SEQUENCE LISTING

<110> Pompejus, Markus
Kroger, Burkhard
Schroder, Hartwig
Zelder, Oskar
Haberhauer, Gregor
<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL PROTEINS
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Met Ser Thr Gln Thr
1 5

atc acc atc aca gtc cta gaa acc gcc acc atc ttt gac ggc cct gaa 163
Ile Thr Ile Thr Val Leu Glu Thr Ala Thr Ile Phe Asp Gly Pro Glu
10 15 20

acc atc tac cgc tat gac ctg gct gcc gaa ggc atc ctt gat gga tgg 211
Thr Ile Tyr Arg Tyr Asp Leu Ala Ala Glu Gly Ile Leu Asp Gly Trp
25 30 35

gct cac tct gct gtg ctg gat caa gtg aaa caa ata gca ggt gaa aac 259
Ala His Ser Ala Val Leu Asp Gln Val Lys Gln Ile Ala Gly Glu Asn
40 45 50

tgg ccg act gtt gag atc gtg gtg gat ggc acc gac aac gta gtc aat 307
Trp Pro Thr Val Glu Ile Val Val Asp Gly Thr Asp Asn Val Val Asn
55 60 65

gca ctc acc tcc atg ttt gct tcc aaa ggc gtg acc tgc ggt ggg gtt 355
Ala Leu Thr Ser Met Phe Ala Ser Lys Gly Val Thr Cys Gly Gly Val
70 75 80 85

gga gta gaa gca cct ccc gtt gcg gag gaa cca ccg aaa att aaa cgg 403
Gly Val Glu Ala Pro Pro Val Ala Glu Glu Pro Pro Lys Ile Lys Arg
90 95 100

ccc acg agt gga aaa caa gtc cgc cag ttc tac ggc atc aag cca cta 451
Pro Thr Ser Gly Lys Gln Val Arg Gln Phe Tyr Gly Ile Lys Pro Leu
105 110 115

cac ctg ttg ttg gtc agc ata ttg gtt ggt tct att gct ggt att tgg 499
His Leu Leu Leu Val Ser Ile Leu Val Gly Ser Ile Ala Gly Ile Trp

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        120                 125                 130

gtg att tcg ggt ttc act ggg cca gtg gac tca cgg ccg gta gat aag   547
Val Ile Ser Gly Phe Thr Gly Pro Val Asp Ser Arg Pro Val Asp Lys
    135                 140                 145

gtg gcg gag att tca acg cag ggg gag acg tcg ata agc aat caa ccc   595
Val Ala Glu Ile Ser Thr Gln Gly Glu Thr Ser Ile Ser Asn Gln Pro
150                 155                 160                 165

caa ccc cag ccc acc gtg ctc gtg acc gag gac ctg ctt att gag gcg   643
Gln Pro Gln Pro Thr Val Leu Val Thr Glu Asp Leu Leu Ile Glu Ala
                170                 175                 180

cca ttt ggt ttt gaa atg cga agc gac gaa cag tcg cgc tac ctg gaa   691
Pro Phe Gly Phe Glu Met Arg Ser Asp Glu Gln Ser Arg Tyr Leu Glu
            185                 190                 195

ggc ccc gac ccg aat ctg cgc atc cac gtg ggc gtc gat ccg ctg cac   739
Gly Pro Asp Pro Asn Leu Arg Ile His Val Gly Val Asp Pro Leu His
        200                 205                 210

ggc gcg gac gcc gcg ctg gtt gcc gaa gag ctg cgc cgc ctg atc acc   787
Gly Ala Asp Ala Ala Leu Val Ala Glu Glu Leu Arg Arg Leu Ile Thr
    215                 220                 225

gag gat cct tcg ctg gag gaa att ccc gca ggg gag tgg ggc gag aaa   835
Glu Asp Pro Ser Leu Glu Glu Ile Pro Ala Gly Glu Trp Gly Glu Lys
230                 235                 240                 245

acc acc atc gac tac cgc gaa aca ccc ggc gat ggc tct cat gtg ctg   883
Thr Thr Ile Asp Tyr Arg Glu Thr Pro Gly Asp Gly Ser His Val Leu
                250                 255                 260

tgg gtg acc tgg ttt gac acc gac cga caa ctc aac gtt ggg tgc cat   931
Trp Val Thr Trp Phe Asp Thr Asp Arg Gln Leu Asn Val Gly Cys His
            265                 270                 275

agc aaa gcc gcc gaa acc ctt gtt cac aag gca caa tgc cga aat gtg   979
Ser Lys Ala Ala Glu Thr Leu Val His Lys Ala Gln Cys Arg Asn Val
        280                 285                 290

att gag cat ctg acg ctg aaa tgatgccggt ttctatccgg aat            1023
Ile Glu His Leu Thr Leu Lys
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Phe Asp Gly Pro Glu Thr Ile Tyr Arg Tyr Asp Leu Ala Ala Glu Gly
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Ile Leu Asp Gly Trp Ala His Ser Ala Val Leu Asp Gln Val Lys Gln
         35                  40                  45
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Ile Ala Gly Glu Asn Trp Pro Thr Val Glu Ile Val Val Asp Gly Thr
     50                  55                  60

Asp Asn Val Val Asn Ala Leu Thr Ser Met Phe Ala Ser Lys Gly Val
 65                  70                  75                  80

Thr Cys Gly Gly Val Gly Val Glu Ala Pro Pro Val Ala Glu Glu Pro
                 85                  90                  95

Pro Lys Ile Lys Arg Pro Thr Ser Gly Lys Gln Val Arg Gln Phe Tyr
            100                 105                 110

Gly Ile Lys Pro Leu His Leu Leu Leu Val Ser Ile Leu Val Gly Ser
        115                 120                 125

Ile Ala Gly Ile Trp Val Ile Ser Gly Phe Thr Gly Pro Val Asp Ser
    130                 135                 140

Arg Pro Val Asp Lys Val Ala Glu Ile Ser Thr Gln Gly Glu Thr Ser
145                 150                 155                 160

Ile Ser Asn Gln Pro Gln Pro Gln Pro Thr Val Leu Val Thr Glu Asp
                165                 170                 175

Leu Leu Ile Glu Ala Pro Phe Gly Phe Glu Met Arg Ser Asp Glu Gln
            180                 185                 190

Ser Arg Tyr Leu Glu Gly Pro Asp Pro Asn Leu Arg Ile His Val Gly
        195                 200                 205

Val Asp Pro Leu His Gly Ala Asp Ala Ala Leu Val Ala Glu Glu Leu
    210                 215                 220

Arg Arg Leu Ile Thr Glu Asp Pro Ser Leu Glu Glu Ile Pro Ala Gly
225                 230                 235                 240

Glu Trp Gly Glu Lys Thr Thr Ile Asp Tyr Arg Glu Thr Pro Gly Asp
                245                 250                 255

Gly Ser His Val Leu Trp Val Thr Trp Phe Asp Thr Asp Arg Gln Leu
            260                 265                 270

Asn Val Gly Cys His Ser Lys Ala Ala Glu Thr Leu Val His Lys Ala
        275                 280                 285

Gln Cys Arg Asn Val Ile Glu His Leu Thr Leu Lys
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ggagacgtcg ataagcaatc aaccccaacc ccagcccacc gtg ctc gtg acc gag   115
                                              Val Leu Val Thr Glu
                                                1               5

gac ctg ctt att gag gcg cca ttt ggt ttt gaa atg cga agc gac gaa   163
Asp Leu Leu Ile Glu Ala Pro Phe Gly Phe Glu Met Arg Ser Asp Glu
                 10                  15                  20

cag tcg cgc tac ctg gaa ggc ccc gac ccg aat ctg cgc atc cac gtg   211
Gln Ser Arg Tyr Leu Glu Gly Pro Asp Pro Asn Leu Arg Ile His Val
             25                  30                  35

ggc gtc gat ccg ctg cac ggc gcg gac gcc gcg ctg gtt gcc gaa gag   259
Gly Val Asp Pro Leu His Gly Ala Asp Ala Ala Leu Val Ala Glu Glu
         40                  45                  50

ctg cgc cgc ctg atc acc gag gat cct tcg ctg gag gaa att ccc gca   307
Leu Arg Arg Leu Ile Thr Glu Asp Pro Ser Leu Glu Glu Ile Pro Ala
     55                  60                  65

ggg gag tgg ggc gag aaa acc acc atc gac tac cgc gaa aca ccc ggc   355
Gly Glu Trp Gly Glu Lys Thr Thr Ile Asp Tyr Arg Glu Thr Pro Gly
 70                  75                  80                  85

gat ggc tct cat gtg ctg tgg gtg acc tgg ttt gac acc gac cga caa   403
Asp Gly Ser His Val Leu Trp Val Thr Trp Phe Asp Thr Asp Arg Gln
                 90                  95                 100

ctc aac gtt ggg tgc cat agc aaa gcc gcc gaa acc ctt gtt cac aag   451
Leu Asn Val Gly Cys His Ser Lys Ala Ala Glu Thr Leu Val His Lys
            105                 110                 115

gca caa tgc cga aat gtg att gag cat ctg acg ctg aaa tgatgccggt    500
Ala Gln Cys Arg Asn Val Ile Glu His Leu Thr Leu Lys
        120                 125                 130

ttctatccgg aat                                                   513


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Val Leu Val Thr Glu Asp Leu Leu Ile Glu Ala Pro Phe Gly Phe Glu
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Met Arg Ser Asp Glu Gln Ser Arg Tyr Leu Glu Gly Pro Asp Pro Asn
             20                  25                  30

Leu Arg Ile His Val Gly Val Asp Pro Leu His Gly Ala Asp Ala Ala
         35                  40                  45

Leu Val Ala Glu Glu Leu Arg Arg Leu Ile Thr Glu Asp Pro Ser Leu
     50                  55                  60

Glu Glu Ile Pro Ala Gly Glu Trp Gly Glu Lys Thr Thr Ile Asp Tyr
 65                  70                  75                  80
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Arg Glu Thr Pro Gly Asp Gly Ser His Val Leu Trp Val Thr Trp Phe
                 85                  90                  95

Asp Thr Asp Arg Gln Leu Asn Val Gly Cys His Ser Lys Ala Ala Glu
            100                 105                 110

Thr Leu Val His Lys Ala Gln Cys Arg Asn Val Ile Glu His Leu Thr
        115                 120                 125

Leu Lys
    130
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                                            Met Ser Thr Gln Thr
                                              1               5

atc acc atc aca gtc cta gaa acc gcc acc atc ttt gac ggc cct gaa   163
Ile Thr Ile Thr Val Leu Glu Thr Ala Thr Ile Phe Asp Gly Pro Glu
                 10                  15                  20

acc atc tac cgc tat gac ctg gct gcc gaa ggc atc ctt gat gga tgg   211
Thr Ile Tyr Arg Tyr Asp Leu Ala Ala Glu Gly Ile Leu Asp Gly Trp
             25                  30                  35

gct cac tct gct gtg ctg gat caa gtg aaa caa ata gca ggt gaa aac   259
Ala His Ser Ala Val Leu Asp Gln Val Lys Gln Ile Ala Gly Glu Asn
         40                  45                  50

tgg ccg act gtt gag atc gtg gtg gat ggc acc gac aac gta gtc aat   307
Trp Pro Thr Val Glu Ile Val Val Asp Gly Thr Asp Asn Val Val Asn
     55                  60                  65

gca ctc acc tcc atg ttt gct tcc aaa ggc gtg acc tgc ggt ggg gtt   355
Ala Leu Thr Ser Met Phe Ala Ser Lys Gly Val Thr Cys Gly Gly Val
 70                  75                  80                  85

gga gta gaa gca cct ccc gtt gcg gag gaa cca ccg aaa att aaa cgg   403
Gly Val Glu Ala Pro Pro Val Ala Glu Glu Pro Pro Lys Ile Lys Arg
                 90                  95                 100

ccc acg agt gga aaa caa gtc cgc cag ttc tac ggc atc aag cca cta   451
Pro Thr Ser Gly Lys Gln Val Arg Gln Phe Tyr Gly Ile Lys Pro Leu
            105                 110                 115

cac ctg ttg ttg gtc agc ata ttg gtt ggt tct att gct ggt att tgg   499
His Leu Leu Leu Val Ser Ile Leu Val Gly Ser Ile Ala Gly Ile Trp
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        120                 125                 130

gga ttt cgg gtt tca ctg ggc cag tgg act cac ggc cgg tagataaggt    548
Gly Phe Arg Val Ser Leu Gly Gln Trp Thr His Gly Arg
    135                 140                 145

ggcggagatt tca                                                  561


<210> 6
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<213> Corynebacterium glutamicum

<400> 6
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Phe Asp Gly Pro Glu Thr Ile Tyr Arg Tyr Asp Leu Ala Ala Glu Gly
             20                  25                  30

Ile Leu Asp Gly Trp Ala His Ser Ala Val Leu Asp Gln Val Lys Gln
         35                  40                  45

Ile Ala Gly Glu Asn Trp Pro Thr Val Glu Ile Val Val Asp Gly Thr
     50                  55                  60

Asp Asn Val Val Asn Ala Leu Thr Ser Met Phe Ala Ser Lys Gly Val
 65                  70                  75                  80

Thr Cys Gly Gly Val Gly Val Glu Ala Pro Pro Val Ala Glu Glu Pro
                 85                  90                  95

Pro Lys Ile Lys Arg Pro Thr Ser Gly Lys Gln Val Arg Gln Phe Tyr
            100                 105                 110

Gly Ile Lys Pro Leu His Leu Leu Leu Val Ser Ile Leu Val Gly Ser
        115                 120                 125

Ile Ala Gly Ile Trp Gly Phe Arg Val Ser Leu Gly Gln Trp Thr His
    130                 135                 140

Gly Arg
145


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<213> Corynebacterium glutamicum

<220>
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Trp Gly Gln Lys Asp His Trp Gly Lys Ala Pro Leu Gly Asp His Asp
  1               5                  10                  15
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```
gct gtg cgt atc tat agg caa gca gaa gcc ttg atg aaa cag cgc gca    96
Ala Val Arg Ile Tyr Arg Gln Ala Glu Ala Leu Met Lys Gln Arg Ala
             20                  25                  30

gca aac aat aag ggc tta gac ctc aat gat gaa gcg acc tat ggc gcc   144
Ala Asn Asn Lys Gly Leu Asp Leu Asn Asp Glu Ala Thr Tyr Gly Ala
         35                  40                  45

atc atg ttt gcg tct ttc gat gat gcc ttc gcc gct gat gcc gaa gct   192
Ile Met Phe Ala Ser Phe Asp Asp Ala Phe Ala Ala Asp Ala Glu Ala
     50                  55                  60

cat ggc tgt gta cac cga cca cag ttc gcg aag gta act agg cga aat   240
His Gly Cys Val His Arg Pro Gln Phe Ala Lys Val Thr Arg Arg Asn
 65                  70                  75                  80

att ctt aat tca ccg caa tac acg gcg att aag tca tct tat gac gcg   288
Ile Leu Asn Ser Pro Gln Tyr Thr Ala Ile Lys Ser Ser Tyr Asp Ala
                 85                  90                  95

ctg gtg cag cag gat ctc gtg gcc caa cag cag cag gca caa gcg cta   336
Leu Val Gln Gln Asp Leu Val Ala Gln Gln Gln Gln Ala Gln Ala Leu
            100                 105                 110

cag caa gct gct tat gag caa gag cag gca gct att ttc cag gca cgt   384
Gln Gln Ala Ala Tyr Glu Gln Glu Gln Ala Ala Ile Phe Gln Ala Arg
        115                 120                 125

gat caa gca aca ttc cag gct gaa caa acg ctc gcg caa gag tcc gtt   432
Asp Gln Ala Thr Phe Gln Ala Glu Gln Thr Leu Ala Gln Glu Ser Val
    130                 135                 140

cgc caa tca gag ggt gtg ggt tta cct gtc att gat ccg atg gag agc   480
Arg Gln Ser Glu Gly Val Gly Leu Pro Val Ile Asp Pro Met Glu Ser
145                 150                 155                 160

tat ttc cgg gag tac gcc ttc tat gaa ggt gtc gag atg ttt ggt acc   528
Tyr Phe Arg Glu Tyr Ala Phe Tyr Glu Gly Val Glu Met Phe Gly Thr
                165                 170                 175

tgg ggt acg cac gtt gat gct ggt gtg tcg cag ttt agc acc tct gat   576
Trp Gly Thr His Val Asp Ala Gly Val Ser Gln Phe Ser Thr Ser Asp
            180                 185                 190

ggc cgt gcg atc cga gcg ctt gtt gat gag cat ctc gca acc tat gaa   624
Gly Arg Ala Ile Arg Ala Leu Val Asp Glu His Leu Ala Thr Tyr Glu
        195                 200                 205

cca gta gag cag cgg ggg agt act cag gca ttc ttc gcc tct gtc aat   672
Pro Val Glu Gln Arg Gly Ser Thr Gln Ala Phe Phe Ala Ser Val Asn
    210                 215                 220

gct gcc ttt gct gag gtg gca cct cac gca gca ccc atg ttt agt gcg   720
Ala Ala Phe Ala Glu Val Ala Pro His Ala Ala Pro Met Phe Ser Ala
225                 230                 235                 240

att gct cgc gag ggt gag ggt tca aag ggg tac cag gcg ctg cgt cac   768
Ile Ala Arg Glu Gly Glu Gly Ser Lys Gly Tyr Gln Ala Leu Arg His
                245                 250                 255

cgt ttc gac aag atg gtc ggc act gca att gga cct aat ggt ttg cct   816
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Arg Phe Asp Lys Met Val Gly Thr Ala Ile Gly Pro Asn Gly Leu Pro
            260                 265                 270

gag gga cct gat ctg ggt ggt cgt cgt tta cct att tcg cct tat gat   864
Glu Gly Pro Asp Leu Gly Gly Arg Arg Leu Pro Ile Ser Pro Tyr Asp
        275                 280                 285

cca cgc tgg tca gac cgc gaa gta gtc cgt gtg cac ggt acc aag ctg   912
Pro Arg Trp Ser Asp Arg Glu Val Val Arg Val His Gly Thr Lys Leu
    290                 295                 300

cta tca ctg tcc gaa gag agt gtt ggc atg atc agg gac ctt gat cta   960
Leu Ser Leu Ser Glu Glu Ser Val Gly Met Ile Arg Asp Leu Asp Leu
305                 310                 315                 320

gca acg atc cac cta caa gat aat gat gtt tac gag ggc act cat cga  1008
Ala Thr Ile His Leu Gln Asp Asn Asp Val Tyr Glu Gly Thr His Arg
                325                 330                 335

gaa gac gac act aaa ggc ggt gtg cga ccg ttg act caa tgg gtc aat  1056
Glu Asp Asp Thr Lys Gly Gly Val Arg Pro Leu Thr Gln Trp Val Asn
            340                 345                 350

ggt gaa gct att gcc tgg cgc act atc acc gag aat gac cag atg cga  1104
Gly Glu Ala Ile Ala Trp Arg Thr Ile Thr Glu Asn Asp Gln Met Arg
        355                 360                 365

ctg ccc aat att ggt cag ttt atg acg gct aaa gaa tac cgt gcc gca  1152
Leu Pro Asn Ile Gly Gln Phe Met Thr Ala Lys Glu Tyr Arg Ala Ala
    370                 375                 380

gcg tca tgg ctg cgt gct gga ctc att gat acc gca gat gtt gcg agt  1200
Ala Ser Trp Leu Arg Ala Gly Leu Ile Asp Thr Ala Asp Val Ala Ser
385                 390                 395                 400

cag aaa att gac ccc aac aag gtc atg tct gat gag ggt atc gcg cgc  1248
Gln Lys Ile Asp Pro Asn Lys Val Met Ser Asp Glu Gly Ile Ala Arg
                405                 410                 415

tcg gaa gct att ttg acg tat ctg tcg gat gag ggt gtg gat ttt agg  1296
Ser Glu Ala Ile Leu Thr Tyr Leu Ser Asp Glu Gly Val Asp Phe Arg
            420                 425                 430

atc gag cca gat cgt gag ccg gga cag ctt aaa gtg cgt att gag ggc  1344
Ile Glu Pro Asp Arg Glu Pro Gly Gln Leu Lys Val Arg Ile Glu Gly
        435                 440                 445

acc cgt att gat att cgt ctc act gat act cgc gcc aat gaa cag tgg  1392
Thr Arg Ile Asp Ile Arg Leu Thr Asp Thr Arg Ala Asn Glu Gln Trp
    450                 455                 460

gtg ggt cgt gtc tat gat tct ggc act gtg att aag tat tcc gcc gaa  1440
Val Gly Arg Val Tyr Asp Ser Gly Thr Val Ile Lys Tyr Ser Ala Glu
465                 470                 475                 480

caa aca gcg gaa gaa cgt cta cga gct cgt gag cgc atg gag aac ggt  1488
Gln Thr Ala Glu Glu Arg Leu Arg Ala Arg Glu Arg Met Glu Asn Gly
                485                 490                 495

gat gga acg tgg aca ccg gct act gat tat gaa cca agc cca act gaa  1536
Asp Gly Thr Trp Thr Pro Ala Thr Asp Tyr Glu Pro Ser Pro Thr Glu
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                500                 505                 510

gtt gtc gat ctc gtg aaa ttt gct ctc ggt cga gag gtt gag cga cag   1584
Val Val Asp Leu Val Lys Phe Ala Leu Gly Arg Glu Val Glu Arg Gln
        515                 520                 525

gat ggc aaa ggt ctt gtt ggt gtg cct aat gct cga cac cca cgt gct   1632
Asp Gly Lys Gly Leu Val Gly Val Pro Asn Ala Arg His Pro Arg Ala
    530                 535                 540

tta gag cag gca cag gat gca tat ttc act aag aat cgt tcc gca ttc   1680
Leu Glu Gln Ala Gln Asp Ala Tyr Phe Thr Lys Asn Arg Ser Ala Phe
545                 550                 555                 560

atg gtg cgt gaa ggg ctc tcg atc gtt cag gat gca cgt gat cga agt   1728
Met Val Arg Glu Gly Leu Ser Ile Val Gln Asp Ala Arg Asp Arg Ser
                565                 570                 575

gct ggt cct gga aag tgg ttt gat aat gaa gcg aaa gca tcg gag tgg   1776
Ala Gly Pro Gly Lys Trp Phe Asp Asn Glu Ala Lys Ala Ser Glu Trp
            580                 585                 590

ctt ggt aac aat atc gcc ctt act cgt gcg cgt gtg gcc gaa gag ctc   1824
Leu Gly Asn Asn Ile Ala Leu Thr Arg Ala Arg Val Ala Glu Glu Leu
        595                 600                 605

ggc gtt gaa gaa ctg att gcg ctt tct gca cag tac gcc gat gat cct   1872
Gly Val Glu Glu Leu Ile Ala Leu Ser Ala Gln Tyr Ala Asp Asp Pro
    610                 615                 620

gac ttc atg ccg gct ttt gct ggt gag gat gag ctc atg gcg ata aag   1920
Asp Phe Met Pro Ala Phe Ala Gly Glu Asp Glu Leu Met Ala Ile Lys
625                 630                 635                 640

cag gac tat tgg gcg atg ctg cga ggt gag gaa acc gat ctg ctt aac   1968
Gln Asp Tyr Trp Ala Met Leu Arg Gly Glu Glu Thr Asp Leu Leu Asn
                645                 650                 655

cct ggg gtt aac cgc gat gat tat atg gct gct atc cgc gat ggt gat   2016
Pro Gly Val Asn Arg Asp Asp Tyr Met Ala Ala Ile Arg Asp Gly Asp
            660                 665                 670

cat gag cag att gct gcg atg acc tca gca atg aat gct gtg acc gtg   2064
His Glu Gln Ile Ala Ala Met Thr Ser Ala Met Asn Ala Val Thr Val
        675                 680                 685

gag gat cgt gtg cgt cag cac gcg gcc ctt gtt ctt gat gat tat gtc   2112
Glu Asp Arg Val Arg Gln His Ala Ala Leu Val Leu Asp Asp Tyr Val
    690                 695                 700

ggc acg gtg gag cct gat cct gtt acc ggc ttg cgt ttt aat ccg gtg   2160
Gly Thr Val Glu Pro Asp Pro Val Thr Gly Leu Arg Phe Asn Pro Val
705                 710                 715                 720

aca gtt gct cag cac atg ccg agt gct aaa tcc ctg tgg tca aac cat   2208
Thr Val Ala Gln His Met Pro Ser Ala Lys Ser Leu Trp Ser Asn His
                725                 730                 735

gac gat att att gcc gcg ttg cga gcg act tcg att act ggc gat gaa   2256
Asp Asp Ile Ile Ala Ala Leu Arg Ala Thr Ser Ile Thr Gly Asp Glu
            740                 745                 750
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ctg cgc ggt gac gaa ttc tat aac gat gtt att aat caa cag ttg ctc   2304
Leu Arg Gly Asp Glu Phe Tyr Asn Asp Val Ile Asn Gln Gln Leu Leu
        755                 760                 765

aaa ttt aat cct gag acc gcg cag aaa atg gtt aat aac cct gat ctt   2352
Lys Phe Asn Pro Glu Thr Ala Gln Lys Met Val Asn Asn Pro Asp Leu
    770                 775                 780

gac ccg cag ttg gct cga ttt ggc act gtc att gcc gag act att tcc   2400
Asp Pro Gln Leu Ala Arg Phe Gly Thr Val Ile Ala Glu Thr Ile Ser
785                 790                 795                 800

cgc aat ggt gct gat gtg gtc gat att gct gtt gac gat aac ggt gtg   2448
Arg Asn Gly Ala Asp Val Val Asp Ile Ala Val Asp Asp Asn Gly Val
                805                 810                 815

gtg cgg tgg acc gca cag cga cgt gtt ggt gcg aag gat agt cgt gca   2496
Val Arg Trp Thr Ala Gln Arg Arg Val Gly Ala Lys Asp Ser Arg Ala
            820                 825                 830

gta gat agt aag ggg cag gtt cgc ggt gaa cgc acc cgt cat gtg cag   2544
Val Asp Ser Lys Gly Gln Val Arg Gly Glu Arg Thr Arg His Val Gln
        835                 840                 845

ggt gag ata ggt cag att ttt act cgc ggt gag cat ggt gaa att gtc   2592
Gly Glu Ile Gly Gln Ile Phe Thr Arg Gly Glu His Gly Glu Ile Val
    850                 855                 860

acc aaa ttt aat ggt ggc gag aac tat atg ttt gcc cct ggc tac acc   2640
Thr Lys Phe Asn Gly Gly Glu Asn Tyr Met Phe Ala Pro Gly Tyr Thr
865                 870                 875                 880

gcg tct gtg gta cca caa aag cct ggt gag aca aag agt tta gaa gag   2688
Ala Ser Val Val Pro Gln Lys Pro Gly Glu Thr Lys Ser Leu Glu Glu
                885                 890                 895

cgt acc aag ctc aaa ggc tat gag cag gtg atg tca gag gcg ttg gtg   2736
Arg Thr Lys Leu Lys Gly Tyr Glu Gln Val Met Ser Glu Ala Leu Val
            900                 905                 910

tac cgt gtg cga gaa gat ttg atg ttc act gag cga tcc cga gtg ggt   2784
Tyr Arg Val Arg Glu Asp Leu Met Phe Thr Glu Arg Ser Arg Val Gly
        915                 920                 925

gct aca acc agc atc aac agt gca tat aag cga ctg tat gac aat cgc   2832
Ala Thr Thr Ser Ile Asn Ser Ala Tyr Lys Arg Leu Tyr Asp Asn Arg
    930                 935                 940

ttc cct gtg gac ttc ttc gag cgc agc gcc gaa gaa ggt ttg agc gat   2880
Phe Pro Val Asp Phe Phe Glu Arg Ser Ala Glu Glu Gly Leu Ser Asp
945                 950                 955                 960

gag tgg cgt gct gcg ttg ctt gag act gcg agt ttg cgt gtg cgc tac   2928
Glu Trp Arg Ala Ala Leu Leu Glu Thr Ala Ser Leu Arg Val Arg Tyr
                965                 970                 975

gac aac tct att cgt gat ggt gcg aat gtg atg gag gat att cga gca   2976
Asp Asn Ser Ile Arg Asp Gly Ala Asn Val Met Glu Asp Ile Arg Ala
            980                 985                 990
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cag cag cgt ggt ttt gat gcg cgt aat gat aac tcc cgt gat gcg ctg   3024
Gln Gln Arg Gly Phe Asp Ala Arg Asn Asp Asn Ser Arg Asp Ala Leu
        995                 1000                1005

gtg ctt acc ggt ggg cgt aac att tct gta ctt gat gtt gat gcg ggt   3072
Val Leu Thr Gly Gly Arg Asn Ile Ser Val Leu Asp Val Asp Ala Gly
    1010                1015                1020

aaa ggt ttc ttt gat ccc atg atg act ggt atg gcg gcg aac cag ggt   3120
Lys Gly Phe Phe Asp Pro Met Met Thr Gly Met Ala Ala Asn Gln Gly
1025                1030                1035                1040

tct gtt cgc tat ttg ttg cct tct gcg aag gtg ggc gct gat ggc atg   3168
Ser Val Arg Tyr Leu Leu Pro Ser Ala Lys Val Gly Ala Asp Gly Met
                1045                1050                1055

att acc cct ggt gat ccg gct gat cga gta cct gtt gca gcg cat cca   3216
Ile Thr Pro Gly Asp Pro Ala Asp Arg Val Pro Val Ala Ala His Pro
            1060                1065                1070

gaa tca tgg gcg atg ggc ttt gac cca cat gac cgt cag aac atg act   3264
Glu Ser Trp Ala Met Gly Phe Asp Pro His Asp Arg Gln Asn Met Thr
        1075                1080                1085

ttc tcg aac atc atg cag gct agc gct gtg act ggt ggt gca cgc act   3312
Phe Ser Asn Ile Met Gln Ala Ser Ala Val Thr Gly Gly Ala Arg Thr
    1090                1095                1100

gcg atg ata cag ctg ggc ggt tgg aac ttt gaa gat ggc att att gtc   3360
Ala Met Ile Gln Leu Gly Gly Trp Asn Phe Glu Asp Gly Ile Ile Val
1105                1110                1115                1120

tct gcc gat ttt gcg aat acc cat gtt att cgc gat acg gaa gat gag   3408
Ser Ala Asp Phe Ala Asn Thr His Val Ile Arg Asp Thr Glu Asp Glu
                1125                1130                1135

atg cgc ccc ttg gtt gcc ggc gat aag ctg tct gat ttt cac ggt aat   3456
Met Arg Pro Leu Val Ala Gly Asp Lys Leu Ser Asp Phe His Gly Asn
            1140                1145                1150

aag ggt gtg acc gct ctt gtt gtt gat cca gcg atg agt gat gct gat   3504
Lys Gly Val Thr Ala Leu Val Val Asp Pro Ala Met Ser Asp Ala Asp
        1155                1160                1165

gca cgt gca gca ggg ctg gaa tca gag gtg gcg ttt ttc cga gac aac   3552
Ala Arg Ala Ala Gly Leu Glu Ser Glu Val Ala Phe Phe Arg Asp Asn
    1170                1175                1180

cct gat cta gag gtt gtc atg agt ccg ttt tct gcc att tct cgt ttt   3600
Pro Asp Leu Glu Val Val Met Ser Pro Phe Ser Ala Ile Ser Arg Phe
1185                1190                1195                1200

aat ggt ggc acg gca cgt gag ctc atg acc aac ccg cag gat gtg gtg   3648
Asn Gly Gly Thr Ala Arg Glu Leu Met Thr Asn Pro Gln Asp Val Val
                1205                1210                1215

ttc agg aat aat gat ggt tct act cgt gtt caa cca ggt gcc tct ggt   3696
Phe Arg Asn Asn Asp Gly Ser Thr Arg Val Gln Pro Gly Ala Ser Gly
            1220                1225                1230

gat ctc aac ttc atc gtc acg cat atg gct gtt gat gcg aaa acc aat   3744
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Asp Leu Asn Phe Ile Val Thr His Met Ala Val Asp Ala Lys Thr Asn
        1235                1240                1245

gtc tat gat gaa gaa gct gtt cgt gag ggc caa gga cgt aaa gcg tct   3792
Val Tyr Asp Glu Glu Ala Val Arg Glu Gly Gln Gly Arg Lys Ala Ser
    1250                1255                1260

tct cag ctg gcg tgg gtg ctc caa gcc cag gaa tgt cat gag att atg   3840
Ser Gln Leu Ala Trp Val Leu Gln Ala Gln Glu Cys His Glu Ile Met
1265                1270                1275                1280

gag cac ttt tat ggc aac aac gtc tct gca ttg gct aac ttc cag gaa   3888
Glu His Phe Tyr Gly Asn Asn Val Ser Ala Leu Ala Asn Phe Gln Glu
                1285                1290                1295

tat ctt cgc gtc acg ggg ctt gat gtc acc ccg tat ggt gag ttg cgc   3936
Tyr Leu Arg Val Thr Gly Leu Asp Val Thr Pro Tyr Gly Glu Leu Arg
            1300                1305                1310

gag ggg ttc agc gag tcc aat gag cag cgc aat atc atc gag atg cca   3984
Glu Gly Phe Ser Glu Ser Asn Glu Gln Arg Asn Ile Ile Glu Met Pro
        1315                1320                1325

agc att tac gat gag aac ggt gag ctg aat aat cgt gtt aat cgt gca   4032
Ser Ile Tyr Asp Glu Asn Gly Glu Leu Asn Asn Arg Val Asn Arg Ala
    1330                1335                1340

cag gtg cgc gaa gct ttt gtt gag cag atc agt cgc gct ggt ggt gtt   4080
Gln Val Arg Glu Ala Phe Val Glu Gln Ile Ser Arg Ala Gly Gly Val
1345                1350                1355                1360

atg gag att cct ttc cag tta cag ttg cgc aat ggt gca cag cta gaa   4128
Met Glu Ile Pro Phe Gln Leu Gln Leu Arg Asn Gly Ala Gln Leu Glu
                1365                1370                1375

gag tca cct aat aat cca gac atg tat cag ttg cca cta ctg agc ccg   4176
Glu Ser Pro Asn Asn Pro Asp Met Tyr Gln Leu Pro Leu Leu Ser Pro
            1380                1385                1390

cat ttg cgc agt gat gag gat tta gcg gac ggt agt acc tct cga cat   4224
His Leu Arg Ser Asp Glu Asp Leu Ala Asp Gly Ser Thr Ser Arg His
        1395                1400                1405

gag tac acc acg cgg tat atg gct att ttt gat acg tgc tac aag ctg   4272
Glu Tyr Thr Thr Arg Tyr Met Ala Ile Phe Asp Thr Cys Tyr Lys Leu
    1410                1415                1420

gca gaa gag caa gcc aag att gac gca ttg cgc cag gag gaa gcg cag   4320
Ala Glu Glu Gln Ala Lys Ile Asp Ala Leu Arg Gln Glu Glu Ala Gln
1425                1430                1435                1440

cac ggc acg ttg cct cgt gct gcg gaa aag cga ctg agc gag tca cag   4368
His Gly Thr Leu Pro Arg Ala Ala Glu Lys Arg Leu Ser Glu Ser Gln
                1445                1450                1455

aag ttt gtt gat caa gca cag aaa aag gtg cag gca agc ttt gat gga   4416
Lys Phe Val Asp Gln Ala Gln Lys Lys Val Gln Ala Ser Phe Asp Gly
            1460                1465                1470

att gct aat gat att gtc gcc agc cgg atc gag acc aag aac aat gtg   4464
Ile Ala Asn Asp Ile Val Ala Ser Arg Ile Glu Thr Lys Asn Asn Val
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        1475                1480                1485

ttc aag gac ggc ttt atg tcg gcg cga cag tca cac tcc gct act gct   4512
Phe Lys Asp Gly Phe Met Ser Ala Arg Gln Ser His Ser Ala Thr Ala
    1490                1495                1500

gtg tgg aca ggt gat cca cgc ctg tca gtt gat gaa gta gcc atg aac   4560
Val Trp Thr Gly Asp Pro Arg Leu Ser Val Asp Glu Val Ala Met Asn
1505                1510                1515                1520

tct tcg atg gca cgt gaa ctc ggc gtt ctc gat aac ggt tat gca atg   4608
Ser Ser Met Ala Arg Glu Leu Gly Val Leu Asp Asn Gly Tyr Ala Met
                1525                1530                1535

gtg tgg cgt gat ccg gtg atc cgc gat ggt ggt gtg cgc tat ttg cgt   4656
Val Trp Arg Asp Pro Val Ile Arg Asp Gly Gly Val Arg Tyr Leu Arg
            1540                1545                1550

gtg gtt att aat gat gat ctg cac ggt gtg gca gtc aac cct gtg tcg   4704
Val Val Ile Asn Asp Asp Leu His Gly Val Ala Val Asn Pro Val Ser
        1555                1560                1565

gtg aag agc ttt gac ggt gac ttc gat ggt gac tct gta ggt ctg gtc   4752
Val Lys Ser Phe Asp Gly Asp Phe Asp Gly Asp Ser Val Gly Leu Val
    1570                1575                1580

ggc aat ctg ccg aaa aag gcg cat gag gag gca ttg tcc agg ctc aca   4800
Gly Asn Leu Pro Lys Lys Ala His Glu Glu Ala Leu Ser Arg Leu Thr
1585                1590                1595                1600

gtt gag gca aac atg ctt gat ctt ggt gat ggt aag cgt atg gag gac   4848
Val Glu Ala Asn Met Leu Asp Leu Gly Asp Gly Lys Arg Met Glu Asp
                1605                1610                1615

ggc act atg ttt tat ggg cta act ctg cat gac agc ctc gat gta cag   4896
Gly Thr Met Phe Tyr Gly Leu Thr Leu His Asp Ser Leu Asp Val Gln
            1620                1625                1630

gta gcg cag cac cat gat ccg gca atg gcc gag aac atg aag gtt att   4944
Val Ala Gln His His Asp Pro Ala Met Ala Glu Asn Met Lys Val Ile
        1635                1640                1645

gtc tct gag ctt aac cgc tac cag cgt gaa tac gag gcc ggc gag att   4992
Val Ser Glu Leu Asn Arg Tyr Gln Arg Glu Tyr Glu Ala Gly Glu Ile
    1650                1655                1660

agc cgc gaa gaa ttg cta gag gtc aac cgt gca cac atg gat gat ctc   5040
Ser Arg Glu Glu Leu Leu Glu Val Asn Arg Ala His Met Asp Asp Leu
1665                1670                1675                1680

aat gag cac tat gca cag gct ttt gcc aac cgc gat ggt ttg gtg acc   5088
Asn Glu His Tyr Ala Gln Ala Phe Ala Asn Arg Asp Gly Leu Val Thr
                1685                1690                1695

ttg cgt ttt gac ggt atg gaa aac cat atg gct tct gtt gcg cag tgc   5136
Leu Arg Phe Asp Gly Met Glu Asn His Met Ala Ser Val Ala Gln Cys
            1700                1705                1710

ttc gag acg ggt gcg aaa ggt tcg cct ggc aag ctg aag gaa tat gcc   5184
Phe Glu Thr Gly Ala Lys Gly Ser Pro Gly Lys Leu Lys Glu Tyr Ala
        1715                1720                1725
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acc tat atc ggc gct gat ccg gcg cag ggt ttt aaa gac gta ggt caa   5232
Thr Tyr Ile Gly Ala Asp Pro Ala Gln Gly Phe Lys Asp Val Gly Gln
    1730                1735                1740

cca acg cca gaa gcg ctg cgt agc cac tat gag ggt tcg cag aag gcg   5280
Pro Thr Pro Glu Ala Leu Arg Ser His Tyr Glu Gly Ser Gln Lys Ala
1745                1750                1755                1760

act gca att aag gtg ctc ttt acc ggt gtg gct ggt aaa aaa gag cag   5328
Thr Ala Ile Lys Val Leu Phe Thr Gly Val Ala Gly Lys Lys Glu Gln
                1765                1770                1775

gaa atg gtg gca ttg tgc cgc aat ctt ggt ctg acc aag gaa gct atg   5376
Glu Met Val Ala Leu Cys Arg Asn Leu Gly Leu Thr Lys Glu Ala Met
            1780                1785                1790

gct gca tca gca ccg gca cag cag tcg att ctg cag gcg aag cac gac   5424
Ala Ala Ser Ala Pro Ala Gln Gln Ser Ile Leu Gln Ala Lys His Asp
        1795                1800                1805

ccg att gac gcg ctc tat cgt gca gaa act ctt atg gga cca gta ggt   5472
Pro Ile Asp Ala Leu Tyr Arg Ala Glu Thr Leu Met Gly Pro Val Gly
    1810                1815                1820

gat ctc tac caa ggt cgc aag atg cgt cgt ggt gag aat gag caa ggt   5520
Asp Leu Tyr Gln Gly Arg Lys Met Arg Arg Gly Glu Asn Glu Gln Gly
1825                1830                1835                1840

cgc tat gag tgg gaa gtc gtt agg gac gag aac cac cag cct atc cag   5568
Arg Tyr Glu Trp Glu Val Val Arg Asp Glu Asn His Gln Pro Ile Gln
                1845                1850                1855

gcc acc aag gat gaa tgg gta cag cag tac atg gag atg tac gcc gat   5616
Ala Thr Lys Asp Glu Trp Val Gln Gln Tyr Met Glu Met Tyr Ala Asp
            1860                1865                1870

gac aag ggt atg ggt gtc tcg gtt ggc gtt gac cag gtg gag aag atc   5664
Asp Lys Gly Met Gly Val Ser Val Gly Val Asp Gln Val Glu Lys Ile
        1875                1880                1885

gcg gaa gaa ttc tct gat gag cag ggt tat atg cgt gtg ctt agc cat   5712
Ala Glu Glu Phe Ser Asp Glu Gln Gly Tyr Met Arg Val Leu Ser His
    1890                1895                1900

gat gag cta ccc act gag att aag cca cta gca ctt gat cag ctt gcc   5760
Asp Glu Leu Pro Thr Glu Ile Lys Pro Leu Ala Leu Asp Gln Leu Ala
1905                1910                1915                1920

tat ggc gat aag aag aac cgc ttt gat ttg ttg tgc gag atg gca aag   5808
Tyr Gly Asp Lys Lys Asn Arg Phe Asp Leu Leu Cys Glu Met Ala Lys
                1925                1930                1935

cag cag gtc aac atc tac gac ggt gat gct tat gac ttt gcc cct cgt   5856
Gln Gln Val Asn Ile Tyr Asp Gly Asp Ala Tyr Asp Phe Ala Pro Arg
            1940                1945                1950

gtg gtg cgc gcc aat atg aag gca atg gag gat gca gcg cgt ttt ggt   5904
Val Val Arg Ala Asn Met Lys Ala Met Glu Asp Ala Ala Arg Phe Gly
        1955                1960                1965
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atc cct gat gtg gag att cag tcg att tct gca cag cag tca ttg gcg   5952
Ile Pro Asp Val Glu Ile Gln Ser Ile Ser Ala Gln Gln Ser Leu Ala
    1970                1975                1980

agc ttt gag cga gtc cca caa cgt tct ggt ttc cgt att gag cgt cgt   6000
Ser Phe Glu Arg Val Pro Gln Arg Ser Gly Phe Arg Ile Glu Arg Arg
1985                1990                1995                2000

gtg ccg gca gaa gta ggt aca ggg att gct gca cca gca ccg tta cct   6048
Val Pro Ala Glu Val Gly Thr Gly Ile Ala Ala Pro Ala Pro Leu Pro
                2005                2010                2015

gat gca ggt gta cag ggg aat tat gtt cag cag cag gtg cct gcg acc   6096
Asp Ala Gly Val Gln Gly Asn Tyr Val Gln Gln Gln Val Pro Ala Thr
            2020                2025                2030

ccg cca gtt atg cct gtc aca cct ccg gca cag caa cct gtt tcg cct   6144
Pro Pro Val Met Pro Val Thr Pro Pro Ala Gln Gln Pro Val Ser Pro
        2035                2040                2045

gct cag acg gac ttc cgg ggc gtt ggt cag cca ctc gac cag ggc gga   6192
Ala Gln Thr Asp Phe Arg Gly Val Gly Gln Pro Leu Asp Gln Gly Gly
    2050                2055                2060

aaa atc ggg aat tat gga cat cag gga cct gca atg ggg gcg caa cag   6240
Lys Ile Gly Asn Tyr Gly His Gln Gly Pro Ala Met Gly Ala Gln Gln
2065                2070                2075                2080

cca gtt gtg cct cag cag cag aat att ccg cct gtg cat aat ccg gta   6288
Pro Val Val Pro Gln Gln Gln Asn Ile Pro Pro Val His Asn Pro Val
                2085                2090                2095

cca cag aat tct gtt ccg cct act ccg gtt gtg ccg aag cca ggt aca   6336
Pro Gln Asn Ser Val Pro Pro Thr Pro Val Val Pro Lys Pro Gly Thr
            2100                2105                2110

gga aac ccg ttt act cat ggt ggt gcg aac aat cag ttt atg ggt cga   6384
Gly Asn Pro Phe Thr His Gly Gly Ala Asn Asn Gln Phe Met Gly Arg
        2115                2120                2125

ttt gat aca agc cgt tac aac caa cag gaa cca cca caa cga cag gat   6432
Phe Asp Thr Ser Arg Tyr Asn Gln Gln Glu Pro Pro Gln Arg Gln Asp
    2130                2135                2140

ggc ggg ttt gag ctc taaataatgg cagtagattt cag                    6470
Gly Gly Phe Glu Leu
2145
```

<210> 8
<211> 2149
<212> PRT
<213> Corynebacterium glutamicum

<400> 8

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Trp Gly Gln Lys Asp His Trp Gly Lys Ala Pro Leu Gly Asp His Asp
  1               5                  10                  15

Ala Val Arg Ile Tyr Arg Gln Ala Glu Ala Leu Met Lys Gln Arg Ala
            20                  25                  30
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Ala Asn Asn Lys Gly Leu Asp Leu Asn Asp Glu Ala Thr Tyr Gly Ala
          35                  40                  45

Ile Met Phe Ala Ser Phe Asp Asp Ala Phe Ala Ala Asp Ala Glu Ala
      50                  55                  60

His Gly Cys Val His Arg Pro Gln Phe Ala Lys Val Thr Arg Arg Asn
 65                  70                  75                  80

Ile Leu Asn Ser Pro Gln Tyr Thr Ala Ile Lys Ser Ser Tyr Asp Ala
                 85                  90                  95

Leu Val Gln Gln Asp Leu Val Ala Gln Gln Gln Gln Ala Gln Ala Leu
            100                 105                 110

Gln Gln Ala Ala Tyr Glu Gln Glu Gln Ala Ala Ile Phe Gln Ala Arg
        115                 120                 125

Asp Gln Ala Thr Phe Gln Ala Glu Gln Thr Leu Ala Gln Glu Ser Val
    130                 135                 140

Arg Gln Ser Glu Gly Val Gly Leu Pro Val Ile Asp Pro Met Glu Ser
145                 150                 155                 160

Tyr Phe Arg Glu Tyr Ala Phe Tyr Glu Gly Val Glu Met Phe Gly Thr
                165                 170                 175

Trp Gly Thr His Val Asp Ala Gly Val Ser Gln Phe Ser Thr Ser Asp
            180                 185                 190

Gly Arg Ala Ile Arg Ala Leu Val Asp Glu His Leu Ala Thr Tyr Glu
        195                 200                 205

Pro Val Glu Gln Arg Gly Ser Thr Gln Ala Phe Phe Ala Ser Val Asn
    210                 215                 220

Ala Ala Phe Ala Glu Val Ala Pro His Ala Ala Pro Met Phe Ser Ala
225                 230                 235                 240

Ile Ala Arg Glu Gly Glu Gly Ser Lys Gly Tyr Gln Ala Leu Arg His
                245                 250                 255

Arg Phe Asp Lys Met Val Gly Thr Ala Ile Gly Pro Asn Gly Leu Pro
            260                 265                 270

Glu Gly Pro Asp Leu Gly Gly Arg Arg Leu Pro Ile Ser Pro Tyr Asp
        275                 280                 285

Pro Arg Trp Ser Asp Arg Glu Val Val Arg Val His Gly Thr Lys Leu
    290                 295                 300

Leu Ser Leu Ser Glu Glu Ser Val Gly Met Ile Arg Asp Leu Asp Leu
305                 310                 315                 320

Ala Thr Ile His Leu Gln Asp Asn Asp Val Tyr Glu Gly Thr His Arg
                325                 330                 335

Glu Asp Asp Thr Lys Gly Gly Val Arg Pro Leu Thr Gln Trp Val Asn
            340                 345                 350

Gly Glu Ala Ile Ala Trp Arg Thr Ile Thr Glu Asn Asp Gln Met Arg
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        355                 360                 365

Leu Pro Asn Ile Gly Gln Phe Met Thr Ala Lys Glu Tyr Arg Ala Ala
    370                 375                 380

Ala Ser Trp Leu Arg Ala Gly Leu Ile Asp Thr Ala Asp Val Ala Ser
385                 390                 395                 400

Gln Lys Ile Asp Pro Asn Lys Val Met Ser Asp Glu Gly Ile Ala Arg
                405                 410                 415

Ser Glu Ala Ile Leu Thr Tyr Leu Ser Asp Glu Gly Val Asp Phe Arg
            420                 425                 430

Ile Glu Pro Asp Arg Glu Pro Gly Gln Leu Lys Val Arg Ile Glu Gly
        435                 440                 445

Thr Arg Ile Asp Ile Arg Leu Thr Asp Thr Arg Ala Asn Glu Gln Trp
    450                 455                 460

Val Gly Arg Val Tyr Asp Ser Gly Thr Val Ile Lys Tyr Ser Ala Glu
465                 470                 475                 480

Gln Thr Ala Glu Glu Arg Leu Arg Ala Arg Glu Arg Met Glu Asn Gly
                485                 490                 495

Asp Gly Thr Trp Thr Pro Ala Thr Asp Tyr Glu Pro Ser Pro Thr Glu
            500                 505                 510

Val Val Asp Leu Val Lys Phe Ala Leu Gly Arg Glu Val Glu Arg Gln
        515                 520                 525

Asp Gly Lys Gly Leu Val Gly Val Pro Asn Ala Arg His Pro Arg Ala
    530                 535                 540

Leu Glu Gln Ala Gln Asp Ala Tyr Phe Thr Lys Asn Arg Ser Ala Phe
545                 550                 555                 560

Met Val Arg Glu Gly Leu Ser Ile Val Gln Asp Ala Arg Asp Arg Ser
                565                 570                 575

Ala Gly Pro Gly Lys Trp Phe Asp Asn Glu Ala Lys Ala Ser Glu Trp
            580                 585                 590

Leu Gly Asn Asn Ile Ala Leu Thr Arg Ala Arg Val Ala Glu Glu Leu
        595                 600                 605

Gly Val Glu Glu Leu Ile Ala Leu Ser Ala Gln Tyr Ala Asp Asp Pro
    610                 615                 620

Asp Phe Met Pro Ala Phe Ala Gly Glu Asp Glu Leu Met Ala Ile Lys
625                 630                 635                 640

Gln Asp Tyr Trp Ala Met Leu Arg Gly Glu Glu Thr Asp Leu Leu Asn
                645                 650                 655

Pro Gly Val Asn Arg Asp Asp Tyr Met Ala Ala Ile Arg Asp Gly Asp
            660                 665                 670

His Glu Gln Ile Ala Ala Met Thr Ser Ala Met Asn Ala Val Thr Val
        675                 680                 685
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Glu Asp Arg Val Arg Gln His Ala Ala Leu Val Leu Asp Asp Tyr Val
    690                 695                 700

Gly Thr Val Glu Pro Asp Pro Val Thr Gly Leu Arg Phe Asn Pro Val
705                 710                 715                 720

Thr Val Ala Gln His Met Pro Ser Ala Lys Ser Leu Trp Ser Asn His
                725                 730                 735

Asp Asp Ile Ile Ala Ala Leu Arg Ala Thr Ser Ile Thr Gly Asp Glu
            740                 745                 750

Leu Arg Gly Asp Glu Phe Tyr Asn Asp Val Ile Asn Gln Gln Leu Leu
        755                 760                 765

Lys Phe Asn Pro Glu Thr Ala Gln Lys Met Val Asn Asn Pro Asp Leu
    770                 775                 780

Asp Pro Gln Leu Ala Arg Phe Gly Thr Val Ile Ala Glu Thr Ile Ser
785                 790                 795                 800

Arg Asn Gly Ala Asp Val Val Asp Ile Ala Val Asp Asp Asn Gly Val
                805                 810                 815

Val Arg Trp Thr Ala Gln Arg Arg Val Gly Ala Lys Asp Ser Arg Ala
            820                 825                 830

Val Asp Ser Lys Gly Gln Val Arg Gly Glu Arg Thr Arg His Val Gln
        835                 840                 845

Gly Glu Ile Gly Gln Ile Phe Thr Arg Gly Glu His Gly Glu Ile Val
    850                 855                 860

Thr Lys Phe Asn Gly Gly Glu Asn Tyr Met Phe Ala Pro Gly Tyr Thr
865                 870                 875                 880

Ala Ser Val Val Pro Gln Lys Pro Gly Glu Thr Lys Ser Leu Glu Glu
                885                 890                 895

Arg Thr Lys Leu Lys Gly Tyr Glu Gln Val Met Ser Glu Ala Leu Val
            900                 905                 910

Tyr Arg Val Arg Glu Asp Leu Met Phe Thr Glu Arg Ser Arg Val Gly
        915                 920                 925

Ala Thr Thr Ser Ile Asn Ser Ala Tyr Lys Arg Leu Tyr Asp Asn Arg
    930                 935                 940

Phe Pro Val Asp Phe Phe Glu Arg Ser Ala Glu Glu Gly Leu Ser Asp
945                 950                 955                 960

Glu Trp Arg Ala Ala Leu Leu Glu Thr Ala Ser Leu Arg Val Arg Tyr
                965                 970                 975

Asp Asn Ser Ile Arg Asp Gly Ala Asn Val Met Glu Asp Ile Arg Ala
            980                 985                 990

Gln Gln Arg Gly Phe Asp Ala Arg Asn Asp Asn Ser Arg Asp Ala Leu
        995                 1000                1005
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Val Leu Thr Gly Gly Arg Asn Ile Ser Val Leu Asp Val Asp Ala Gly
    1010                1015                1020

Lys Gly Phe Phe Asp Pro Met Met Thr Gly Met Ala Ala Asn Gln Gly
1025                1030                1035                1040

Ser Val Arg Tyr Leu Leu Pro Ser Ala Lys Val Gly Ala Asp Gly Met
                1045                1050                1055

Ile Thr Pro Gly Asp Pro Ala Asp Arg Val Pro Val Ala Ala His Pro
            1060                1065                1070

Glu Ser Trp Ala Met Gly Phe Asp Pro His Asp Arg Gln Asn Met Thr
        1075                1080                1085

Phe Ser Asn Ile Met Gln Ala Ser Ala Val Thr Gly Gly Ala Arg Thr
    1090                1095                1100

Ala Met Ile Gln Leu Gly Gly Trp Asn Phe Glu Asp Gly Ile Ile Val
1105                1110                1115                1120

Ser Ala Asp Phe Ala Asn Thr His Val Ile Arg Asp Thr Glu Asp Glu
                1125                1130                1135

Met Arg Pro Leu Val Ala Gly Asp Lys Leu Ser Asp Phe His Gly Asn
            1140                1145                1150

Lys Gly Val Thr Ala Leu Val Val Asp Pro Ala Met Ser Asp Ala Asp
        1155                1160                1165

Ala Arg Ala Ala Gly Leu Glu Ser Glu Val Ala Phe Phe Arg Asp Asn
    1170                1175                1180

Pro Asp Leu Glu Val Val Met Ser Pro Phe Ser Ala Ile Ser Arg Phe
1185                1190                1195                1200

Asn Gly Gly Thr Ala Arg Glu Leu Met Thr Asn Pro Gln Asp Val Val
                1205                1210                1215

Phe Arg Asn Asn Asp Gly Ser Thr Arg Val Gln Pro Gly Ala Ser Gly
            1220                1225                1230

Asp Leu Asn Phe Ile Val Thr His Met Ala Val Asp Ala Lys Thr Asn
        1235                1240                1245

Val Tyr Asp Glu Glu Ala Val Arg Glu Gly Gln Gly Arg Lys Ala Ser
    1250                1255                1260

Ser Gln Leu Ala Trp Val Leu Gln Ala Gln Glu Cys His Glu Ile Met
1265                1270                1275                1280

Glu His Phe Tyr Gly Asn Asn Val Ser Ala Leu Ala Asn Phe Gln Glu
                1285                1290                1295

Tyr Leu Arg Val Thr Gly Leu Asp Val Thr Pro Tyr Gly Glu Leu Arg
            1300                1305                1310

Glu Gly Phe Ser Glu Ser Asn Glu Gln Arg Asn Ile Ile Glu Met Pro
        1315                1320                1325

Ser Ile Tyr Asp Glu Asn Gly Glu Leu Asn Asn Arg Val Asn Arg Ala
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    1330                1335                1340

Gln Val Arg Glu Ala Phe Val Glu Gln Ile Ser Arg Ala Gly Gly Val
1345                1350                1355                1360

Met Glu Ile Pro Phe Gln Leu Gln Leu Arg Asn Gly Ala Gln Leu Glu
                1365                1370                1375

Glu Ser Pro Asn Asn Pro Asp Met Tyr Gln Leu Pro Leu Leu Ser Pro
            1380                1385                1390

His Leu Arg Ser Asp Glu Asp Leu Ala Asp Gly Ser Thr Ser Arg His
        1395                1400                1405

Glu Tyr Thr Thr Arg Tyr Met Ala Ile Phe Asp Thr Cys Tyr Lys Leu
    1410                1415                1420

Ala Glu Glu Gln Ala Lys Ile Asp Ala Leu Arg Gln Glu Glu Ala Gln
1425                1430                1435                1440

His Gly Thr Leu Pro Arg Ala Ala Glu Lys Arg Leu Ser Glu Ser Gln
                1445                1450                1455

Lys Phe Val Asp Gln Ala Gln Lys Lys Val Gln Ala Ser Phe Asp Gly
            1460                1465                1470

Ile Ala Asn Asp Ile Val Ala Ser Arg Ile Glu Thr Lys Asn Asn Val
        1475                1480                1485

Phe Lys Asp Gly Phe Met Ser Ala Arg Gln Ser His Ser Ala Thr Ala
    1490                1495                1500

Val Trp Thr Gly Asp Pro Arg Leu Ser Val Asp Glu Val Ala Met Asn
1505                1510                1515                1520

Ser Ser Met Ala Arg Glu Leu Gly Val Leu Asp Asn Gly Tyr Ala Met
                1525                1530                1535

Val Trp Arg Asp Pro Val Ile Arg Asp Gly Gly Val Arg Tyr Leu Arg
            1540                1545                1550

Val Val Ile Asn Asp Asp Leu His Gly Val Ala Val Asn Pro Val Ser
        1555                1560                1565

Val Lys Ser Phe Asp Gly Asp Phe Asp Gly Asp Ser Val Gly Leu Val
    1570                1575                1580

Gly Asn Leu Pro Lys Lys Ala His Glu Glu Ala Leu Ser Arg Leu Thr
1585                1590                1595                1600

Val Glu Ala Asn Met Leu Asp Leu Gly Asp Gly Lys Arg Met Glu Asp
                1605                1610                1615

Gly Thr Met Phe Tyr Gly Leu Thr Leu His Asp Ser Leu Asp Val Gln
            1620                1625                1630

Val Ala Gln His His Asp Pro Ala Met Ala Glu Asn Met Lys Val Ile
        1635                1640                1645

Val Ser Glu Leu Asn Arg Tyr Gln Arg Glu Tyr Glu Ala Gly Glu Ile
    1650                1655                1660
```

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Ser Arg Glu Glu Leu Leu Glu Val Asn Arg Ala His Met Asp Asp Leu
1665                1670                1675                1680

Asn Glu His Tyr Ala Gln Ala Phe Ala Asn Arg Asp Gly Leu Val Thr
                1685                1690                1695

Leu Arg Phe Asp Gly Met Glu Asn His Met Ala Ser Val Ala Gln Cys
            1700                1705                1710

Phe Glu Thr Gly Ala Lys Gly Ser Pro Gly Lys Leu Lys Glu Tyr Ala
        1715                1720                1725

Thr Tyr Ile Gly Ala Asp Pro Ala Gln Gly Phe Lys Asp Val Gly Gln
    1730                1735                1740

Pro Thr Pro Glu Ala Leu Arg Ser His Tyr Glu Gly Ser Gln Lys Ala
1745                1750                1755                1760

Thr Ala Ile Lys Val Leu Phe Thr Gly Val Ala Gly Lys Lys Glu Gln
                1765                1770                1775

Glu Met Val Ala Leu Cys Arg Asn Leu Gly Leu Thr Lys Glu Ala Met
            1780                1785                1790

Ala Ala Ser Ala Pro Ala Gln Gln Ser Ile Leu Gln Ala Lys His Asp
        1795                1800                1805

Pro Ile Asp Ala Leu Tyr Arg Ala Glu Thr Leu Met Gly Pro Val Gly
    1810                1815                1820

Asp Leu Tyr Gln Gly Arg Lys Met Arg Arg Gly Glu Asn Glu Gln Gly
1825                1830                1835                1840

Arg Tyr Glu Trp Glu Val Val Arg Asp Glu Asn His Gln Pro Ile Gln
                1845                1850                1855

Ala Thr Lys Asp Glu Trp Val Gln Gln Tyr Met Glu Met Tyr Ala Asp
            1860                1865                1870

Asp Lys Gly Met Gly Val Ser Val Gly Val Asp Gln Val Glu Lys Ile
        1875                1880                1885

Ala Glu Glu Phe Ser Asp Glu Gln Gly Tyr Met Arg Val Leu Ser His
    1890                1895                1900

Asp Glu Leu Pro Thr Glu Ile Lys Pro Leu Ala Leu Asp Gln Leu Ala
1905                1910                1915                1920

Tyr Gly Asp Lys Lys Asn Arg Phe Asp Leu Leu Cys Glu Met Ala Lys
                1925                1930                1935

Gln Gln Val Asn Ile Tyr Asp Gly Asp Ala Tyr Asp Phe Ala Pro Arg
            1940                1945                1950

Val Val Arg Ala Asn Met Lys Ala Met Glu Asp Ala Ala Arg Phe Gly
        1955                1960                1965

Ile Pro Asp Val Glu Ile Gln Ser Ile Ser Ala Gln Gln Ser Leu Ala
    1970                1975                1980
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Ser Phe Glu Arg Val Pro Gln Arg Ser Gly Phe Arg Ile Glu Arg Arg
1985                1990                1995                2000

Val Pro Ala Glu Val Gly Thr Gly Ile Ala Ala Pro Ala Pro Leu Pro
                2005                2010                2015

Asp Ala Gly Val Gln Gly Asn Tyr Val Gln Gln Gln Val Pro Ala Thr
            2020                2025                2030

Pro Pro Val Met Pro Val Thr Pro Pro Ala Gln Gln Pro Val Ser Pro
        2035                2040                2045

Ala Gln Thr Asp Phe Arg Gly Val Gly Gln Pro Leu Asp Gln Gly Gly
    2050                2055                2060

Lys Ile Gly Asn Tyr Gly His Gln Gly Pro Ala Met Gly Ala Gln Gln
2065                2070                2075                2080

Pro Val Val Pro Gln Gln Gln Asn Ile Pro Pro Val His Asn Pro Val
                2085                2090                2095

Pro Gln Asn Ser Val Pro Pro Thr Pro Val Val Pro Lys Pro Gly Thr
            2100                2105                2110

Gly Asn Pro Phe Thr His Gly Gly Ala Asn Asn Gln Phe Met Gly Arg
        2115                2120                2125

Phe Asp Thr Ser Arg Tyr Asn Gln Gln Glu Pro Pro Gln Arg Gln Asp
    2130                2135                2140

Gly Gly Phe Glu Leu
2145
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<210> 9
<211> 1307
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1284)
<223> FRXA01590

<400> 9

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ggc aag ttg aag gaa tat gcc acc tat atc ggc gct gat ccg gcg cag   48
Gly Lys Leu Lys Glu Tyr Ala Thr Tyr Ile Gly Ala Asp Pro Ala Gln
  1               5                  10                  15

ggt ttt aaa gac gta ggt caa cca acg cca gaa gcg ctg cgt agc cac   96
Gly Phe Lys Asp Val Gly Gln Pro Thr Pro Glu Ala Leu Arg Ser His
             20                  25                  30

tat gag ggt tcg cag aag gcg act gca att aag gtg ctc ttt acc ggt   144
Tyr Glu Gly Ser Gln Lys Ala Thr Ala Ile Lys Val Leu Phe Thr Gly
         35                  40                  45

gtg gct ggt aaa aaa gag cag gaa atg gtg gca ttg tgc cgc aat ctt   192
Val Ala Gly Lys Lys Glu Gln Glu Met Val Ala Leu Cys Arg Asn Leu
     50                  55                  60
```

```
ggt ctg acc aag gaa gct atg gct gca tca gca ccg gca cag cag tcg   240
Gly Leu Thr Lys Glu Ala Met Ala Ala Ser Ala Pro Ala Gln Gln Ser
 65                  70                  75                  80

att ctg cag gcg aag cac gac ccg att gac gcg ctc tat cgt gca gaa   288
Ile Leu Gln Ala Lys His Asp Pro Ile Asp Ala Leu Tyr Arg Ala Glu
                85                  90                  95

act ctt atg gga cca gta ggt gat ctc tac caa ggt cgc aag atg cgt   336
Thr Leu Met Gly Pro Val Gly Asp Leu Tyr Gln Gly Arg Lys Met Arg
            100                 105                 110

cgt ggt gag aat gag caa ggt cgc tat gag tgg gaa gtc gtt agg gac   384
Arg Gly Glu Asn Glu Gln Gly Arg Tyr Glu Trp Glu Val Val Arg Asp
        115                 120                 125

gag aac cac cag cct atc cag gcc acc aag gat gaa tgg gta cag cag   432
Glu Asn His Gln Pro Ile Gln Ala Thr Lys Asp Glu Trp Val Gln Gln
    130                 135                 140

tac atg gag atg tac gcc gat gac aag ggt atg ggt gtc tcg gtt ggc   480
Tyr Met Glu Met Tyr Ala Asp Asp Lys Gly Met Gly Val Ser Val Gly
145                 150                 155                 160

gtt gac cag gtg gag aag atc gcg gaa gaa ttc tct gat gag cag ggt   528
Val Asp Gln Val Glu Lys Ile Ala Glu Glu Phe Ser Asp Glu Gln Gly
                165                 170                 175

tat atg cgt gtg ctt agc cat gat gag cta ccc act gag att aag cca   576
Tyr Met Arg Val Leu Ser His Asp Glu Leu Pro Thr Glu Ile Lys Pro
            180                 185                 190

cta gca ctt gat cag ctt gcc tat ggc gat aag aag aac cgc ttt gat   624
Leu Ala Leu Asp Gln Leu Ala Tyr Gly Asp Lys Lys Asn Arg Phe Asp
        195                 200                 205

ttg ttg tgc gag atg gca aag cag cag gtc aac atc tac gac ggt gat   672
Leu Leu Cys Glu Met Ala Lys Gln Gln Val Asn Ile Tyr Asp Gly Asp
    210                 215                 220

gct tat gac ttt gcc cct cgt gtg gtg cgc gcc aat atg aag gca atg   720
Ala Tyr Asp Phe Ala Pro Arg Val Val Arg Ala Asn Met Lys Ala Met
225                 230                 235                 240

gag gat gca gcg cgt ttt ggt atc cct gat gtg gag att cag tcg att   768
Glu Asp Ala Ala Arg Phe Gly Ile Pro Asp Val Glu Ile Gln Ser Ile
                245                 250                 255

tct gca cag cag tca ttg gcg agc ttt gag cga gtc cca caa cgt tct   816
Ser Ala Gln Gln Ser Leu Ala Ser Phe Glu Arg Val Pro Gln Arg Ser
            260                 265                 270

ggt ttc cgt att gag cgt cgt gtg ccg gca gaa gta ggt aca ggg att   864
Gly Phe Arg Ile Glu Arg Arg Val Pro Ala Glu Val Gly Thr Gly Ile
        275                 280                 285

gct gca cca gca ccg tta cct gat gca ggt gta cag ggg aat tat gtt   912
Ala Ala Pro Ala Pro Leu Pro Asp Ala Gly Val Gln Gly Asn Tyr Val
    290                 295                 300

cag cag cag gtg cct gcg acc ccg cca gtt atg cct gtc aca cct ccg   960
```

```
Gln Gln Gln Val Pro Ala Thr Pro Pro Val Met Pro Val Thr Pro Pro
305                 310                 315                 320

gca cag caa cct gtt tcg cct gct cag acg gac ttc cgg ggc gtt ggt   1008
Ala Gln Gln Pro Val Ser Pro Ala Gln Thr Asp Phe Arg Gly Val Gly
                325                 330                 335

cag cca ctc gac cag ggc gga aaa atc ggg aat tat gga cat cag gga   1056
Gln Pro Leu Asp Gln Gly Gly Lys Ile Gly Asn Tyr Gly His Gln Gly
            340                 345                 350

cct gca atg ggg gcg caa cag cca gtt gtg cct cag cag cag aat att   1104
Pro Ala Met Gly Ala Gln Gln Pro Val Val Pro Gln Gln Gln Asn Ile
        355                 360                 365

ccg cct gtg cat aat ccg gta cca cag aat tct gtt ccg cct act ccg   1152
Pro Pro Val His Asn Pro Val Pro Gln Asn Ser Val Pro Pro Thr Pro
    370                 375                 380

gtt gtg ccg aag cca ggt aca gga aac ccg ttt act cat ggt ggt gcg   1200
Val Val Pro Lys Pro Gly Thr Gly Asn Pro Phe Thr His Gly Gly Ala
385                 390                 395                 400

aac aat cag ttt atg ggt cga ttt gat aca agc cgt tac aac caa cag   1248
Asn Asn Gln Phe Met Gly Arg Phe Asp Thr Ser Arg Tyr Asn Gln Gln
                405                 410                 415

gaa cca cca caa cga cag gat ggc ggg ttt gag ctc taaataatgg        1294
Glu Pro Pro Gln Arg Gln Asp Gly Gly Phe Glu Leu
            420                 425

cagtagattt cag                                                   1307


<210> 10
<211> 428
<212> PRT
<213> Corynebacterium glutamicum

<400> 10
Gly Lys Leu Lys Glu Tyr Ala Thr Tyr Ile Gly Ala Asp Pro Ala Gln
  1               5                  10                  15

Gly Phe Lys Asp Val Gly Gln Pro Thr Pro Glu Ala Leu Arg Ser His
            20                  25                  30

Tyr Glu Gly Ser Gln Lys Ala Thr Ala Ile Lys Val Leu Phe Thr Gly
        35                  40                  45

Val Ala Gly Lys Lys Glu Gln Glu Met Val Ala Leu Cys Arg Asn Leu
    50                  55                  60

Gly Leu Thr Lys Glu Ala Met Ala Ala Ser Ala Pro Ala Gln Gln Ser
65                  70                  75                  80

Ile Leu Gln Ala Lys His Asp Pro Ile Asp Ala Leu Tyr Arg Ala Glu
                85                  90                  95

Thr Leu Met Gly Pro Val Gly Asp Leu Tyr Gln Gly Arg Lys Met Arg
            100                 105                 110
```

```
Arg Gly Glu Asn Glu Gln Gly Arg Tyr Glu Trp Glu Val Val Arg Asp
        115                 120                 125

Glu Asn His Gln Pro Ile Gln Ala Thr Lys Asp Glu Trp Val Gln Gln
    130                 135                 140

Tyr Met Glu Met Tyr Ala Asp Asp Lys Gly Met Gly Val Ser Val Gly
145                 150                 155                 160

Val Asp Gln Val Glu Lys Ile Ala Glu Glu Phe Ser Asp Glu Gln Gly
                165                 170                 175

Tyr Met Arg Val Leu Ser His Asp Glu Leu Pro Thr Glu Ile Lys Pro
            180                 185                 190

Leu Ala Leu Asp Gln Leu Ala Tyr Gly Asp Lys Lys Asn Arg Phe Asp
        195                 200                 205

Leu Leu Cys Glu Met Ala Lys Gln Gln Val Asn Ile Tyr Asp Gly Asp
    210                 215                 220

Ala Tyr Asp Phe Ala Pro Arg Val Val Arg Ala Asn Met Lys Ala Met
225                 230                 235                 240

Glu Asp Ala Ala Arg Phe Gly Ile Pro Asp Val Glu Ile Gln Ser Ile
                245                 250                 255

Ser Ala Gln Gln Ser Leu Ala Ser Phe Glu Arg Val Pro Gln Arg Ser
            260                 265                 270

Gly Phe Arg Ile Glu Arg Arg Val Pro Ala Glu Val Gly Thr Gly Ile
        275                 280                 285

Ala Ala Pro Ala Pro Leu Pro Asp Ala Gly Val Gln Gly Asn Tyr Val
    290                 295                 300

Gln Gln Gln Val Pro Ala Thr Pro Pro Val Met Pro Val Thr Pro Pro
305                 310                 315                 320

Ala Gln Gln Pro Val Ser Pro Ala Gln Thr Asp Phe Arg Gly Val Gly
                325                 330                 335

Gln Pro Leu Asp Gln Gly Gly Lys Ile Gly Asn Tyr Gly His Gln Gly
            340                 345                 350

Pro Ala Met Gly Ala Gln Gln Pro Val Val Pro Gln Gln Gln Asn Ile
        355                 360                 365

Pro Pro Val His Asn Pro Val Pro Gln Asn Ser Val Pro Pro Thr Pro
    370                 375                 380

Val Val Pro Lys Pro Gly Thr Gly Asn Pro Phe Thr His Gly Gly Ala
385                 390                 395                 400

Asn Asn Gln Phe Met Gly Arg Phe Asp Thr Ser Arg Tyr Asn Gln Gln
                405                 410                 415

Glu Pro Pro Gln Arg Gln Asp Gly Gly Phe Glu Leu
            420                 425
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<210> 11
<211> 5061
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(5061)
<223> FRXA01542

<400> 11

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tgg ggt caa aaa gat cac tgg ggc aaa gct cca ctg ggt gat cac gat   48
Trp Gly Gln Lys Asp His Trp Gly Lys Ala Pro Leu Gly Asp His Asp
  1               5                  10                  15

gct gtg cgt atc tat agg caa gca gaa gcc ttg atg aaa cag cgc gca   96
Ala Val Arg Ile Tyr Arg Gln Ala Glu Ala Leu Met Lys Gln Arg Ala
             20                  25                  30

gca aac aat aag ggc tta gac ctc aat gat gaa gcg acc tat ggc gcc   144
Ala Asn Asn Lys Gly Leu Asp Leu Asn Asp Glu Ala Thr Tyr Gly Ala
         35                  40                  45

atc atg ttt gcg tct ttc gat gat gcc ttc gcc gct gat gcc gaa gct   192
Ile Met Phe Ala Ser Phe Asp Asp Ala Phe Ala Ala Asp Ala Glu Ala
     50                  55                  60

cat ggc tgt gta cac cga cca cag ttc gcg aag gta act agg cga aat   240
His Gly Cys Val His Arg Pro Gln Phe Ala Lys Val Thr Arg Arg Asn
 65                  70                  75                  80

att ctt aat tca ccg caa tac acg gcg att aag tca tct tat gac gcg   288
Ile Leu Asn Ser Pro Gln Tyr Thr Ala Ile Lys Ser Ser Tyr Asp Ala
                 85                  90                  95

ctg gtg cag cag gat ctc gtg gcc caa cag cag cag gca caa gcg cta   336
Leu Val Gln Gln Asp Leu Val Ala Gln Gln Gln Gln Ala Gln Ala Leu
            100                 105                 110

cag caa gct gct tat gag caa gag cag gca gct att ttc cag gca cgt   384
Gln Gln Ala Ala Tyr Glu Gln Glu Gln Ala Ala Ile Phe Gln Ala Arg
        115                 120                 125

gat caa gca aca ttc cag gct gaa caa acg ctc gcg caa gag tcc gtt   432
Asp Gln Ala Thr Phe Gln Ala Glu Gln Thr Leu Ala Gln Glu Ser Val
    130                 135                 140

cgc caa tca gag ggt gtg ggt tta cct gtc att gat ccg atg gag agc   480
Arg Gln Ser Glu Gly Val Gly Leu Pro Val Ile Asp Pro Met Glu Ser
145                 150                 155                 160

tat ttc cgg gag tac gcc ttc tat gaa ggt gtc gag atg ttt ggt acc   528
Tyr Phe Arg Glu Tyr Ala Phe Tyr Glu Gly Val Glu Met Phe Gly Thr
                165                 170                 175

tgg ggt acg cac gtt gat gct ggt gtg tcg cag ttt agc acc tct gat   576
Trp Gly Thr His Val Asp Ala Gly Val Ser Gln Phe Ser Thr Ser Asp
            180                 185                 190

ggc cgt gcg atc cga gcg ctt gtt gat gag cat ctc gca acc tat gaa   624
Gly Arg Ala Ile Arg Ala Leu Val Asp Glu His Leu Ala Thr Tyr Glu
```

```
        195                 200                 205

cca gta gag cag cgg ggg agt act cag gca ttc ttc gcc tct gtc aat   672
Pro Val Glu Gln Arg Gly Ser Thr Gln Ala Phe Phe Ala Ser Val Asn
    210                 215                 220

gct gcc ttt gct gag gtg gca cct cac gca gca ccc atg ttt agt gcg   720
Ala Ala Phe Ala Glu Val Ala Pro His Ala Ala Pro Met Phe Ser Ala
225                 230                 235                 240

att gct cgc gag ggt gag ggt tca aag ggg tac cag gcg ctg cgt cac   768
Ile Ala Arg Glu Gly Glu Gly Ser Lys Gly Tyr Gln Ala Leu Arg His
                245                 250                 255

cgt ttc gac aag atg gtc ggc act gca att gga cct aat ggt ttg cct   816
Arg Phe Asp Lys Met Val Gly Thr Ala Ile Gly Pro Asn Gly Leu Pro
            260                 265                 270

gag gga cct gat ctg ggt ggt cgt cgt tta cct att tcg cct tat gat   864
Glu Gly Pro Asp Leu Gly Gly Arg Arg Leu Pro Ile Ser Pro Tyr Asp
        275                 280                 285

cca cgc tgg tca gac cgc gaa gta gtc cgt gtg cac ggt acc aag ctg   912
Pro Arg Trp Ser Asp Arg Glu Val Val Arg Val His Gly Thr Lys Leu
    290                 295                 300

cta tca ctg tcc gaa gag agt gtt ggc atg atc agg gac ctt gat cta   960
Leu Ser Leu Ser Glu Glu Ser Val Gly Met Ile Arg Asp Leu Asp Leu
305                 310                 315                 320

gca acg atc cac cta caa gat aat gat gtt tac gag ggc act cat cga  1008
Ala Thr Ile His Leu Gln Asp Asn Asp Val Tyr Glu Gly Thr His Arg
                325                 330                 335

gaa gac gac act aaa ggc ggt gtg cga ccg ttg act caa tgg gtc aat  1056
Glu Asp Asp Thr Lys Gly Gly Val Arg Pro Leu Thr Gln Trp Val Asn
            340                 345                 350

ggt gaa gct att gcc tgg cgc act atc acc gag aat gac cag atg cga  1104
Gly Glu Ala Ile Ala Trp Arg Thr Ile Thr Glu Asn Asp Gln Met Arg
        355                 360                 365

ctg ccc aat att ggt cag ttt atg acg gct aaa gaa tac cgt gcc gca  1152
Leu Pro Asn Ile Gly Gln Phe Met Thr Ala Lys Glu Tyr Arg Ala Ala
    370                 375                 380

gcg tca tgg ctg cgt gct gga ctc att gat acc gca gat gtt gcg agt  1200
Ala Ser Trp Leu Arg Ala Gly Leu Ile Asp Thr Ala Asp Val Ala Ser
385                 390                 395                 400

cag aaa att gac ccc aac aag gtc atg tct gat gag ggt atc gcg cgc  1248
Gln Lys Ile Asp Pro Asn Lys Val Met Ser Asp Glu Gly Ile Ala Arg
                405                 410                 415

tcg gaa gct att ttg acg tat ctg tcg gat gag ggt gtg gat ttt agg  1296
Ser Glu Ala Ile Leu Thr Tyr Leu Ser Asp Glu Gly Val Asp Phe Arg
            420                 425                 430

atc gag cca gat cgt gag ccg gga cag ctt aaa gtg cgt att gag ggc  1344
Ile Glu Pro Asp Arg Glu Pro Gly Gln Leu Lys Val Arg Ile Glu Gly
        435                 440                 445
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```
acc cgt att gat att cgt ctc act gat act cgc gcc aat gaa cag tgg   1392
Thr Arg Ile Asp Ile Arg Leu Thr Asp Thr Arg Ala Asn Glu Gln Trp
    450                 455                 460

gtg ggt cgt gtc tat gat tct ggc act gtg att aag tat tcc gcc gaa   1440
Val Gly Arg Val Tyr Asp Ser Gly Thr Val Ile Lys Tyr Ser Ala Glu
465                 470                 475                 480

caa aca gcg gaa gaa cgt cta cga gct cgt gag cgc atg gag aac ggt   1488
Gln Thr Ala Glu Glu Arg Leu Arg Ala Arg Glu Arg Met Glu Asn Gly
                485                 490                 495

gat gga acg tgg aca ccg gct act gat tat gaa cca agc cca act gaa   1536
Asp Gly Thr Trp Thr Pro Ala Thr Asp Tyr Glu Pro Ser Pro Thr Glu
            500                 505                 510

gtt gtc gat ctc gtg aaa ttt gct ctc ggt cga gag gtt gag cga cag   1584
Val Val Asp Leu Val Lys Phe Ala Leu Gly Arg Glu Val Glu Arg Gln
        515                 520                 525

gat ggc aaa ggt ctt gtt ggt gtg cct aat gct cga cac cca cgt gct   1632
Asp Gly Lys Gly Leu Val Gly Val Pro Asn Ala Arg His Pro Arg Ala
    530                 535                 540

tta gag cag gca cag gat gca tat ttc act aag aat cgt tcc gca ttc   1680
Leu Glu Gln Ala Gln Asp Ala Tyr Phe Thr Lys Asn Arg Ser Ala Phe
545                 550                 555                 560

atg gtg cgt gaa ggg ctc tcg atc gtt cag gat gca cgt gat cga agt   1728
Met Val Arg Glu Gly Leu Ser Ile Val Gln Asp Ala Arg Asp Arg Ser
                565                 570                 575

gct ggt cct gga aag tgg ttt gat aat gaa gcg aaa gca tcg gag tgg   1776
Ala Gly Pro Gly Lys Trp Phe Asp Asn Glu Ala Lys Ala Ser Glu Trp
            580                 585                 590

ctt ggt aac aat atc gcc ctt act cgt gcg cgt gtg gcc gaa gag ctc   1824
Leu Gly Asn Asn Ile Ala Leu Thr Arg Ala Arg Val Ala Glu Glu Leu
        595                 600                 605

ggc gtt gaa gaa ctg att gcg ctt tct gca cag tac gcc gat gat cct   1872
Gly Val Glu Glu Leu Ile Ala Leu Ser Ala Gln Tyr Ala Asp Asp Pro
    610                 615                 620

gac ttc atg ccg gct ttt gct ggt gag gat gag ctc atg gcg ata aag   1920
Asp Phe Met Pro Ala Phe Ala Gly Glu Asp Glu Leu Met Ala Ile Lys
625                 630                 635                 640

cag gac tat tgg gcg atg ctg cga ggt gag gaa acc gat ctg ctt aac   1968
Gln Asp Tyr Trp Ala Met Leu Arg Gly Glu Glu Thr Asp Leu Leu Asn
                645                 650                 655

cct ggg gtt aac cgc gat gat tat atg gct gct atc cgc gat ggt gat   2016
Pro Gly Val Asn Arg Asp Asp Tyr Met Ala Ala Ile Arg Asp Gly Asp
            660                 665                 670

cat gag cag att gct gcg atg acc tca gca atg aat gct gtg acc gtg   2064
His Glu Gln Ile Ala Ala Met Thr Ser Ala Met Asn Ala Val Thr Val
        675                 680                 685
```

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gag gat cgt gtg cgt cag cac gcg gcc ctt gtt ctt gat gat tat gtc   2112
Glu Asp Arg Val Arg Gln His Ala Ala Leu Val Leu Asp Asp Tyr Val
    690                 695                 700

ggc acg gtg gag cct gat cct gtt acc ggc ttg cgt ttt aat ccg gtg   2160
Gly Thr Val Glu Pro Asp Pro Val Thr Gly Leu Arg Phe Asn Pro Val
705                 710                 715                 720

aca gtt gct cag cac atg ccg agt gct aaa tcc ctg tgg tca aac cat   2208
Thr Val Ala Gln His Met Pro Ser Ala Lys Ser Leu Trp Ser Asn His
                725                 730                 735

gac gat att att gcc gcg ttg cga gcg act tcg att act ggc gat gaa   2256
Asp Asp Ile Ile Ala Ala Leu Arg Ala Thr Ser Ile Thr Gly Asp Glu
            740                 745                 750

ctg cgc ggt gac gaa ttc tat aac gat gtt att aat caa cag ttg ctc   2304
Leu Arg Gly Asp Glu Phe Tyr Asn Asp Val Ile Asn Gln Gln Leu Leu
        755                 760                 765

aaa ttt aat cct gag acc gcg cag aaa atg gtt aat aac cct gat ctt   2352
Lys Phe Asn Pro Glu Thr Ala Gln Lys Met Val Asn Asn Pro Asp Leu
    770                 775                 780

gac ccg cag ttg gct cga ttt ggc act gtc att gcc gag act att tcc   2400
Asp Pro Gln Leu Ala Arg Phe Gly Thr Val Ile Ala Glu Thr Ile Ser
785                 790                 795                 800

cgc aat ggt gct gat gtg gtc gat att gct gtt gac gat aac ggt gtg   2448
Arg Asn Gly Ala Asp Val Val Asp Ile Ala Val Asp Asp Asn Gly Val
                805                 810                 815

gtg cgg tgg acc gca cag cga cgt gtt ggt gcg aag gat agt cgt gca   2496
Val Arg Trp Thr Ala Gln Arg Arg Val Gly Ala Lys Asp Ser Arg Ala
            820                 825                 830

gta gat agt aag ggg cag gtt cgc ggt gaa cgc acc cgt cat gtg cag   2544
Val Asp Ser Lys Gly Gln Val Arg Gly Glu Arg Thr Arg His Val Gln
        835                 840                 845

ggt gag ata ggt cag att ttt act cgc ggt gag cat ggt gaa att gtc   2592
Gly Glu Ile Gly Gln Ile Phe Thr Arg Gly Glu His Gly Glu Ile Val
    850                 855                 860

acc aaa ttt aat ggt ggc gag aac tat atg ttt gcc cct ggc tac acc   2640
Thr Lys Phe Asn Gly Gly Glu Asn Tyr Met Phe Ala Pro Gly Tyr Thr
865                 870                 875                 880

gcg tct gtg gta cca caa aag cct ggt gag aca aag agt tta gaa gag   2688
Ala Ser Val Val Pro Gln Lys Pro Gly Glu Thr Lys Ser Leu Glu Glu
                885                 890                 895

cgt acc aag ctc aaa ggc tat gag cag gtg atg tca gag gcg ttg gtg   2736
Arg Thr Lys Leu Lys Gly Tyr Glu Gln Val Met Ser Glu Ala Leu Val
            900                 905                 910

tac cgt gtg cga gaa gat ttg atg ttc act gag cga tcc cga gtg ggt   2784
Tyr Arg Val Arg Glu Asp Leu Met Phe Thr Glu Arg Ser Arg Val Gly
        915                 920                 925

gct aca acc agc atc aac agt gca tat aag cga ctg tat gac aat cgc   2832
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```
Ala Thr Thr Ser Ile Asn Ser Ala Tyr Lys Arg Leu Tyr Asp Asn Arg
    930                 935                 940

ttc cct gtg gac ttc ttc gag cgc agc gcc gaa gaa ggt ttg agc gat   2880
Phe Pro Val Asp Phe Phe Glu Arg Ser Ala Glu Glu Gly Leu Ser Asp
945                 950                 955                 960

gag tgg cgt gct gcg ttg ctt gag act gcg agt ttg cgt gtg cgc tac   2928
Glu Trp Arg Ala Ala Leu Leu Glu Thr Ala Ser Leu Arg Val Arg Tyr
                965                 970                 975

gac aac tct att cgt gat ggt gcg aat gtg atg gag gat att cga gca   2976
Asp Asn Ser Ile Arg Asp Gly Ala Asn Val Met Glu Asp Ile Arg Ala
            980                 985                 990

cag cag cgt ggt ttt gat gcg cgt aat gat aac tcc cgt gat gcg ctg   3024
Gln Gln Arg Gly Phe Asp Ala Arg Asn Asp Asn Ser Arg Asp Ala Leu
        995                 1000                1005

gtg ctt acc ggt ggg cgt aac att tct gta ctt gat gtt gat gcg ggt   3072
Val Leu Thr Gly Gly Arg Asn Ile Ser Val Leu Asp Val Asp Ala Gly
    1010                1015                1020

aaa ggt ttc ttt gat ccc atg atg act ggt atg gcg gcg aac cag ggt   3120
Lys Gly Phe Phe Asp Pro Met Met Thr Gly Met Ala Ala Asn Gln Gly
1025                1030                1035                1040

tct gtt cgc tat ttg ttg cct tct gcg aag gtg ggc gct gat ggc atg   3168
Ser Val Arg Tyr Leu Leu Pro Ser Ala Lys Val Gly Ala Asp Gly Met
                1045                1050                1055

att acc cct ggt gat ccg gct gat cga gta cct gtt gca gcg cat cca   3216
Ile Thr Pro Gly Asp Pro Ala Asp Arg Val Pro Val Ala Ala His Pro
            1060                1065                1070

gaa tca tgg gcg atg ggc ttt gac cca cat gac cgt cag aac atg act   3264
Glu Ser Trp Ala Met Gly Phe Asp Pro His Asp Arg Gln Asn Met Thr
        1075                1080                1085

ttc tcg aac atc atg cag gct agc gct gtg act ggt ggt gca cgc act   3312
Phe Ser Asn Ile Met Gln Ala Ser Ala Val Thr Gly Gly Ala Arg Thr
    1090                1095                1100

gcg atg ata cag ctg ggc ggt tgg aac ttt gaa gat ggc att att gtc   3360
Ala Met Ile Gln Leu Gly Gly Trp Asn Phe Glu Asp Gly Ile Ile Val
1105                1110                1115                1120

tct gcc gat ttt gcg aat acc cat gtt att cgc gat acg gaa gat gag   3408
Ser Ala Asp Phe Ala Asn Thr His Val Ile Arg Asp Thr Glu Asp Glu
                1125                1130                1135

atg cgc ccc ttg gtt gcc ggc gat aag ctg tct gat ttt cac ggt aat   3456
Met Arg Pro Leu Val Ala Gly Asp Lys Leu Ser Asp Phe His Gly Asn
            1140                1145                1150

aag ggt gtg acc gct ctt gtt gtt gat cca gcg atg agt gat gct gat   3504
Lys Gly Val Thr Ala Leu Val Val Asp Pro Ala Met Ser Asp Ala Asp
        1155                1160                1165

gca cgt gca gca ggg ctg gaa tca gag gtg gcg ttt ttc cga gac aac   3552
Ala Arg Ala Ala Gly Leu Glu Ser Glu Val Ala Phe Phe Arg Asp Asn
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1170 1175 1180

cct gat cta gag gtt gtc atg agt ccg ttt tct gcc att tct cgt ttt 3600
Pro Asp Leu Glu Val Val Met Ser Pro Phe Ser Ala Ile Ser Arg Phe
1185 1190 1195 1200

aat ggt ggc acg gca cgt gag ctc atg acc aac ccg cag gat gtg gtg 3648
Asn Gly Gly Thr Ala Arg Glu Leu Met Thr Asn Pro Gln Asp Val Val
1205 1210 1215

ttc agg aat aat gat ggt tct act cgt gtt caa cca ggt gcc tct ggt 3696
Phe Arg Asn Asn Asp Gly Ser Thr Arg Val Gln Pro Gly Ala Ser Gly
1220 1225 1230

gat ctc aac ttc atc gtc acg cat atg gct gtt gat gcg aaa acc aat 3744
Asp Leu Asn Phe Ile Val Thr His Met Ala Val Asp Ala Lys Thr Asn
1235 1240 1245

gtc tat gat gaa gaa gct gtt cgt gag ggc caa gga cgt aaa gcg tct 3792
Val Tyr Asp Glu Glu Ala Val Arg Glu Gly Gln Gly Arg Lys Ala Ser
1250 1255 1260

tct cag ctg gcg tgg gtg ctc caa gcc cag gaa tgt cat gag att atg 3840
Ser Gln Leu Ala Trp Val Leu Gln Ala Gln Glu Cys His Glu Ile Met
1265 1270 1275 1280

gag cac ttt tat ggc aac aac gtc tct gca ttg gct aac ttc cag gaa 3888
Glu His Phe Tyr Gly Asn Asn Val Ser Ala Leu Ala Asn Phe Gln Glu
1285 1290 1295

tat ctt cgc gtc acg ggg ctt gat gtc acc ccg tat ggt gag ttg cgc 3936
Tyr Leu Arg Val Thr Gly Leu Asp Val Thr Pro Tyr Gly Glu Leu Arg
1300 1305 1310

gag ggg ttc agc gag tcc aat gag cag cgc aat atc atc gag atg cca 3984
Glu Gly Phe Ser Glu Ser Asn Glu Gln Arg Asn Ile Ile Glu Met Pro
1315 1320 1325

agc att tac gat gag aac ggt gag ctg aat aat cgt gtt aat cgt gca 4032
Ser Ile Tyr Asp Glu Asn Gly Glu Leu Asn Asn Arg Val Asn Arg Ala
1330 1335 1340

cag gtg cgc gaa gct ttt gtt gag cag atc agt cgc gct ggt ggt gtt 4080
Gln Val Arg Glu Ala Phe Val Glu Gln Ile Ser Arg Ala Gly Gly Val
1345 1350 1355 1360

atg gag att cct ttc cag tta cag ttg cgc aat ggt gca cag cta gaa 4128
Met Glu Ile Pro Phe Gln Leu Gln Leu Arg Asn Gly Ala Gln Leu Glu
1365 1370 1375

gag tca cct aat aat cca gac atg tat cag ttg cca cta ctg agc ccg 4176
Glu Ser Pro Asn Asn Pro Asp Met Tyr Gln Leu Pro Leu Leu Ser Pro
1380 1385 1390

cat ttg cgc agt gat gag gat tta gcg gac ggt agt acc tct cga cat 4224
His Leu Arg Ser Asp Glu Asp Leu Ala Asp Gly Ser Thr Ser Arg His
1395 1400 1405

gag tac acc acg cgg tat atg gct att ttt gat acg tgc tac aag ctg 4272
Glu Tyr Thr Thr Arg Tyr Met Ala Ile Phe Asp Thr Cys Tyr Lys Leu
1410 1415 1420

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gca gaa gag caa gcc aag att gac gca ttg cgc cag gag gaa gcg cag   4320
Ala Glu Glu Gln Ala Lys Ile Asp Ala Leu Arg Gln Glu Glu Ala Gln
1425                1430                1435                1440

cac ggc acg ttg cct cgt gct gcg gaa aag cga ctg agc gag tca cag   4368
His Gly Thr Leu Pro Arg Ala Ala Glu Lys Arg Leu Ser Glu Ser Gln
                1445                1450                1455

aag ttt gtt gat caa gca cag aaa aag gtg cag gca agc ttt gat gga   4416
Lys Phe Val Asp Gln Ala Gln Lys Lys Val Gln Ala Ser Phe Asp Gly
            1460                1465                1470

att gct aat gat att gtc gcc agc cgg atc gag acc aag aac aat gtg   4464
Ile Ala Asn Asp Ile Val Ala Ser Arg Ile Glu Thr Lys Asn Asn Val
        1475                1480                1485

ttc aag gac ggc ttt atg tcg gcg cga cag tca cac tcc gct act gct   4512
Phe Lys Asp Gly Phe Met Ser Ala Arg Gln Ser His Ser Ala Thr Ala
    1490                1495                1500

gtg tgg aca ggt gat cca cgc ctg tca gtt gat gaa gta gcc atg aac   4560
Val Trp Thr Gly Asp Pro Arg Leu Ser Val Asp Glu Val Ala Met Asn
1505                1510                1515                1520

tct tcg atg gca cgt gaa ctc ggc gtt ctc gat aac ggt tat gca atg   4608
Ser Ser Met Ala Arg Glu Leu Gly Val Leu Asp Asn Gly Tyr Ala Met
                1525                1530                1535

gtg tgg cgt gat ccg gtg atc cgc gat ggt ggt gtg cgc tat ttg cgt   4656
Val Trp Arg Asp Pro Val Ile Arg Asp Gly Gly Val Arg Tyr Leu Arg
            1540                1545                1550

gtg gtt att aat gat gat ctg cac ggt gtg gca gtc aac cct gtg tcg   4704
Val Val Ile Asn Asp Asp Leu His Gly Val Ala Val Asn Pro Val Ser
        1555                1560                1565

gtg aag agc ttt gac ggt gac ttc gat ggt gac tct gta ggt ctg gtc   4752
Val Lys Ser Phe Asp Gly Asp Phe Asp Gly Asp Ser Val Gly Leu Val
    1570                1575                1580

ggc aat ctg ccg aaa aag gcg cat gag gag gca ttg tcc agg ctc aca   4800
Gly Asn Leu Pro Lys Lys Ala His Glu Glu Ala Leu Ser Arg Leu Thr
1585                1590                1595                1600

gtt gag gca aac atg ctt gat ctt ggt gat ggt aag cgt atg gag gac   4848
Val Glu Ala Asn Met Leu Asp Leu Gly Asp Gly Lys Arg Met Glu Asp
                1605                1610                1615

ggc act atg ttt tat ggg cta act ctg cat gac agc ctc gat gta cag   4896
Gly Thr Met Phe Tyr Gly Leu Thr Leu His Asp Ser Leu Asp Val Gln
            1620                1625                1630

gta gcg cag cac cat gat ccg gca atg gcc gag aac atg aag gtt att   4944
Val Ala Gln His His Asp Pro Ala Met Ala Glu Asn Met Lys Val Ile
        1635                1640                1645

gtc tct gag ctt aac cgc tac cag cgt gaa tac gag gcc ggc gag att   4992
Val Ser Glu Leu Asn Arg Tyr Gln Arg Glu Tyr Glu Ala Gly Glu Ile
    1650                1655                1660
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agc cgc gaa gaa ttg cta gag gtc aac cgt gca cac atg gat gat ctc   5040
Ser Arg Glu Glu Leu Leu Glu Val Asn Arg Ala His Met Asp Asp Leu
1665                 1670                 1675                 1680

aat gag cac tat gca cag gct                                      5061
Asn Glu His Tyr Ala Gln Ala
               1685
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<210> 12
<211> 1687
<212> PRT
<213> Corynebacterium glutamicum

<400> 12

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Trp Gly Gln Lys Asp His Trp Gly Lys Ala Pro Leu Gly Asp His Asp
  1               5                  10                  15

Ala Val Arg Ile Tyr Arg Gln Ala Glu Ala Leu Met Lys Gln Arg Ala
             20                  25                  30

Ala Asn Asn Lys Gly Leu Asp Leu Asn Asp Glu Ala Thr Tyr Gly Ala
         35                  40                  45

Ile Met Phe Ala Ser Phe Asp Asp Ala Phe Ala Ala Asp Ala Glu Ala
     50                  55                  60

His Gly Cys Val His Arg Pro Gln Phe Ala Lys Val Thr Arg Arg Asn
 65                  70                  75                  80

Ile Leu Asn Ser Pro Gln Tyr Thr Ala Ile Lys Ser Ser Tyr Asp Ala
                 85                  90                  95

Leu Val Gln Gln Asp Leu Val Ala Gln Gln Gln Gln Ala Gln Ala Leu
            100                 105                 110

Gln Gln Ala Ala Tyr Glu Gln Glu Gln Ala Ala Ile Phe Gln Ala Arg
        115                 120                 125

Asp Gln Ala Thr Phe Gln Ala Glu Gln Thr Leu Ala Gln Glu Ser Val
    130                 135                 140

Arg Gln Ser Glu Gly Val Gly Leu Pro Val Ile Asp Pro Met Glu Ser
145                 150                 155                 160

Tyr Phe Arg Glu Tyr Ala Phe Tyr Glu Gly Val Glu Met Phe Gly Thr
                165                 170                 175

Trp Gly Thr His Val Asp Ala Gly Val Ser Gln Phe Ser Thr Ser Asp
            180                 185                 190

Gly Arg Ala Ile Arg Ala Leu Val Asp Glu His Leu Ala Thr Tyr Glu
        195                 200                 205

Pro Val Glu Gln Arg Gly Ser Thr Gln Ala Phe Phe Ala Ser Val Asn
    210                 215                 220

Ala Ala Phe Ala Glu Val Ala Pro His Ala Ala Pro Met Phe Ser Ala
225                 230                 235                 240

Ile Ala Arg Glu Gly Glu Gly Ser Lys Gly Tyr Gln Ala Leu Arg His
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                  245                 250                 255

Arg Phe Asp Lys Met Val Gly Thr Ala Ile Gly Pro Asn Gly Leu Pro
            260                 265                 270

Glu Gly Pro Asp Leu Gly Gly Arg Arg Leu Pro Ile Ser Pro Tyr Asp
        275                 280                 285

Pro Arg Trp Ser Asp Arg Glu Val Val Arg Val His Gly Thr Lys Leu
    290                 295                 300

Leu Ser Leu Ser Glu Glu Ser Val Gly Met Ile Arg Asp Leu Asp Leu
305                 310                 315                 320

Ala Thr Ile His Leu Gln Asp Asn Asp Val Tyr Glu Gly Thr His Arg
                325                 330                 335

Glu Asp Asp Thr Lys Gly Gly Val Arg Pro Leu Thr Gln Trp Val Asn
            340                 345                 350

Gly Glu Ala Ile Ala Trp Arg Thr Ile Thr Glu Asn Asp Gln Met Arg
        355                 360                 365

Leu Pro Asn Ile Gly Gln Phe Met Thr Ala Lys Glu Tyr Arg Ala Ala
    370                 375                 380

Ala Ser Trp Leu Arg Ala Gly Leu Ile Asp Thr Ala Asp Val Ala Ser
385                 390                 395                 400

Gln Lys Ile Asp Pro Asn Lys Val Met Ser Asp Glu Gly Ile Ala Arg
                405                 410                 415

Ser Glu Ala Ile Leu Thr Tyr Leu Ser Asp Glu Gly Val Asp Phe Arg
            420                 425                 430

Ile Glu Pro Asp Arg Glu Pro Gly Gln Leu Lys Val Arg Ile Glu Gly
        435                 440                 445

Thr Arg Ile Asp Ile Arg Leu Thr Asp Thr Arg Ala Asn Glu Gln Trp
    450                 455                 460

Val Gly Arg Val Tyr Asp Ser Gly Thr Val Ile Lys Tyr Ser Ala Glu
465                 470                 475                 480

Gln Thr Ala Glu Glu Arg Leu Arg Ala Arg Glu Arg Met Glu Asn Gly
                485                 490                 495

Asp Gly Thr Trp Thr Pro Ala Thr Asp Tyr Glu Pro Ser Pro Thr Glu
            500                 505                 510

Val Val Asp Leu Val Lys Phe Ala Leu Gly Arg Glu Val Glu Arg Gln
        515                 520                 525

Asp Gly Lys Gly Leu Val Gly Val Pro Asn Ala Arg His Pro Arg Ala
    530                 535                 540

Leu Glu Gln Ala Gln Asp Ala Tyr Phe Thr Lys Asn Arg Ser Ala Phe
545                 550                 555                 560

Met Val Arg Glu Gly Leu Ser Ile Val Gln Asp Ala Arg Asp Arg Ser
                565                 570                 575
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Ala Gly Pro Gly Lys Trp Phe Asp Asn Glu Ala Lys Ala Ser Glu Trp
            580                 585                 590

Leu Gly Asn Asn Ile Ala Leu Thr Arg Ala Arg Val Ala Glu Glu Leu
        595                 600                 605

Gly Val Glu Glu Leu Ile Ala Leu Ser Ala Gln Tyr Ala Asp Asp Pro
    610                 615                 620

Asp Phe Met Pro Ala Phe Ala Gly Glu Asp Glu Leu Met Ala Ile Lys
625                 630                 635                 640

Gln Asp Tyr Trp Ala Met Leu Arg Gly Glu Glu Thr Asp Leu Leu Asn
                645                 650                 655

Pro Gly Val Asn Arg Asp Asp Tyr Met Ala Ala Ile Arg Asp Gly Asp
            660                 665                 670

His Glu Gln Ile Ala Ala Met Thr Ser Ala Met Asn Ala Val Thr Val
        675                 680                 685

Glu Asp Arg Val Arg Gln His Ala Ala Leu Val Leu Asp Asp Tyr Val
    690                 695                 700

Gly Thr Val Glu Pro Asp Pro Val Thr Gly Leu Arg Phe Asn Pro Val
705                 710                 715                 720

Thr Val Ala Gln His Met Pro Ser Ala Lys Ser Leu Trp Ser Asn His
                725                 730                 735

Asp Asp Ile Ile Ala Ala Leu Arg Ala Thr Ser Ile Thr Gly Asp Glu
            740                 745                 750

Leu Arg Gly Asp Glu Phe Tyr Asn Asp Val Ile Asn Gln Gln Leu Leu
        755                 760                 765

Lys Phe Asn Pro Glu Thr Ala Gln Lys Met Val Asn Asn Pro Asp Leu
    770                 775                 780

Asp Pro Gln Leu Ala Arg Phe Gly Thr Val Ile Ala Glu Thr Ile Ser
785                 790                 795                 800

Arg Asn Gly Ala Asp Val Val Asp Ile Ala Val Asp Asp Asn Gly Val
                805                 810                 815

Val Arg Trp Thr Ala Gln Arg Arg Val Gly Ala Lys Asp Ser Arg Ala
            820                 825                 830

Val Asp Ser Lys Gly Gln Val Arg Gly Glu Arg Thr Arg His Val Gln
        835                 840                 845

Gly Glu Ile Gly Gln Ile Phe Thr Arg Gly Glu His Gly Glu Ile Val
    850                 855                 860

Thr Lys Phe Asn Gly Gly Glu Asn Tyr Met Phe Ala Pro Gly Tyr Thr
865                 870                 875                 880

Ala Ser Val Val Pro Gln Lys Pro Gly Glu Thr Lys Ser Leu Glu Glu
                885                 890                 895
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Arg Thr Lys Leu Lys Gly Tyr Glu Gln Val Met Ser Glu Ala Leu Val
            900                 905                 910

Tyr Arg Val Arg Glu Asp Leu Met Phe Thr Glu Arg Ser Arg Val Gly
        915                 920                 925

Ala Thr Thr Ser Ile Asn Ser Ala Tyr Lys Arg Leu Tyr Asp Asn Arg
    930                 935                 940

Phe Pro Val Asp Phe Phe Glu Arg Ser Ala Glu Glu Gly Leu Ser Asp
945                 950                 955                 960

Glu Trp Arg Ala Ala Leu Leu Glu Thr Ala Ser Leu Arg Val Arg Tyr
                965                 970                 975

Asp Asn Ser Ile Arg Asp Gly Ala Asn Val Met Glu Asp Ile Arg Ala
            980                 985                 990

Gln Gln Arg Gly Phe Asp Ala Arg Asn Asp Asn Ser Arg Asp Ala Leu
        995                 1000                1005

Val Leu Thr Gly Gly Arg Asn Ile Ser Val Leu Asp Val Asp Ala Gly
    1010                1015                1020

Lys Gly Phe Phe Asp Pro Met Met Thr Gly Met Ala Ala Asn Gln Gly
1025                1030                1035                1040

Ser Val Arg Tyr Leu Leu Pro Ser Ala Lys Val Gly Ala Asp Gly Met
                1045                1050                1055

Ile Thr Pro Gly Asp Pro Ala Asp Arg Val Pro Val Ala Ala His Pro
            1060                1065                1070

Glu Ser Trp Ala Met Gly Phe Asp Pro His Asp Arg Gln Asn Met Thr
        1075                1080                1085

Phe Ser Asn Ile Met Gln Ala Ser Ala Val Thr Gly Gly Ala Arg Thr
    1090                1095                1100

Ala Met Ile Gln Leu Gly Gly Trp Asn Phe Glu Asp Gly Ile Ile Val
1105                1110                1115                1120

Ser Ala Asp Phe Ala Asn Thr His Val Ile Arg Asp Thr Glu Asp Glu
                1125                1130                1135

Met Arg Pro Leu Val Ala Gly Asp Lys Leu Ser Asp Phe His Gly Asn
            1140                1145                1150

Lys Gly Val Thr Ala Leu Val Val Asp Pro Ala Met Ser Asp Ala Asp
        1155                1160                1165

Ala Arg Ala Ala Gly Leu Glu Ser Glu Val Ala Phe Phe Arg Asp Asn
    1170                1175                1180

Pro Asp Leu Glu Val Val Met Ser Pro Phe Ser Ala Ile Ser Arg Phe
1185                1190                1195                1200

Asn Gly Gly Thr Ala Arg Glu Leu Met Thr Asn Pro Gln Asp Val Val
                1205                1210                1215

Phe Arg Asn Asn Asp Gly Ser Thr Arg Val Gln Pro Gly Ala Ser Gly
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            1220                1225                1230

Asp Leu Asn Phe Ile Val Thr His Met Ala Val Asp Ala Lys Thr Asn
        1235                1240                1245

Val Tyr Asp Glu Glu Ala Val Arg Glu Gly Gln Gly Arg Lys Ala Ser
    1250                1255                1260

Ser Gln Leu Ala Trp Val Leu Gln Ala Gln Glu Cys His Glu Ile Met
1265                1270                1275                1280

Glu His Phe Tyr Gly Asn Asn Val Ser Ala Leu Ala Asn Phe Gln Glu
                1285                1290                1295

Tyr Leu Arg Val Thr Gly Leu Asp Val Thr Pro Tyr Gly Glu Leu Arg
            1300                1305                1310

Glu Gly Phe Ser Glu Ser Asn Glu Gln Arg Asn Ile Ile Glu Met Pro
        1315                1320                1325

Ser Ile Tyr Asp Glu Asn Gly Glu Leu Asn Asn Arg Val Asn Arg Ala
    1330                1335                1340

Gln Val Arg Glu Ala Phe Val Glu Gln Ile Ser Arg Ala Gly Gly Val
1345                1350                1355                1360

Met Glu Ile Pro Phe Gln Leu Gln Leu Arg Asn Gly Ala Gln Leu Glu
                1365                1370                1375

Glu Ser Pro Asn Asn Pro Asp Met Tyr Gln Leu Pro Leu Leu Ser Pro
            1380                1385                1390

His Leu Arg Ser Asp Glu Asp Leu Ala Asp Gly Ser Thr Ser Arg His
        1395                1400                1405

Glu Tyr Thr Thr Arg Tyr Met Ala Ile Phe Asp Thr Cys Tyr Lys Leu
    1410                1415                1420

Ala Glu Glu Gln Ala Lys Ile Asp Ala Leu Arg Gln Glu Glu Ala Gln
1425                1430                1435                1440

His Gly Thr Leu Pro Arg Ala Ala Glu Lys Arg Leu Ser Glu Ser Gln
                1445                1450                1455

Lys Phe Val Asp Gln Ala Gln Lys Lys Val Gln Ala Ser Phe Asp Gly
            1460                1465                1470

Ile Ala Asn Asp Ile Val Ala Ser Arg Ile Glu Thr Lys Asn Asn Val
        1475                1480                1485

Phe Lys Asp Gly Phe Met Ser Ala Arg Gln Ser His Ser Ala Thr Ala
    1490                1495                1500

Val Trp Thr Gly Asp Pro Arg Leu Ser Val Asp Glu Val Ala Met Asn
1505                1510                1515                1520

Ser Ser Met Ala Arg Glu Leu Gly Val Leu Asp Asn Gly Tyr Ala Met
                1525                1530                1535

Val Trp Arg Asp Pro Val Ile Arg Asp Gly Gly Val Arg Tyr Leu Arg
            1540                1545                1550
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Val Val Ile Asn Asp Asp Leu His Gly Val Ala Val Asn Pro Val Ser
        1555                1560                1565

Val Lys Ser Phe Asp Gly Asp Phe Asp Gly Asp Ser Val Gly Leu Val
    1570                1575                1580

Gly Asn Leu Pro Lys Lys Ala His Glu Glu Ala Leu Ser Arg Leu Thr
1585                1590                1595                1600

Val Glu Ala Asn Met Leu Asp Leu Gly Asp Gly Lys Arg Met Glu Asp
                1605                1610                1615

Gly Thr Met Phe Tyr Gly Leu Thr Leu His Asp Ser Leu Asp Val Gln
            1620                1625                1630

Val Ala Gln His His Asp Pro Ala Met Ala Glu Asn Met Lys Val Ile
        1635                1640                1645

Val Ser Glu Leu Asn Arg Tyr Gln Arg Glu Tyr Glu Ala Gly Glu Ile
    1650                1655                1660

Ser Arg Glu Glu Leu Leu Glu Val Asn Arg Ala His Met Asp Asp Leu
1665                1670                1675                1680

Asn Glu His Tyr Ala Gln Ala
                1685
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Sequence Listing

<210> 13
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<212> DNA
<213> Corynebacterium glutamicum

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<221> CDS
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<223> RXN01539

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                                          Val Val Thr Val Ala
                                            1               5

ggg aat gag aag aat aag ata cga gaa gag cgg gtg gct cgg cgt gcc   163
Gly Asn Glu Lys Asn Lys Ile Arg Glu Glu Arg Val Ala Arg Arg Ala
                  10                  15                  20

cag gca gtc gta gag gcg gag att agt ctt gct gca caa gca agt gag   211
Gln Ala Val Val Glu Ala Glu Ile Ser Leu Ala Ala Gln Ala Ser Glu
              25                  30                  35

cag gtg cgt gaa caa gca gag gcg cct gat gta aat gaa cag gta gaa   259
Gln Val Arg Glu Gln Ala Glu Ala Pro Asp Val Asn Glu Gln Val Glu
          40                  45                  50

gag gtt agt gtc gag gta tct tct gtc cag tca tta acc cag cct aag   307
Glu Val Ser Val Glu Val Ser Ser Val Gln Ser Leu Thr Gln Pro Lys
      55                  60                  65
```

```
acg ttg ggg cag ctg cat gac cca agg aaa aat gtc atg agt agc agc   355
Thr Leu Gly Gln Leu His Asp Pro Arg Lys Asn Val Met Ser Ser Ser
 70                  75                  80                  85

gac ttg gct tct att att ggt gta gag caa cag cct gtt gct tat ggt   403
Asp Leu Ala Ser Ile Ile Gly Val Glu Gln Gln Pro Val Ala Tyr Gly
                 90                  95                 100

gag tct gag gaa cca gaa aca ctg cgt gat gtg ttg cct cgg cga aag   451
Glu Ser Glu Glu Pro Glu Thr Leu Arg Asp Val Leu Pro Arg Arg Lys
            105                 110                 115

ctt cac cca tct gag ata aca ccg agt tat gag gtt gct gat ggt gaa   499
Leu His Pro Ser Glu Ile Thr Pro Ser Tyr Glu Val Ala Asp Gly Glu
        120                 125                 130

cag cgc agc att ttt ggt gaa tca gct ccg tct gat ttt gat gac ctc   547
Gln Arg Ser Ile Phe Gly Glu Ser Ala Pro Ser Asp Phe Asp Asp Leu
    135                 140                 145

agt gat gtc gaa gaa ttt gat acc agt cat tgg gtg cgt gct gga caa   595
Ser Asp Val Glu Glu Phe Asp Thr Ser His Trp Val Arg Ala Gly Gln
150                 155                 160                 165

gat gat cgt agt gat gat gat cga ctc gct gat gag gct ggt gta ccg   643
Asp Asp Arg Ser Asp Asp Asp Arg Leu Ala Asp Glu Ala Gly Val Pro
                170                 175                 180

cgt agt ggc gca caa gat gta gct gat aat gag gct aat ctt tct ggt   691
Arg Ser Gly Ala Gln Asp Val Ala Asp Asn Glu Ala Asn Leu Ser Gly
            185                 190                 195

gtg gat gag cag ctg cac atg cgt gaa gtc cat gca cag agt ttt gac   739
Val Asp Glu Gln Leu His Met Arg Glu Val His Ala Gln Ser Phe Asp
        200                 205                 210

cct att gac gtt gcc aaa aag gaa cgc aaa gca gcg gaa aag aag tat   787
Pro Ile Asp Val Ala Lys Lys Glu Arg Lys Ala Ala Glu Lys Lys Tyr
    215                 220                 225

gcc aag cca cca aaa agt gat aat ccg tac cta gca cgg gat gcc aaa   835
Ala Lys Pro Pro Lys Ser Asp Asn Pro Tyr Leu Ala Arg Asp Ala Lys
230                 235                 240                 245

gat gca gct gct cgt aag cgg aag atc aat gca gct cat gat aat ttt   883
Asp Ala Ala Ala Arg Lys Arg Lys Ile Asn Ala Ala His Asp Asn Phe
                250                 255                 260

gcc caa gag atg gca cag gct gcg atg gga cca ctg cgc aaa ggg gtc   931
Ala Gln Glu Met Ala Gln Ala Ala Met Gly Pro Leu Arg Lys Gly Val
            265                 270                 275

aac act caa acg gtg atg gcc gcg tgt acg act gct gcg gtg atg tgg   979
Asn Thr Gln Thr Val Met Ala Ala Cys Thr Thr Ala Ala Val Met Trp
        280                 285                 290

tgc atg agc cca cgt atg acc ggt gtg aac gtg gat atg aag cgc aag   1027
Cys Met Ser Pro Arg Met Thr Gly Val Asn Val Asp Met Lys Arg Lys
    295                 300                 305
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ttt aac aag gat ctg gaa cag gct aaa gac act aag ttg tcg aag tat   1075
Phe Asn Lys Asp Leu Glu Gln Ala Lys Asp Thr Lys Leu Ser Lys Tyr
310                 315                 320                 325

gtg tcc aaa gat ttt tgg aag tca aag ctg acg cgc gat aag acg gag   1123
Val Ser Lys Asp Phe Trp Lys Ser Lys Leu Thr Arg Asp Lys Thr Glu
                330                 335                 340

aag gaa gcg aag tcg ctc tct gat gcg ttc atg cag cag aaa aca gcg   1171
Lys Glu Ala Lys Ser Leu Ser Asp Ala Phe Met Gln Gln Lys Thr Ala
            345                 350                 355

atc atc agc aac cgt gaa cga atc ccc atg agt gtt gct tct gcc gcg   1219
Ile Ile Ser Asn Arg Glu Arg Ile Pro Met Ser Val Ala Ser Ala Ala
        360                 365                 370

cag acc gtg gtt cgg ttg tct gat caa gcg tat gag gcg atg cgt gaa   1267
Gln Thr Val Val Arg Leu Ser Asp Gln Ala Tyr Glu Ala Met Arg Glu
    375                 380                 385

gta gat acg gat ggt caa gcg ata gtg gat gcg aag gat gtc tct gca   1315
Val Asp Thr Asp Gly Gln Ala Ile Val Asp Ala Lys Asp Val Ser Ala
390                 395                 400                 405

cag gtg gca gaa gat att gac atg gtg gtc aag cag ggt gaa gag cat   1363
Gln Val Ala Glu Asp Ile Asp Met Val Val Lys Gln Gly Glu Glu His
                410                 415                 420

ggc ctg aag tcg aag gat att tat ggc gct gcc cgc gat att gtg ggt   1411
Gly Leu Lys Ser Lys Asp Ile Tyr Gly Ala Ala Arg Asp Ile Val Gly
            425                 430                 435

cgt cgc atg gag cgc gat cca ggc tat gct gcc cgg ttt aat gag acg   1459
Arg Arg Met Glu Arg Asp Pro Gly Tyr Ala Ala Arg Phe Asn Glu Thr
        440                 445                 450

gct ttt ggc acc gtg cgc ctg ggt gaa caa cga cgt ggc atg gtg att   1507
Ala Phe Gly Thr Val Arg Leu Gly Glu Gln Arg Arg Gly Met Val Ile
    455                 460                 465

tca aag acc ccg aca tgg caa ttc cct gat ggt gca ggt ttg agt aaa   1555
Ser Lys Thr Pro Thr Trp Gln Phe Pro Asp Gly Ala Gly Leu Ser Lys
470                 475                 480                 485

aac gcc ggc tgg ttt agt gtt cgt gag ccg atg ggt aat gcg cag aac   1603
Asn Ala Gly Trp Phe Ser Val Arg Glu Pro Met Gly Asn Ala Gln Asn
                490                 495                 500

ttc gct gac aac ctg gct gcg act ttg gcg aca gaa atg cgg gta gct   1651
Phe Ala Asp Asn Leu Ala Ala Thr Leu Ala Thr Glu Met Arg Val Ala
            505                 510                 515

ggt gag cag tac ggt tcc gat ggc gtt cgt gat gta gtt gcc ggc ttc   1699
Gly Glu Gln Tyr Gly Ser Asp Gly Val Arg Asp Val Val Ala Gly Phe
        520                 525                 530

atg aca gcg act gat gtc tca gaa agt ggc ctc gcc tct gcg aag aaa   1747
Met Thr Ala Thr Asp Val Ser Glu Ser Gly Leu Ala Ser Ala Lys Lys
    535                 540                 545

ctg tta cct gac ttt gat aca cgt ggt cgc agt gct tct cgg gtg cgc   1795
```

```
Leu Leu Pro Asp Phe Asp Thr Arg Gly Arg Ser Ala Ser Arg Val Arg
550                 555                 560                 565

cag att gct atg gca cag cgc aca cag gca gcg atc aag gtg ttg cag   1843
Gln Ile Ala Met Ala Gln Arg Thr Gln Ala Ala Ile Lys Val Leu Gln
                570                 575                 580

gat gat ggt aat cag acc gcg atg acg act gag cag gtc aag gag gtt   1891
Asp Asp Gly Asn Gln Thr Ala Met Thr Thr Glu Gln Val Lys Glu Val
            585                 590                 595

cag gta tgg gcg atg gat cag gct gag aag gtg atg cag cgt gat cat   1939
Gln Val Trp Ala Met Asp Gln Ala Glu Lys Val Met Gln Arg Asp His
        600                 605                 610

cca gcg att ctg gat aag ttt gtg cgc aaa cat ggg cag aca ttt ggg   1987
Pro Ala Ile Leu Asp Lys Phe Val Arg Lys His Gly Gln Thr Phe Gly
    615                 620                 625

cag gat gcg gac gct ttt gtt aaa tcc ata act atg gaa aaa gac acg   2035
Gln Asp Ala Asp Ala Phe Val Lys Ser Ile Thr Met Glu Lys Asp Thr
630                 635                 640                 645

agc agc gag tac act gat gct atg gtt cga cct caa gaa aat cgt gga   2083
Ser Ser Glu Tyr Thr Asp Ala Met Val Arg Pro Gln Glu Asn Arg Gly
                650                 655                 660

tca ggt cga gaa ctg gca gct cgt cgt cgt gta caa gca gcg caa atc   2131
Ser Gly Arg Glu Leu Ala Ala Arg Arg Arg Val Gln Ala Ala Gln Ile
            665                 670                 675

aat cag gca gca cag ctg gat atg aat gtt cat gat ttc cgt gaa tcg   2179
Asn Gln Ala Ala Gln Leu Asp Met Asn Val His Asp Phe Arg Glu Ser
        680                 685                 690

aat ctg cca gag gaa cga ccc gcg aat cct tat gaa gcg tat gtt cgt   2227
Asn Leu Pro Glu Glu Arg Pro Ala Asn Pro Tyr Glu Ala Tyr Val Arg
    695                 700                 705

gag act gaa gcg aaa acc aat gat ccg cag tac ggt tat taatagaaaa   2276
Glu Thr Glu Ala Lys Thr Asn Asp Pro Gln Tyr Gly Tyr
710                 715                 720

tgatagaaag aag                                                  2289


<210> 14
<211> 722
<212> PRT
<213> Corynebacterium glutamicum

<400> 14
Val Val Thr Val Ala Gly Asn Glu Lys Asn Lys Ile Arg Glu Glu Arg
  1               5                  10                  15

Val Ala Arg Arg Ala Gln Ala Val Val Glu Ala Glu Ile Ser Leu Ala
            20                  25                  30

Ala Gln Ala Ser Glu Gln Val Arg Glu Gln Ala Glu Ala Pro Asp Val
        35                  40                  45
```

```
Asn Glu Gln Val Glu Glu Val Ser Val Glu Val Ser Ser Val Gln Ser
     50                  55                  60

Leu Thr Gln Pro Lys Thr Leu Gly Gln Leu His Asp Pro Arg Lys Asn
 65                  70                  75                  80

Val Met Ser Ser Ser Asp Leu Ala Ser Ile Ile Gly Val Glu Gln Gln
                 85                  90                  95

Pro Val Ala Tyr Gly Glu Ser Glu Glu Pro Glu Thr Leu Arg Asp Val
            100                 105                 110

Leu Pro Arg Arg Lys Leu His Pro Ser Glu Ile Thr Pro Ser Tyr Glu
        115                 120                 125

Val Ala Asp Gly Glu Gln Arg Ser Ile Phe Gly Glu Ser Ala Pro Ser
    130                 135                 140

Asp Phe Asp Asp Leu Ser Asp Val Glu Glu Phe Asp Thr Ser His Trp
145                 150                 155                 160

Val Arg Ala Gly Gln Asp Asp Arg Ser Asp Asp Asp Arg Leu Ala Asp
                165                 170                 175

Glu Ala Gly Val Pro Arg Ser Gly Ala Gln Asp Val Ala Asp Asn Glu
            180                 185                 190

Ala Asn Leu Ser Gly Val Asp Glu Gln Leu His Met Arg Glu Val His
        195                 200                 205

Ala Gln Ser Phe Asp Pro Ile Asp Val Ala Lys Lys Glu Arg Lys Ala
    210                 215                 220

Ala Glu Lys Lys Tyr Ala Lys Pro Pro Lys Ser Asp Asn Pro Tyr Leu
225                 230                 235                 240

Ala Arg Asp Ala Lys Asp Ala Ala Ala Arg Lys Arg Lys Ile Asn Ala
                245                 250                 255

Ala His Asp Asn Phe Ala Gln Glu Met Ala Gln Ala Ala Met Gly Pro
            260                 265                 270

Leu Arg Lys Gly Val Asn Thr Gln Thr Val Met Ala Ala Cys Thr Thr
        275                 280                 285

Ala Ala Val Met Trp Cys Met Ser Pro Arg Met Thr Gly Val Asn Val
    290                 295                 300

Asp Met Lys Arg Lys Phe Asn Lys Asp Leu Glu Gln Ala Lys Asp Thr
305                 310                 315                 320

Lys Leu Ser Lys Tyr Val Ser Lys Asp Phe Trp Lys Ser Lys Leu Thr
                325                 330                 335

Arg Asp Lys Thr Glu Lys Glu Ala Lys Ser Leu Ser Asp Ala Phe Met
            340                 345                 350

Gln Gln Lys Thr Ala Ile Ile Ser Asn Arg Glu Arg Ile Pro Met Ser
        355                 360                 365

Val Ala Ser Ala Ala Gln Thr Val Val Arg Leu Ser Asp Gln Ala Tyr
```

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    370                 375                 380

Glu Ala Met Arg Glu Val Asp Thr Asp Gly Gln Ala Ile Val Asp Ala
385                 390                 395                 400

Lys Asp Val Ser Ala Gln Val Ala Glu Asp Ile Asp Met Val Val Lys
                405                 410                 415

Gln Gly Glu Glu His Gly Leu Lys Ser Lys Asp Ile Tyr Gly Ala Ala
            420                 425                 430

Arg Asp Ile Val Gly Arg Arg Met Glu Arg Asp Pro Gly Tyr Ala Ala
        435                 440                 445

Arg Phe Asn Glu Thr Ala Phe Gly Thr Val Arg Leu Gly Glu Gln Arg
    450                 455                 460

Arg Gly Met Val Ile Ser Lys Thr Pro Thr Trp Gln Phe Pro Asp Gly
465                 470                 475                 480

Ala Gly Leu Ser Lys Asn Ala Gly Trp Phe Ser Val Arg Glu Pro Met
                485                 490                 495

Gly Asn Ala Gln Asn Phe Ala Asp Asn Leu Ala Ala Thr Leu Ala Thr
            500                 505                 510

Glu Met Arg Val Ala Gly Glu Gln Tyr Gly Ser Asp Gly Val Arg Asp
        515                 520                 525

Val Val Ala Gly Phe Met Thr Ala Thr Asp Val Ser Glu Ser Gly Leu
    530                 535                 540

Ala Ser Ala Lys Lys Leu Leu Pro Asp Phe Asp Thr Arg Gly Arg Ser
545                 550                 555                 560

Ala Ser Arg Val Arg Gln Ile Ala Met Ala Gln Arg Thr Gln Ala Ala
                565                 570                 575

Ile Lys Val Leu Gln Asp Asp Gly Asn Gln Thr Ala Met Thr Thr Glu
            580                 585                 590

Gln Val Lys Glu Val Gln Val Trp Ala Met Asp Gln Ala Glu Lys Val
        595                 600                 605

Met Gln Arg Asp His Pro Ala Ile Leu Asp Lys Phe Val Arg Lys His
    610                 615                 620

Gly Gln Thr Phe Gly Gln Asp Ala Asp Ala Phe Val Lys Ser Ile Thr
625                 630                 635                 640

Met Glu Lys Asp Thr Ser Ser Glu Tyr Thr Asp Ala Met Val Arg Pro
                645                 650                 655

Gln Glu Asn Arg Gly Ser Gly Arg Glu Leu Ala Ala Arg Arg Arg Val
            660                 665                 670

Gln Ala Ala Gln Ile Asn Gln Ala Ala Gln Leu Asp Met Asn Val His
        675                 680                 685

Asp Phe Arg Glu Ser Asn Leu Pro Glu Glu Arg Pro Ala Asn Pro Tyr
    690                 695                 700
```

```
Glu Ala Tyr Val Arg Glu Thr Glu Ala Lys Thr Asn Asp Pro Gln Tyr
705                 710                 715                 720

Gly Tyr
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<210> 15
<211> 2046
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2023)
<223> FRXA01539

<400> 15

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aaatgaacag gtagaagagg ttagtgtcga ggtatcttct gtccagtcat taacccagcc 60

taagacgttg gggcagctgc atgacccaag gaaaaatgtc atg agt agc agc gac   115
                                            Met Ser Ser Ser Asp
                                              1               5

ttg gct tct att att ggt gta gag caa cag cct gtt gct tat ggt gag   163
Leu Ala Ser Ile Ile Gly Val Glu Gln Gln Pro Val Ala Tyr Gly Glu
                 10                  15                  20

tct gag gaa cca gaa aca ctg cgt gat gtg ttg cct cgg cga aag ctt   211
Ser Glu Glu Pro Glu Thr Leu Arg Asp Val Leu Pro Arg Arg Lys Leu
             25                  30                  35

cac cca tct gag ata aca ccg agt tat gag gtt gct gat ggt gaa cag   259
His Pro Ser Glu Ile Thr Pro Ser Tyr Glu Val Ala Asp Gly Glu Gln
         40                  45                  50

cgc agc att ttt ggt gaa tca gct ccg tct gat ttt gat gac ctc agt   307
Arg Ser Ile Phe Gly Glu Ser Ala Pro Ser Asp Phe Asp Asp Leu Ser
     55                  60                  65

gat gtc gaa gaa ttt gat acc agt cat tgg gtg cgt gct gga caa gat   355
Asp Val Glu Glu Phe Asp Thr Ser His Trp Val Arg Ala Gly Gln Asp
 70                  75                  80                  85

gat cgt agt gat gat gat cga ctc gct gat gag gct ggt gta ccg cct   403
Asp Arg Ser Asp Asp Asp Arg Leu Ala Asp Glu Ala Gly Val Pro Pro
                 90                  95                 100

agt ggc gca caa gat gta gct gat aat gag gct aat ctt tct ggt gtg   451
Ser Gly Ala Gln Asp Val Ala Asp Asn Glu Ala Asn Leu Ser Gly Val
            105                 110                 115

gat gag cag ctg cac atg cgt gaa gtc cat gca cag agt ttt gac cct   499
Asp Glu Gln Leu His Met Arg Glu Val His Ala Gln Ser Phe Asp Pro
        120                 125                 130

att gac gtt gcc aaa aag gaa cgc aaa gca gcg gaa aag aag tat gcc   547
Ile Asp Val Ala Lys Lys Glu Arg Lys Ala Ala Glu Lys Lys Tyr Ala
    135                 140                 145
```

```
aag cca cca aaa agt gat aat ccg tac cta gca cgg gat gcc aaa gat   595
Lys Pro Pro Lys Ser Asp Asn Pro Tyr Leu Ala Arg Asp Ala Lys Asp
150                 155                 160                 165

gca gct gct cgt aag cgg aag atc aat gca gct cat gat aat ttt gcc   643
Ala Ala Ala Arg Lys Arg Lys Ile Asn Ala Ala His Asp Asn Phe Ala
                170                 175                 180

caa gag atg gca cag gct gcg atg gga cca ctg cgc aaa ggg gtc aac   691
Gln Glu Met Ala Gln Ala Ala Met Gly Pro Leu Arg Lys Gly Val Asn
            185                 190                 195

act caa acg gtg atg gcc gcg tgt acg act gct gcg gtg atg tgg tgc   739
Thr Gln Thr Val Met Ala Ala Cys Thr Thr Ala Ala Val Met Trp Cys
        200                 205                 210

atg agc cca cgt atg acc ggt gtg aac gtg gat atg aag cgc aag ttt   787
Met Ser Pro Arg Met Thr Gly Val Asn Val Asp Met Lys Arg Lys Phe
    215                 220                 225

aac aag gat ctg gaa cag gct aaa gac act aag ttg tcg aag tat gtg   835
Asn Lys Asp Leu Glu Gln Ala Lys Asp Thr Lys Leu Ser Lys Tyr Val
230                 235                 240                 245

tcc aaa gat ttt tgg aag tca aag ctg acg cgc gat aag acg gag aag   883
Ser Lys Asp Phe Trp Lys Ser Lys Leu Thr Arg Asp Lys Thr Glu Lys
                250                 255                 260

gaa gcg aag tcg ctc tct gat gcg ttc atg cag cag aaa aca gcg atc   931
Glu Ala Lys Ser Leu Ser Asp Ala Phe Met Gln Gln Lys Thr Ala Ile
            265                 270                 275

atc agc aac cgt gaa cga atc ccc atg agt gtt gct tct gcc gcg cag   979
Ile Ser Asn Arg Glu Arg Ile Pro Met Ser Val Ala Ser Ala Ala Gln
        280                 285                 290

acc gtg gtt cgg ttg tct gat caa gcg tat gag gcg atg cgt gaa gta   1027
Thr Val Val Arg Leu Ser Asp Gln Ala Tyr Glu Ala Met Arg Glu Val
    295                 300                 305

gat acg gat ggt caa gcg ata gtg gat gcg aag gat gtc tct gca cag   1075
Asp Thr Asp Gly Gln Ala Ile Val Asp Ala Lys Asp Val Ser Ala Gln
310                 315                 320                 325

gtg gca gaa gat att gac atg gtg gtc aag cag ggt gaa gag cat ggc   1123
Val Ala Glu Asp Ile Asp Met Val Val Lys Gln Gly Glu Glu His Gly
                330                 335                 340

ctg aag tcg aag gat att tat ggc gct gcc cgc gat att gtg ggt cgt   1171
Leu Lys Ser Lys Asp Ile Tyr Gly Ala Ala Arg Asp Ile Val Gly Arg
            345                 350                 355

cgc atg gag cgc gat cca ggc tat gct gcc cgg ttt aat gag acg gct   1219
Arg Met Glu Arg Asp Pro Gly Tyr Ala Ala Arg Phe Asn Glu Thr Ala
        360                 365                 370

ttt ggc acc gtg cgc ctg ggt gaa caa cga cgt ggc atg gtg att tca   1267
Phe Gly Thr Val Arg Leu Gly Glu Gln Arg Arg Gly Met Val Ile Ser
    375                 380                 385

aag acc ccg aca tgg caa ttc cct gat ggt gca ggt ttg agt aaa aac   1315
```

```
Lys Thr Pro Thr Trp Gln Phe Pro Asp Gly Ala Gly Leu Ser Lys Asn
390                 395                 400                 405

gcc ggc tgg ttt agt gtt cgt gag ccg atg ggt aat gcg cag aac ttc   1363
Ala Gly Trp Phe Ser Val Arg Glu Pro Met Gly Asn Ala Gln Asn Phe
                410                 415                 420

gct gac aac ctg gct gcg act ttg gcg aca gaa atg cgg gta gct ggt   1411
Ala Asp Asn Leu Ala Ala Thr Leu Ala Thr Glu Met Arg Val Ala Gly
            425                 430                 435

gag cag tac ggt tcc gat ggc gtt cgt gat gta gtt gcc ggc ttc atg   1459
Glu Gln Tyr Gly Ser Asp Gly Val Arg Asp Val Val Ala Gly Phe Met
        440                 445                 450

aca gcg act gat gtc tca gaa agt ggc ctc gcc tct gcg aag aaa ctg   1507
Thr Ala Thr Asp Val Ser Glu Ser Gly Leu Ala Ser Ala Lys Lys Leu
    455                 460                 465

tta cct gac ttt gat aca cgt ggt cgc agt gct tct cgg gtg cgc cag   1555
Leu Pro Asp Phe Asp Thr Arg Gly Arg Ser Ala Ser Arg Val Arg Gln
470                 475                 480                 485

att gct atg gca cag cgc aca cag gca gcg atc aag gtg ttg cag gat   1603
Ile Ala Met Ala Gln Arg Thr Gln Ala Ala Ile Lys Val Leu Gln Asp
                490                 495                 500

gat ggt aat cag acc gcg atg acg act gag cag gtc aag gag gtt cag   1651
Asp Gly Asn Gln Thr Ala Met Thr Thr Glu Gln Val Lys Glu Val Gln
            505                 510                 515

gta tgg gcg atg gat cag gct gag aag gtg atg cag cgt gat cat cca   1699
Val Trp Ala Met Asp Gln Ala Glu Lys Val Met Gln Arg Asp His Pro
        520                 525                 530

gcg att ctg gat aag ttt gtg cgc aaa cat ggg cag aca ttt ggg cag   1747
Ala Ile Leu Asp Lys Phe Val Arg Lys His Gly Gln Thr Phe Gly Gln
    535                 540                 545

gat gcg gac gct ttt gtt aaa tcc ata act atg gaa aaa gac acg agc   1795
Asp Ala Asp Ala Phe Val Lys Ser Ile Thr Met Glu Lys Asp Thr Ser
550                 555                 560                 565

agc gag tac act gat gct atg gtt cga cct caa gaa aat cgt gga tca   1843
Ser Glu Tyr Thr Asp Ala Met Val Arg Pro Gln Glu Asn Arg Gly Ser
                570                 575                 580

ggt cga gaa ctg gca gct cgt cgt cgt gta caa gca gcg caa atc aat   1891
Gly Arg Glu Leu Ala Ala Arg Arg Arg Val Gln Ala Ala Gln Ile Asn
            585                 590                 595

cag gca gca cag ctg gat atg aat gtt cat gat ttc cgt gaa tcg aat   1939
Gln Ala Ala Gln Leu Asp Met Asn Val His Asp Phe Arg Glu Ser Asn
        600                 605                 610

ctg cca gag gaa cga ccc gcg aat cct tat gaa gcg tat gtt cgt gag   1987
Leu Pro Glu Glu Arg Pro Ala Asn Pro Tyr Glu Ala Tyr Val Arg Glu
    615                 620                 625

act gaa gcg aaa acc aat gat ccg cag tac ggt tat taatagaaaa        2033
Thr Glu Ala Lys Thr Asn Asp Pro Gln Tyr Gly Tyr
```

630 635 640

tgatagaaag aag 2046

<210> 16
<211> 641
<212> PRT
<213> Corynebacterium glutamicum

<400> 16

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Met Ser Ser Ser Asp Leu Ala Ser Ile Ile Gly Val Glu Gln Gln Pro
  1               5                  10                  15

Val Ala Tyr Gly Glu Ser Glu Glu Pro Glu Thr Leu Arg Asp Val Leu
             20                  25                  30

Pro Arg Arg Lys Leu His Pro Ser Glu Ile Thr Pro Ser Tyr Glu Val
         35                  40                  45

Ala Asp Gly Glu Gln Arg Ser Ile Phe Gly Glu Ser Ala Pro Ser Asp
     50                  55                  60

Phe Asp Asp Leu Ser Asp Val Glu Glu Phe Asp Thr Ser His Trp Val
 65                  70                  75                  80

Arg Ala Gly Gln Asp Asp Arg Ser Asp Asp Asp Arg Leu Ala Asp Glu
                 85                  90                  95

Ala Gly Val Pro Pro Ser Gly Ala Gln Asp Val Ala Asp Asn Glu Ala
            100                 105                 110

Asn Leu Ser Gly Val Asp Glu Gln Leu His Met Arg Glu Val His Ala
        115                 120                 125

Gln Ser Phe Asp Pro Ile Asp Val Ala Lys Lys Glu Arg Lys Ala Ala
    130                 135                 140

Glu Lys Lys Tyr Ala Lys Pro Pro Lys Ser Asp Asn Pro Tyr Leu Ala
145                 150                 155                 160

Arg Asp Ala Lys Asp Ala Ala Ala Arg Lys Arg Lys Ile Asn Ala Ala
                165                 170                 175

His Asp Asn Phe Ala Gln Glu Met Ala Gln Ala Ala Met Gly Pro Leu
            180                 185                 190

Arg Lys Gly Val Asn Thr Gln Thr Val Met Ala Ala Cys Thr Thr Ala
        195                 200                 205

Ala Val Met Trp Cys Met Ser Pro Arg Met Thr Gly Val Asn Val Asp
    210                 215                 220

Met Lys Arg Lys Phe Asn Lys Asp Leu Glu Gln Ala Lys Asp Thr Lys
225                 230                 235                 240

Leu Ser Lys Tyr Val Ser Lys Asp Phe Trp Lys Ser Lys Leu Thr Arg
                245                 250                 255

Asp Lys Thr Glu Lys Glu Ala Lys Ser Leu Ser Asp Ala Phe Met Gln
            260                 265                 270
```

```
Gln Lys Thr Ala Ile Ile Ser Asn Arg Glu Arg Ile Pro Met Ser Val
        275                 280                 285

Ala Ser Ala Ala Gln Thr Val Val Arg Leu Ser Asp Gln Ala Tyr Glu
    290                 295                 300

Ala Met Arg Glu Val Asp Thr Asp Gly Gln Ala Ile Val Asp Ala Lys
305                 310                 315                 320

Asp Val Ser Ala Gln Val Ala Glu Asp Ile Asp Met Val Val Lys Gln
                325                 330                 335

Gly Glu Glu His Gly Leu Lys Ser Lys Asp Ile Tyr Gly Ala Ala Arg
            340                 345                 350

Asp Ile Val Gly Arg Arg Met Glu Arg Asp Pro Gly Tyr Ala Ala Arg
        355                 360                 365

Phe Asn Glu Thr Ala Phe Gly Thr Val Arg Leu Gly Glu Gln Arg Arg
    370                 375                 380

Gly Met Val Ile Ser Lys Thr Pro Thr Trp Gln Phe Pro Asp Gly Ala
385                 390                 395                 400

Gly Leu Ser Lys Asn Ala Gly Trp Phe Ser Val Arg Glu Pro Met Gly
                405                 410                 415

Asn Ala Gln Asn Phe Ala Asp Asn Leu Ala Ala Thr Leu Ala Thr Glu
            420                 425                 430

Met Arg Val Ala Gly Glu Gln Tyr Gly Ser Asp Gly Val Arg Asp Val
        435                 440                 445

Val Ala Gly Phe Met Thr Ala Thr Asp Val Ser Glu Ser Gly Leu Ala
    450                 455                 460

Ser Ala Lys Lys Leu Leu Pro Asp Phe Asp Thr Arg Gly Arg Ser Ala
465                 470                 475                 480

Ser Arg Val Arg Gln Ile Ala Met Ala Gln Arg Thr Gln Ala Ala Ile
                485                 490                 495

Lys Val Leu Gln Asp Asp Gly Asn Gln Thr Ala Met Thr Thr Glu Gln
            500                 505                 510

Val Lys Glu Val Gln Val Trp Ala Met Asp Gln Ala Glu Lys Val Met
        515                 520                 525

Gln Arg Asp His Pro Ala Ile Leu Asp Lys Phe Val Arg Lys His Gly
    530                 535                 540

Gln Thr Phe Gly Gln Asp Ala Asp Ala Phe Val Lys Ser Ile Thr Met
545                 550                 555                 560

Glu Lys Asp Thr Ser Ser Glu Tyr Thr Asp Ala Met Val Arg Pro Gln
                565                 570                 575

Glu Asn Arg Gly Ser Gly Arg Glu Leu Ala Ala Arg Arg Arg Val Gln
            580                 585                 590
```

```
Ala Ala Gln Ile Asn Gln Ala Ala Gln Leu Asp Met Asn Val His Asp
        595                 600                 605

Phe Arg Glu Ser Asn Leu Pro Glu Glu Arg Pro Ala Asn Pro Tyr Glu
    610                 615                 620

Ala Tyr Val Arg Glu Thr Glu Ala Lys Thr Asn Asp Pro Gln Tyr Gly
625                 630                 635                 640

Tyr
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<210> 17
<211> 1095
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1072)
<223> RXN01422

<400> 17

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aatgcattga aatcgtgatc gcctgttatt gttttgtacg tcgaataaca gtcccacaac 60

agttccccaa aaggtgcgag cgggaaaagg agaagcaaac atg gct cag cga aaa   115
                                            Met Ala Gln Arg Lys
                                              1               5

ctg gcc tct gtg atc ggt gca gca ttg gca gca tct gct gta ctg gtt   163
Leu Ala Ser Val Ile Gly Ala Ala Leu Ala Ala Ser Ala Val Leu Val
                  10                  15                  20

gga tta atg aca ccc gca aca gca caa agt agt ggc agc tca tca aca   211
Gly Leu Met Thr Pro Ala Thr Ala Gln Ser Ser Gly Ser Ser Ser Thr
              25                  30                  35

gac atc act cga gca ctc acc tca agt ggt ggt gtg gct gat agc cgt   259
Asp Ile Thr Arg Ala Leu Thr Ser Ser Gly Gly Val Ala Asp Ser Arg
          40                  45                  50

gct cct gaa ggt ggc gca aag gtc gtt gtt ttc ggt gac tcc cac acc   307
Ala Pro Glu Gly Gly Ala Lys Val Val Val Phe Gly Asp Ser His Thr
      55                  60                  65

tct ggc acc aat gct cca ttc cgt acc gat gag cgt ggc tgc ctc aag   355
Ser Gly Thr Asn Ala Pro Phe Arg Thr Asp Glu Arg Gly Cys Leu Lys
  70                  75                  80                  85

ggt gca aac aac tgg gca gat cag ctg cag tct cag ctg gga ctt ggc   403
Gly Ala Asn Asn Trp Ala Asp Gln Leu Gln Ser Gln Leu Gly Leu Gly
                  90                  95                 100

gcg gga gac ctc att gat gtc tcc tgc tcc ggt gca tcg atc aac tct   451
Ala Gly Asp Leu Ile Asp Val Ser Cys Ser Gly Ala Ser Ile Asn Ser
              105                 110                 115

gat gga ttc cac ttc tct gat gaa gtc cgc cat gct gaa gct cgt ggc   499
Asp Gly Phe His Phe Ser Asp Glu Val Arg His Ala Glu Ala Arg Gly
          120                 125                 130
```

```
gca atc ggc cca aac acc acc gat att ttt gtt cag ttg ggc aag aat   547
Ala Ile Gly Pro Asn Thr Thr Asp Ile Phe Val Gln Leu Gly Lys Asn
    135                 140                 145

gat cag tgg ggc ctt tcc aat gtg aac ctt ctg cag tct gtt cag acc   595
Asp Gln Trp Gly Leu Ser Asn Val Asn Leu Leu Gln Ser Val Gln Thr
150                 155                 160                 165

tgc ttg act gat gtg ttc gct ggt tgt ggc gat gct gcg gtt gct gct   643
Cys Leu Thr Asp Val Phe Ala Gly Cys Gly Asp Ala Ala Val Ala Ala
                170                 175                 180

ggc aag atg cag gat cca aat gca gtt act gct gaa aac tat gca gag   691
Gly Lys Met Gln Asp Pro Asn Ala Val Thr Ala Glu Asn Tyr Ala Glu
            185                 190                 195

cgc atg aag cca gtc att gac tac ttg aag tac tac gca cca aac gca   739
Arg Met Lys Pro Val Ile Asp Tyr Leu Lys Tyr Tyr Ala Pro Asn Ala
        200                 205                 210

gag atc acc ttg gtt ggt tac cag gaa tac acc gct cgc agc gga agt   787
Glu Ile Thr Leu Val Gly Tyr Gln Glu Tyr Thr Ala Arg Ser Gly Ser
    215                 220                 225

cag gta tgt gtt cgc ctt ggt gga acc cca ctg gtg aaa aat gat gca   835
Gln Val Cys Val Arg Leu Gly Gly Thr Pro Leu Val Lys Asn Asp Ala
230                 235                 240                 245

cct gcg ctg gtt tcg ttc atg aac aag ttg gac atg gcg att gat ggt   883
Pro Ala Leu Val Ser Phe Met Asn Lys Leu Asp Met Ala Ile Asp Gly
                250                 255                 260

gct gct gga atc ctc ggc gtc agc cac gtt gat ctg cgt agc gcg act   931
Ala Ala Gly Ile Leu Gly Val Ser His Val Asp Leu Arg Ser Ala Thr
            265                 270                 275

gaa ggg cac gac agc tgc tcc aac gat cct tgg gtc aac ggt gtc ttt   979
Glu Gly His Asp Ser Cys Ser Asn Asp Pro Trp Val Asn Gly Val Phe
        280                 285                 290

gat gca cgt gca gaa atc gtc ggc ggt ccg tgg cac cca tct gtt aag   1027
Asp Ala Arg Ala Glu Ile Val Gly Gly Pro Trp His Pro Ser Val Lys
    295                 300                 305

gga gac tcg gtt act gca ggg atc ctg cga gat cga gta aac gcc       1072
Gly Asp Ser Val Thr Ala Gly Ile Leu Arg Asp Arg Val Asn Ala
310                 315                 320

taaagatgac gtcgaaaagc att                                       1095
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<210> 18
<211> 324
<212> PRT
<213> Corynebacterium glutamicum

<400> 18

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Met Ala Gln Arg Lys Leu Ala Ser Val Ile Gly Ala Ala Leu Ala Ala
  1               5                  10                  15
```

```
Ser Ala Val Leu Val Gly Leu Met Thr Pro Ala Thr Ala Gln Ser Ser
            20                  25                  30

Gly Ser Ser Ser Thr Asp Ile Thr Arg Ala Leu Thr Ser Ser Gly Gly
        35                  40                  45

Val Ala Asp Ser Arg Ala Pro Glu Gly Gly Ala Lys Val Val Val Phe
    50                  55                  60

Gly Asp Ser His Thr Ser Gly Thr Asn Ala Pro Phe Arg Thr Asp Glu
65                  70                  75                  80

Arg Gly Cys Leu Lys Gly Ala Asn Asn Trp Ala Asp Gln Leu Gln Ser
                85                  90                  95

Gln Leu Gly Leu Gly Ala Gly Asp Leu Ile Asp Val Ser Cys Ser Gly
            100                 105                 110

Ala Ser Ile Asn Ser Asp Gly Phe His Phe Ser Asp Glu Val Arg His
        115                 120                 125

Ala Glu Ala Arg Gly Ala Ile Gly Pro Asn Thr Thr Asp Ile Phe Val
    130                 135                 140

Gln Leu Gly Lys Asn Asp Gln Trp Gly Leu Ser Asn Val Asn Leu Leu
145                 150                 155                 160

Gln Ser Val Gln Thr Cys Leu Thr Asp Val Phe Ala Gly Cys Gly Asp
                165                 170                 175

Ala Ala Val Ala Ala Gly Lys Met Gln Asp Pro Asn Ala Val Thr Ala
            180                 185                 190

Glu Asn Tyr Ala Glu Arg Met Lys Pro Val Ile Asp Tyr Leu Lys Tyr
        195                 200                 205

Tyr Ala Pro Asn Ala Glu Ile Thr Leu Val Gly Tyr Gln Glu Tyr Thr
    210                 215                 220

Ala Arg Ser Gly Ser Gln Val Cys Val Arg Leu Gly Gly Thr Pro Leu
225                 230                 235                 240

Val Lys Asn Asp Ala Pro Ala Leu Val Ser Phe Met Asn Lys Leu Asp
                245                 250                 255

Met Ala Ile Asp Gly Ala Ala Gly Ile Leu Gly Val Ser His Val Asp
            260                 265                 270

Leu Arg Ser Ala Thr Glu Gly His Asp Ser Cys Ser Asn Asp Pro Trp
        275                 280                 285

Val Asn Gly Val Phe Asp Ala Arg Ala Glu Ile Val Gly Gly Pro Trp
    290                 295                 300

His Pro Ser Val Lys Gly Asp Ser Val Thr Ala Gly Ile Leu Arg Asp
305                 310                 315                 320

Arg Val Asn Ala
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<210> 19
<211> 806
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(783)
<223> FRXA01422

<400> 19

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ttc ggt gac tcc cac acc tct ggc acc aat gct cca ttc cgt acc gat   48
Phe Gly Asp Ser His Thr Ser Gly Thr Asn Ala Pro Phe Arg Thr Asp
  1               5                  10                  15

gag cgt ggc tgc ctc aag ggt gca aac aac tgg gca gat cag ctg cag   96
Glu Arg Gly Cys Leu Lys Gly Ala Asn Asn Trp Ala Asp Gln Leu Gln
             20                  25                  30

tct cag ctg gga ctt ggc gcg gga gac ctc att gat gtc tcc tgc tcc  144
Ser Gln Leu Gly Leu Gly Ala Gly Asp Leu Ile Asp Val Ser Cys Ser
         35                  40                  45

ggt gca tcg atc aac tct gat gga ttc cac ttc tct gat gaa gtc cgc  192
Gly Ala Ser Ile Asn Ser Asp Gly Phe His Phe Ser Asp Glu Val Arg
     50                  55                  60

cat gct gaa gct cgt ggc gca atc ggc cca aac acc acc gat att ttt  240
His Ala Glu Ala Arg Gly Ala Ile Gly Pro Asn Thr Thr Asp Ile Phe
 65                  70                  75                  80

gtt cag ttg ggc aag aat gat cag tgg ggc ctt tcc aat gtg aac ctt  288
Val Gln Leu Gly Lys Asn Asp Gln Trp Gly Leu Ser Asn Val Asn Leu
                 85                  90                  95

ctg cag tct gtt cag acc tgc ttg act gat gtg ttc gct ggt tgt ggc  336
Leu Gln Ser Val Gln Thr Cys Leu Thr Asp Val Phe Ala Gly Cys Gly
            100                 105                 110

gat gct gcg gtt gct gct ggc aag atg cag gat cca aat gca gtt act  384
Asp Ala Ala Val Ala Ala Gly Lys Met Gln Asp Pro Asn Ala Val Thr
        115                 120                 125

gct gaa aac tat gca gag cgc atg aag cca gtc att gac tac ttg aag  432
Ala Glu Asn Tyr Ala Glu Arg Met Lys Pro Val Ile Asp Tyr Leu Lys
    130                 135                 140

tac tac gca cca aac gca gag atc acc ttg gtt ggt tac cag gaa tac  480
Tyr Tyr Ala Pro Asn Ala Glu Ile Thr Leu Val Gly Tyr Gln Glu Tyr
145                 150                 155                 160

acc gct cgc agc gga agt cag gta tgt gtt cgc ctt ggt gga acc cca  528
Thr Ala Arg Ser Gly Ser Gln Val Cys Val Arg Leu Gly Gly Thr Pro
                165                 170                 175

ctg gtg aaa aat gat gca cct gcg ctg gtt tcg ttc atg aac aag ttg  576
Leu Val Lys Asn Asp Ala Pro Ala Leu Val Ser Phe Met Asn Lys Leu
            180                 185                 190

gac atg gcg att gat ggt gct gct gga atc ctc ggc gtc agc cac gtt  624
Asp Met Ala Ile Asp Gly Ala Ala Gly Ile Leu Gly Val Ser His Val
```

```
        195                 200                 205

gat ctg cgt agc gcg act gaa ggg cac gac agc tgc tcc aac gat cct   672
Asp Leu Arg Ser Ala Thr Glu Gly His Asp Ser Cys Ser Asn Asp Pro
    210                 215                 220

tgg gtc aac ggt gtc ttt gat gca cgt gca gaa atc gtc ggc ggt ccg   720
Trp Val Asn Gly Val Phe Asp Ala Arg Ala Glu Ile Val Gly Gly Pro
225                 230                 235                 240

tgg cac cca tct gtt aag gga gac tcg gtt act gca ggg atc ctg cga   768
Trp His Pro Ser Val Lys Gly Asp Ser Val Thr Ala Gly Ile Leu Arg
                245                 250                 255

gat cga gta aac gcc taaagatgac gtcgaaaagc att                    806
Asp Arg Val Asn Ala
            260
```

<210> 20
<211> 261
<212> PRT
<213> Corynebacterium glutamicum

<400> 20

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Phe Gly Asp Ser His Thr Ser Gly Thr Asn Ala Pro Phe Arg Thr Asp
  1               5                  10                  15

Glu Arg Gly Cys Leu Lys Gly Ala Asn Asn Trp Ala Asp Gln Leu Gln
             20                  25                  30

Ser Gln Leu Gly Leu Gly Ala Gly Asp Leu Ile Asp Val Ser Cys Ser
         35                  40                  45

Gly Ala Ser Ile Asn Ser Asp Gly Phe His Phe Ser Asp Glu Val Arg
     50                  55                  60

His Ala Glu Ala Arg Gly Ala Ile Gly Pro Asn Thr Thr Asp Ile Phe
 65                  70                  75                  80

Val Gln Leu Gly Lys Asn Asp Gln Trp Gly Leu Ser Asn Val Asn Leu
                85                  90                  95

Leu Gln Ser Val Gln Thr Cys Leu Thr Asp Val Phe Ala Gly Cys Gly
            100                 105                 110

Asp Ala Ala Val Ala Ala Gly Lys Met Gln Asp Pro Asn Ala Val Thr
        115                 120                 125

Ala Glu Asn Tyr Ala Glu Arg Met Lys Pro Val Ile Asp Tyr Leu Lys
    130                 135                 140

Tyr Tyr Ala Pro Asn Ala Glu Ile Thr Leu Val Gly Tyr Gln Glu Tyr
145                 150                 155                 160

Thr Ala Arg Ser Gly Ser Gln Val Cys Val Arg Leu Gly Gly Thr Pro
                165                 170                 175

Leu Val Lys Asn Asp Ala Pro Ala Leu Val Ser Phe Met Asn Lys Leu
            180                 185                 190
```

```
Asp Met Ala Ile Asp Gly Ala Ala Gly Ile Leu Gly Val Ser His Val
        195                 200                 205

Asp Leu Arg Ser Ala Thr Glu Gly His Asp Ser Cys Ser Asn Asp Pro
    210                 215                 220

Trp Val Asn Gly Val Phe Asp Ala Arg Ala Glu Ile Val Gly Gly Pro
225                 230                 235                 240

Trp His Pro Ser Val Lys Gly Asp Ser Val Thr Ala Gly Ile Leu Arg
                245                 250                 255

Asp Arg Val Asn Ala
            260


<210> 21
<211> 771
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> RXN01403

<400> 21
gtgcgtcgca tacggtgaat tatctttcgg cggatcgttt ccgcacggtg tcgagtttcg 60

tagagtttgc ggccgatcgc ggtattcagg aattcagcca ttg gtg cgc ggt cgg   115
                                        Leu Val Arg Gly Arg
                                          1               5

ggc tat ttc aat gcg gtg gat att tat gag acc tcc acg caa cct gac   163
Gly Tyr Phe Asn Ala Val Asp Ile Tyr Glu Thr Ser Thr Gln Pro Asp
                  10                  15                  20

cag gaa ttt cct ttc gat ttt gac act ttt tca gcc gac ccc acg ccg   211
Gln Glu Phe Pro Phe Asp Phe Asp Thr Phe Ser Ala Asp Pro Thr Pro
              25                  30                  35

ttt caa ctc tct gcg gtg cgt gcc gat acc ggc gag acc gtt ttt tgg   259
Phe Gln Leu Ser Ala Val Arg Ala Asp Thr Gly Glu Thr Val Phe Trp
          40                  45                  50

ggc agg gaa gac acc ccg gat ttg agc gct ctg atg aag cgg gtt cgc   307
Gly Arg Glu Asp Thr Pro Asp Leu Ser Ala Leu Met Lys Arg Val Arg
      55                  60                  65

gcg tcg tcg acc atg cct ggt ttc atg ccg atc acc tac atc gac ggc   355
Ala Ser Ser Thr Met Pro Gly Phe Met Pro Ile Thr Tyr Ile Asp Gly
  70                  75                  80                  85

cat cca tat gtc gat ggc gcg gtc ggg gag acc ggc ggt ttg atg cta   403
His Pro Tyr Val Asp Gly Ala Val Gly Glu Thr Gly Gly Leu Met Leu
                  90                  95                 100

cag ccg gcc atc gat gcg ggc ttc acc cgc ttt ttc gtt atc gcc tcc   451
Gln Pro Ala Ile Asp Ala Gly Phe Thr Arg Phe Phe Val Ile Ala Ser
              105                 110                 115
```

```
cgt ccg cgc gat tat tgg cgc aag gag atc ggg cgc ccg ggt ttc atc   499
Arg Pro Arg Asp Tyr Trp Arg Lys Glu Ile Gly Arg Pro Gly Phe Ile
        120                 125                 130

aaa gct gct tta cga cgt ttc ccc aca atc gcc gac ctc acc atc gcg   547
Lys Ala Ala Leu Arg Arg Phe Pro Thr Ile Ala Asp Leu Thr Ile Ala
    135                 140                 145

cgt cct gca ctg tat aac tcg gta aag caa cag atc ctc gac cta gag   595
Arg Pro Ala Leu Tyr Asn Ser Val Lys Gln Gln Ile Leu Asp Leu Glu
150                 155                 160                 165

aaa caa ggc agc gcc tat gtg ttc ttt gcg gac aac atg aac atc cag   643
Lys Gln Gly Ser Ala Tyr Val Phe Phe Ala Asp Asn Met Asn Ile Gln
                170                 175                 180

aac acg gaa atc aat ctg aag aaa ctc cgt gca tct ttc gat gca ggc   691
Asn Thr Glu Ile Asn Leu Lys Lys Leu Arg Ala Ser Phe Asp Ala Gly
            185                 190                 195

atg cag cag acc cgc aaa gat tgg ccg gag atc atg agc ttc ctg aac   739
Met Gln Gln Thr Arg Lys Asp Trp Pro Glu Ile Met Ser Phe Leu Asn
        200                 205                 210

caa acc aga taatgaaggt ttttagtcca act                            771
Gln Thr Arg
    215
```

20050170410.0

<210> 22
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 22

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Leu Val Arg Gly Arg Gly Tyr Phe Asn Ala Val Asp Ile Tyr Glu Thr
  1               5                  10                  15

Ser Thr Gln Pro Asp Gln Glu Phe Pro Phe Asp Phe Asp Thr Phe Ser
             20                  25                  30

Ala Asp Pro Thr Pro Phe Gln Leu Ser Ala Val Arg Ala Asp Thr Gly
         35                  40                  45

Glu Thr Val Phe Trp Gly Arg Glu Asp Thr Pro Asp Leu Ser Ala Leu
     50                  55                  60

Met Lys Arg Val Arg Ala Ser Ser Thr Met Pro Gly Phe Met Pro Ile
 65                  70                  75                  80

Thr Tyr Ile Asp Gly His Pro Tyr Val Asp Gly Ala Val Gly Glu Thr
                 85                  90                  95

Gly Gly Leu Met Leu Gln Pro Ala Ile Asp Ala Gly Phe Thr Arg Phe
            100                 105                 110

Phe Val Ile Ala Ser Arg Pro Arg Asp Tyr Trp Arg Lys Glu Ile Gly
        115                 120                 125

Arg Pro Gly Phe Ile Lys Ala Ala Leu Arg Arg Phe Pro Thr Ile Ala
    130                 135                 140
```

```
Asp Leu Thr Ile Ala Arg Pro Ala Leu Tyr Asn Ser Val Lys Gln Gln
145                 150                 155                 160

Ile Leu Asp Leu Glu Lys Gln Gly Ser Ala Tyr Val Phe Phe Ala Asp
                165                 170                 175

Asn Met Asn Ile Gln Asn Thr Glu Ile Asn Leu Lys Lys Leu Arg Ala
            180                 185                 190

Ser Phe Asp Ala Gly Met Gln Gln Thr Arg Lys Asp Trp Pro Glu Ile
        195                 200                 205

Met Ser Phe Leu Asn Gln Thr Arg
    210                 215


<210> 23
<211> 437
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(414)
<223> FRXA01403

<400> 23
ccg atc acc tac atc gac ggc cat cca tat gtc gat ggc gcg gtc ggg   48
Pro Ile Thr Tyr Ile Asp Gly His Pro Tyr Val Asp Gly Ala Val Gly
  1               5                  10                  15

gag acc ggc ggt ttg atg cta cag ccg gcc atc gat gcg ggc ttc acc   96
Glu Thr Gly Gly Leu Met Leu Gln Pro Ala Ile Asp Ala Gly Phe Thr
             20                  25                  30

cgc ttt ttc gtt atc gcc tcc cgt ccg cgc gat tat tgg cgc aag gag   144
Arg Phe Phe Val Ile Ala Ser Arg Pro Arg Asp Tyr Trp Arg Lys Glu
         35                  40                  45

atc ggg cgc ccg ggt ttc atc aaa gct gct tta cga cgt ttc ccc aca   192
Ile Gly Arg Pro Gly Phe Ile Lys Ala Ala Leu Arg Arg Phe Pro Thr
     50                  55                  60

atc gcc gac ctc acc atc gcg cgt cct gca ctg tat aac tcg gta aag   240
Ile Ala Asp Leu Thr Ile Ala Arg Pro Ala Leu Tyr Asn Ser Val Lys
 65                  70                  75                  80

caa cag atc ctc gac cta gag aaa caa ggc agc gcc tat gtg ttc ttt   288
Gln Gln Ile Leu Asp Leu Glu Lys Gln Gly Ser Ala Tyr Val Phe Phe
                 85                  90                  95

gcg gac aac atg aac atc cag aac acg gaa atc aat ctg aag aaa ctc   336
Ala Asp Asn Met Asn Ile Gln Asn Thr Glu Ile Asn Leu Lys Lys Leu
            100                 105                 110

cgt gca tct ttc gat gca ggc atg cag cag acc cgc aaa gat tgg ccg   384
Arg Ala Ser Phe Asp Ala Gly Met Gln Gln Thr Arg Lys Asp Trp Pro
        115                 120                 125

gag atc atg agc ttc ctg aac caa acc aga taatgaaggt ttttagtcca     434
```

```
Glu Ile Met Ser Phe Leu Asn Gln Thr Arg
    130                 135

act                                                                  437


<210> 24
<211> 138
<212> PRT
<213> Corynebacterium glutamicum

<400> 24
Pro Ile Thr Tyr Ile Asp Gly His Pro Tyr Val Asp Gly Ala Val Gly
  1               5                  10                  15

Glu Thr Gly Gly Leu Met Leu Gln Pro Ala Ile Asp Ala Gly Phe Thr
             20                  25                  30

Arg Phe Phe Val Ile Ala Ser Arg Pro Arg Asp Tyr Trp Arg Lys Glu
         35                  40                  45

Ile Gly Arg Pro Gly Phe Ile Lys Ala Ala Leu Arg Arg Phe Pro Thr
     50                  55                  60

Ile Ala Asp Leu Thr Ile Ala Arg Pro Ala Leu Tyr Asn Ser Val Lys
 65                  70                  75                  80

Gln Gln Ile Leu Asp Leu Glu Lys Gln Gly Ser Ala Tyr Val Phe Phe
                 85                  90                  95

Ala Asp Asn Met Asn Ile Gln Asn Thr Glu Ile Asn Leu Lys Lys Leu
            100                 105                 110

Arg Ala Ser Phe Asp Ala Gly Met Gln Gln Thr Arg Lys Asp Trp Pro
        115                 120                 125

Glu Ile Met Ser Phe Leu Asn Gln Thr Arg
    130                 135


<210> 25
<211> 489
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(466)
<223> RXN01326

<400> 25
gtccttgagg ctgcttacac tctacttatt gtagaaatgg gagggtcgtg gcgtcgaaaa 60

gcaaacatct tttaacgctt ttggcccgta ttatggtggc atg gct ttc ccc gtg   115
                                              Met Ala Phe Pro Val
                                                1               5

aca gaa gac aaa atc ctg gca gct gag gaa acc ctt ggc agg cgc ctc   163
Thr Glu Asp Lys Ile Leu Ala Ala Glu Glu Thr Leu Gly Arg Arg Leu
            10                  15                  20
```

```
ccc gaa act ttg cgc gaa cga cta ctt caa aac aat ggt ggc gaa gtc   211
Pro Glu Thr Leu Arg Glu Arg Leu Leu Gln Asn Asn Gly Gly Glu Val
            25                  30                  35

atc gac aat gaa aac aac gac tgg att ctc cat cca gtt cgt gat gac   259
Ile Asp Asn Glu Asn Asn Asp Trp Ile Leu His Pro Val Arg Asp Asp
        40                  45                  50

agc gac cga aaa agg ctt gtc cga act gcc aac gac atc atc cgc gag   307
Ser Asp Arg Lys Arg Leu Val Arg Thr Ala Asn Asp Ile Ile Arg Glu
    55                  60                  65

acc gaa tct gca cgt gaa tgg gac aat ttc ccc gaa aat gcg atc gca   355
Thr Glu Ser Ala Arg Glu Trp Asp Asn Phe Pro Glu Asn Ala Ile Ala
70                  75                  80                  85

att gca aat gac gga acg ggc gac tta ata att ctg ctt ccc gac gat   403
Ile Ala Asn Asp Gly Thr Gly Asp Leu Ile Ile Leu Leu Pro Asp Asp
                90                  95                  100

gat gct ttc tac atc tgg tcg cac gaa gat gaa ccc ctg atc gaa act   451
Asp Ala Phe Tyr Ile Trp Ser His Glu Asp Glu Pro Leu Ile Glu Thr
            105                 110                 115

gaa ctt gag gat gcc taaaacagct ggacagaatt cga                    489
Glu Leu Glu Asp Ala
        120
```

<210> 26
<211> 122
<212> PRT
<213> Corynebacterium glutamicum

```
<400> 26
Met Ala Phe Pro Val Thr Glu Asp Lys Ile Leu Ala Ala Glu Glu Thr
  1               5                  10                  15

Leu Gly Arg Arg Leu Pro Glu Thr Leu Arg Glu Arg Leu Leu Gln Asn
            20                  25                  30

Asn Gly Gly Glu Val Ile Asp Asn Glu Asn Asn Asp Trp Ile Leu His
        35                  40                  45

Pro Val Arg Asp Asp Ser Asp Arg Lys Arg Leu Val Arg Thr Ala Asn
    50                  55                  60

Asp Ile Ile Arg Glu Thr Glu Ser Ala Arg Glu Trp Asp Asn Phe Pro
65                  70                  75                  80

Glu Asn Ala Ile Ala Ile Ala Asn Asp Gly Thr Gly Asp Leu Ile Ile
                85                  90                  95

Leu Leu Pro Asp Asp Asp Ala Phe Tyr Ile Trp Ser His Glu Asp Glu
            100                 105                 110

Pro Leu Ile Glu Thr Glu Leu Glu Asp Ala
        115                 120
```

<210> 27

<211> 361
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (45)..(338)
<223> FRXA01326

<400> 27
ccggctggcg ctgaggaaac cttggcaggc gcctccccga aactttg cgc gaa cga 56
Leu Arg Glu Arg
1

cta ctt caa aac aat ggt ggc gaa gtc atc gac aat gaa aac aac gac 104
Leu Leu Gln Asn Asn Gly Gly Glu Val Ile Asp Asn Glu Asn Asn Asp
5 10 15 20

tgg att ctc cat cca gtt cgt gat gac agc gac cga aaa agg ctt gtc 152
Trp Ile Leu His Pro Val Arg Asp Asp Ser Asp Arg Lys Arg Leu Val
25 30 35

cga act gcc aac gac atc atc cgc gag acc gaa tct gca cgt gaa tgg 200
Arg Thr Ala Asn Asp Ile Ile Arg Glu Thr Glu Ser Ala Arg Glu Trp
40 45 50

gac aat ttc ccc gaa aat gcg atc gca att gca aat gac gga acg ggc 248
Asp Asn Phe Pro Glu Asn Ala Ile Ala Ile Ala Asn Asp Gly Thr Gly
55 60 65

gac tta ata att ctg ctt ccc gac gat gat gct ttc tac atc tgg tcg 296
Asp Leu Ile Ile Leu Leu Pro Asp Asp Asp Ala Phe Tyr Ile Trp Ser
70 75 80

cac gaa gat gaa ccc ctg atc gaa act gaa ctt gag gat gcc 338
His Glu Asp Glu Pro Leu Ile Glu Thr Glu Leu Glu Asp Ala
85 90 95

taaaacagct ggacagaatt cga 361

<210> 28
<211> 98
<212> PRT
<213> Corynebacterium glutamicum

<400> 28
Leu Arg Glu Arg Leu Leu Gln Asn Asn Gly Gly Glu Val Ile Asp Asn
1 5 10 15

Glu Asn Asn Asp Trp Ile Leu His Pro Val Arg Asp Asp Ser Asp Arg
20 25 30

Lys Arg Leu Val Arg Thr Ala Asn Asp Ile Ile Arg Glu Thr Glu Ser
35 40 45

Ala Arg Glu Trp Asp Asn Phe Pro Glu Asn Ala Ile Ala Ile Ala Asn
50 55 60

Asp Gly Thr Gly Asp Leu Ile Ile Leu Leu Pro Asp Asp Asp Ala Phe
65 70 75 80

```
Tyr Ile Trp Ser His Glu Asp Glu Pro Leu Ile Glu Thr Glu Leu Glu
                 85                  90                  95

Asp Ala
```

<210> 29
<211> 648
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(625)
<223> RXN01301

<400> 29

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aggcaagaac gcaaagttct agtacgctgc taaagtatgc agcttggccc gcacggtttc 60

cgcgtgcggg acgtgttcat ttctgtatag gaaaactacc ttg atc gtt gat acc   115
                                          Leu Ile Val Asp Thr
                                            1               5

cag ttt gag aag atc cct gct cac gac gtc gtg ggc atc cgg gta atc   163
Gln Phe Glu Lys Ile Pro Ala His Asp Val Val Gly Ile Arg Val Ile
                10                  15                  20

ctt tcc tct gag gat ctc cct gag ctc ttt aaa cgc ggc tac gcg gaa   211
Leu Ser Ser Glu Asp Leu Pro Glu Leu Phe Lys Arg Gly Tyr Ala Glu
            25                  30                  35

gta aag aaa ttc ctc cgc cta gaa ggc atc gaa cct aaa ggt cct gcc   259
Val Lys Lys Phe Leu Arg Leu Glu Gly Ile Glu Pro Lys Gly Pro Ala
        40                  45                  50

cgc gcc tac tac ttt ggc gat gtc tct gac acc gta gac atc ctg att   307
Arg Ala Tyr Tyr Phe Gly Asp Val Ser Asp Thr Val Asp Ile Leu Ile
    55                  60                  65

ggt ttc ccc gtc agc ccc gcg caa gca gaa tcc ctg cgc cgc ggc gca   355
Gly Phe Pro Val Ser Pro Ala Gln Ala Glu Ser Leu Arg Arg Gly Ala
70                  75                  80                  85

ttg agc caa tcc ggt ggc gac atc gat gac gtt gtc ctc cac cac ttc   403
Leu Ser Gln Ser Gly Gly Asp Ile Asp Asp Val Val Leu His His Phe
                90                  95                  100

cgc gac atg aaa acc atg cac agc cgc cac tcc ggc ccc ttc gat gga   451
Arg Asp Met Lys Thr Met His Ser Arg His Ser Gly Pro Phe Asp Gly
            105                 110                 115

gtc gag cgc gtc tgg gac gaa atc ctc gat gaa gtc gaa gac ctc gga   499
Val Glu Arg Val Trp Asp Glu Ile Leu Asp Glu Val Glu Asp Leu Gly
        120                 125                 130

tgc act ctg cca tcc agc agc atc ggt tgg gaa gaa tac atc gag ggc   547
Cys Thr Leu Pro Ser Ser Ser Ile Gly Trp Glu Glu Tyr Ile Glu Gly
    135                 140                 145
```

```
cca gcc acc gct gat acc tgc gac caa ctg gcc tct gaa gtt tat gtt   595
Pro Ala Thr Ala Asp Thr Cys Asp Gln Leu Ala Ser Glu Val Tyr Val
150                 155                 160                 165

cag gtg tgc caa gca ccg gtg aag tct gca taaagattca cccggaattt     645
Gln Val Cys Gln Ala Pro Val Lys Ser Ala
                170                 175

ccc                                                               648
```

<210> 30
<211> 175
<212> PRT
<213> Corynebacterium glutamicum

<400> 30

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Leu Ile Val Asp Thr Gln Phe Glu Lys Ile Pro Ala His Asp Val Val
  1               5                  10                  15

Gly Ile Arg Val Ile Leu Ser Ser Glu Asp Leu Pro Glu Leu Phe Lys
             20                  25                  30

Arg Gly Tyr Ala Glu Val Lys Lys Phe Leu Arg Leu Glu Gly Ile Glu
         35                  40                  45

Pro Lys Gly Pro Ala Arg Ala Tyr Tyr Phe Gly Asp Val Ser Asp Thr
     50                  55                  60

Val Asp Ile Leu Ile Gly Phe Pro Val Ser Pro Ala Gln Ala Glu Ser
 65                  70                  75                  80

Leu Arg Arg Gly Ala Leu Ser Gln Ser Gly Gly Asp Ile Asp Asp Val
                 85                  90                  95

Val Leu His His Phe Arg Asp Met Lys Thr Met His Ser Arg His Ser
            100                 105                 110

Gly Pro Phe Asp Gly Val Glu Arg Val Trp Asp Glu Ile Leu Asp Glu
        115                 120                 125

Val Glu Asp Leu Gly Cys Thr Leu Pro Ser Ser Ser Ile Gly Trp Glu
    130                 135                 140

Glu Tyr Ile Glu Gly Pro Ala Thr Ala Asp Thr Cys Asp Gln Leu Ala
145                 150                 155                 160

Ser Glu Val Tyr Val Gln Val Cys Gln Ala Pro Val Lys Ser Ala
                165                 170                 175
```

<210> 31
<211> 428
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(405)
<223> FRXA01301

<400> 31
ttc ctc cgc cta gaa ggc atc gaa cct aaa ggt cct gcc cgc gcc tac 48
Phe Leu Arg Leu Glu Gly Ile Glu Pro Lys Gly Pro Ala Arg Ala Tyr
1 5 10 15

tac ttt ggc gat gtc tct gac acc gta gac atc ctg att ggt ttc ccc 96
Tyr Phe Gly Asp Val Ser Asp Thr Val Asp Ile Leu Ile Gly Phe Pro
20 25 30

gtc agc ccc gcg caa gca gaa tcc ctg cgc cgc ggc gca ttg agc caa 144
Val Ser Pro Ala Gln Ala Glu Ser Leu Arg Arg Gly Ala Leu Ser Gln
35 40 45

tcc ggt ggc gac atc gat gac gtt gtc ctc cac cac ttc cgc gac atg 192
Ser Gly Gly Asp Ile Asp Asp Val Val Leu His His Phe Arg Asp Met
50 55 60

aaa acc atg cac agc cgc cac tcc ggc ccc ttc gat gga gtc gag cgc 240
Lys Thr Met His Ser Arg His Ser Gly Pro Phe Asp Gly Val Glu Arg
65 70 75 80

gtc tgg gac gaa atc ctc gat gaa gtc gaa gac ctc gga tgc act ctg 288
Val Trp Asp Glu Ile Leu Asp Glu Val Glu Asp Leu Gly Cys Thr Leu
85 90 95

cca tcc agc agc atc ggt tgg gaa gaa tac atc gag ggc cca gcc acc 336
Pro Ser Ser Ser Ile Gly Trp Glu Glu Tyr Ile Glu Gly Pro Ala Thr
100 105 110

gct gat acc tgc gac caa ctg gcc tct gaa gtt tat gtt cag gtg tgc 384
Ala Asp Thr Cys Asp Gln Leu Ala Ser Glu Val Tyr Val Gln Val Cys
115 120 125

caa gca ccg gtg aag tct gca taaagattca cccggaattt ccc 428
Gln Ala Pro Val Lys Ser Ala
130 135

<210> 32
<211> 135
<212> PRT
<213> Corynebacterium glutamicum

<400> 32
Phe Leu Arg Leu Glu Gly Ile Glu Pro Lys Gly Pro Ala Arg Ala Tyr
1 5 10 15

Tyr Phe Gly Asp Val Ser Asp Thr Val Asp Ile Leu Ile Gly Phe Pro
20 25 30

Val Ser Pro Ala Gln Ala Glu Ser Leu Arg Arg Gly Ala Leu Ser Gln
35 40 45

Ser Gly Gly Asp Ile Asp Asp Val Val Leu His His Phe Arg Asp Met
50 55 60

Lys Thr Met His Ser Arg His Ser Gly Pro Phe Asp Gly Val Glu Arg
65 70 75 80

Val Trp Asp Glu Ile Leu Asp Glu Val Glu Asp Leu Gly Cys Thr Leu
85 90 95

```
Pro Ser Ser Ser Ile Gly Trp Glu Glu Tyr Ile Glu Gly Pro Ala Thr
            100                 105                 110

Ala Asp Thr Cys Asp Gln Leu Ala Ser Glu Val Tyr Val Gln Val Cys
        115                 120                 125

Gln Ala Pro Val Lys Ser Ala
    130                 135


<210> 33
<211> 567
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(544)
<223> RXN01276

<400> 33
tgcgtaaaac cctcatcacc atgctcgcga ccaccgcgat cgccttttcc gccatctcac 60

cagtgcaggc gcaaaccgtg gacacagaca ctgacgcctc gtg tca tct gag ctg   115
                                            Val Ser Ser Glu Leu
                                              1               5

agc agc ggc aca agc tca gga agt tca gag gat tcc gaa gat tct gac   163
Ser Ser Gly Thr Ser Ser Gly Ser Ser Glu Asp Ser Glu Asp Ser Asp
                10                  15                  20

atc tcc aac cgg gac atc atc ttc ggc atc gca gct atc gct gca gtc   211
Ile Ser Asn Arg Asp Ile Ile Phe Gly Ile Ala Ala Ile Ala Ala Val
            25                  30                  35

ggc gga ctt atc gca agt ggt gtg cac tgg gca gta caa cag cgc atg   259
Gly Gly Leu Ile Ala Ser Gly Val His Trp Ala Val Gln Gln Arg Met
        40                  45                  50

atc cca aat ccc ctc cca gga atc att cca aat ccc cct gca ctg gca   307
Ile Pro Asn Pro Leu Pro Gly Ile Ile Pro Asn Pro Pro Ala Leu Ala
    55                  60                  65

cct cag gcg cct gcc cca gca cct gct ccc gct cct gcc cct cag gca   355
Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Gln Ala
70                  75                  80                  85

gtc gcg ccc cag gtt gtc gct ccc cag gtt gtc gcg cct gct cca gcc   403
Val Ala Pro Gln Val Val Ala Pro Gln Val Val Ala Pro Ala Pro Ala
                90                  95                  100

cca gta cag acc aac cgc acc tac aaa aac tgc acc gaa gta tgg aac   451
Pro Val Gln Thr Asn Arg Thr Tyr Lys Asn Cys Thr Glu Val Trp Asn
            105                 110                 115

gtc ctg gga agg tcc atc cgc caa agc gat cca ggc tac ggc aca cac   499
Val Leu Gly Arg Ser Ile Arg Gln Ser Asp Pro Gly Tyr Gly Thr His
        120                 125                 130

ctc gac cgc gac cgc gac ggc atc ggc tgc gaa tca cgc cct agg       544
```

Leu Asp Arg Asp Arg Asp Gly Ile Gly Cys Glu Ser Arg Pro Arg
135 140 145

tagtttgggt tttggggatc ttc 567

<210> 34
<211> 148
<212> PRT
<213> Corynebacterium glutamicum

<400> 34
Val Ser Ser Glu Leu Ser Ser Gly Thr Ser Ser Gly Ser Ser Glu Asp
1 5 10 15

Ser Glu Asp Ser Asp Ile Ser Asn Arg Asp Ile Ile Phe Gly Ile Ala
20 25 30

Ala Ile Ala Ala Val Gly Gly Leu Ile Ala Ser Gly Val His Trp Ala
35 40 45

Val Gln Gln Arg Met Ile Pro Asn Pro Leu Pro Gly Ile Ile Pro Asn
50 55 60

Pro Pro Ala Leu Ala Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala
65 70 75 80

Pro Ala Pro Gln Ala Val Ala Pro Gln Val Val Ala Pro Gln Val Val
85 90 95

Ala Pro Ala Pro Ala Pro Val Gln Thr Asn Arg Thr Tyr Lys Asn Cys
100 105 110

Thr Glu Val Trp Asn Val Leu Gly Arg Ser Ile Arg Gln Ser Asp Pro
115 120 125

Gly Tyr Gly Thr His Leu Asp Arg Asp Arg Asp Gly Ile Gly Cys Glu
130 135 140

Ser Arg Pro Arg
145

<210> 35
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(646)
<223> FRXA01276

<400> 35
ctagatgccc ggaaaatagc atctcctata cacccaaaaa aaaggggagc gctgacagaa 60

aatagtaata attttgacag ctcgtgcaaa gatgattggc atg cgt aaa acc ctc 115
Met Arg Lys Thr Leu
1 5

atc acc atg ctc gcg acc acc gcg atc gcc ttt tcc gcc atc tca cca 163

```
Ile Thr Met Leu Ala Thr Thr Ala Ile Ala Phe Ser Ala Ile Ser Pro
                 10                  15                  20

gtg cag gcg caa acc gtg gac aca gac act gac gcc tcc gtg tca tct   211
Val Gln Ala Gln Thr Val Asp Thr Asp Thr Asp Ala Ser Val Ser Ser
             25                  30                  35

gag ctg agc agc ggc aca agc tca gga agt tca gag gat tcc gaa gat   259
Glu Leu Ser Ser Gly Thr Ser Ser Gly Ser Ser Glu Asp Ser Glu Asp
         40                  45                  50

tct gac atc tcc aac cgg gac atc atc ttc ggc atc gca gct atc gct   307
Ser Asp Ile Ser Asn Arg Asp Ile Ile Phe Gly Ile Ala Ala Ile Ala
     55                  60                  65

gca gtc ggc gga ctt atc gca ggt ggt gtg cac tgg gca gta caa cag   355
Ala Val Gly Gly Leu Ile Ala Gly Gly Val His Trp Ala Val Gln Gln
 70                  75                  80                  85

cgc atg atc cca aat ccc ctc cca gga atc att cca aat ccc cct gca   403
Arg Met Ile Pro Asn Pro Leu Pro Gly Ile Ile Pro Asn Pro Pro Ala
                 90                  95                 100

ctg gca cct cag gcg cct gcc cca gca cct gct ccc gct cct gcc cct   451
Leu Ala Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
            105                 110                 115

cag gca gtc gcg ccc cag gtt gtc gct ccc cag gtt gtc gcg cct gct   499
Gln Ala Val Ala Pro Gln Val Val Ala Pro Gln Val Val Ala Pro Ala
        120                 125                 130

cca gcc cca gta cag acc aac cgc acc tac aaa aac tgc acc gaa gta   547
Pro Ala Pro Val Gln Thr Asn Arg Thr Tyr Lys Asn Cys Thr Glu Val
    135                 140                 145

tgg aac gtc ctg gga agg tcc atc cgc caa agc gat cca ggc tac ggc   595
Trp Asn Val Leu Gly Arg Ser Ile Arg Gln Ser Asp Pro Gly Tyr Gly
150                 155                 160                 165

aca cac ctc gac cgc gac cgc gac ggc atc ggc tgc gaa tca cgc cct   643
Thr His Leu Asp Arg Asp Arg Asp Gly Ile Gly Cys Glu Ser Arg Pro
                170                 175                 180

agg tagtttgggt tttggggatc ttc                                    669
Arg
```

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<210> 36
<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 36

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Met Arg Lys Thr Leu Ile Thr Met Leu Ala Thr Thr Ala Ile Ala Phe
  1               5                  10                  15

Ser Ala Ile Ser Pro Val Gln Ala Gln Thr Val Asp Thr Asp Thr Asp
             20                  25                  30

Ala Ser Val Ser Ser Glu Leu Ser Ser Gly Thr Ser Ser Gly Ser Ser
```

```
         35                  40                  45

Glu Asp Ser Glu Asp Ser Asp Ile Ser Asn Arg Asp Ile Ile Phe Gly
     50                  55                  60

Ile Ala Ala Ile Ala Ala Val Gly Gly Leu Ile Ala Gly Gly Val His
 65                  70                  75                  80

Trp Ala Val Gln Gln Arg Met Ile Pro Asn Pro Leu Pro Gly Ile Ile
                 85                  90                  95

Pro Asn Pro Pro Ala Leu Ala Pro Gln Ala Pro Ala Pro Ala Pro Ala
            100                 105                 110

Pro Ala Pro Ala Pro Gln Ala Val Ala Pro Gln Val Val Ala Pro Gln
        115                 120                 125

Val Val Ala Pro Ala Pro Ala Pro Val Gln Thr Asn Arg Thr Tyr Lys
    130                 135                 140

Asn Cys Thr Glu Val Trp Asn Val Leu Gly Arg Ser Ile Arg Gln Ser
145                 150                 155                 160

Asp Pro Gly Tyr Gly Thr His Leu Asp Arg Asp Arg Asp Gly Ile Gly
                165                 170                 175

Cys Glu Ser Arg Pro Arg
            180
```

<210> 37
<211> 366
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(343)
<223> RXN01231

<400> 37

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tcctgggacg tcttccccga ggcgtgggag acattgaagg tttacctggg ctttcgtgcc 60

ccaggcatcg agcacttcac ccccctatga cgccttgcaa atg ctg ggc tac acc   115
                                              Met Leu Gly Tyr Thr
                                                1               5

ttc gtc atc ttt atc ctg gcg ccg ttt ctc atc ctc acc gga ata gcg   163
Phe Val Ile Phe Ile Leu Ala Pro Phe Leu Ile Leu Thr Gly Ile Ala
                 10                  15                  20

atg gcc ccg gcc atc cgg tcc cgc ttc ccg tgg tac gtc aaa ctc ttc   211
Met Ala Pro Ala Ile Arg Ser Arg Phe Pro Trp Tyr Val Lys Leu Phe
             25                  30                  35

ggc ggc cac cag ggt gca cgt tcc ctg cac ttc atc gcc atg gtg ttg   259
Gly Gly His Gln Gly Ala Arg Ser Leu His Phe Ile Ala Met Val Leu
         40                  45                  50

atg acg ggc ttt gtc atc atg cac gtc ggc ctg gtt ttt tgg tcc atg   307
Met Thr Gly Phe Val Ile Met His Val Gly Leu Val Phe Trp Ser Met
```

```
     55                  60                  65

gcg act aca aca tgg tcc aca tgg tct tcg gcg ata tgaacactga        353
Ala Thr Thr Thr Trp Ser Thr Trp Ser Ser Ala Ile
 70                  75                  80

ccgtgcggcg cag                                                    366


<210> 38
<211> 81
<212> PRT
<213> Corynebacterium glutamicum

<400> 38
Met Leu Gly Tyr Thr Phe Val Ile Phe Ile Leu Ala Pro Phe Leu Ile
  1               5                  10                  15

Leu Thr Gly Ile Ala Met Ala Pro Ala Ile Arg Ser Arg Phe Pro Trp
             20                  25                  30

Tyr Val Lys Leu Phe Gly Gly His Gln Gly Ala Arg Ser Leu His Phe
         35                  40                  45

Ile Ala Met Val Leu Met Thr Gly Phe Val Ile Met His Val Gly Leu
     50                  55                  60

Val Phe Trp Ser Met Ala Thr Thr Thr Trp Ser Thr Trp Ser Ser Ala
 65                  70                  75                  80

Ile


<210> 39
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> FRXA01231

<400> 39
cctgggacgt cttccccgag gcgtgggang acattgaagg tttacctggg ctttcgtgcc 60

ccaggcatcg agcacttcac ccccctatga cgccttgcaa atg ctg ggc tac acc   115
                                              Met Leu Gly Tyr Thr
                                                1               5

ttc gtc atc ttt atc ctg gcg ccg ttt ctc atc ctc acc gga ata gcg   163
Phe Val Ile Phe Ile Leu Ala Pro Phe Leu Ile Leu Thr Gly Ile Ala
                 10                  15                  20

atg gcc ccg gcc atc cgg tcc cgc ttc ccg tgg tac gtc aaa ctc ttc   211
Met Ala Pro Ala Ile Arg Ser Arg Phe Pro Trp Tyr Val Lys Leu Phe
             25                  30                  35

ggc ggc cac cag ggt gca cgt tcc ctg cac ttc atc gcc atg gtg ttg   259
Gly Gly His Gln Gly Ala Arg Ser Leu His Phe Ile Ala Met Val Leu
```

```
         40                  45                  50

atg acg ggc ttt gtc atc atg cac ngt cgg cct ggt ttt ttg gtc cat   307
Met Thr Gly Phe Val Ile Met His Xaa Arg Pro Gly Phe Leu Val His
     55                  60                  65

ggc gac tac aac atg gtc cac atg gtc ttc ggc gat atg aac act gac   355
Gly Asp Tyr Asn Met Val His Met Val Phe Gly Asp Met Asn Thr Asp
 70                  75                  80                  85

cgt gcg gcg cag gcc tac atc atc gtg atc acc acc atc gtc ant ggt   403
Arg Ala Ala Gln Ala Tyr Ile Ile Val Ile Thr Thr Ile Val Xaa Gly
                 90                  95                 100

ggt gtt ktt ctg rat cgk gct cag tat att kgt mrc tgg ctk acc grg   451
Gly Val Xaa Leu Xaa Xaa Ala Gln Tyr Ile Xaa Xaa Trp Xaa Thr Xaa
            105                 110                 115

mcc gcg ccm wgc ggt tya ccg cca gcw tca tck gag wtm ggw cgc aaa   499
Xaa Ala Xaa Xaa Gly Xaa Pro Pro Xaa Ser Xaa Glu Xaa Xaa Arg Lys
        120                 125                 130

atc ttt nct caw ccg gct gcg tcc ccg gat gag cag gca gan nan cac   547
Ile Phe Xaa Xaa Pro Ala Ala Ser Pro Asp Glu Gln Ala Xaa Xaa His
    135                 140                 145

cta cac gga caa gga cat ctc gca gtt cca ctg gac caa tgg cct gcc   595
Leu His Gly Gln Gly His Leu Ala Val Pro Leu Asp Gln Trp Pro Ala
150                 155                 160                 165

gcc gac cga tgatgaatcc cccgagtgga tcg                            627
Ala Asp Arg
```

<210> 40
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 40

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Met Leu Gly Tyr Thr Phe Val Ile Phe Ile Leu Ala Pro Phe Leu Ile
  1               5                  10                  15

Leu Thr Gly Ile Ala Met Ala Pro Ala Ile Arg Ser Arg Phe Pro Trp
             20                  25                  30

Tyr Val Lys Leu Phe Gly Gly His Gln Gly Ala Arg Ser Leu His Phe
         35                  40                  45

Ile Ala Met Val Leu Met Thr Gly Phe Val Ile Met His Xaa Arg Pro
     50                  55                  60

Gly Phe Leu Val His Gly Asp Tyr Asn Met Val His Met Val Phe Gly
 65                  70                  75                  80

Asp Met Asn Thr Asp Arg Ala Ala Gln Ala Tyr Ile Ile Val Ile Thr
                 85                  90                  95

Thr Ile Val Xaa Gly Gly Val Xaa Leu Xaa Xaa Ala Gln Tyr Ile Xaa
            100                 105                 110
```

```
Xaa Trp Xaa Thr Xaa Xaa Ala Xaa Xaa Gly Xaa Pro Pro Xaa Ser Xaa
        115                 120                 125

Glu Xaa Xaa Arg Lys Ile Phe Xaa Xaa Pro Ala Ala Ser Pro Asp Glu
    130                 135                 140

Gln Ala Xaa Xaa His Leu His Gly Gln Gly His Leu Ala Val Pro Leu
145                 150                 155                 160

Asp Gln Trp Pro Ala Ala Asp Arg
                165
```

<210> 41
<211> 954
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(931)
<223> RXN01210

<400> 41

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ttcgctgcaa aacccgccac cttggaatcc gtattcatgg acatcgcctc actcgagaac 60

acctcgctgc aaaccgccta gaatctttaa ggagaccaca atg acc acg tca cac   115
                                              Met Thr Thr Ser His
                                                1               5

acc gcc cgc ggg ctg caa cat gca acc ccg gag cgc cgc aag act tca   163
Thr Ala Arg Gly Leu Gln His Ala Thr Pro Glu Arg Arg Lys Thr Ser
                  10                  15                  20

ttt ttc aaa acc tct ctg ttt aag gcc gaa tgg ctc cag ttc cgc aga   211
Phe Phe Lys Thr Ser Leu Phe Lys Ala Glu Trp Leu Gln Phe Arg Arg
             25                  30                  35

aat aaa acc ctg ttg ttc atg gcc acc gta ttc cca gtc gga atc cct   259
Asn Lys Thr Leu Leu Phe Met Ala Thr Val Phe Pro Val Gly Ile Pro
         40                  45                  50

ttg ttg ctc ttt ctc atc gga aat ggt ggg gca gca gag tcc gcg aac   307
Leu Leu Leu Phe Leu Ile Gly Asn Gly Gly Ala Ala Glu Ser Ala Asn
     55                  60                  65

tcc ttc gac tac ttc gtc atg tac acc ctg cta ttt gtg cag ttc tac   355
Ser Phe Asp Tyr Phe Val Met Tyr Thr Leu Leu Phe Val Gln Phe Tyr
 70                  75                  80                  85

acg gtg ctg tcc atg gca acc acc cgc cgt gat gaa cgt gtg ctg aaa   403
Thr Val Leu Ser Met Ala Thr Thr Arg Arg Asp Glu Arg Val Leu Lys
                  90                  95                 100

agg ctg cgc acg gga gaa gcc cgc gac atc gat atc atc ggt gcc atc   451
Arg Leu Arg Thr Gly Glu Ala Arg Asp Ile Asp Ile Ile Gly Ala Ile
             105                 110                 115

tgt ttc ccc ggc gcg ctc ctc aca ctg atc ttc acc gtg gtg atc att   499
Cys Phe Pro Gly Ala Leu Leu Thr Leu Ile Phe Thr Val Val Ile Ile
```

```
        120                 125                 130

cca ttg ctc atg gtt ttg gga gct ccc gcg ccc atc aac ctt gtg ccc   547
Pro Leu Leu Met Val Leu Gly Ala Pro Ala Pro Ile Asn Leu Val Pro
    135                 140                 145

att gtg ttt gcc gta ctg atc gga cta ctt ctt tgt agt gct ctt gcc   595
Ile Val Phe Ala Val Leu Ile Gly Leu Leu Leu Cys Ser Ala Leu Ala
150                 155                 160                 165

ttg atg acc agc ggt ttc acc cga aac gcc gaa gcc gca cag atg acc   643
Leu Met Thr Ser Gly Phe Thr Arg Asn Ala Glu Ala Ala Gln Met Thr
                170                 175                 180

tcc atg ccc gtg ttc atg ctt gcg atg ggt gga ctt gga tca atc cgc   691
Ser Met Pro Val Phe Met Leu Ala Met Gly Gly Leu Gly Ser Ile Arg
            185                 190                 195

ttc gta ttc ggc gac agc att gtg gct gat atc ttg gcc tac acc cca   739
Phe Val Phe Gly Asp Ser Ile Val Ala Asp Ile Leu Ala Tyr Thr Pro
        200                 205                 210

ttc gcc gcg atc agt gac ctt gtc caa atc ggc tgg gct ggc gcc acc   787
Phe Ala Ala Ile Ser Asp Leu Val Gln Ile Gly Trp Ala Gly Ala Thr
    215                 220                 225

ttc gcc gac agc gtt ggt gga gta gag gca gca aac ttc gct gga att   835
Phe Ala Asp Ser Val Gly Gly Val Glu Ala Ala Asn Phe Ala Gly Ile
230                 235                 240                 245

ttc caa gac atg ctc ata cca ctt gga att ctg gca gcg tgg aca gct   883
Phe Gln Asp Met Leu Ile Pro Leu Gly Ile Leu Ala Ala Trp Thr Ala
                250                 255                 260

gca gcg gtg tgg gcg gcg aac cgc tac atg cgc tgg gac tcg tac cgc   931
Ala Ala Val Trp Ala Ala Asn Arg Tyr Met Arg Trp Asp Ser Tyr Arg
            265                 270                 275

taagcctgca gccgacggga tta                                        954
```

CCGCGGCGCGCCGCGCG

```
Phe Val Gln Phe Tyr Thr Val Leu Ser Met Ala Thr Thr Arg Arg Asp
                 85                  90                  95

Glu Arg Val Leu Lys Arg Leu Arg Thr Gly Glu Ala Arg Asp Ile Asp
            100                 105                 110

Ile Ile Gly Ala Ile Cys Phe Pro Gly Ala Leu Leu Thr Leu Ile Phe
        115                 120                 125

Thr Val Val Ile Ile Pro Leu Leu Met Val Leu Gly Ala Pro Ala Pro
    130                 135                 140

Ile Asn Leu Val Pro Ile Val Phe Ala Val Leu Ile Gly Leu Leu Leu
145                 150                 155                 160

Cys Ser Ala Leu Ala Leu Met Thr Ser Gly Phe Thr Arg Asn Ala Glu
            165                 170                 175

Ala Ala Gln Met Thr Ser Met Pro Val Phe Met Leu Ala Met Gly Gly
            180                 185                 190

Leu Gly Ser Ile Arg Phe Val Phe Gly Asp Ser Ile Val Ala Asp Ile
        195                 200                 205

Leu Ala Tyr Thr Pro Phe Ala Ala Ile Ser Asp Leu Val Gln Ile Gly
    210                 215                 220

Trp Ala Gly Ala Thr Phe Ala Asp Ser Val Gly Gly Val Glu Ala Ala
225                 230                 235                 240

Asn Phe Ala Gly Ile Phe Gln Asp Met Leu Ile Pro Leu Gly Ile Leu
                245                 250                 255

Ala Ala Trp Thr Ala Ala Ala Val Trp Ala Ala Asn Arg Tyr Met Arg
            260                 265                 270

Trp Asp Ser Tyr Arg
        275
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<210> 43
<211> 716
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(693)
<223> FRXA01210

<400> 43

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gta ttc cca gtc gga atc cct ttg ttg ctc ttt ctc atc gga aat ggt   48
Val Phe Pro Val Gly Ile Pro Leu Leu Leu Phe Leu Ile Gly Asn Gly
  1               5                  10                  15

ggg gca gca gag tcc gcg aac tcc ttc gac tac ttc gtc atg tac acc   96
Gly Ala Ala Glu Ser Ala Asn Ser Phe Asp Tyr Phe Val Met Tyr Thr
             20                  25                  30

ctg cta ttt gtg cag ttc tac acg gtg ctg tcc atg gca acc acc cgc   144
```

```
Leu Leu Phe Val Gln Phe Tyr Thr Val Leu Ser Met Ala Thr Thr Arg
         35                  40                  45

cgt gat gaa cgt gtg ctg aaa agg ctg cgc acg gga gaa gcc cgc gac   192
Arg Asp Glu Arg Val Leu Lys Arg Leu Arg Thr Gly Glu Ala Arg Asp
     50                  55                  60

atc gat atc atc ggt gcc atc tgt ttc ccc ggc gcg ctc ctc aca ctg   240
Ile Asp Ile Ile Gly Ala Ile Cys Phe Pro Gly Ala Leu Leu Thr Leu
 65                  70                  75                  80

atc ttc acc gtg gtg atc att cca ttg ctc atg gtt ttg gga gct ccc   288
Ile Phe Thr Val Val Ile Ile Pro Leu Leu Met Val Leu Gly Ala Pro
                 85                  90                  95

gcg ccc atc aac ctt gtg ccc att gtg ttt gcc gta ctg atc gga cta   336
Ala Pro Ile Asn Leu Val Pro Ile Val Phe Ala Val Leu Ile Gly Leu
            100                 105                 110

ctt ctt tgt agt gct ctt gcc ttg atg acc agc ggt ttc acc cga aac   384
Leu Leu Cys Ser Ala Leu Ala Leu Met Thr Ser Gly Phe Thr Arg Asn
        115                 120                 125

gcc gaa gcc gca cag atg acc tcc atg ccc gtg ttc atg ctt gcg atg   432
Ala Glu Ala Ala Gln Met Thr Ser Met Pro Val Phe Met Leu Ala Met
    130                 135                 140

ggt gga ctt gga tca atc cgc ttc gta ttc ggc gac agc att gtg gct   480
Gly Gly Leu Gly Ser Ile Arg Phe Val Phe Gly Asp Ser Ile Val Ala
145                 150                 155                 160

gat atc ttg gcc tac acc cca ttc gcc gcg atc agt gac ctt gtc caa   528
Asp Ile Leu Ala Tyr Thr Pro Phe Ala Ala Ile Ser Asp Leu Val Gln
                165                 170                 175

atc ggc tgg gct ggc gcc acc ttc gcc gac agc gtt ggt gga gta gag   576
Ile Gly Trp Ala Gly Ala Thr Phe Ala Asp Ser Val Gly Gly Val Glu
            180                 185                 190

gca gca aac ttc gct gga att ttc caa gac atg ctc ata cca ctt gga   624
Ala Ala Asn Phe Ala Gly Ile Phe Gln Asp Met Leu Ile Pro Leu Gly
        195                 200                 205

att ctg gca gcg tgg aca gct gca gcg gtg tgg gcg gcg aac cgc tac   672
Ile Leu Ala Ala Trp Thr Ala Ala Ala Val Trp Ala Ala Asn Arg Tyr
    210                 215                 220

atg cgc tgg gac tcg tac cgc taagcctgca gccgacggga tta             716
Met Arg Trp Asp Ser Tyr Arg
225                 230
```

<210> 44
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 44

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Val Phe Pro Val Gly Ile Pro Leu Leu Leu Phe Leu Ile Gly Asn Gly
  1               5                  10                  15
```

```
Gly Ala Ala Glu Ser Ala Asn Ser Phe Asp Tyr Phe Val Met Tyr Thr
            20                  25                  30

Leu Leu Phe Val Gln Phe Tyr Thr Val Leu Ser Met Ala Thr Thr Arg
        35                  40                  45

Arg Asp Glu Arg Val Leu Lys Arg Leu Arg Thr Gly Glu Ala Arg Asp
    50                  55                  60

Ile Asp Ile Ile Gly Ala Ile Cys Phe Pro Gly Ala Leu Leu Thr Leu
65                  70                  75                  80

Ile Phe Thr Val Val Ile Ile Pro Leu Leu Met Val Leu Gly Ala Pro
                85                  90                  95

Ala Pro Ile Asn Leu Val Pro Ile Val Phe Ala Val Leu Ile Gly Leu
            100                 105                 110

Leu Leu Cys Ser Ala Leu Ala Leu Met Thr Ser Gly Phe Thr Arg Asn
        115                 120                 125

Ala Glu Ala Ala Gln Met Thr Ser Met Pro Val Phe Met Leu Ala Met
    130                 135                 140

Gly Gly Leu Gly Ser Ile Arg Phe Val Phe Gly Asp Ser Ile Val Ala
145                 150                 155                 160

Asp Ile Leu Ala Tyr Thr Pro Phe Ala Ala Ile Ser Asp Leu Val Gln
                165                 170                 175

Ile Gly Trp Ala Gly Ala Thr Phe Ala Asp Ser Val Gly Gly Val Glu
            180                 185                 190

Ala Ala Asn Phe Ala Gly Ile Phe Gln Asp Met Leu Ile Pro Leu Gly
        195                 200                 205

Ile Leu Ala Ala Trp Thr Ala Ala Ala Val Trp Ala Ala Asn Arg Tyr
    210                 215                 220

Met Arg Trp Asp Ser Tyr Arg
225                 230
```

CCGTGCCAGTGATGAAAAGCCGGCGAGCCGCCAAACTTGATTAAGTGATTGTCACTTTGG

<210> 45
<211> 400
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(400)
<223> RXN01206

<400> 45

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ccgtgccagt gatgaaaagc cggcgagccg ccaaacttga ttaagtgatt gtcactttgg 60

attgtcatat tgggcgaata aaccggtagg attccccttc gtg agc gcc gaa aat   115
                                               Val Ser Ala Glu Asn
                                                 1               5

acc gag aac aca gat tcc cca ttt gaa atc tcc gag ttt gat gat cac   163
```

```
Thr Glu Asn Thr Asp Ser Pro Phe Glu Ile Ser Glu Phe Asp Asp His
                 10                  15                  20

cga cgc ccc ctc cag cgg gcc ctc aaa ttc ggt tcc atc gcc cta att   211
Arg Arg Pro Leu Gln Arg Ala Leu Lys Phe Gly Ser Ile Ala Leu Ile
            25                  30                  35

gtc ttc acc ctg atc tcc cta gcg atc tgg ggt gca act cgt ggc gta   259
Val Phe Thr Leu Ile Ser Leu Ala Ile Trp Gly Ala Thr Arg Gly Val
        40                  45                  50

ccc ggc gta tca gca gtt gtt atc ggc gca gca gtt ggc gca ggc ttt   307
Pro Gly Val Ser Ala Val Val Ile Gly Ala Ala Val Gly Ala Gly Phe
    55                  60                  65

gtc ctc tta acg gct ctc agc gtc ctg ttt aca act aat tcc aac gtc   355
Val Leu Leu Thr Ala Leu Ser Val Leu Phe Thr Thr Asn Ser Asn Val
70                  75                  80                  85

acc acc acc ggt gcg gtg gtg ctc ggt ggc tgg ctg ctg aag atc       400
Thr Thr Thr Gly Ala Val Val Leu Gly Gly Trp Leu Leu Lys Ile
                90                  95                  100
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<210> 46
<211> 100
<212> PRT
<213> Corynebacterium glutamicum

<400> 46

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Val Ser Ala Glu Asn Thr Glu Asn Thr Asp Ser Pro Phe Glu Ile Ser
  1               5                  10                  15

Glu Phe Asp Asp His Arg Arg Pro Leu Gln Arg Ala Leu Lys Phe Gly
            20                  25                  30

Ser Ile Ala Leu Ile Val Phe Thr Leu Ile Ser Leu Ala Ile Trp Gly
        35                  40                  45

Ala Thr Arg Gly Val Pro Gly Val Ser Ala Val Val Ile Gly Ala Ala
    50                  55                  60

Val Gly Ala Gly Phe Val Leu Leu Thr Ala Leu Ser Val Leu Phe Thr
65                  70                  75                  80

Thr Asn Ser Asn Val Thr Thr Thr Gly Ala Val Val Leu Gly Gly Trp
                85                  90                  95

Leu Leu Lys Ile
            100
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<210> 47
<211> 361
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(361)
<223> FRXA01206

<400> 47
ccgtgccagt gatgaaaagc cggcgagccg ccaaacttga ttaagtgatt gtcactttgg 60

attgtcatat tgggcgaata aaccggtagg attccccttc gtg agc gcc gaa aat 115
Val Ser Ala Glu Asn
1 5

acc gag aac aca gat tcc cca ttt gaa atc tcc gag ttt gat gat cac 163
Thr Glu Asn Thr Asp Ser Pro Phe Glu Ile Ser Glu Phe Asp Asp His
10 15 20

cga cgc ccc ctc cag cgg gcc ctc aaa ttc ggt tcc atc gcc cta att 211
Arg Arg Pro Leu Gln Arg Ala Leu Lys Phe Gly Ser Ile Ala Leu Ile
25 30 35

gtc ttc acc ctg atc tcc cta gcg atc tgg ggt gca act cgt ggc gta 259
Val Phe Thr Leu Ile Ser Leu Ala Ile Trp Gly Ala Thr Arg Gly Val
40 45 50

ccc ggc gta tca gca gtt gtt atc ggc gca gca gtt ggc gca ggc ttt 307
Pro Gly Val Ser Ala Val Val Ile Gly Ala Ala Val Gly Ala Gly Phe
55 60 65

gtc ctc tta acg gct ctc agc gtc ctg ttt aca act aat tcc aac gtc 355
Val Leu Leu Thr Ala Leu Ser Val Leu Phe Thr Thr Asn Ser Asn Val
70 75 80 85

acc acc 361
Thr Thr

<210> 48
<211> 87
<212> PRT
<213> Corynebacterium glutamicum

<400> 48
Val Ser Ala Glu Asn Thr Glu Asn Thr Asp Ser Pro Phe Glu Ile Ser
1 5 10 15

Glu Phe Asp Asp His Arg Arg Pro Leu Gln Arg Ala Leu Lys Phe Gly
20 25 30

Ser Ile Ala Leu Ile Val Phe Thr Leu Ile Ser Leu Ala Ile Trp Gly
35 40 45

Ala Thr Arg Gly Val Pro Gly Val Ser Ala Val Val Ile Gly Ala Ala
50 55 60

Val Gly Ala Gly Phe Val Leu Leu Thr Ala Leu Ser Val Leu Phe Thr
65 70 75 80

Thr Asn Ser Asn Val Thr Thr
85

<210> 49
<211> 1209
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1186)
<223> RXN01121

<400> 49
aaagatttac tgcgtacaac tctaaccaac aatattggca atgggttgtt ccatcttagc 60

gctttacctg tgaactctgc agagcggtac gcttaagcta atg aat ccc gaa ttt 115
Met Asn Pro Glu Phe
1 5

att cac ggc gca acc gaa att gaa acc aca aac agg ggc ctt cgc ccg 163
Ile His Gly Ala Thr Glu Ile Glu Thr Thr Asn Arg Gly Leu Arg Pro
10 15 20

cat cga ctc agc aaa gaa ata gta gaa cgc tac tgt gat ccc cag ttt 211
His Arg Leu Ser Lys Glu Ile Val Glu Arg Tyr Cys Asp Pro Gln Phe
25 30 35

agc gcg atg gaa cgc caa cca tcg ggc gtg cgc gtt gtg tgt cgc acc 259
Ser Ala Met Glu Arg Gln Pro Ser Gly Val Arg Val Val Cys Arg Thr
40 45 50

acc gcc acc tcc gtc acg ctg acc acg tat tcc acg cgg gtg gtg tac 307
Thr Ala Thr Ser Val Thr Leu Thr Thr Tyr Ser Thr Arg Val Val Tyr
55 60 65

ctc gat tcc ggc cgg ccg ggc ggc aag att gat gtg ctt atc gac ggc 355
Leu Asp Ser Gly Arg Pro Gly Gly Lys Ile Asp Val Leu Ile Asp Gly
70 75 80 85

gcc ccc aca tct tcc acg cca act tcc ggg ggc gag acc acg gaa gtc 403
Ala Pro Thr Ser Ser Thr Pro Thr Ser Gly Gly Glu Thr Thr Glu Val
90 95 100

aat ttc atc acc ggc gcc acg gaa cgg cgc ctg aaa gat ccg cag gtg 451
Asn Phe Ile Thr Gly Ala Thr Glu Arg Arg Leu Lys Asp Pro Gln Val
105 110 115

ctc aca gtg gat gga ctt tca gag cag gaa aag gtg gtg gag ttc tgg 499
Leu Thr Val Asp Gly Leu Ser Glu Gln Glu Lys Val Val Glu Phe Trp
120 125 130

ctg cct cac aat gaa gaa att gaa gtg atc tcc ctt aaa gcc aac gca 547
Leu Pro His Asn Glu Glu Ile Glu Val Ile Ser Leu Lys Ala Asn Ala
135 140 145

gct tta aac act gtc gaa gac acc cgt ccc gtg tgg atc aat tac ggc 595
Ala Leu Asn Thr Val Glu Asp Thr Arg Pro Val Trp Ile Asn Tyr Gly
150 155 160 165

agc tcc att agc cac ggt tcg gtt gcc act gcc cca acc aaa att tgg 643
Ser Ser Ile Ser His Gly Ser Val Ala Thr Ala Pro Thr Lys Ile Trp
170 175 180

cca gcc att gtt gcc cag tcc aaa aac tac aac ctg cgt aac ttc ggt 691
Pro Ala Ile Val Ala Gln Ser Lys Asn Tyr Asn Leu Arg Asn Phe Gly
185 190 195

```
ttt ggt ggc agc gcc atg ttg gat cct ttt atg gcg agg cta atc agg   739
Phe Gly Gly Ser Ala Met Leu Asp Pro Phe Met Ala Arg Leu Ile Arg
        200                 205                 210

gat act cca gct gat ctg atc acc ttg gaa att ggc atc aat att gtc   787
Asp Thr Pro Ala Asp Leu Ile Thr Leu Glu Ile Gly Ile Asn Ile Val
    215                 220                 225

aat ggt gat gtg atg cgt cgc cgc gga cta gag gct gct gtg gat ggg   835
Asn Gly Asp Val Met Arg Arg Arg Gly Leu Glu Ala Ala Val Asp Gly
230                 235                 240                 245

ttc atc aat acc atc cgc gat ggc cac ccc acc acg ccg atc aag att   883
Phe Ile Asn Thr Ile Arg Asp Gly His Pro Thr Thr Pro Ile Lys Ile
                250                 255                 260

gtg tcg ccg ttc tac tgc ccc att cat gag aaa act cca gga ccc ggc   931
Val Ser Pro Phe Tyr Cys Pro Ile His Glu Lys Thr Pro Gly Pro Gly
            265                 270                 275

gcg ttt gat acc tca tcg ttt ggc agt ggt cag att agg ttc atc gcc   979
Ala Phe Asp Thr Ser Ser Phe Gly Ser Gly Gln Ile Arg Phe Ile Ala
        280                 285                 290

act ggt gaa cct gat gag cat ggt cga ctg acg ctg gag atg gtg cgt   1027
Thr Gly Glu Pro Asp Glu His Gly Arg Leu Thr Leu Glu Met Val Arg
    295                 300                 305

gag gtg ttg gag ggg ttc gtc gaa aag caa aaa gac ccg cac ctg acc   1075
Glu Val Leu Glu Gly Phe Val Glu Lys Gln Lys Asp Pro His Leu Thr
310                 315                 320                 325

tac gtc gat ggt gcg agc ctt tat cag gcc agc gat gcg ccg ttg ctg   1123
Tyr Val Asp Gly Ala Ser Leu Tyr Gln Ala Ser Asp Ala Pro Leu Leu
                330                 335                 340

gat aat ttg cac cca gac gag gcg tcg cac gcc tta att gcg cag cgt   1171
Asp Asn Leu His Pro Asp Glu Ala Ser His Ala Leu Ile Ala Gln Arg
            345                 350                 355

ttg ctt aag caa ctt tgaaatcggc ttcggtgatt tcg                    1209
Leu Leu Lys Gln Leu
        360
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<210> 50
<211> 362
<212> PRT
<213> Corynebacterium glutamicum

<400> 50

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Met Asn Pro Glu Phe Ile His Gly Ala Thr Glu Ile Glu Thr Thr Asn
  1               5                  10                  15

Arg Gly Leu Arg Pro His Arg Leu Ser Lys Glu Ile Val Glu Arg Tyr
            20                  25                  30

Cys Asp Pro Gln Phe Ser Ala Met Glu Arg Gln Pro Ser Gly Val Arg
         35                  40                  45
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```
Val Val Cys Arg Thr Thr Ala Thr Ser Val Thr Leu Thr Thr Tyr Ser
     50                  55                  60

Thr Arg Val Val Tyr Leu Asp Ser Gly Arg Pro Gly Gly Lys Ile Asp
 65                  70                  75                  80

Val Leu Ile Asp Gly Ala Pro Thr Ser Ser Thr Pro Thr Ser Gly Gly
                 85                  90                  95

Glu Thr Thr Glu Val Asn Phe Ile Thr Gly Ala Thr Glu Arg Arg Leu
            100                 105                 110

Lys Asp Pro Gln Val Leu Thr Val Asp Gly Leu Ser Glu Gln Glu Lys
        115                 120                 125

Val Val Glu Phe Trp Leu Pro His Asn Glu Glu Ile Glu Val Ile Ser
    130                 135                 140

Leu Lys Ala Asn Ala Ala Leu Asn Thr Val Glu Asp Thr Arg Pro Val
145                 150                 155                 160

Trp Ile Asn Tyr Gly Ser Ser Ile Ser His Gly Ser Val Ala Thr Ala
                165                 170                 175

Pro Thr Lys Ile Trp Pro Ala Ile Val Ala Gln Ser Lys Asn Tyr Asn
            180                 185                 190

Leu Arg Asn Phe Gly Phe Gly Gly Ser Ala Met Leu Asp Pro Phe Met
        195                 200                 205

Ala Arg Leu Ile Arg Asp Thr Pro Ala Asp Leu Ile Thr Leu Glu Ile
    210                 215                 220

Gly Ile Asn Ile Val Asn Gly Asp Val Met Arg Arg Arg Gly Leu Glu
225                 230                 235                 240

Ala Ala Val Asp Gly Phe Ile Asn Thr Ile Arg Asp Gly His Pro Thr
                245                 250                 255

Thr Pro Ile Lys Ile Val Ser Pro Phe Tyr Cys Pro Ile His Glu Lys
            260                 265                 270

Thr Pro Gly Pro Gly Ala Phe Asp Thr Ser Ser Phe Gly Ser Gly Gln
        275                 280                 285

Ile Arg Phe Ile Ala Thr Gly Glu Pro Asp Glu His Gly Arg Leu Thr
    290                 295                 300

Leu Glu Met Val Arg Glu Val Leu Glu Gly Phe Val Glu Lys Gln Lys
305                 310                 315                 320

Asp Pro His Leu Thr Tyr Val Asp Gly Ala Ser Leu Tyr Gln Ala Ser
                325                 330                 335

Asp Ala Pro Leu Leu Asp Asn Leu His Pro Asp Glu Ala Ser His Ala
            340                 345                 350

Leu Ile Ala Gln Arg Leu Leu Lys Gln Leu
        355                 360
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<210> 51
<211> 778
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(778)
<223> FRXA01121

<400> 51
aaagatttac tgcgtacaac tctaaccaac aatattggca atgggttgtt ccatcttagc 60

gctttacctg tgaactctgc agagcggtac gcttaagcta atg aat ccc gaa ttt 115
Met Asn Pro Glu Phe
1 5

att cac ggc gca acc gaa att gaa acc aca aac agg ggc ctt cgc ccg 163
Ile His Gly Ala Thr Glu Ile Glu Thr Thr Asn Arg Gly Leu Arg Pro
10 15 20

cat cga ctc agc aaa gaa ata gta gaa cgc tac tgt gat ccc cag ttt 211
His Arg Leu Ser Lys Glu Ile Val Glu Arg Tyr Cys Asp Pro Gln Phe
25 30 35

agc gcg atg gaa cgc caa cca tcg ggc gtg cgc gtt gtg tgt cgc acc 259
Ser Ala Met Glu Arg Gln Pro Ser Gly Val Arg Val Val Cys Arg Thr
40 45 50

acc gcc acc tcc gtc acg ctg acc acg tat tcc acg cgg gtg gtg tac 307
Thr Ala Thr Ser Val Thr Leu Thr Thr Tyr Ser Thr Arg Val Val Tyr
55 60 65

ctc gat tcc ggc cgg ccg ggc ggc aag att gat gtg ctt atc gac ggc 355
Leu Asp Ser Gly Arg Pro Gly Gly Lys Ile Asp Val Leu Ile Asp Gly
70 75 80 85

gcc ccc aca tct tcc acg cca act tcc ggg ggc gag acc acg gaa gtc 403
Ala Pro Thr Ser Ser Thr Pro Thr Ser Gly Gly Glu Thr Thr Glu Val
90 95 100

aat ttc atc acc ggc gcc acg gaa cgg cgc ctg aaa gat ccg cag gtg 451
Asn Phe Ile Thr Gly Ala Thr Glu Arg Arg Leu Lys Asp Pro Gln Val
105 110 115

ctc aca gtg gat gga ctt tca gag cag gaa aag gtg gtg gag ttc tgg 499
Leu Thr Val Asp Gly Leu Ser Glu Gln Glu Lys Val Val Glu Phe Trp
120 125 130

ctg cct cac aat gaa gaa att gaa gtg atc tcc ctt aaa gcc aac gca 547
Leu Pro His Asn Glu Glu Ile Glu Val Ile Ser Leu Lys Ala Asn Ala
135 140 145

gct tta aac act gtc gaa gac acc cgt ccc gtg tgg atc aat tac ggc 595
Ala Leu Asn Thr Val Glu Asp Thr Arg Pro Val Trp Ile Asn Tyr Gly
150 155 160 165

agc tcc att agc cac ggt tcg gtt gcc act gcc cca acc aaa att tgg 643
Ser Ser Ile Ser His Gly Ser Val Ala Thr Ala Pro Thr Lys Ile Trp
170 175 180

```
cca gcc att gtt gcc cag tcc aaa aac tac aac ctg cgt aac ttc ggt   691
Pro Ala Ile Val Ala Gln Ser Lys Asn Tyr Asn Leu Arg Asn Phe Gly
            185                 190                 195

ttt ggt ggc agc gcc atg ttg gat cct ttt atg gcg agg cta atc agg   739
Phe Gly Gly Ser Ala Met Leu Asp Pro Phe Met Ala Arg Leu Ile Arg
        200                 205                 210

gat act cca gct gat ctg atc acc ttg gaa att ggc atc               778
Asp Thr Pro Ala Asp Leu Ile Thr Leu Glu Ile Gly Ile
    215                 220                 225
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<210> 52
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 52

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Met Asn Pro Glu Phe Ile His Gly Ala Thr Glu Ile Glu Thr Thr Asn
  1               5                  10                  15

Arg Gly Leu Arg Pro His Arg Leu Ser Lys Glu Ile Val Glu Arg Tyr
             20                  25                  30

Cys Asp Pro Gln Phe Ser Ala Met Glu Arg Gln Pro Ser Gly Val Arg
         35                  40                  45

Val Val Cys Arg Thr Thr Ala Thr Ser Val Thr Leu Thr Thr Tyr Ser
     50                  55                  60

Thr Arg Val Val Tyr Leu Asp Ser Gly Arg Pro Gly Gly Lys Ile Asp
 65                  70                  75                  80

Val Leu Ile Asp Gly Ala Pro Thr Ser Ser Thr Pro Thr Ser Gly Gly
                 85                  90                  95

Glu Thr Thr Glu Val Asn Phe Ile Thr Gly Ala Thr Glu Arg Arg Leu
            100                 105                 110

Lys Asp Pro Gln Val Leu Thr Val Asp Gly Leu Ser Glu Gln Glu Lys
        115                 120                 125

Val Val Glu Phe Trp Leu Pro His Asn Glu Glu Ile Glu Val Ile Ser
    130                 135                 140

Leu Lys Ala Asn Ala Ala Leu Asn Thr Val Glu Asp Thr Arg Pro Val
145                 150                 155                 160

Trp Ile Asn Tyr Gly Ser Ser Ile Ser His Gly Ser Val Ala Thr Ala
                165                 170                 175

Pro Thr Lys Ile Trp Pro Ala Ile Val Ala Gln Ser Lys Asn Tyr Asn
            180                 185                 190

Leu Arg Asn Phe Gly Phe Gly Gly Ser Ala Met Leu Asp Pro Phe Met
        195                 200                 205

Ala Arg Leu Ile Arg Asp Thr Pro Ala Asp Leu Ile Thr Leu Glu Ile
    210                 215                 220
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Gly Ile
225

<210> 53
<211> 902
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(879)
<223> RXN01085

<400> 53

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cga aag cgt ggt gaa gga ctt gat ccc aac tca cca gaa gct att gag   48
Arg Lys Arg Gly Glu Gly Leu Asp Pro Asn Ser Pro Glu Ala Ile Glu
  1               5                  10                  15

cag gcg aag aag aaa ggg gaa cgg aag gct cgt aat gag cgt tgc cgc   96
Gln Ala Lys Lys Lys Gly Glu Arg Lys Ala Arg Asn Glu Arg Cys Arg
             20                  25                  30

aaa aac ttc aaa ggt ggt ggc acc aaa gat ctt aag cag act gat cgg   144
Lys Asn Phe Lys Gly Gly Gly Thr Lys Asp Leu Lys Gln Thr Asp Arg
         35                  40                  45

acc ttt gat cag ctg cga aaa cag cgg gtg acg gat aaa gcc cgc aac   192
Thr Phe Asp Gln Leu Arg Lys Gln Arg Val Thr Asp Lys Ala Arg Asn
     50                  55                  60

cgt gac gta cac aat gag cag caa ctg gca cgc ggt gaa atc gga gaa   240
Arg Asp Val His Asn Glu Gln Gln Leu Ala Arg Gly Glu Ile Gly Glu
 65                  70                  75                  80

atg cgc tca ccg atg tgg gtt gag gtg ggt gct gcg att ctg ggc gtg   288
Met Arg Ser Pro Met Trp Val Glu Val Gly Ala Ala Ile Leu Gly Val
                 85                  90                  95

ttt gtc ctg gtt gtg atg tgg ctg gcc tgg ggc ggt atc ggg ctg ctg   336
Phe Val Leu Val Val Met Trp Leu Ala Trp Gly Gly Ile Gly Leu Leu
            100                 105                 110

atc cag acc atg atg aat act ggc tca cct aat gac aaa gag ctt ttt   384
Ile Gln Thr Met Met Asn Thr Gly Ser Pro Asn Asp Lys Glu Leu Phe
        115                 120                 125

gat gag ctt ggt gtg aga ccc tat tat gtt gct gtc gaa cag caa atc   432
Asp Glu Leu Gly Val Arg Pro Tyr Tyr Val Ala Val Glu Gln Gln Ile
    130                 135                 140

ggc acc agt agt gct cac acc acg tgc tac caa ccg ctt gat gaa ttt   480
Gly Thr Ser Ser Ala His Thr Thr Cys Tyr Gln Pro Leu Asp Glu Phe
145                 150                 155                 160

ggc aat aat ttt ggc gac tgt acg cgt agc gtg cct aaa gag cca gtg   528
Gly Asn Asn Phe Gly Asp Cys Thr Arg Ser Val Pro Lys Glu Pro Val
                165                 170                 175

tgg tac gcc gat tat gta gct agt gtg ttc gca gaa cat ggc ttt gat   576
Trp Tyr Ala Asp Tyr Val Ala Ser Val Phe Ala Glu His Gly Phe Asp
```

```
            180                 185                 190

gca cca gaa cct att gat aat tcg gtg ggt agc tgg ctg tta ttt ggt   624
Ala Pro Glu Pro Ile Asp Asn Ser Val Gly Ser Trp Leu Leu Phe Gly
        195                 200                 205

cat gtg ggc att att cgg gtg acg ttt gtg att gcg gtt gca gcg ggt   672
His Val Gly Ile Ile Arg Val Thr Phe Val Ile Ala Val Ala Ala Gly
    210                 215                 220

gtg tat gcg atg tca cgc gca gca atg atg cgt cag cta gaa aca caa   720
Val Tyr Ala Met Ser Arg Ala Ala Met Met Arg Gln Leu Glu Thr Gln
225                 230                 235                 240

aac gtc gct gtg gac acc acc gat att aac cag cac acc aat gac gca   768
Asn Val Ala Val Asp Thr Thr Asp Ile Asn Gln His Thr Asn Asp Ala
                245                 250                 255

cgt ttg gcg att ccg cag gag att gtg cgc gat ttg agt ctg ttc ccc   816
Arg Leu Ala Ile Pro Gln Glu Ile Val Arg Asp Leu Ser Leu Phe Pro
            260                 265                 270

gat gtc ggt gca cac ttc acc agt cca gcc ctc aag cat gat ttc cca   864
Asp Val Gly Ala His Phe Thr Ser Pro Ala Leu Lys His Asp Phe Pro
        275                 280                 285

tgt gat gct gtc gaa taagggcttt gaaaaaggtg gat                    902
Cys Asp Ala Val Glu
    290
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Sequence Listing

<210> 54
<211> 293
<212> PRT
<213> Corynebacterium glutamicum

<400> 54

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Arg Lys Arg Gly Glu Gly Leu Asp Pro Asn Ser Pro Glu Ala Ile Glu
  1               5                  10                  15

Gln Ala Lys Lys Lys Gly Glu Arg Lys Ala Arg Asn Glu Arg Cys Arg
            20                  25                  30

Lys Asn Phe Lys Gly Gly Gly Thr Lys Asp Leu Lys Gln Thr Asp Arg
        35                  40                  45

Thr Phe Asp Gln Leu Arg Lys Gln Arg Val Thr Asp Lys Ala Arg Asn
    50                  55                  60

Arg Asp Val His Asn Glu Gln Gln Leu Ala Arg Gly Glu Ile Gly Glu
65                  70                  75                  80

Met Arg Ser Pro Met Trp Val Glu Val Gly Ala Ala Ile Leu Gly Val
                85                  90                  95

Phe Val Leu Val Val Met Trp Leu Ala Trp Gly Gly Ile Gly Leu Leu
            100                 105                 110

Ile Gln Thr Met Met Asn Thr Gly Ser Pro Asn Asp Lys Glu Leu Phe
        115                 120                 125
```

```
Asp Glu Leu Gly Val Arg Pro Tyr Tyr Val Ala Val Glu Gln Gln Ile
    130                 135                 140

Gly Thr Ser Ser Ala His Thr Thr Cys Tyr Gln Pro Leu Asp Glu Phe
145                 150                 155                 160

Gly Asn Asn Phe Gly Asp Cys Thr Arg Ser Val Pro Lys Glu Pro Val
                165                 170                 175

Trp Tyr Ala Asp Tyr Val Ala Ser Val Phe Ala Glu His Gly Phe Asp
            180                 185                 190

Ala Pro Glu Pro Ile Asp Asn Ser Val Gly Ser Trp Leu Leu Phe Gly
        195                 200                 205

His Val Gly Ile Ile Arg Val Thr Phe Val Ile Ala Val Ala Ala Gly
    210                 215                 220

Val Tyr Ala Met Ser Arg Ala Ala Met Met Arg Gln Leu Glu Thr Gln
225                 230                 235                 240

Asn Val Ala Val Asp Thr Thr Asp Ile Asn Gln His Thr Asn Asp Ala
                245                 250                 255

Arg Leu Ala Ile Pro Gln Glu Ile Val Arg Asp Leu Ser Leu Phe Pro
            260                 265                 270

Asp Val Gly Ala His Phe Thr Ser Pro Ala Leu Lys His Asp Phe Pro
        275                 280                 285

Cys Asp Ala Val Glu
    290
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<210> 55
<211> 1057
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1057)
<223> FRXA01085

<400> 55
gaagggtcgt aatgagcgtt gccgcaaaaa cttcaaaggt ggtggcacca aagatcttaa 60

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gcagactgat cggacctttg atcagctgcg aaaacagcgg gtg acg gat aaa gcc   115
                                            Val Thr Asp Lys Ala
                                              1               5

cgc aac cgt gac gta cac aat gag cag caa ctg gca cgc ggt gaa atc   163
Arg Asn Arg Asp Val His Asn Glu Gln Gln Leu Ala Arg Gly Glu Ile
                 10                  15                  20

gga gaa atg cgc tca ccg atg tgg gtt gag gtg ggt gct gcg att ctg   211
Gly Glu Met Arg Ser Pro Met Trp Val Glu Val Gly Ala Ala Ile Leu
             25                  30                  35

ggc gtg ttt gtc ctg gtt gtg atg tgg ctg gcc tgg ggc ggt atc ggg   259
Gly Val Phe Val Leu Val Val Met Trp Leu Ala Trp Gly Gly Ile Gly
```

```
         40                  45                  50

ctg ctg atc cag acc atg atg aat act ggc tca cct aat gac aaa gag   307
Leu Leu Ile Gln Thr Met Met Asn Thr Gly Ser Pro Asn Asp Lys Glu
     55                  60                  65

ctt ttt gat gag ctt ggt gtg aga ccc tat tat gtt gct gtc gaa cag   355
Leu Phe Asp Glu Leu Gly Val Arg Pro Tyr Tyr Val Ala Val Glu Gln
 70                  75                  80                  85

caa atc ggc acc agt agt gct cac acc acg tgc tac caa ccg ctt gat   403
Gln Ile Gly Thr Ser Ser Ala His Thr Thr Cys Tyr Gln Pro Leu Asp
                 90                  95                 100

gaa ttt ggc aat aat ttt ggc gac tgt acg cgt agc gtg cct aaa gag   451
Glu Phe Gly Asn Asn Phe Gly Asp Cys Thr Arg Ser Val Pro Lys Glu
            105                 110                 115

cca gtg tgg tac gcc gat tat gta gct agt gtg ttc gca gaa cat ggc   499
Pro Val Trp Tyr Ala Asp Tyr Val Ala Ser Val Phe Ala Glu His Gly
        120                 125                 130

ttt gat gca cca gaa cct att gat aat tcg gtg ggt agc tgg ctg tta   547
Phe Asp Ala Pro Glu Pro Ile Asp Asn Ser Val Gly Ser Trp Leu Leu
    135                 140                 145

ttt ggt cat gtg ggc att att cgg gtg acg ttt gtg att gcg gtt gca   595
Phe Gly His Val Gly Ile Ile Arg Val Thr Phe Val Ile Ala Val Ala
150                 155                 160                 165

gcg ggt gtg tat gcg atg tca cgc gca gca atg atg cgt cag cta gaa   643
Ala Gly Val Tyr Ala Met Ser Arg Ala Ala Met Met Arg Gln Leu Glu
                170                 175                 180

aca caa aac gtc gct gtg gac acc acc gat att aac cag cac acc aat   691
Thr Gln Asn Val Ala Val Asp Thr Thr Asp Ile Asn Gln His Thr Asn
            185                 190                 195

gac gca cgt ttg gcg att ccg cag gag att gtg cgc gat ttg agt ctg   739
Asp Ala Arg Leu Ala Ile Pro Gln Glu Ile Val Arg Asp Leu Ser Leu
        200                 205                 210

ttc ccc gat gtc ggt gca cac tca cca gtc cag ccc tca agc atg att   787
Phe Pro Asp Val Gly Ala His Ser Pro Val Gln Pro Ser Ser Met Ile
    215                 220                 225

tcc cat gtg atg ctg tcg aat aag ggc ttg aaa aag gtg gat gta acg   835
Ser His Val Met Leu Ser Asn Lys Gly Leu Lys Lys Val Asp Val Thr
230                 235                 240                 245

cag ttt gca cag gag aca att atc gac aat gac act ggt gaa att gtc   883
Gln Phe Ala Gln Glu Thr Ile Ile Asp Asn Asp Thr Gly Glu Ile Val
                250                 255                 260

tct gaa aag ggt gaa gtg ctc tat gac ggt gca gga caa ccg atc aca   931
Ser Glu Lys Gly Glu Val Leu Tyr Asp Gly Ala Gly Gln Pro Ile Thr
            265                 270                 275

aag agc ttg ccg atg att gac aac gaa ttt agc cat gcg att ttt gac   979
Lys Ser Leu Pro Met Ile Asp Asn Glu Phe Ser His Ala Ile Phe Asp
        280                 285                 290
```

```
aaa tca gat gtc ccg aat ctt ccc gag ctg cga cgg ttc ttt aat cca   1027
Lys Ser Asp Val Pro Asn Leu Pro Glu Leu Arg Arg Phe Phe Asn Pro
    295                 300                 305

gca aag att gag tgg aat cct ggt ggt agt                          1057
Ala Lys Ile Glu Trp Asn Pro Gly Gly Ser
310                 315
```

<210> 56
<211> 319
<212> PRT
<213> Corynebacterium glutamicum

<400> 56

```
Val Thr Asp Lys Ala Arg Asn Arg Asp Val His Asn Glu Gln Gln Leu
  1               5                  10                  15

Ala Arg Gly Glu Ile Gly Glu Met Arg Ser Pro Met Trp Val Glu Val
            20                  25                  30

Gly Ala Ala Ile Leu Gly Val Phe Val Leu Val Val Met Trp Leu Ala
        35                  40                  45

Trp Gly Gly Ile Gly Leu Leu Ile Gln Thr Met Met Asn Thr Gly Ser
    50                  55                  60

Pro Asn Asp Lys Glu Leu Phe Asp Glu Leu Gly Val Arg Pro Tyr Tyr
65                  70                  75                  80

Val Ala Val Glu Gln Gln Ile Gly Thr Ser Ser Ala His Thr Thr Cys
                85                  90                  95

Tyr Gln Pro Leu Asp Glu Phe Gly Asn Asn Phe Gly Asp Cys Thr Arg
            100                 105                 110

Ser Val Pro Lys Glu Pro Val Trp Tyr Ala Asp Tyr Val Ala Ser Val
        115                 120                 125

Phe Ala Glu His Gly Phe Asp Ala Pro Glu Pro Ile Asp Asn Ser Val
    130                 135                 140

Gly Ser Trp Leu Leu Phe Gly His Val Gly Ile Ile Arg Val Thr Phe
145                 150                 155                 160

Val Ile Ala Val Ala Ala Gly Val Tyr Ala Met Ser Arg Ala Ala Met
                165                 170                 175

Met Arg Gln Leu Glu Thr Gln Asn Val Ala Val Asp Thr Thr Asp Ile
            180                 185                 190

Asn Gln His Thr Asn Asp Ala Arg Leu Ala Ile Pro Gln Glu Ile Val
        195                 200                 205

Arg Asp Leu Ser Leu Phe Pro Asp Val Gly Ala His Ser Pro Val Gln
    210                 215                 220

Pro Ser Ser Met Ile Ser His Val Met Leu Ser Asn Lys Gly Leu Lys
225                 230                 235                 240
```

```
Lys Val Asp Val Thr Gln Phe Ala Gln Glu Thr Ile Ile Asp Asn Asp
               245                 250                 255

Thr Gly Glu Ile Val Ser Glu Lys Gly Glu Val Leu Tyr Asp Gly Ala
            260                 265                 270

Gly Gln Pro Ile Thr Lys Ser Leu Pro Met Ile Asp Asn Glu Phe Ser
        275                 280                 285

His Ala Ile Phe Asp Lys Ser Asp Val Pro Asn Leu Pro Glu Leu Arg
    290                 295                 300

Arg Phe Phe Asn Pro Ala Lys Ile Glu Trp Asn Pro Gly Gly Ser
305                 310                 315


<210> 57
<211> 1824
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1801)
<223> RXN00022

<400> 57
aggactgctc cgcaaacctc taacaacacc tgctactccc cctgcagcgc cggtcaaccc 60

cacaccaccc acccccttaac aaccacaaga aagatttatc atg tcc gct cca acc   115
                                              Met Ser Ala Pro Thr
                                                1               5

atc tac ccc ggc acc aaa aca tct att gat ccg atc acc atg gat gac   163
Ile Tyr Pro Gly Thr Lys Thr Ser Ile Asp Pro Ile Thr Met Asp Asp
                10                  15                  20

gct cgc atc atc ttt ttc gat att gag tcg ctc cac aat att ttc acg   211
Ala Arg Ile Ile Phe Phe Asp Ile Glu Ser Leu His Asn Ile Phe Thr
            25                  30                  35

gta gca acc tac gat tct ctg tcc cac cac gtc gat gtc ttt tac ctg   259
Val Ala Thr Tyr Asp Ser Leu Ser His His Val Asp Val Phe Tyr Leu
        40                  45                  50

ctc gat cac aca acc agc cct cag atc acg gtg ctg ccg cac tca atg   307
Leu Asp His Thr Thr Ser Pro Gln Ile Thr Val Leu Pro His Ser Met
    55                  60                  65

gat tat ttc gat caa acg cgc agc gat gct gtt atg gct gcc atc att   355
Asp Tyr Phe Asp Gln Thr Arg Ser Asp Ala Val Met Ala Ala Ile Ile
70                  75                  80                  85

gag caa aac cct gcg ttc gca gaa att aaa ggc tca ccc att aca acc   403
Glu Gln Asn Pro Ala Phe Ala Glu Ile Lys Gly Ser Pro Ile Thr Thr
                90                  95                  100

gca gat gta gcc ctc cac aat ctc ggt gac acc aac gcc aac cga cgc   451
Ala Asp Val Ala Leu His Asn Leu Gly Asp Thr Asn Ala Asn Arg Arg
            105                 110                 115
```

```
tgg cag tct aac gtg ctg ctt gcc cgg cta ctc ggg ggt att agt gtg   499
Trp Gln Ser Asn Val Leu Leu Ala Arg Leu Leu Gly Gly Ile Ser Val
        120                 125                 130

cgc gga gag gta cct gag cac cag agc cac aac cat ctc gcc aag cag   547
Arg Gly Glu Val Pro Glu His Gln Ser His Asn His Leu Ala Lys Gln
    135                 140                 145

ttt gcc gag gca acc ttg gtc acc agg gac ttc gat gtg aat tat gat   595
Phe Ala Glu Ala Thr Leu Val Thr Arg Asp Phe Asp Val Asn Tyr Asp
150                 155                 160                 165

cca aca agc gct cac cct ttt act gct ggc ttc aac tcg atc aac tat   643
Pro Thr Ser Ala His Pro Phe Thr Ala Gly Phe Asn Ser Ile Asn Tyr
                170                 175                 180

gac acc acc ttg ctc agc ctg tac ttc gca atg ttg acc tca aat atc   691
Asp Thr Thr Leu Leu Ser Leu Tyr Phe Ala Met Leu Thr Ser Asn Ile
            185                 190                 195

gga agt aca ccg acg tat ttc ccg gtg atc acc gca cag gaa ctt cgt   739
Gly Ser Thr Pro Thr Tyr Phe Pro Val Ile Thr Ala Gln Glu Leu Arg
        200                 205                 210

gcg cat aac gac aag ctc ttt agc cct gag ttc atc aaa aac atg cca   787
Ala His Asn Asp Lys Leu Phe Ser Pro Glu Phe Ile Lys Asn Met Pro
    215                 220                 225

aag tat ctc tgg gat cgc gac agc ggt gct gga ctc aga gct gca tcg   835
Lys Tyr Leu Trp Asp Arg Asp Ser Gly Ala Gly Leu Arg Ala Ala Ser
230                 235                 240                 245

ggt ttc cgc aac gcc atg ctc aaa tcg ggt cgc cac att gat att caa   883
Gly Phe Arg Asn Ala Met Leu Lys Ser Gly Arg His Ile Asp Ile Gln
                250                 255                 260

cgc ctc aat gaa aaa cag ctc ttt gtt gga ctc aag cgc ctg ctt ggt   931
Arg Leu Asn Glu Lys Gln Leu Phe Val Gly Leu Lys Arg Leu Leu Gly
            265                 270                 275

ctc ctc ggt cac cag att ctc gaa tct gat cgt ctc tct ggt gat gat   979
Leu Leu Gly His Gln Ile Leu Glu Ser Asp Arg Leu Ser Gly Asp Asp
        280                 285                 290

gcc cat gtt gat act aac gag gat gta ctt gat ctc att gcc tac aac   1027
Ala His Val Asp Thr Asn Glu Asp Val Leu Asp Leu Ile Ala Tyr Asn
    295                 300                 305

gtc tca gac gtg gtg ggc acc aga ctg ctc gct gag gac ccg gtg tac   1075
Val Ser Asp Val Val Gly Thr Arg Leu Leu Ala Glu Asp Pro Val Tyr
310                 315                 320                 325

tcc ggc tct ttc gat ctg cgg gca ggt cta ctg agc acc tac cca gag   1123
Ser Gly Ser Phe Asp Leu Arg Ala Gly Leu Leu Ser Thr Tyr Pro Glu
                330                 335                 340

act gtt ttt gat cat gat ggt act ttc cgt cag cca tcc acg cag atg   1171
Thr Val Phe Asp His Asp Gly Thr Phe Arg Gln Pro Ser Thr Gln Met
            345                 350                 355

cgt aaa gat cgc cta acg att aat acc tca tca gct cag ttc gca gcg   1219
```

```
Arg Lys Asp Arg Leu Thr Ile Asn Thr Ser Ser Ala Gln Phe Ala Ala
        360                 365                 370

cgt att ttg gcg cca tat cgc cca ctc cgc gat gtc cct gat gcg att   1267
Arg Ile Leu Ala Pro Tyr Arg Pro Leu Arg Asp Val Pro Asp Ala Ile
    375                 380                 385

ggc gac atg ccg gtg gtg tct tac ttg tac ccg gat gca gca gtc gcc   1315
Gly Asp Met Pro Val Val Ser Tyr Leu Tyr Pro Asp Ala Ala Val Ala
390                 395                 400                 405

gaa gca aca ggt caa aaa caa gtc aac gtg ctt gat gag tca aag aag   1363
Glu Ala Thr Gly Gln Lys Gln Val Asn Val Leu Asp Glu Ser Lys Lys
                410                 415                 420

ttc ttc tat gac aac atc acc gac ccg gaa gca cgt gct gcc ttt gat   1411
Phe Phe Tyr Asp Asn Ile Thr Asp Pro Glu Ala Arg Ala Ala Phe Asp
            425                 430                 435

gag gtc ttt gct ttt tac gct gat att gag ggt cgc aac ttc aac agt   1459
Glu Val Phe Ala Phe Tyr Ala Asp Ile Glu Gly Arg Asn Phe Asn Ser
        440                 445                 450

cac aat gag gct att gat acc cag att aac caa tta cgt gct tat ctc   1507
His Asn Glu Ala Ile Asp Thr Gln Ile Asn Gln Leu Arg Ala Tyr Leu
    455                 460                 465

aac cag gtt gtc gca ttc gat gca gct ggg tat gcg ctc tat gat gta   1555
Asn Gln Val Val Ala Phe Asp Ala Ala Gly Tyr Ala Leu Tyr Asp Val
470                 475                 480                 485

cgt aca cgt ttt gag cag atc ttc ccc aag gat cgc agc tac atc aac   1603
Arg Thr Arg Phe Glu Gln Ile Phe Pro Lys Asp Arg Ser Tyr Ile Asn
                490                 495                 500

gat gct acg gat atg acc cct cgc gca gta tcg agc ttt gac gat ctg   1651
Asp Ala Thr Asp Met Thr Pro Arg Ala Val Ser Ser Phe Asp Asp Leu
            505                 510                 515

gtt gca ctc tgt gat gat att cgc ggt gta ctt gat cga ggt tta gag   1699
Val Ala Leu Cys Asp Asp Ile Arg Gly Val Leu Asp Arg Gly Leu Glu
        520                 525                 530

atc tca tct ccg aat cat cat gag atg gtg gat gct atg cgc aag cag   1747
Ile Ser Ser Pro Asn His His Glu Met Val Asp Ala Met Arg Lys Gln
    535                 540                 545

ctg cac tat att cag gca ttt tac cgt gcc tgg gac cca tca acg ccg   1795
Leu His Tyr Ile Gln Ala Phe Tyr Arg Ala Trp Asp Pro Ser Thr Pro
550                 555                 560                 565

ctt caa tgacgctgac ccagcggtga ccc                                1824
Leu Gln
```

<210> 58
<211> 567
<212> PRT
<213> Corynebacterium glutamicum

<400> 58

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Met Ser Ala Pro Thr Ile Tyr Pro Gly Thr Lys Thr Ser Ile Asp Pro
 1               5                  10                  15

Ile Thr Met Asp Asp Ala Arg Ile Ile Phe Phe Asp Ile Glu Ser Leu
            20                  25                  30

His Asn Ile Phe Thr Val Ala Thr Tyr Asp Ser Leu Ser His His Val
        35                  40                  45

Asp Val Phe Tyr Leu Leu Asp His Thr Thr Ser Pro Gln Ile Thr Val
    50                  55                  60

Leu Pro His Ser Met Asp Tyr Phe Asp Gln Thr Arg Ser Asp Ala Val
65                  70                  75                  80

Met Ala Ala Ile Ile Glu Gln Asn Pro Ala Phe Ala Glu Ile Lys Gly
                85                  90                  95

Ser Pro Ile Thr Thr Ala Asp Val Ala Leu His Asn Leu Gly Asp Thr
            100                 105                 110

Asn Ala Asn Arg Arg Trp Gln Ser Asn Val Leu Leu Ala Arg Leu Leu
        115                 120                 125

Gly Gly Ile Ser Val Arg Gly Glu Val Pro Glu His Gln Ser His Asn
    130                 135                 140

His Leu Ala Lys Gln Phe Ala Glu Ala Thr Leu Val Thr Arg Asp Phe
145                 150                 155                 160

Asp Val Asn Tyr Asp Pro Thr Ser Ala His Pro Phe Thr Ala Gly Phe
                165                 170                 175

Asn Ser Ile Asn Tyr Asp Thr Thr Leu Leu Ser Leu Tyr Phe Ala Met
            180                 185                 190

Leu Thr Ser Asn Ile Gly Ser Thr Pro Thr Tyr Phe Pro Val Ile Thr
        195                 200                 205

Ala Gln Glu Leu Arg Ala His Asn Asp Lys Leu Phe Ser Pro Glu Phe
    210                 215                 220

Ile Lys Asn Met Pro Lys Tyr Leu Trp Asp Arg Asp Ser Gly Ala Gly
225                 230                 235                 240

Leu Arg Ala Ala Ser Gly Phe Arg Asn Ala Met Leu Lys Ser Gly Arg
                245                 250                 255

His Ile Asp Ile Gln Arg Leu Asn Glu Lys Gln Leu Phe Val Gly Leu
            260                 265                 270

Lys Arg Leu Leu Gly Leu Leu Gly His Gln Ile Leu Glu Ser Asp Arg
        275                 280                 285

Leu Ser Gly Asp Asp Ala His Val Asp Thr Asn Glu Asp Val Leu Asp
    290                 295                 300

Leu Ile Ala Tyr Asn Val Ser Asp Val Val Gly Thr Arg Leu Leu Ala
305                 310                 315                 320
```

```
Glu Asp Pro Val Tyr Ser Gly Ser Phe Asp Leu Arg Ala Gly Leu Leu
                325                 330                 335

Ser Thr Tyr Pro Glu Thr Val Phe Asp His Asp Gly Thr Phe Arg Gln
            340                 345                 350

Pro Ser Thr Gln Met Arg Lys Asp Arg Leu Thr Ile Asn Thr Ser Ser
        355                 360                 365

Ala Gln Phe Ala Ala Arg Ile Leu Ala Pro Tyr Arg Pro Leu Arg Asp
    370                 375                 380

Val Pro Asp Ala Ile Gly Asp Met Pro Val Val Ser Tyr Leu Tyr Pro
385                 390                 395                 400

Asp Ala Ala Val Ala Glu Ala Thr Gly Gln Lys Gln Val Asn Val Leu
                405                 410                 415

Asp Glu Ser Lys Lys Phe Phe Tyr Asp Asn Ile Thr Asp Pro Glu Ala
            420                 425                 430

Arg Ala Ala Phe Asp Glu Val Phe Ala Phe Tyr Ala Asp Ile Glu Gly
        435                 440                 445

Arg Asn Phe Asn Ser His Asn Glu Ala Ile Asp Thr Gln Ile Asn Gln
    450                 455                 460

Leu Arg Ala Tyr Leu Asn Gln Val Val Ala Phe Asp Ala Ala Gly Tyr
465                 470                 475                 480

Ala Leu Tyr Asp Val Arg Thr Arg Phe Glu Gln Ile Phe Pro Lys Asp
                485                 490                 495

Arg Ser Tyr Ile Asn Asp Ala Thr Asp Met Thr Pro Arg Ala Val Ser
            500                 505                 510

Ser Phe Asp Asp Leu Val Ala Leu Cys Asp Asp Ile Arg Gly Val Leu
        515                 520                 525

Asp Arg Gly Leu Glu Ile Ser Ser Pro Asn His His Glu Met Val Asp
    530                 535                 540

Ala Met Arg Lys Gln Leu His Tyr Ile Gln Ala Phe Tyr Arg Ala Trp
545                 550                 555                 560

Asp Pro Ser Thr Pro Leu Gln
                565
```

<210> 59
<211> 835
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(835)
<223> FRXA00022

<400> 59
aggactgctc cgcaaacctc taacaacacc tgctactccc cctgcagcgc cggtcaaccc 60

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cacaccaccc acccttaac aaccacaaga aagatttatc atg tcc gct cca acc   115
                                           Met Ser Ala Pro Thr
                                             1               5

atc tac ccc ggc acc aaa aca tct att gat ccg atc acc atg gat gac   163
Ile Tyr Pro Gly Thr Lys Thr Ser Ile Asp Pro Ile Thr Met Asp Asp
                10                  15                  20

gct cgc atc atc ttt ttc gat att gag tcg ctc cac aat att ttc acg   211
Ala Arg Ile Ile Phe Phe Asp Ile Glu Ser Leu His Asn Ile Phe Thr
            25                  30                  35

gta gca acc tac gat tct ctg tcc cac cac gtc gat gtc ttt tac ctg   259
Val Ala Thr Tyr Asp Ser Leu Ser His His Val Asp Val Phe Tyr Leu
        40                  45                  50

ctc gat cac aca acc agc cct cag atc acg gtg ctg ccg cac tca atg   307
Leu Asp His Thr Thr Ser Pro Gln Ile Thr Val Leu Pro His Ser Met
    55                  60                  65

gat tat ttc gat caa acg cgc agc gat gct gtt atg gct gcc atc att   355
Asp Tyr Phe Asp Gln Thr Arg Ser Asp Ala Val Met Ala Ala Ile Ile
70                  75                  80                  85

gag caa aac cct gcg ttc gca gaa att aaa ggc tca ccc att aca acc   403
Glu Gln Asn Pro Ala Phe Ala Glu Ile Lys Gly Ser Pro Ile Thr Thr
                90                  95                  100

gca gat gta gcc ctc cac aat ctc ggt gac acc aac gcc aac cga cgc   451
Ala Asp Val Ala Leu His Asn Leu Gly Asp Thr Asn Ala Asn Arg Arg
            105                 110                 115

tgg cag tct aac gtg ctg ctt gcc cgg cta ctc ggg ggt att agt gtg   499
Trp Gln Ser Asn Val Leu Leu Ala Arg Leu Leu Gly Gly Ile Ser Val
        120                 125                 130

cgc gga gag gta cct gag cac cag agc cac aac cat ctc gcc aag cag   547
Arg Gly Glu Val Pro Glu His Gln Ser His Asn His Leu Ala Lys Gln
    135                 140                 145

ttt gcc gag gca acc ttg gtc acc agg gac ttc gat gtg aat tat gat   595
Phe Ala Glu Ala Thr Leu Val Thr Arg Asp Phe Asp Val Asn Tyr Asp
150                 155                 160                 165

cca aca agc gct cac cct ttt act gct ggc ttc aac tcg atc aac tat   643
Pro Thr Ser Ala His Pro Phe Thr Ala Gly Phe Asn Ser Ile Asn Tyr
                170                 175                 180

gac acc acc ttg ctc agc ctg tac ttc gca atg ttg acc tca aat atc   691
Asp Thr Thr Leu Leu Ser Leu Tyr Phe Ala Met Leu Thr Ser Asn Ile
            185                 190                 195

gga agt aca ccg acg tat ttc ccg gtg atc acc gca caa gaa ctt cgt   739
Gly Ser Thr Pro Thr Tyr Phe Pro Val Ile Thr Ala Gln Glu Leu Arg
        200                 205                 210

gcg cat aac gac aag ctc ttt agc cct gag ttc atc aaa aac atg cca   787
Ala His Asn Asp Lys Leu Phe Ser Pro Glu Phe Ile Lys Asn Met Pro
    215                 220                 225
```

```
aag tat ttc tgg gat cgc gac agc ggt gct gga ctc aga gct gca tcg   835
Lys Tyr Phe Trp Asp Arg Asp Ser Gly Ala Gly Leu Arg Ala Ala Ser
230                 235                 240                 245
```

<210> 60
<211> 245
<212> PRT
<213> Corynebacterium glutamicum

<400> 60

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Met Ser Ala Pro Thr Ile Tyr Pro Gly Thr Lys Thr Ser Ile Asp Pro
  1               5                  10                  15

Ile Thr Met Asp Asp Ala Arg Ile Ile Phe Phe Asp Ile Glu Ser Leu
             20                  25                  30

His Asn Ile Phe Thr Val Ala Thr Tyr Asp Ser Leu Ser His His Val
         35                  40                  45

Asp Val Phe Tyr Leu Leu Asp His Thr Thr Ser Pro Gln Ile Thr Val
     50                  55                  60

Leu Pro His Ser Met Asp Tyr Phe Asp Gln Thr Arg Ser Asp Ala Val
 65                  70                  75                  80

Met Ala Ala Ile Ile Glu Gln Asn Pro Ala Phe Ala Glu Ile Lys Gly
                 85                  90                  95

Ser Pro Ile Thr Thr Ala Asp Val Ala Leu His Asn Leu Gly Asp Thr
            100                 105                 110

Asn Ala Asn Arg Arg Trp Gln Ser Asn Val Leu Leu Ala Arg Leu Leu
        115                 120                 125

Gly Gly Ile Ser Val Arg Gly Glu Val Pro Glu His Gln Ser His Asn
    130                 135                 140

His Leu Ala Lys Gln Phe Ala Glu Ala Thr Leu Val Thr Arg Asp Phe
145                 150                 155                 160

Asp Val Asn Tyr Asp Pro Thr Ser Ala His Pro Phe Thr Ala Gly Phe
                165                 170                 175

Asn Ser Ile Asn Tyr Asp Thr Thr Leu Leu Ser Leu Tyr Phe Ala Met
            180                 185                 190

Leu Thr Ser Asn Ile Gly Ser Thr Pro Thr Tyr Phe Pro Val Ile Thr
        195                 200                 205

Ala Gln Glu Leu Arg Ala His Asn Asp Lys Leu Phe Ser Pro Glu Phe
    210                 215                 220

Ile Lys Asn Met Pro Lys Tyr Phe Trp Asp Arg Asp Ser Gly Ala Gly
225                 230                 235                 240

Leu Arg Ala Ala Ser
                245
```

<210> 61

<211> 939
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(939)
<223> FRXA01921

<400> 61

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cac att gat att caa cgc ctc aat gaa aaa cag ctc ttt gtt gga ctc   48
His Ile Asp Ile Gln Arg Leu Asn Glu Lys Gln Leu Phe Val Gly Leu
  1               5                  10                  15

aag cgc ctg ctt ggt ctc ctc ggt cac cag att ctc gaa tct gat cgt   96
Lys Arg Leu Leu Gly Leu Leu Gly His Gln Ile Leu Glu Ser Asp Arg
             20                  25                  30

ctc tct ggt gat gat gcc cat gtt gat act aac gag gat gta ctt gat   144
Leu Ser Gly Asp Asp Ala His Val Asp Thr Asn Glu Asp Val Leu Asp
         35                  40                  45

ctc att gcc tac aac gtc tca gac gtg gtg ggc acc aga ctg ctc gct   192
Leu Ile Ala Tyr Asn Val Ser Asp Val Val Gly Thr Arg Leu Leu Ala
     50                  55                  60

gag gac ccg gtg tac tcc ggc tct ttc gat ctg cgg gca ggt cta ctg   240
Glu Asp Pro Val Tyr Ser Gly Ser Phe Asp Leu Arg Ala Gly Leu Leu
 65                  70                  75                  80

agc acc tac cca gag act gtt ttt gat cat gat ggt act ttc cgt cag   288
Ser Thr Tyr Pro Glu Thr Val Phe Asp His Asp Gly Thr Phe Arg Gln
                 85                  90                  95

cca tcc acg cag atg cgt aaa gat cgc cta acg att aat acc tca tca   336
Pro Ser Thr Gln Met Arg Lys Asp Arg Leu Thr Ile Asn Thr Ser Ser
            100                 105                 110

gct cag ttc gca gcg cgt att ttg gcg cca tat cgc cca ctc cgc gat   384
Ala Gln Phe Ala Ala Arg Ile Leu Ala Pro Tyr Arg Pro Leu Arg Asp
        115                 120                 125

gtc cct gat gcg att ggc gac atg ccg gtg gtg tct tac ttg tac ccg   432
Val Pro Asp Ala Ile Gly Asp Met Pro Val Val Ser Tyr Leu Tyr Pro
    130                 135                 140

gat gca gca gtc gcc gaa gca aca ggt caa aaa caa gtc aac gtg ctt   480
Asp Ala Ala Val Ala Glu Ala Thr Gly Gln Lys Gln Val Asn Val Leu
145                 150                 155                 160

gat gag tca aag aag ttc ttc tat gac aac atc acc gac ccg gaa gca   528
Asp Glu Ser Lys Lys Phe Phe Tyr Asp Asn Ile Thr Asp Pro Glu Ala
                165                 170                 175

cgt gct gcc ttt gat gag gtc ttt gct ttt tac gct gat att gag ggt   576
Arg Ala Ala Phe Asp Glu Val Phe Ala Phe Tyr Ala Asp Ile Glu Gly
            180                 185                 190

cgc aac ttc aac agt cac aat gag gct att gat acc cag att aac caa   624
Arg Asn Phe Asn Ser His Asn Glu Ala Ile Asp Thr Gln Ile Asn Gln
        195                 200                 205
```

```
tta cgt gct tat ctc aac cag gtt gtc gca ttc gat gca gct ggg tat   672
Leu Arg Ala Tyr Leu Asn Gln Val Val Ala Phe Asp Ala Ala Gly Tyr
    210                 215                 220

gcg ctc tat gat gta cgt aca cgt ttt gag cag atc ttc ccc aag gat   720
Ala Leu Tyr Asp Val Arg Thr Arg Phe Glu Gln Ile Phe Pro Lys Asp
225                 230                 235                 240

cgc agc tac atc aac gat gct acg gat atg acc cct cgc gca gta tcg   768
Arg Ser Tyr Ile Asn Asp Ala Thr Asp Met Thr Pro Arg Ala Val Ser
                245                 250                 255

agc ttt gac gat ctg gtt gca ctc tgt gat gat att cgc ggt gta ctt   816
Ser Phe Asp Asp Leu Val Ala Leu Cys Asp Asp Ile Arg Gly Val Leu
            260                 265                 270

gat cga ggt tta gag atc tca tct ccg aat cat cat gag atg gtg gat   864
Asp Arg Gly Leu Glu Ile Ser Ser Pro Asn His His Glu Met Val Asp
        275                 280                 285

gct atg cgc aag cag ctg cac tat att cag gca ttt acc gtg cct ggg   912
Ala Met Arg Lys Gln Leu His Tyr Ile Gln Ala Phe Thr Val Pro Gly
    290                 295                 300

acc cat caa cgc cgc ttc aat gac gct                              939
Thr His Gln Arg Arg Phe Asn Asp Ala
305                 310
```

<210> 62
<211> 313
<212> PRT
<213> Corynebacterium glutamicum

<400> 62

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His Ile Asp Ile Gln Arg Leu Asn Glu Lys Gln Leu Phe Val Gly Leu
  1               5                  10                  15

Lys Arg Leu Leu Gly Leu Leu Gly His Gln Ile Leu Glu Ser Asp Arg
             20                  25                  30

Leu Ser Gly Asp Asp Ala His Val Asp Thr Asn Glu Asp Val Leu Asp
         35                  40                  45

Leu Ile Ala Tyr Asn Val Ser Asp Val Val Gly Thr Arg Leu Leu Ala
     50                  55                  60

Glu Asp Pro Val Tyr Ser Gly Ser Phe Asp Leu Arg Ala Gly Leu Leu
 65                  70                  75                  80

Ser Thr Tyr Pro Glu Thr Val Phe Asp His Asp Gly Thr Phe Arg Gln
                 85                  90                  95

Pro Ser Thr Gln Met Arg Lys Asp Arg Leu Thr Ile Asn Thr Ser Ser
            100                 105                 110

Ala Gln Phe Ala Ala Arg Ile Leu Ala Pro Tyr Arg Pro Leu Arg Asp
        115                 120                 125

Val Pro Asp Ala Ile Gly Asp Met Pro Val Val Ser Tyr Leu Tyr Pro
```

```
    130                 135                 140

Asp Ala Ala Val Ala Glu Ala Thr Gly Gln Lys Gln Val Asn Val Leu
145                 150                 155                 160

Asp Glu Ser Lys Lys Phe Phe Tyr Asp Asn Ile Thr Asp Pro Glu Ala
                165                 170                 175

Arg Ala Ala Phe Asp Glu Val Phe Ala Phe Tyr Ala Asp Ile Glu Gly
            180                 185                 190

Arg Asn Phe Asn Ser His Asn Glu Ala Ile Asp Thr Gln Ile Asn Gln
        195                 200                 205

Leu Arg Ala Tyr Leu Asn Gln Val Val Ala Phe Asp Ala Ala Gly Tyr
    210                 215                 220

Ala Leu Tyr Asp Val Arg Thr Arg Phe Glu Gln Ile Phe Pro Lys Asp
225                 230                 235                 240

Arg Ser Tyr Ile Asn Asp Ala Thr Asp Met Thr Pro Arg Ala Val Ser
                245                 250                 255

Ser Phe Asp Asp Leu Val Ala Leu Cys Asp Asp Ile Arg Gly Val Leu
            260                 265                 270

Asp Arg Gly Leu Glu Ile Ser Ser Pro Asn His His Glu Met Val Asp
        275                 280                 285

Ala Met Arg Lys Gln Leu His Tyr Ile Gln Ala Phe Thr Val Pro Gly
    290                 295                 300

Thr His Gln Arg Arg Phe Asn Asp Ala
305                 310


<210> 63
<211> 489
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(466)
<223> RXN00027

<400> 63
ttaggcaacg actccgaaac cttcaagaac gtgtggcact aacaattgcg gactatcctt 60

gggaactgtt ttagatttta ttcagggtag ggagattgtt gtg gat gaa cga agc   115
                                              Val Asp Glu Arg Ser
                                                1               5

cgg ttt gcg cgc agc gtt ttc ccg gac ggt gaa gaa cca gat cca cgt   163
Arg Phe Ala Arg Ser Val Phe Pro Asp Gly Glu Glu Pro Asp Pro Arg
                  10                  15                  20

ttc act ttg gcc aat gag cgc acg ttt cta gca tgg acg cgt acg tct   211
Phe Thr Leu Ala Asn Glu Arg Thr Phe Leu Ala Trp Thr Arg Thr Ser
             25                  30                  35
```

```
ttg gcg ttt ctt gcc ggt ggt att gct ttt gag gcg ttc cag atc agt   259
Leu Ala Phe Leu Ala Gly Gly Ile Ala Phe Glu Ala Phe Gln Ile Ser
         40                  45                  50

gga cta tcg gat act gtc cgt aca aca atc gcg gtt ttt atc att gcg   307
Gly Leu Ser Asp Thr Val Arg Thr Thr Ile Ala Val Phe Ile Ile Ala
     55                  60                  65

gtt ggc atg atc att gcc gct ggt gct gcg gtg agg tgg atg aat gtg   355
Val Gly Met Ile Ile Ala Ala Gly Ala Ala Val Arg Trp Met Asn Val
 70                  75                  80                  85

gag cgt gca atg cgt aaa cag aag cca ctt ccc gta cct gcg att att   403
Glu Arg Ala Met Arg Lys Gln Lys Pro Leu Pro Val Pro Ala Ile Ile
                 90                  95                 100

ccg ttt ctg tct att gcg gct ttg gtg gcc tct gcg gct gtc ttg gtt   451
Pro Phe Leu Ser Ile Ala Ala Leu Val Ala Ser Ala Ala Val Leu Val
            105                 110                 115

ctg att att gtt cag tagctatgcg cattcatgag gat                    489
Leu Ile Ile Val Gln
        120
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0307070307

<210> 64
<211> 122
<212> PRT
<213> Corynebacterium glutamicum

<400> 64

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Val Asp Glu Arg Ser Arg Phe Ala Arg Ser Val Phe Pro Asp Gly Glu
  1               5                  10                  15

Glu Pro Asp Pro Arg Phe Thr Leu Ala Asn Glu Arg Thr Phe Leu Ala
             20                  25                  30

Trp Thr Arg Thr Ser Leu Ala Phe Leu Ala Gly Gly Ile Ala Phe Glu
         35                  40                  45

Ala Phe Gln Ile Ser Gly Leu Ser Asp Thr Val Arg Thr Thr Ile Ala
     50                  55                  60

Val Phe Ile Ile Ala Val Gly Met Ile Ile Ala Ala Gly Ala Ala Val
 65                  70                  75                  80

Arg Trp Met Asn Val Glu Arg Ala Met Arg Lys Gln Lys Pro Leu Pro
                 85                  90                  95

Val Pro Ala Ile Ile Pro Phe Leu Ser Ile Ala Ala Leu Val Ala Ser
            100                 105                 110

Ala Ala Val Leu Val Leu Ile Ile Val Gln
        115                 120
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<210> 65
<211> 489
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(466)
<223> FRXA00027

<400> 65
ttaggcaacg actccgaaac cttcaagaac gtgtggcact aacaattgcg gactatcctt 60

gggaactgtt ttagatttta ttcagggtag ggagattgtt gtg gat gaa cga agc 115
Val Asp Glu Arg Ser
1 5

cgg ttt gcg cgc agc gtt ttc ccg gac ggt gaa gaa cca gat cca cgt 163
Arg Phe Ala Arg Ser Val Phe Pro Asp Gly Glu Glu Pro Asp Pro Arg
10 15 20

ttc act ttg gcc aat gag cgc acg ttt cta gca tgg acg cgt acg tct 211
Phe Thr Leu Ala Asn Glu Arg Thr Phe Leu Ala Trp Thr Arg Thr Ser
25 30 35

ttg gcg ttt ctt gcc ggt ggt att gct ttt gag gcg ttc cag atc agt 259
Leu Ala Phe Leu Ala Gly Gly Ile Ala Phe Glu Ala Phe Gln Ile Ser
40 45 50

gga cta tcg gat act gtc cgt aca aca atc gcg gtt ttt atc att gcg 307
Gly Leu Ser Asp Thr Val Arg Thr Thr Ile Ala Val Phe Ile Ile Ala
55 60 65

gtt ggc atg atc att gcc gct ggt gct gcg gtg agg tgg atg aat gtg 355
Val Gly Met Ile Ile Ala Ala Gly Ala Ala Val Arg Trp Met Asn Val
70 75 80 85

gag cgt gca atg cgt aaa cag aag cca ctt ccc gta cct gcg att att 403
Glu Arg Ala Met Arg Lys Gln Lys Pro Leu Pro Val Pro Ala Ile Ile
90 95 100

ccg ttt ctg tct att gcg gct ttg gtg gcc tct gcg gct gtc ttg gtt 451
Pro Phe Leu Ser Ile Ala Ala Leu Val Ala Ser Ala Ala Val Leu Val
105 110 115

ctg att att gtt cag tagctatgcg cattcatgag gat 489
Leu Ile Ile Val Gln
120

<210> 66
<211> 122
<212> PRT
<213> Corynebacterium glutamicum

<400> 66
Val Asp Glu Arg Ser Arg Phe Ala Arg Ser Val Phe Pro Asp Gly Glu
1 5 10 15

Glu Pro Asp Pro Arg Phe Thr Leu Ala Asn Glu Arg Thr Phe Leu Ala
20 25 30

Trp Thr Arg Thr Ser Leu Ala Phe Leu Ala Gly Gly Ile Ala Phe Glu
35 40 45

Ala Phe Gln Ile Ser Gly Leu Ser Asp Thr Val Arg Thr Thr Ile Ala

```
     50                  55                  60

Val Phe Ile Ile Ala Val Gly Met Ile Ile Ala Ala Gly Ala Ala Val
 65                  70                  75                  80

Arg Trp Met Asn Val Glu Arg Ala Met Arg Lys Gln Lys Pro Leu Pro
                 85                  90                  95

Val Pro Ala Ile Ile Pro Phe Leu Ser Ile Ala Ala Leu Val Ala Ser
            100                 105                 110

Ala Ala Val Leu Val Leu Ile Ile Val Gln
        115                 120


<210> 67
<211> 2070
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2047)
<223> RXN00028

<400> 67
aaaagtcctg gccagaaaac tctctatact gtgcagcatg gcaccaacga tcaccgacat 60

ccatgttctg cttcgtcgcg gtgagcgaca atcagtgatc atg acc ctc act gcc   115
                                          Met Thr Leu Thr Ala
                                            1               5

tct tcc ttg gag gcc ggg aaa atg tct ttt agt ggc ggg tat atc gtg   163
Ser Ser Leu Glu Ala Gly Lys Met Ser Phe Ser Gly Gly Tyr Ile Val
                10                  15                  20

ggc gag acg atg atc ttc ctc gtc gat ccc gat gaa gtc gag ata cga   211
Gly Glu Thr Met Ile Phe Leu Val Asp Pro Asp Glu Val Glu Ile Arg
            25                  30                  35

cgc agc cct aac agc ctc cac gtc ctg cgt aac ggt agc gat att ctg   259
Arg Ser Pro Asn Ser Leu His Val Leu Arg Asn Gly Ser Asp Ile Leu
        40                  45                  50

cgc cgc aac gag cat cat tgc tgg gta ttt gag aat ttc aat aaa ccc   307
Arg Arg Asn Glu His His Cys Trp Val Phe Glu Asn Phe Asn Lys Pro
    55                  60                  65

att gac cca cct gtt cga ttg ggt cct cgg gat atc atc tgc ccg agc   355
Ile Asp Pro Pro Val Arg Leu Gly Pro Arg Asp Ile Ile Cys Pro Ser
70                  75                  80                  85

gcc ttg gcc tgg gtt ctt caa cag cat tcc atc tcc cgg tcc tta tcc   403
Ala Leu Ala Trp Val Leu Gln Gln His Ser Ile Ser Arg Ser Leu Ser
                90                  95                  100

cac cac ctt cac gcg gat aag atc act gcg gga gag att gct gga cgc   451
His His Leu His Ala Asp Lys Ile Thr Ala Gly Glu Ile Ala Gly Arg
            105                 110                 115

ccc acc tgg atc ctc cgt gag gaa cct act tca gga ggg cag gac cca   499
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Pro Thr Trp Ile Leu Arg Glu Glu Pro Thr Ser Gly Gly Gln Asp Pro
        120                 125                 130

agt cga ttg gtc agt ctt gaa atc gac cag gaa cac ggt gtc atc ctt   547
Ser Arg Leu Val Ser Leu Glu Ile Asp Gln Glu His Gly Val Ile Leu
    135                 140                 145

gca gtg gag act gga caa gaa cga ctc gaa gcc acg gag att tct ttt   595
Ala Val Glu Thr Gly Gln Glu Arg Leu Glu Ala Thr Glu Ile Ser Phe
150                 155                 160                 165

cct gac act ctt cct aat cct tcc tgg gac gga gcc tgg gaa cca ttc   643
Pro Asp Thr Leu Pro Asn Pro Ser Trp Asp Gly Ala Trp Glu Pro Phe
                170                 175                 180

cat tat cca gat tcg aca cca cac act gcc cct gat gtt gct gaa ata   691
His Tyr Pro Asp Ser Thr Pro His Thr Ala Pro Asp Val Ala Glu Ile
            185                 190                 195

ccc ggt tac att cag tca ctg ccg ccg cag tct gaa gat cct cgc aga   739
Pro Gly Tyr Ile Gln Ser Leu Pro Pro Gln Ser Glu Asp Pro Arg Arg
        200                 205                 210

cta cga gtc ttc gtc aat gag ata gca ctc gaa ggt gat ttc cct gac   787
Leu Arg Val Phe Val Asn Glu Ile Ala Leu Glu Gly Asp Phe Pro Asp
    215                 220                 225

tac cgt caa gga caa tct gtg cga ctt act ttg gga att agc tcc tcc   835
Tyr Arg Gln Gly Gln Ser Val Arg Leu Thr Leu Gly Ile Ser Ser Ser
230                 235                 240                 245

cct gtg cca ctc gaa gga atg aca acc aga cgc cgg ggc cgg gta cgc   883
Pro Val Pro Leu Glu Gly Met Thr Thr Arg Arg Arg Gly Arg Val Arg
                250                 255                 260

aac ctt ggg gaa gaa gct agt cca ggc gat gac ggt atg ccc cag tgg   931
Asn Leu Gly Glu Glu Ala Ser Pro Gly Asp Asp Gly Met Pro Gln Trp
            265                 270                 275

cca atc ctg ctc act ggt gat ggg tgg acg gcg ctg gcc tac act ccc   979
Pro Ile Leu Leu Thr Gly Asp Gly Trp Thr Ala Leu Ala Tyr Thr Pro
        280                 285                 290

atc cca aaa cgt gga gat gca gag atc cag ggg tgg ttt tat tat tcc   1027
Ile Pro Lys Arg Gly Asp Ala Glu Ile Gln Gly Trp Phe Tyr Tyr Ser
    295                 300                 305

gcc tac gga att gtt gat gtt ccc aca gat cta cgg gta gag cgt att   1075
Ala Tyr Gly Ile Val Asp Val Pro Thr Asp Leu Arg Val Glu Arg Ile
310                 315                 320                 325

ttc gct ggt atc ggc aca agt ggc acc aac gag cgt ttg tgg cag gag   1123
Phe Ala Gly Ile Gly Thr Ser Gly Thr Asn Glu Arg Leu Trp Gln Glu
                330                 335                 340

ata gac aat act tct tcg gct tat cac tcg gaa gat tgg tgg atc cgc   1171
Ile Asp Asn Thr Ser Ser Ala Tyr His Ser Glu Asp Trp Trp Ile Arg
            345                 350                 355

gat gtc gtt tta gac gtc acg ttg gat gga gct gtt ccg cct ccg ctt   1219
Asp Val Val Leu Asp Val Thr Leu Asp Gly Ala Val Pro Pro Pro Leu
```

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        360                 365                 370

aga cgt gac gtc ttc act gct gtc gat cct att gtg gcg ggt gac aaa   1267
Arg Arg Asp Val Phe Thr Ala Val Asp Pro Ile Val Ala Gly Asp Lys
    375                 380                 385

ttg tgg ctg tgt gac gtg cac ttt ccg gta gcc cgc tgc tgg gag acc   1315
Leu Trp Leu Cys Asp Val His Phe Pro Val Ala Arg Cys Trp Glu Thr
390                 395                 400                 405

acg acc ggc cga tac ttg ggg cag act tta gtc cca gca cca ctg cga   1363
Thr Thr Gly Arg Tyr Leu Gly Gln Thr Leu Val Pro Ala Pro Leu Arg
                410                 415                 420

gat cga tcg tac gtc ctt gag ctg cac agc gac caa caa tta gga gcc   1411
Asp Arg Ser Tyr Val Leu Glu Leu His Ser Asp Gln Gln Leu Gly Ala
            425                 430                 435

gta gcg gca agt ggg aag agt ggt tgg att ctc aca cct ggt caa gca   1459
Val Ala Ala Ser Gly Lys Ser Gly Trp Ile Leu Thr Pro Gly Gln Ala
        440                 445                 450

gta gcc act aaa gct cct gat tgg act cct ccc acc cgg gca acc gat   1507
Val Ala Thr Lys Ala Pro Asp Trp Thr Pro Pro Thr Arg Ala Thr Asp
    455                 460                 465

ctg cct cag gtc ccc tcc ccc tgg gag atc gtc gct gtc cgt ggc caa   1555
Leu Pro Gln Val Pro Ser Pro Trp Glu Ile Val Ala Val Arg Gly Gln
470                 475                 480                 485

ggt ctg ttt gag ctg cag gtg gaa act agt aga cgc acc gcc ctc ggt   1603
Gly Leu Phe Glu Leu Gln Val Glu Thr Ser Arg Arg Thr Ala Leu Gly
                490                 495                 500

cga gtt aat gcg acc ggt ggc gtc gac atc ggt gaa ctc ccg ccc aac   1651
Arg Val Asn Ala Thr Gly Gly Val Asp Ile Gly Glu Leu Pro Pro Asn
            505                 510                 515

ggc tat acc atc agt tct gtg gtt cag atc ggt gat gaa tac atc gtg   1699
Gly Tyr Thr Ile Ser Ser Val Val Gln Ile Gly Asp Glu Tyr Ile Val
        520                 525                 530

ggc agg tgg gta gag gaa tac cgg ctc aac tcc aaa ctg gag gtc att   1747
Gly Arg Trp Val Glu Glu Tyr Arg Leu Asn Ser Lys Leu Glu Val Ile
    535                 540                 545

tct acc aaa gag cta gat atc tcc gca tcc gga tgg aag agc aag ggg   1795
Ser Thr Lys Glu Leu Asp Ile Ser Ala Ser Gly Trp Lys Ser Lys Gly
550                 555                 560                 565

acg gtt gct tat ctg tcg gaa gac act cac ata tgt ttc ttc gac cag   1843
Thr Val Ala Tyr Leu Ser Glu Asp Thr His Ile Cys Phe Phe Asp Gln
                570                 575                 580

gtc agc ggg gcc gag ctt ccc agc ctg ggt atc gcc gag gga cac cag   1891
Val Ser Gly Ala Glu Leu Pro Ser Leu Gly Ile Ala Glu Gly His Gln
            585                 590                 595

ggc gag gtt atg tca gca act tct tca gag agc atc gtg ctt atc tac   1939
Gly Glu Val Met Ser Ala Thr Ser Ser Glu Ser Ile Val Leu Ile Tyr
        600                 605                 610
```

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cgg cgc aac ccg aac aat tca atg tcg att gtc ccg act tcc gtt gcc   1987
Arg Arg Asn Pro Asn Asn Ser Met Ser Ile Val Pro Thr Ser Val Ala
    615                 620                 625

acc tat gac aat ggc acc tgg acg act atg ccg cta cag gaa gct cca   2035
Thr Tyr Asp Asn Gly Thr Trp Thr Thr Met Pro Leu Gln Glu Ala Pro
630                 635                 640                 645

gcg gaa ctg tcc taaactgctc atagactgct gag                        2070
Ala Glu Leu Ser
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<210> 68
<211> 649
<212> PRT
<213> Corynebacterium glutamicum

<400> 68

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Met Thr Leu Thr Ala Ser Ser Leu Glu Ala Gly Lys Met Ser Phe Ser
  1               5                  10                  15

Gly Gly Tyr Ile Val Gly Glu Thr Met Ile Phe Leu Val Asp Pro Asp
             20                  25                  30

Glu Val Glu Ile Arg Arg Ser Pro Asn Ser Leu His Val Leu Arg Asn
         35                  40                  45

Gly Ser Asp Ile Leu Arg Arg Asn Glu His His Cys Trp Val Phe Glu
     50                  55                  60

Asn Phe Asn Lys Pro Ile Asp Pro Pro Val Arg Leu Gly Pro Arg Asp
 65                  70                  75                  80

Ile Ile Cys Pro Ser Ala Leu Ala Trp Val Leu Gln Gln His Ser Ile
                 85                  90                  95

Ser Arg Ser Leu Ser His His Leu His Ala Asp Lys Ile Thr Ala Gly
            100                 105                 110

Glu Ile Ala Gly Arg Pro Thr Trp Ile Leu Arg Glu Glu Pro Thr Ser
        115                 120                 125

Gly Gly Gln Asp Pro Ser Arg Leu Val Ser Leu Glu Ile Asp Gln Glu
    130                 135                 140

His Gly Val Ile Leu Ala Val Glu Thr Gly Gln Glu Arg Leu Glu Ala
145                 150                 155                 160

Thr Glu Ile Ser Phe Pro Asp Thr Leu Pro Asn Pro Ser Trp Asp Gly
                165                 170                 175

Ala Trp Glu Pro Phe His Tyr Pro Asp Ser Thr Pro His Thr Ala Pro
            180                 185                 190

Asp Val Ala Glu Ile Pro Gly Tyr Ile Gln Ser Leu Pro Pro Gln Ser
        195                 200                 205

Glu Asp Pro Arg Arg Leu Arg Val Phe Val Asn Glu Ile Ala Leu Glu
    210                 215                 220
```

```
Gly Asp Phe Pro Asp Tyr Arg Gln Gly Gln Ser Val Arg Leu Thr Leu
225                 230                 235                 240

Gly Ile Ser Ser Ser Pro Val Pro Leu Glu Gly Met Thr Thr Arg Arg
                245                 250                 255

Arg Gly Arg Val Arg Asn Leu Gly Glu Glu Ala Ser Pro Gly Asp Asp
            260                 265                 270

Gly Met Pro Gln Trp Pro Ile Leu Leu Thr Gly Asp Gly Trp Thr Ala
        275                 280                 285

Leu Ala Tyr Thr Pro Ile Pro Lys Arg Gly Asp Ala Glu Ile Gln Gly
    290                 295                 300

Trp Phe Tyr Tyr Ser Ala Tyr Gly Ile Val Asp Val Pro Thr Asp Leu
305                 310                 315                 320

Arg Val Glu Arg Ile Phe Ala Gly Ile Gly Thr Ser Gly Thr Asn Glu
                325                 330                 335

Arg Leu Trp Gln Glu Ile Asp Asn Thr Ser Ser Ala Tyr His Ser Glu
            340                 345                 350

Asp Trp Trp Ile Arg Asp Val Val Leu Asp Val Thr Leu Asp Gly Ala
        355                 360                 365

Val Pro Pro Pro Leu Arg Arg Asp Val Phe Thr Ala Val Asp Pro Ile
    370                 375                 380

Val Ala Gly Asp Lys Leu Trp Leu Cys Asp Val His Phe Pro Val Ala
385                 390                 395                 400

Arg Cys Trp Glu Thr Thr Thr Gly Arg Tyr Leu Gly Gln Thr Leu Val
                405                 410                 415

Pro Ala Pro Leu Arg Asp Arg Ser Tyr Val Leu Glu Leu His Ser Asp
            420                 425                 430

Gln Gln Leu Gly Ala Val Ala Ala Ser Gly Lys Ser Gly Trp Ile Leu
        435                 440                 445

Thr Pro Gly Gln Ala Val Ala Thr Lys Ala Pro Asp Trp Thr Pro Pro
    450                 455                 460

Thr Arg Ala Thr Asp Leu Pro Gln Val Pro Ser Pro Trp Glu Ile Val
465                 470                 475                 480

Ala Val Arg Gly Gln Gly Leu Phe Glu Leu Gln Val Glu Thr Ser Arg
                485                 490                 495

Arg Thr Ala Leu Gly Arg Val Asn Ala Thr Gly Gly Val Asp Ile Gly
            500                 505                 510

Glu Leu Pro Pro Asn Gly Tyr Thr Ile Ser Ser Val Val Gln Ile Gly
        515                 520                 525

Asp Glu Tyr Ile Val Gly Arg Trp Val Glu Glu Tyr Arg Leu Asn Ser
    530                 535                 540
```

```
Lys Leu Glu Val Ile Ser Thr Lys Glu Leu Asp Ile Ser Ala Ser Gly
545                 550                 555                 560

Trp Lys Ser Lys Gly Thr Val Ala Tyr Leu Ser Glu Asp Thr His Ile
                565                 570                 575

Cys Phe Phe Asp Gln Val Ser Gly Ala Glu Leu Pro Ser Leu Gly Ile
            580                 585                 590

Ala Glu Gly His Gln Gly Glu Val Met Ser Ala Thr Ser Ser Glu Ser
        595                 600                 605

Ile Val Leu Ile Tyr Arg Arg Asn Pro Asn Asn Ser Met Ser Ile Val
    610                 615                 620

Pro Thr Ser Val Ala Thr Tyr Asp Asn Gly Thr Trp Thr Thr Met Pro
625                 630                 635                 640

Leu Gln Glu Ala Pro Ala Glu Leu Ser
                645
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CONFIDENTIAL

<210> 69
<211> 2070
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2047)
<223> FRXA00028

<400> 69

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aaaagtcctg gccagaaaac tctctatact gtgcagcatg gcaccaacga tcaccgacat 60

ccatgttctg cttcgtcgcg gtgagcgaca atcagtgatc atg acc ctc act gcc   115
                                            Met Thr Leu Thr Ala
                                              1               5

tct tcc ttg gag gcc ggg aaa atg tct ttt agt ggc ggg tat atc gtg   163
Ser Ser Leu Glu Ala Gly Lys Met Ser Phe Ser Gly Gly Tyr Ile Val
                  10                  15                  20

ggc gag acg atg atc ttc ctc gtc gat ccc gat gaa gtc gag ata cga   211
Gly Glu Thr Met Ile Phe Leu Val Asp Pro Asp Glu Val Glu Ile Arg
              25                  30                  35

cgc agc cct aac agc ctc cac gtc ctg cgt aac ggt agc gat att ctg   259
Arg Ser Pro Asn Ser Leu His Val Leu Arg Asn Gly Ser Asp Ile Leu
          40                  45                  50

cgc cgc aac gag cat cat tgc tgg gta ttt gag aat ttc aat aaa ccc   307
Arg Arg Asn Glu His His Cys Trp Val Phe Glu Asn Phe Asn Lys Pro
      55                  60                  65

att gac cca cct gtt cga ttg ggt cct cgg gat atc atc tgc ccg agc   355
Ile Asp Pro Pro Val Arg Leu Gly Pro Arg Asp Ile Ile Cys Pro Ser
  70                  75                  80                  85

gcc ttg gcc tgg gtt ctt caa cag cat tcc atc tcc cgg tcc tta tcc   403
Ala Leu Ala Trp Val Leu Gln Gln His Ser Ile Ser Arg Ser Leu Ser
```

```
                    90                  95                 100

cac cac ctt cac gcg gat aag atc act gcg gga gag att gct gga cgc   451
His His Leu His Ala Asp Lys Ile Thr Ala Gly Glu Ile Ala Gly Arg
            105                 110                 115

ccc acc tgg atc ctc cgt gag gaa cct act tca gga ggg cag gac cca   499
Pro Thr Trp Ile Leu Arg Glu Glu Pro Thr Ser Gly Gly Gln Asp Pro
        120                 125                 130

agt cga ttg gtc agt ctt gaa atc gac cag gaa cac ggt gtc atc ctt   547
Ser Arg Leu Val Ser Leu Glu Ile Asp Gln Glu His Gly Val Ile Leu
    135                 140                 145

gca gtg gag act gga caa gaa cga ctc gaa gcc acg gag att tct ttt   595
Ala Val Glu Thr Gly Gln Glu Arg Leu Glu Ala Thr Glu Ile Ser Phe
150                 155                 160                 165

cct gac act ctt cct aat cct tcc tgg gac gga gcc tgg gaa cca ttc   643
Pro Asp Thr Leu Pro Asn Pro Ser Trp Asp Gly Ala Trp Glu Pro Phe
                170                 175                 180

cat tat cca gat tcg aca cca cac act gcc cct gat gtt gct gaa ata   691
His Tyr Pro Asp Ser Thr Pro His Thr Ala Pro Asp Val Ala Glu Ile
            185                 190                 195

ccc ggt tac att cag tca ctg ccg ccg cag tct gaa gat cct cgc aga   739
Pro Gly Tyr Ile Gln Ser Leu Pro Pro Gln Ser Glu Asp Pro Arg Arg
        200                 205                 210

cta cga gtc ttc gtc aat gag ata gca ctc gaa ggt gat ttc cct gac   787
Leu Arg Val Phe Val Asn Glu Ile Ala Leu Glu Gly Asp Phe Pro Asp
    215                 220                 225

tac cgt caa gga caa tct gtg cga ctt act ttg gga att agc tcc tcc   835
Tyr Arg Gln Gly Gln Ser Val Arg Leu Thr Leu Gly Ile Ser Ser Ser
230                 235                 240                 245

cct gtg cca ctc gaa gga atg aca acc aga cgc cgg ggc cgg gta cgc   883
Pro Val Pro Leu Glu Gly Met Thr Thr Arg Arg Arg Gly Arg Val Arg
                250                 255                 260

aac ctt ggg gaa gaa gct agt cca ggc gat gac ggt atg ccc cag tgg   931
Asn Leu Gly Glu Glu Ala Ser Pro Gly Asp Asp Gly Met Pro Gln Trp
            265                 270                 275

cca atc ctg ctc act ggt gat ggg tgg acg gcg ctg gcc tac act ccc   979
Pro Ile Leu Leu Thr Gly Asp Gly Trp Thr Ala Leu Ala Tyr Thr Pro
        280                 285                 290

atc cca aaa cgt gga gat gca gag atc cag ggg tgg ttt tat tat tcc   1027
Ile Pro Lys Arg Gly Asp Ala Glu Ile Gln Gly Trp Phe Tyr Tyr Ser
    295                 300                 305

gcc tac gga att gtt gat gtt ccc aca gat cta cgg gta gag cgt att   1075
Ala Tyr Gly Ile Val Asp Val Pro Thr Asp Leu Arg Val Glu Arg Ile
310                 315                 320                 325

ttc gct ggt atc ggc aca agt ggc acc aac gag cgt ttg tgg cag gag   1123
Phe Ala Gly Ile Gly Thr Ser Gly Thr Asn Glu Arg Leu Trp Gln Glu
                330                 335                 340
```

```
ata gac aat act tct tcg gct tat cac tcg gaa gat tgg tgg atc cgc   1171
Ile Asp Asn Thr Ser Ser Ala Tyr His Ser Glu Asp Trp Trp Ile Arg
            345                 350                 355

gat gtc gtt tta gac gtc acg ttg gat gga gct gtt ccg cct ccg ctt   1219
Asp Val Val Leu Asp Val Thr Leu Asp Gly Ala Val Pro Pro Pro Leu
        360                 365                 370

aga cgt gac gtc ttc act gct gtc gat cct att gtg gcg ggt gac aaa   1267
Arg Arg Asp Val Phe Thr Ala Val Asp Pro Ile Val Ala Gly Asp Lys
    375                 380                 385

ttg tgg ctg tgt gac gtg cac ttt ccg gta gcc cgc tgc tgg gag acc   1315
Leu Trp Leu Cys Asp Val His Phe Pro Val Ala Arg Cys Trp Glu Thr
390                 395                 400                 405

acg acc ggc cga tac ttg ggg cag act tta ktc cca gca cca ctg cga   1363
Thr Thr Gly Arg Tyr Leu Gly Gln Thr Leu Xaa Pro Ala Pro Leu Arg
                410                 415                 420

gat cga tcg tac gtc ctt gag ctg cac agc gac caa caa tta gga gcc   1411
Asp Arg Ser Tyr Val Leu Glu Leu His Ser Asp Gln Gln Leu Gly Ala
            425                 430                 435

gta gcg gca agt ggg aag agt ggt tgg att ctc aca cct ggt caa gca   1459
Val Ala Ala Ser Gly Lys Ser Gly Trp Ile Leu Thr Pro Gly Gln Ala
        440                 445                 450

gta gcc act aaa gct cct gat tgg act cct ccc acc cgg gca acc gat   1507
Val Ala Thr Lys Ala Pro Asp Trp Thr Pro Pro Thr Arg Ala Thr Asp
    455                 460                 465

ctg cct cag gtc ccc tcc ccc tgg gag atc gtc gct gtc cgt ggc caa   1555
Leu Pro Gln Val Pro Ser Pro Trp Glu Ile Val Ala Val Arg Gly Gln
470                 475                 480                 485

ggt ctg ttt gag ctg cag gtg gaa act agt aga cgc acc gcc ctc ggt   1603
Gly Leu Phe Glu Leu Gln Val Glu Thr Ser Arg Arg Thr Ala Leu Gly
                490                 495                 500

cga gtt aat gcg acc ggt ggc gtc gac atc ggt gaa ctc ccg ccc aac   1651
Arg Val Asn Ala Thr Gly Gly Val Asp Ile Gly Glu Leu Pro Pro Asn
            505                 510                 515

ggc tat acc atc agt tct gtg gtt cag atc ggt gat gaa tac atc gtg   1699
Gly Tyr Thr Ile Ser Ser Val Val Gln Ile Gly Asp Glu Tyr Ile Val
        520                 525                 530

ggc agg tgg gta gag gaa tac cgg ctc aac tcc aaa ctg gag gtc att   1747
Gly Arg Trp Val Glu Glu Tyr Arg Leu Asn Ser Lys Leu Glu Val Ile
    535                 540                 545

tct acc aaa gag cta gat atc tcc gca tcc gga tgg aag agc aag ggg   1795
Ser Thr Lys Glu Leu Asp Ile Ser Ala Ser Gly Trp Lys Ser Lys Gly
550                 555                 560                 565

acg gtt gct tat ctg tcg gaa gac act cac ata tgt ttc ttc gac cag   1843
Thr Val Ala Tyr Leu Ser Glu Asp Thr His Ile Cys Phe Phe Asp Gln
                570                 575                 580
```

```
gtc agc ggg gcc gag ctt ccc agc ctg ggt atc gcc gag gga cac cag   1891
Val Ser Gly Ala Glu Leu Pro Ser Leu Gly Ile Ala Glu Gly His Gln
            585                 590                 595

ggc gag gtt atg tca gca act tct tca gag agc atc gtg ctt atc tac   1939
Gly Glu Val Met Ser Ala Thr Ser Ser Glu Ser Ile Val Leu Ile Tyr
        600                 605                 610

cgg cgc aac ccg aac aat tca atg tcg att gtc ccg act tcc gtt gcc   1987
Arg Arg Asn Pro Asn Asn Ser Met Ser Ile Val Pro Thr Ser Val Ala
    615                 620                 625

acc tat gac aat ggc acc tgg acg act atg ccg cta cag gaa gct cca   2035
Thr Tyr Asp Asn Gly Thr Trp Thr Thr Met Pro Leu Gln Glu Ala Pro
630                 635                 640                 645

gcg gaa ctg tcc taaactgctc atagactgct gag                        2070
Ala Glu Leu Ser
```

<210> 70
<211> 649
<212> PRT
<213> Corynebacterium glutamicum

<400> 70

```
Met Thr Leu Thr Ala Ser Ser Leu Glu Ala Gly Lys Met Ser Phe Ser
  1               5                  10                  15

Gly Gly Tyr Ile Val Gly Glu Thr Met Ile Phe Leu Val Asp Pro Asp
            20                  25                  30

Glu Val Glu Ile Arg Arg Ser Pro Asn Ser Leu His Val Leu Arg Asn
        35                  40                  45

Gly Ser Asp Ile Leu Arg Arg Asn Glu His His Cys Trp Val Phe Glu
    50                  55                  60

Asn Phe Asn Lys Pro Ile Asp Pro Pro Val Arg Leu Gly Pro Arg Asp
65                  70                  75                  80

Ile Ile Cys Pro Ser Ala Leu Ala Trp Val Leu Gln Gln His Ser Ile
                85                  90                  95

Ser Arg Ser Leu Ser His His Leu His Ala Asp Lys Ile Thr Ala Gly
            100                 105                 110

Glu Ile Ala Gly Arg Pro Thr Trp Ile Leu Arg Glu Glu Pro Thr Ser
        115                 120                 125

Gly Gly Gln Asp Pro Ser Arg Leu Val Ser Leu Glu Ile Asp Gln Glu
    130                 135                 140

His Gly Val Ile Leu Ala Val Glu Thr Gly Gln Glu Arg Leu Glu Ala
145                 150                 155                 160

Thr Glu Ile Ser Phe Pro Asp Thr Leu Pro Asn Pro Ser Trp Asp Gly
                165                 170                 175

Ala Trp Glu Pro Phe His Tyr Pro Asp Ser Thr Pro His Thr Ala Pro
```

```
            180                 185                 190

Asp Val Ala Glu Ile Pro Gly Tyr Ile Gln Ser Leu Pro Pro Gln Ser
        195                 200                 205

Glu Asp Pro Arg Arg Leu Arg Val Phe Val Asn Glu Ile Ala Leu Glu
    210                 215                 220

Gly Asp Phe Pro Asp Tyr Arg Gln Gly Gln Ser Val Arg Leu Thr Leu
225                 230                 235                 240

Gly Ile Ser Ser Ser Pro Val Pro Leu Glu Gly Met Thr Thr Arg Arg
                245                 250                 255

Arg Gly Arg Val Arg Asn Leu Gly Glu Glu Ala Ser Pro Gly Asp Asp
            260                 265                 270

Gly Met Pro Gln Trp Pro Ile Leu Leu Thr Gly Asp Gly Trp Thr Ala
        275                 280                 285

Leu Ala Tyr Thr Pro Ile Pro Lys Arg Gly Asp Ala Glu Ile Gln Gly
    290                 295                 300

Trp Phe Tyr Tyr Ser Ala Tyr Gly Ile Val Asp Val Pro Thr Asp Leu
305                 310                 315                 320

Arg Val Glu Arg Ile Phe Ala Gly Ile Gly Thr Ser Gly Thr Asn Glu
                325                 330                 335

Arg Leu Trp Gln Glu Ile Asp Asn Thr Ser Ser Ala Tyr His Ser Glu
            340                 345                 350

Asp Trp Trp Ile Arg Asp Val Val Leu Asp Val Thr Leu Asp Gly Ala
        355                 360                 365

Val Pro Pro Pro Leu Arg Arg Asp Val Phe Thr Ala Val Asp Pro Ile
    370                 375                 380

Val Ala Gly Asp Lys Leu Trp Leu Cys Asp Val His Phe Pro Val Ala
385                 390                 395                 400

Arg Cys Trp Glu Thr Thr Thr Gly Arg Tyr Leu Gly Gln Thr Leu Xaa
                405                 410                 415

Pro Ala Pro Leu Arg Asp Arg Ser Tyr Val Leu Glu Leu His Ser Asp
            420                 425                 430

Gln Gln Leu Gly Ala Val Ala Ala Ser Gly Lys Ser Gly Trp Ile Leu
        435                 440                 445

Thr Pro Gly Gln Ala Val Ala Thr Lys Ala Pro Asp Trp Thr Pro Pro
    450                 455                 460

Thr Arg Ala Thr Asp Leu Pro Gln Val Pro Ser Pro Trp Glu Ile Val
465                 470                 475                 480

Ala Val Arg Gly Gln Gly Leu Phe Glu Leu Gln Val Glu Thr Ser Arg
                485                 490                 495

Arg Thr Ala Leu Gly Arg Val Asn Ala Thr Gly Gly Val Asp Ile Gly
            500                 505                 510
```

```
Glu Leu Pro Pro Asn Gly Tyr Thr Ile Ser Ser Val Val Gln Ile Gly
        515                 520                 525

Asp Glu Tyr Ile Val Gly Arg Trp Val Glu Glu Tyr Arg Leu Asn Ser
    530                 535                 540

Lys Leu Glu Val Ile Ser Thr Lys Glu Leu Asp Ile Ser Ala Ser Gly
545                 550                 555                 560

Trp Lys Ser Lys Gly Thr Val Ala Tyr Leu Ser Glu Asp Thr His Ile
                565                 570                 575

Cys Phe Phe Asp Gln Val Ser Gly Ala Glu Leu Pro Ser Leu Gly Ile
            580                 585                 590

Ala Glu Gly His Gln Gly Glu Val Met Ser Ala Thr Ser Ser Glu Ser
        595                 600                 605

Ile Val Leu Ile Tyr Arg Arg Asn Pro Asn Asn Ser Met Ser Ile Val
    610                 615                 620

Pro Thr Ser Val Ala Thr Tyr Asp Asn Gly Thr Trp Thr Thr Met Pro
625                 630                 635                 640

Leu Gln Glu Ala Pro Ala Glu Leu Ser
                645
```

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<210> 71
<211> 1458
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1435)
<223> RXN00033

<400> 71

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acacggattt aacgtgacgg tttctcagtg tttttagctt ctggcttttg gcttctgatg 60

ctttagcgct ggactcaaca tttaaaacaa aggtgaacac atg tca gta cag caa   115
                                            Met Ser Val Gln Gln
                                              1               5

agc ggg ttg ctc gaa cgt ctc ggc att ccc cga ccc ttg att ttc gga   163
Ser Gly Leu Leu Glu Arg Leu Gly Ile Pro Arg Pro Leu Ile Phe Gly
                 10                  15                  20

ttt atc ggc ctc acc atc ttc atg atc ggt gac ggt gtc gaa acc aac   211
Phe Ile Gly Leu Thr Ile Phe Met Ile Gly Asp Gly Val Glu Thr Asn
             25                  30                  35

att ttg gaa cct ttc ctc agt tcc gaa cat ggt ttc agc gtt tcc ctc   259
Ile Leu Glu Pro Phe Leu Ser Ser Glu His Gly Phe Ser Val Ser Leu
         40                  45                  50

gcg gga acc ctg gtg act gtt tac ggt gtt gcc gtg gcg atc gca gca   307
Ala Gly Thr Leu Val Thr Val Tyr Gly Val Ala Val Ala Ile Ala Ala
     55                  60                  65
```

```
ttc ttc gcg gcg gca ctt tcg gac ctg tgg ggt cca cga aaa gtg atg   355
Phe Phe Ala Ala Ala Leu Ser Asp Leu Trp Gly Pro Arg Lys Val Met
 70                  75                  80                  85

atc ctc ggt gct tca atc tgg atc gtc ttt gag ctg atc ttc ctc acc   403
Ile Leu Gly Ala Ser Ile Trp Ile Val Phe Glu Leu Ile Phe Leu Thr
                 90                  95                 100

gtg gca ctg acc acc gac cat act tgg ttg atc ttc ctt gct tat ggt   451
Val Ala Leu Thr Thr Asp His Thr Trp Leu Ile Phe Leu Ala Tyr Gly
            105                 110                 115

ctc cgc ggc ttt ggt tat cca ttc ttc gcc tac gga ttc ttg gtg tgg   499
Leu Arg Gly Phe Gly Tyr Pro Phe Phe Ala Tyr Gly Phe Leu Val Trp
        120                 125                 130

atc acc gca act gcc tca cct aag caa ttg ggt acc ggt gtg ggt tgg   547
Ile Thr Ala Thr Ala Ser Pro Lys Gln Leu Gly Thr Gly Val Gly Trp
    135                 140                 145

ttc tac gtt gcc ttc tct gca ggt ctt cct acc ttg ggt gcg ctg gtt   595
Phe Tyr Val Ala Phe Ser Ala Gly Leu Pro Thr Leu Gly Ala Leu Val
150                 155                 160                 165

gcc acc att tcc atg cag tac gtg aac ttg acc ttc tat gaa acg ttg   643
Ala Thr Ile Ser Met Gln Tyr Val Asn Leu Thr Phe Tyr Glu Thr Leu
                170                 175                 180

tgg gtt tcc ctc gtg ctg gtg gtc atc gga tcg ctc atc gca ctg ctg   691
Trp Val Ser Leu Val Leu Val Val Ile Gly Ser Leu Ile Ala Leu Leu
            185                 190                 195

gga gtg aag gaa cgt cgc gga cgc cac cca ctg gtt gcc aac ccc gac   739
Gly Val Lys Glu Arg Arg Gly Arg His Pro Leu Val Ala Asn Pro Asp
        200                 205                 210

gat gtg aag caa aca ctt ggc cag ggc ttc aaa ctt ctg cgc aat gat   787
Asp Val Lys Gln Thr Leu Gly Gln Gly Phe Lys Leu Leu Arg Asn Asp
    215                 220                 225

cga cgt gca cgt ttt gtc acc tac atc cgc acc atc aac tcc att ccg   835
Arg Arg Ala Arg Phe Val Thr Tyr Ile Arg Thr Ile Asn Ser Ile Pro
230                 235                 240                 245

acc tac gcg atg gct gtg ttc ttc cca tca ttt ttc act gac gat ctg   883
Thr Tyr Ala Met Ala Val Phe Phe Pro Ser Phe Phe Thr Asp Asp Leu
                250                 255                 260

aag tgg cag cta agc tgg ttc ctc atc ctc acc act gta att tac gca   931
Lys Trp Gln Leu Ser Trp Phe Leu Ile Leu Thr Thr Val Ile Tyr Ala
            265                 270                 275

gtc aac ctg ccg ttc aat cct ttc ttc ggt agc ttc ggc gac cgc cac   979
Val Asn Leu Pro Phe Asn Pro Phe Phe Gly Ser Phe Gly Asp Arg His
        280                 285                 290

ggt tgg gca cga act gtg ttc tgg ggc gga tca atc ggt ggc gca gtc   1027
Gly Trp Ala Arg Thr Val Phe Trp Gly Gly Ser Ile Gly Gly Ala Val
    295                 300                 305
```

```
acc ctc gcg ttg gtt tac ttc att ccg atg ttc ggc gtt cag gct ggc   1075
Thr Leu Ala Leu Val Tyr Phe Ile Pro Met Phe Gly Val Gln Ala Gly
310                 315                 320                 325

atg tcc aac ggt gtc gtt ttc gga atc acc atc gca gcc ggc gca ctc   1123
Met Ser Asn Gly Val Val Phe Gly Ile Thr Ile Ala Ala Gly Ala Leu
                330                 335                 340

ttt ggt gtg tcc ctc gcg ggc ttc gtg cca ctt tcc gca atc gct gtc   1171
Phe Gly Val Ser Leu Ala Gly Phe Val Pro Leu Ser Ala Ile Ala Val
            345                 350                 355

tcc ctt gat ccc aag cac ccc ggc gca gcg atg gcc aca tac aac ctc   1219
Ser Leu Asp Pro Lys His Pro Gly Ala Ala Met Ala Thr Tyr Asn Leu
        360                 365                 370

ggc gtt ggt ggc gct gta gct gtg gga ccg ctc ctg gtt gca gtc ttc   1267
Gly Val Gly Gly Ala Val Ala Val Gly Pro Leu Leu Val Ala Val Phe
    375                 380                 385

cac cca ctg att ggt cca acc gga ttg atc ctg gtc atg atc gcc ctc   1315
His Pro Leu Ile Gly Pro Thr Gly Leu Ile Leu Val Met Ile Ala Leu
390                 395                 400                 405

tac ctg ctc tcc ggt tgg atg act ctt caa ctt cgc ggc acc caa cca   1363
Tyr Leu Leu Ser Gly Trp Met Thr Leu Gln Leu Arg Gly Thr Gln Pro
                410                 415                 420

gga ttc gac gga gtg cca gca ctt gct gaa gac gcc cac atc gaa gac   1411
Gly Phe Asp Gly Val Pro Ala Leu Ala Glu Asp Ala His Ile Glu Asp
            425                 430                 435

ctt gca gat gta aac gca aac gcc taactgtttt tcgagctaaa ccc         1458
Leu Ala Asp Val Asn Ala Asn Ala
        440                 445
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<210> 72
<211> 445
<212> PRT
<213> Corynebacterium glutamicum

<400> 72

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Met Ser Val Gln Gln Ser Gly Leu Leu Glu Arg Leu Gly Ile Pro Arg
  1               5                  10                  15

Pro Leu Ile Phe Gly Phe Ile Gly Leu Thr Ile Phe Met Ile Gly Asp
             20                  25                  30

Gly Val Glu Thr Asn Ile Leu Glu Pro Phe Leu Ser Ser Glu His Gly
         35                  40                  45

Phe Ser Val Ser Leu Ala Gly Thr Leu Val Thr Val Tyr Gly Val Ala
     50                  55                  60

Val Ala Ile Ala Ala Phe Phe Ala Ala Ala Leu Ser Asp Leu Trp Gly
 65                  70                  75                  80

Pro Arg Lys Val Met Ile Leu Gly Ala Ser Ile Trp Ile Val Phe Glu
                 85                  90                  95
```

```
Leu Ile Phe Leu Thr Val Ala Leu Thr Thr Asp His Thr Trp Leu Ile
            100                 105                 110

Phe Leu Ala Tyr Gly Leu Arg Gly Phe Gly Tyr Pro Phe Phe Ala Tyr
        115                 120                 125

Gly Phe Leu Val Trp Ile Thr Ala Thr Ala Ser Pro Lys Gln Leu Gly
    130                 135                 140

Thr Gly Val Gly Trp Phe Tyr Val Ala Phe Ser Ala Gly Leu Pro Thr
145                 150                 155                 160

Leu Gly Ala Leu Val Ala Thr Ile Ser Met Gln Tyr Val Asn Leu Thr
                165                 170                 175

Phe Tyr Glu Thr Leu Trp Val Ser Leu Val Leu Val Val Ile Gly Ser
            180                 185                 190

Leu Ile Ala Leu Leu Gly Val Lys Glu Arg Arg Gly Arg His Pro Leu
        195                 200                 205

Val Ala Asn Pro Asp Asp Val Lys Gln Thr Leu Gly Gln Gly Phe Lys
    210                 215                 220

Leu Leu Arg Asn Asp Arg Arg Ala Arg Phe Val Thr Tyr Ile Arg Thr
225                 230                 235                 240

Ile Asn Ser Ile Pro Thr Tyr Ala Met Ala Val Phe Phe Pro Ser Phe
                245                 250                 255

Phe Thr Asp Asp Leu Lys Trp Gln Leu Ser Trp Phe Leu Ile Leu Thr
            260                 265                 270

Thr Val Ile Tyr Ala Val Asn Leu Pro Phe Asn Pro Phe Phe Gly Ser
        275                 280                 285

Phe Gly Asp Arg His Gly Trp Ala Arg Thr Val Phe Trp Gly Gly Ser
    290                 295                 300

Ile Gly Gly Ala Val Thr Leu Ala Leu Val Tyr Phe Ile Pro Met Phe
305                 310                 315                 320

Gly Val Gln Ala Gly Met Ser Asn Gly Val Val Phe Gly Ile Thr Ile
                325                 330                 335

Ala Ala Gly Ala Leu Phe Gly Val Ser Leu Ala Gly Phe Val Pro Leu
            340                 345                 350

Ser Ala Ile Ala Val Ser Leu Asp Pro Lys His Pro Gly Ala Ala Met
        355                 360                 365

Ala Thr Tyr Asn Leu Gly Val Gly Gly Ala Val Ala Val Gly Pro Leu
    370                 375                 380

Leu Val Ala Val Phe His Pro Leu Ile Gly Pro Thr Gly Leu Ile Leu
385                 390                 395                 400

Val Met Ile Ala Leu Tyr Leu Leu Ser Gly Trp Met Thr Leu Gln Leu
                405                 410                 415

Arg Gly Thr Gln Pro Gly Phe Asp Gly Val Pro Ala Leu Ala Glu Asp
```

```
            420                 425                 430

Ala His Ile Glu Asp Leu Ala Asp Val Asn Ala Asn Ala
        435                 440                 445


<210> 73
<211> 873
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(850)
<223> RXN00056

<400> 73
atatgaattt aataatagat tccgaacgaa atcggtgtta gcgtctgtgc tgaaacaatc 60

taatcgcgtt tcaggacacc tacatgatca ggagctcttt ttg tta aac aga gtc   115
                                          Leu Leu Asn Arg Val
                                            1               5

agt cgt att gca ggc gct tct gca atc aca cta tgc atc ggc tta acc   163
Ser Arg Ile Ala Gly Ala Ser Ala Ile Thr Leu Cys Ile Gly Leu Thr
                  10                  15                  20

aca ata cta agc cct act tcc act gca caa agc ctc gaa cag atc acc   211
Thr Ile Leu Ser Pro Thr Ser Thr Ala Gln Ser Leu Glu Gln Ile Thr
              25                  30                  35

cct tta cct gaa tct gca atc gac ctc aac gcc gag att cac gta aac   259
Pro Leu Pro Glu Ser Ala Ile Asp Leu Asn Ala Glu Ile His Val Asn
          40                  45                  50

aca agc gac att tca gct gaa cag atc ctt ggt gct caa gat gaa atc   307
Thr Ser Asp Ile Ser Ala Glu Gln Ile Leu Gly Ala Gln Asp Glu Ile
      55                  60                  65

aca act atg tac gat tct cat gac ccc tac gag tac ttc gat acc ctc   355
Thr Thr Met Tyr Asp Ser His Asp Pro Tyr Glu Tyr Phe Asp Thr Leu
  70                  75                  80                  85

acc gac atc gaa cag cgt tca ata ata gca gcg ctt aaa cgg gat ccg   403
Thr Asp Ile Glu Gln Arg Ser Ile Ile Ala Ala Leu Lys Arg Asp Pro
                  90                  95                 100

agt tca ctc caa caa cgc caa gaa acc cgt ctc gcg gca cag tcc gac   451
Ser Ser Leu Gln Gln Arg Gln Glu Thr Arg Leu Ala Ala Gln Ser Asp
             105                 110                 115

ccc tac aaa att tac ata tca ggc ctc gaa atg ctt tca tgc atc aat   499
Pro Tyr Lys Ile Tyr Ile Ser Gly Leu Glu Met Leu Ser Cys Ile Asn
         120                 125                 130

cta gtt gat gtt gta tca tgc ggg att gca aac caa gca gca acc aaa   547
Leu Val Asp Val Val Ser Cys Gly Ile Ala Asn Gln Ala Ala Thr Lys
     135                 140                 145

gca aat aat gag gct gtc gca cga tac cca ggc gat tcc ctt cgc aac   595
Ala Asn Asn Glu Ala Val Ala Arg Tyr Pro Gly Asp Ser Leu Arg Asn
```

```
150                 155                 160                 165

ggc aaa ggc gat gca ttt cgg cat tgc tca tgg aac gct ctg atg acg   643
Gly Lys Gly Asp Ala Phe Arg His Cys Ser Trp Asn Ala Leu Met Thr
                170                 175                 180

ata cga atc ggg agc aat gga gct gaa aga att gca aca aac cac gag   691
Ile Arg Ile Gly Ser Asn Gly Ala Glu Arg Ile Ala Thr Asn His Glu
            185                 190                 195

aca atc ggg gac ggt ccg gcc gat gaa aat gca atg gac cta ttc aat   739
Thr Ile Gly Asp Gly Pro Ala Asp Glu Asn Ala Met Asp Leu Phe Asn
        200                 205                 210

aat gca caa ggc cga cag atc gga gcc gga ttc att aat agt aag gat   787
Asn Ala Gln Gly Arg Gln Ile Gly Ala Gly Phe Ile Asn Ser Lys Asp
    215                 220                 225

gaa act agc gcg ctc gcg ata tgc gcg ctg tgg aca aat ctc ggt aga   835
Glu Thr Ser Ala Leu Ala Ile Cys Ala Leu Trp Thr Asn Leu Gly Arg
230                 235                 240                 245

cta aaa act cta aaa taagcaaggt gccctctgat gct                    873
Leu Lys Thr Leu Lys
                250
```

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<210> 74
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 74

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Leu Leu Asn Arg Val Ser Arg Ile Ala Gly Ala Ser Ala Ile Thr Leu
  1               5                  10                  15

Cys Ile Gly Leu Thr Thr Ile Leu Ser Pro Thr Ser Thr Ala Gln Ser
             20                  25                  30

Leu Glu Gln Ile Thr Pro Leu Pro Glu Ser Ala Ile Asp Leu Asn Ala
         35                  40                  45

Glu Ile His Val Asn Thr Ser Asp Ile Ser Ala Glu Gln Ile Leu Gly
     50                  55                  60

Ala Gln Asp Glu Ile Thr Thr Met Tyr Asp Ser His Asp Pro Tyr Glu
 65                  70                  75                  80

Tyr Phe Asp Thr Leu Thr Asp Ile Glu Gln Arg Ser Ile Ile Ala Ala
                 85                  90                  95

Leu Lys Arg Asp Pro Ser Ser Leu Gln Gln Arg Gln Glu Thr Arg Leu
            100                 105                 110

Ala Ala Gln Ser Asp Pro Tyr Lys Ile Tyr Ile Ser Gly Leu Glu Met
        115                 120                 125

Leu Ser Cys Ile Asn Leu Val Asp Val Val Ser Cys Gly Ile Ala Asn
    130                 135                 140

Gln Ala Ala Thr Lys Ala Asn Asn Glu Ala Val Ala Arg Tyr Pro Gly
```

```
145                 150                 155                 160

Asp Ser Leu Arg Asn Gly Lys Gly Asp Ala Phe Arg His Cys Ser Trp
                165                 170                 175

Asn Ala Leu Met Thr Ile Arg Ile Gly Ser Asn Gly Ala Glu Arg Ile
            180                 185                 190

Ala Thr Asn His Glu Thr Ile Gly Asp Gly Pro Ala Asp Glu Asn Ala
        195                 200                 205

Met Asp Leu Phe Asn Asn Ala Gln Gly Arg Gln Ile Gly Ala Gly Phe
    210                 215                 220

Ile Asn Ser Lys Asp Glu Thr Ser Ala Leu Ala Ile Cys Ala Leu Trp
225                 230                 235                 240

Thr Asn Leu Gly Arg Leu Lys Thr Leu Lys
                245                 250
```

<210> 75
<211> 873
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(850)
<223> FRXA00056

<400> 75

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atatgaattt aataatagat tccgaacgaa atcggtgtta gcgtctgtgc tgaaacaatc 60

taatcgcgtt tcaggacacc tacatgatca ggagctcttt ttg tta aac aga gtc   115
                                              Leu Leu Asn Arg Val
                                                1               5

agt cgt att gca ggc gct tct gca atc aca cta tgc atc ggc tta acc   163
Ser Arg Ile Ala Gly Ala Ser Ala Ile Thr Leu Cys Ile Gly Leu Thr
                10                  15                  20

aca ata cta agc cct act tcc act gca caa agc ctc gaa cag atc acc   211
Thr Ile Leu Ser Pro Thr Ser Thr Ala Gln Ser Leu Glu Gln Ile Thr
            25                  30                  35

cct tta cct gaa tct gca atc gac ctc aac gcc gag att cac gta aac   259
Pro Leu Pro Glu Ser Ala Ile Asp Leu Asn Ala Glu Ile His Val Asn
        40                  45                  50

aca agc gac att tca gct gaa cag atc ctt ggt gct caa gat gaa atc   307
Thr Ser Asp Ile Ser Ala Glu Gln Ile Leu Gly Ala Gln Asp Glu Ile
    55                  60                  65

aca act atg tac gat tct cat gac ccc tac gag tac ttc gat acc ctc   355
Thr Thr Met Tyr Asp Ser His Asp Pro Tyr Glu Tyr Phe Asp Thr Leu
70                  75                  80                  85

acc gac atc gaa cag cgt tca ata ata gca gcg ctt aaa cgg gat ccg   403
Thr Asp Ile Glu Gln Arg Ser Ile Ile Ala Ala Leu Lys Arg Asp Pro
                90                  95                  100
```

```
agt tca ctc caa caa cgc caa gaa acc cgt ctc gcg gca cag tcc gac   451
Ser Ser Leu Gln Gln Arg Gln Glu Thr Arg Leu Ala Ala Gln Ser Asp
            105                 110                 115

ccc tac aaa att tac ata tca ggc ctc gaa atg ctt tca tgc atc aat   499
Pro Tyr Lys Ile Tyr Ile Ser Gly Leu Glu Met Leu Ser Cys Ile Asn
        120                 125                 130

cta gtt gat gtt gta tca tgc ggg att gca aac caa gca gca acc aaa   547
Leu Val Asp Val Val Ser Cys Gly Ile Ala Asn Gln Ala Ala Thr Lys
    135                 140                 145

gca aat aat gag gct gtc gca cga tac cca ggc gat tcc ctt cgc aac   595
Ala Asn Asn Glu Ala Val Ala Arg Tyr Pro Gly Asp Ser Leu Arg Asn
150                 155                 160                 165

ggc aaa ggc gat gca ttt cgg cat tgc tca tgg aac gct ctg atg acg   643
Gly Lys Gly Asp Ala Phe Arg His Cys Ser Trp Asn Ala Leu Met Thr
                170                 175                 180

ata cga atc ggg agc aat gga gct gaa aga att gca aca aac cac gag   691
Ile Arg Ile Gly Ser Asn Gly Ala Glu Arg Ile Ala Thr Asn His Glu
            185                 190                 195

aca atc ggg gac ggt ccg gcc gat gaa aat gca atg gac cta ttc aat   739
Thr Ile Gly Asp Gly Pro Ala Asp Glu Asn Ala Met Asp Leu Phe Asn
        200                 205                 210

aat gca caa ggc cga cag atc gga gcc gga ttc att aat agt aag gat   787
Asn Ala Gln Gly Arg Gln Ile Gly Ala Gly Phe Ile Asn Ser Lys Asp
    215                 220                 225

gaa act agc gcg ctc gcg ata tgc gcg ctg tgg aca aat ctc ggt aga   835
Glu Thr Ser Ala Leu Ala Ile Cys Ala Leu Trp Thr Asn Leu Gly Arg
230                 235                 240                 245

cta aaa act cta aaa taagcaaggt gccctctgat gct                    873
Leu Lys Thr Leu Lys
                250
```

<210> 76
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 76

```
Leu Leu Asn Arg Val Ser Arg Ile Ala Gly Ala Ser Ala Ile Thr Leu
  1               5                  10                  15

Cys Ile Gly Leu Thr Thr Ile Leu Ser Pro Thr Ser Thr Ala Gln Ser
             20                  25                  30

Leu Glu Gln Ile Thr Pro Leu Pro Glu Ser Ala Ile Asp Leu Asn Ala
         35                  40                  45

Glu Ile His Val Asn Thr Ser Asp Ile Ser Ala Glu Gln Ile Leu Gly
     50                  55                  60

Ala Gln Asp Glu Ile Thr Thr Met Tyr Asp Ser His Asp Pro Tyr Glu
```

```
 65                  70                  75                  80

Tyr Phe Asp Thr Leu Thr Asp Ile Glu Gln Arg Ser Ile Ile Ala Ala
                 85                  90                  95

Leu Lys Arg Asp Pro Ser Ser Leu Gln Gln Arg Gln Glu Thr Arg Leu
            100                 105                 110

Ala Ala Gln Ser Asp Pro Tyr Lys Ile Tyr Ile Ser Gly Leu Glu Met
        115                 120                 125

Leu Ser Cys Ile Asn Leu Val Asp Val Val Ser Cys Gly Ile Ala Asn
    130                 135                 140

Gln Ala Ala Thr Lys Ala Asn Asn Glu Ala Val Ala Arg Tyr Pro Gly
145                 150                 155                 160

Asp Ser Leu Arg Asn Gly Lys Gly Asp Ala Phe Arg His Cys Ser Trp
                165                 170                 175

Asn Ala Leu Met Thr Ile Arg Ile Gly Ser Asn Gly Ala Glu Arg Ile
            180                 185                 190

Ala Thr Asn His Glu Thr Ile Gly Asp Gly Pro Ala Asp Glu Asn Ala
        195                 200                 205

Met Asp Leu Phe Asn Asn Ala Gln Gly Arg Gln Ile Gly Ala Gly Phe
    210                 215                 220

Ile Asn Ser Lys Asp Glu Thr Ser Ala Leu Ala Ile Cys Ala Leu Trp
225                 230                 235                 240

Thr Asn Leu Gly Arg Leu Lys Thr Leu Lys
                245                 250


<210> 77
<211> 609
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(586)
<223> RXN00067

<400> 77
ggaatcccgc atgttgggct ccagttgggg actgactctg tttttgatca ttttgacgcc 60

aatcattatt ttcctcactt tcagctaaaa ggaccatgca atg gta gac gct cag   115
                                          Met Val Asp Ala Gln
                                            1               5

cgc ccc aaa gca ggc atc ttc ggt agc cac aca gaa gaa aca tgg gtg   163
Arg Pro Lys Ala Gly Ile Phe Gly Ser His Thr Glu Glu Thr Trp Val
                10                  15                  20

tgg ctc ggt aat gaa ctt ttc gac gag tcc ggc gag gtc atc gcc gac   211
Trp Leu Gly Asn Glu Leu Phe Asp Glu Ser Gly Glu Val Ile Ala Asp
            25                  30                  35
```

```
gtt cgc tcc gac gtc ctc tac gtg gat cgc gaa cga cta ctc atc gaa   259
Val Arg Ser Asp Val Leu Tyr Val Asp Arg Glu Arg Leu Leu Ile Glu
        40                  45                  50

tcc acc ccc ggc acc atg cgt ttt cgt tgc cgc gca aca ctg tcc ggg   307
Ser Thr Pro Gly Thr Met Arg Phe Arg Cys Arg Ala Thr Leu Ser Gly
     55                  60                  65

ggt gag gtc tat acg atg act cag aat tct ttc act gtg ggg gat ctc   355
Gly Glu Val Tyr Thr Met Thr Gln Asn Ser Phe Thr Val Gly Asp Leu
 70                  75                  80                  85

act gcg gtg tgc ggg cgc cgg acg tat tca cta aaa agg gtg tcg ccg   403
Thr Ala Val Cys Gly Arg Arg Thr Tyr Ser Leu Lys Arg Val Ser Pro
                 90                  95                 100

tgg cgt aaa gaa cgc ctg atc acc aac aat ggg gtg gaa gtg gcg cgg   451
Trp Arg Lys Glu Arg Leu Ile Thr Asn Asn Gly Val Glu Val Ala Arg
            105                 110                 115

ctt cgc ccg atg acc agc ggt aaa gtc gaa ttc att gtg ggc acc gcg   499
Leu Arg Pro Met Thr Ser Gly Lys Val Glu Phe Ile Val Gly Thr Ala
        120                 125                 130

ggc agc gag gcg ttg ccg ttc gtc gac gca gta ttt ttg agc tgg gcg   547
Gly Ser Glu Ala Leu Pro Phe Val Asp Ala Val Phe Leu Ser Trp Ala
    135                 140                 145

tgc gtc ctg gtg gat tcg gcc gtg cgc cgg ccg aaa att taaaagcttt    596
Cys Val Leu Val Asp Ser Ala Val Arg Arg Pro Lys Ile
150                 155                 160

ttgcttatcg acg                                                   609


<210> 78
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 78
Met Val Asp Ala Gln Arg Pro Lys Ala Gly Ile Phe Gly Ser His Thr
  1               5                  10                  15

Glu Glu Thr Trp Val Trp Leu Gly Asn Glu Leu Phe Asp Glu Ser Gly
             20                  25                  30

Glu Val Ile Ala Asp Val Arg Ser Asp Val Leu Tyr Val Asp Arg Glu
         35                  40                  45

Arg Leu Leu Ile Glu Ser Thr Pro Gly Thr Met Arg Phe Arg Cys Arg
     50                  55                  60

Ala Thr Leu Ser Gly Gly Glu Val Tyr Thr Met Thr Gln Asn Ser Phe
 65                  70                  75                  80

Thr Val Gly Asp Leu Thr Ala Val Cys Gly Arg Arg Thr Tyr Ser Leu
                 85                  90                  95

Lys Arg Val Ser Pro Trp Arg Lys Glu Arg Leu Ile Thr Asn Asn Gly
            100                 105                 110
```

```
Val Glu Val Ala Arg Leu Arg Pro Met Thr Ser Gly Lys Val Glu Phe
        115                 120                 125

Ile Val Gly Thr Ala Gly Ser Glu Ala Leu Pro Phe Val Asp Ala Val
    130                 135                 140

Phe Leu Ser Trp Ala Cys Val Leu Val Asp Ser Ala Val Arg Arg Pro
145                 150                 155                 160

Lys Ile
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<210> 79
<211> 609
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(586)
<223> FRXA00067

<400> 79

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ggaatcccgc atgttgggct ccagttgggg actgactctg tttttgatca ttttgacgcc 60

aatcattatt ttcctcactt tcagctaaaa ggaccatgca atg gta gac gct cag   115
                                            Met Val Asp Ala Gln
                                              1               5

cgc ccc aaa gca ggc atc ttc ggt agc cac aca gaa gaa aca tgg gtg   163
Arg Pro Lys Ala Gly Ile Phe Gly Ser His Thr Glu Glu Thr Trp Val
                  10                  15                  20

tgg ctc ggt aat gaa ctt ttc gac gag tcc ggc gag gtc atc gcc gac   211
Trp Leu Gly Asn Glu Leu Phe Asp Glu Ser Gly Glu Val Ile Ala Asp
              25                  30                  35

gtt cgc tcc gac gtc ctc tac gtg gat cgc gaa cga cta ctc atc gaa   259
Val Arg Ser Asp Val Leu Tyr Val Asp Arg Glu Arg Leu Leu Ile Glu
          40                  45                  50

tcc acc ccc ggc acc atg cgt ttt cgt tgc cgc gca aca ctg tcc ggg   307
Ser Thr Pro Gly Thr Met Arg Phe Arg Cys Arg Ala Thr Leu Ser Gly
      55                  60                  65

ggt gag gtc tat acg atg act cag aat tct ttc act gtg ggg gat ctc   355
Gly Glu Val Tyr Thr Met Thr Gln Asn Ser Phe Thr Val Gly Asp Leu
  70                  75                  80                  85

act gcg gtg tgc ggg cgc cgg acg tat tca cta aaa agg gtg tcg ccg   403
Thr Ala Val Cys Gly Arg Arg Thr Tyr Ser Leu Lys Arg Val Ser Pro
                  90                  95                 100

tgg cgt aaa gaa cgc ctg atc acc aac aat ggg gtg gaa gtg gcg cgg   451
Trp Arg Lys Glu Arg Leu Ile Thr Asn Asn Gly Val Glu Val Ala Arg
              105                 110                 115

ctt cgc ccg atg acc agc ggt aaa gtc gaa ttc att gtg ggc acc gcg   499
Leu Arg Pro Met Thr Ser Gly Lys Val Glu Phe Ile Val Gly Thr Ala
```

```
        120                 125                 130

ggc agc gag gcg ttg ccg ttc gtc gac gca gta ttt ttg agc tgg gcg   547
Gly Ser Glu Ala Leu Pro Phe Val Asp Ala Val Phe Leu Ser Trp Ala
    135                 140                 145

tgc gtc ctg gtg gat tcg gcc gtg cgc cgg ccg aaa att taaaagcttt   596
Cys Val Leu Val Asp Ser Ala Val Arg Arg Pro Lys Ile
150                 155                 160

ttgcttatcg acg                                                  609


<210> 80
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 80
Met Val Asp Ala Gln Arg Pro Lys Ala Gly Ile Phe Gly Ser His Thr
  1               5                  10                  15

Glu Glu Thr Trp Val Trp Leu Gly Asn Glu Leu Phe Asp Glu Ser Gly
             20                  25                  30

Glu Val Ile Ala Asp Val Arg Ser Asp Val Leu Tyr Val Asp Arg Glu
         35                  40                  45

Arg Leu Leu Ile Glu Ser Thr Pro Gly Thr Met Arg Phe Arg Cys Arg
     50                  55                  60

Ala Thr Leu Ser Gly Gly Glu Val Tyr Thr Met Thr Gln Asn Ser Phe
 65                  70                  75                  80

Thr Val Gly Asp Leu Thr Ala Val Cys Gly Arg Arg Thr Tyr Ser Leu
                 85                  90                  95

Lys Arg Val Ser Pro Trp Arg Lys Glu Arg Leu Ile Thr Asn Asn Gly
            100                 105                 110

Val Glu Val Ala Arg Leu Arg Pro Met Thr Ser Gly Lys Val Glu Phe
        115                 120                 125

Ile Val Gly Thr Ala Gly Ser Glu Ala Leu Pro Phe Val Asp Ala Val
    130                 135                 140

Phe Leu Ser Trp Ala Cys Val Leu Val Asp Ser Ala Val Arg Arg Pro
145                 150                 155                 160

Lys Ile


<210> 81
<211> 1485
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1462)
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<223> RXN00077

<400> 81

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ctaaattgtt ttaacgcgtg aagcagtccc cgcccgattt attcgaggcg gggactttcg 60

ctttccggga taaaaattgc aacgcactac actgagcagt atg aat gat gag aat   115
                                            Met Asn Asp Glu Asn
                                              1               5

att caa agc tcc aac tat cag cca ttc ccg agt ttt gac gat tgg aaa   163
Ile Gln Ser Ser Asn Tyr Gln Pro Phe Pro Ser Phe Asp Asp Trp Lys
                 10                  15                  20

cag atc gag gtg tcg ctc tta gat gtc atc gaa tcc tca cgc cat ttt   211
Gln Ile Glu Val Ser Leu Leu Asp Val Ile Glu Ser Ser Arg His Phe
             25                  30                  35

tct gat ttg aaa gat agc act gat cgt tct gcg tta gat gct gcg cta   259
Ser Asp Leu Lys Asp Ser Thr Asp Arg Ser Ala Leu Asp Ala Ala Leu
         40                  45                  50

gag aga gca aaa aga gct gcc gca gtt gat acc aat gcc ata gaa gga   307
Glu Arg Ala Lys Arg Ala Ala Ala Val Asp Thr Asn Ala Ile Glu Gly
     55                  60                  65

atc ttc caa act gat cgc ggt ttt acc cat aca gtt gca acg cag gta   355
Ile Phe Gln Thr Asp Arg Gly Phe Thr His Thr Val Ala Thr Gln Val
 70                  75                  80                  85

ggg gct tgg gag caa caa atg gcg atg aaa ggc aaa cat gtt aag cct   403
Gly Ala Trp Glu Gln Gln Met Ala Met Lys Gly Lys His Val Lys Pro
                 90                  95                 100

gcg ttt gac gat act cta gaa ggc ttt gag tat gtt ctc gat gca gta   451
Ala Phe Asp Asp Thr Leu Glu Gly Phe Glu Tyr Val Leu Asp Ala Val
             105                 110                 115

act ggt aga act cca atc tct cag caa tgg att aga aat ttg cac gcc   499
Thr Gly Arg Thr Pro Ile Ser Gln Gln Trp Ile Arg Asn Leu His Ala
         120                 125                 130

gtc att ctg cgg agc caa gaa agc cac gag gtt ttt aca gcc gtt gga   547
Val Ile Leu Arg Ser Gln Glu Ser His Glu Val Phe Thr Ala Val Gly
     135                 140                 145

gtc caa aat cag gcg ctt cag aaa ggc gag tat aaa act cag cca aat   595
Val Gln Asn Gln Ala Leu Gln Lys Gly Glu Tyr Lys Thr Gln Pro Asn
150                 155                 160                 165

agt cca cag cgc tca gat gga tct gta cat gca tac gcc cca gtt gaa   643
Ser Pro Gln Arg Ser Asp Gly Ser Val His Ala Tyr Ala Pro Val Glu
                 170                 175                 180

gat act cct gct gaa atg gct aga ttt att tca gaa ctt gaa tct aag   691
Asp Thr Pro Ala Glu Met Ala Arg Phe Ile Ser Glu Leu Glu Ser Lys
             185                 190                 195

gaa ttc tta gca gcc gag aag gtt att caa gct gcc tat gcc cac tat   739
Glu Phe Leu Ala Ala Glu Lys Val Ile Gln Ala Ala Tyr Ala His Tyr
         200                 205                 210
```

```
gct ttc gta tgt att cat cct ttt gca gat ggg aat gga cga gtt gca   787
Ala Phe Val Cys Ile His Pro Phe Ala Asp Gly Asn Gly Arg Val Ala
    215                 220                 225

cga gcc ttg gct agt gtt ttt cta tac aaa gat cct ggt gtc cct ctc   835
Arg Ala Leu Ala Ser Val Phe Leu Tyr Lys Asp Pro Gly Val Pro Leu
230                 235                 240                 245

gta atc tac caa gat caa cgc aga gat tac atc cat gct cta gaa gca   883
Val Ile Tyr Gln Asp Gln Arg Arg Asp Tyr Ile His Ala Leu Glu Ala
                250                 255                 260

gcg gac aag aat aac ccg ctc ctg ctg att aga ttc ttt gct gaa cga   931
Ala Asp Lys Asn Asn Pro Leu Leu Leu Ile Arg Phe Phe Ala Glu Arg
            265                 270                 275

gtg acc gat act att aac tct att atc gtt gat ctc act acc ccg atc   979
Val Thr Asp Thr Ile Asn Ser Ile Ile Val Asp Leu Thr Thr Pro Ile
        280                 285                 290

gcg ggt aaa tct ggt tcg gct aag ctt tcg gat gcg cta cgc ccc act   1027
Ala Gly Lys Ser Gly Ser Ala Lys Leu Ser Asp Ala Leu Arg Pro Thr
    295                 300                 305

cgc gta tta cca gaa tta cat gat gct gca cat agg ctc caa gaa agt   1075
Arg Val Leu Pro Glu Leu His Asp Ala Ala His Arg Leu Gln Glu Ser
310                 315                 320                 325

tta ttt aca gaa atc cga tct cga ttg gat gaa gaa gga aaa agg aat   1123
Leu Phe Thr Glu Ile Arg Ser Arg Leu Asp Glu Glu Gly Lys Arg Asn
                330                 335                 340

ggg ttg gag ttt cta ctt caa cgg att ttt atc ggt tcc cca ttc aat   1171
Gly Leu Glu Phe Leu Leu Gln Arg Ile Phe Ile Gly Ser Pro Phe Asn
            345                 350                 355

ctg cca gag ggc tat aac gct ttc cct gat agc tat tgt ctg acc tta   1219
Leu Pro Glu Gly Tyr Asn Ala Phe Pro Asp Ser Tyr Cys Leu Thr Leu
        360                 365                 370

gct ttc aat agc aac tct cca aaa caa atc ttc cac ccg cta tcc ata   1267
Ala Phe Asn Ser Asn Ser Pro Lys Gln Ile Phe His Pro Leu Ser Ile
    375                 380                 385

gta ata gca gct cga gat ggg aaa aga gcg agc agc gac ctc gtg gca   1315
Val Ile Ala Ala Arg Asp Gly Lys Arg Ala Ser Ser Asp Leu Val Ala
390                 395                 400                 405

gct act tct att gga tac aac ttt cac gct tac gga cgt gaa gtc gag   1363
Ala Thr Ser Ile Gly Tyr Asn Phe His Ala Tyr Gly Arg Glu Val Glu
                410                 415                 420

cct gtt gtt act gaa agc ttt cga gaa cgt gtg aaa att tac gcc gac   1411
Pro Val Val Thr Glu Ser Phe Arg Glu Arg Val Lys Ile Tyr Ala Asp
            425                 430                 435

ggg att gta gat cac ttc tta acc gaa ctg gct aaa aag ttt caa cag   1459
Gly Ile Val Asp His Phe Leu Thr Glu Leu Ala Lys Lys Phe Gln Gln
        440                 445                 450

aat taattagcct atctcggctt tcg                                    1485
```

Asn

<210> 82
<211> 454
<212> PRT
<213> Corynebacterium glutamicum

<400> 82

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Met Asn Asp Glu Asn Ile Gln Ser Ser Asn Tyr Gln Pro Phe Pro Ser
  1               5                  10                  15

Phe Asp Asp Trp Lys Gln Ile Glu Val Ser Leu Leu Asp Val Ile Glu
             20                  25                  30

Ser Ser Arg His Phe Ser Asp Leu Lys Asp Ser Thr Asp Arg Ser Ala
         35                  40                  45

Leu Asp Ala Ala Leu Glu Arg Ala Lys Arg Ala Ala Ala Val Asp Thr
     50                  55                  60

Asn Ala Ile Glu Gly Ile Phe Gln Thr Asp Arg Gly Phe Thr His Thr
 65                  70                  75                  80

Val Ala Thr Gln Val Gly Ala Trp Glu Gln Gln Met Ala Met Lys Gly
                 85                  90                  95

Lys His Val Lys Pro Ala Phe Asp Asp Thr Leu Glu Gly Phe Glu Tyr
            100                 105                 110

Val Leu Asp Ala Val Thr Gly Arg Thr Pro Ile Ser Gln Gln Trp Ile
        115                 120                 125

Arg Asn Leu His Ala Val Ile Leu Arg Ser Gln Glu Ser His Glu Val
    130                 135                 140

Phe Thr Ala Val Gly Val Gln Asn Gln Ala Leu Gln Lys Gly Glu Tyr
145                 150                 155                 160

Lys Thr Gln Pro Asn Ser Pro Gln Arg Ser Asp Gly Ser Val His Ala
                165                 170                 175

Tyr Ala Pro Val Glu Asp Thr Pro Ala Glu Met Ala Arg Phe Ile Ser
            180                 185                 190

Glu Leu Glu Ser Lys Glu Phe Leu Ala Ala Glu Lys Val Ile Gln Ala
        195                 200                 205

Ala Tyr Ala His Tyr Ala Phe Val Cys Ile His Pro Phe Ala Asp Gly
    210                 215                 220

Asn Gly Arg Val Ala Arg Ala Leu Ala Ser Val Phe Leu Tyr Lys Asp
225                 230                 235                 240

Pro Gly Val Pro Leu Val Ile Tyr Gln Asp Gln Arg Arg Asp Tyr Ile
                245                 250                 255

His Ala Leu Glu Ala Ala Asp Lys Asn Asn Pro Leu Leu Leu Ile Arg
            260                 265                 270
```

```
Phe Phe Ala Glu Arg Val Thr Asp Thr Ile Asn Ser Ile Ile Val Asp
        275                 280                 285

Leu Thr Thr Pro Ile Ala Gly Lys Ser Gly Ser Ala Lys Leu Ser Asp
    290                 295                 300

Ala Leu Arg Pro Thr Arg Val Leu Pro Glu Leu His Asp Ala Ala His
305                 310                 315                 320

Arg Leu Gln Glu Ser Leu Phe Thr Glu Ile Arg Ser Arg Leu Asp Glu
                325                 330                 335

Glu Gly Lys Arg Asn Gly Leu Glu Phe Leu Leu Gln Arg Ile Phe Ile
            340                 345                 350

Gly Ser Pro Phe Asn Leu Pro Glu Gly Tyr Asn Ala Phe Pro Asp Ser
        355                 360                 365

Tyr Cys Leu Thr Leu Ala Phe Asn Ser Asn Ser Pro Lys Gln Ile Phe
    370                 375                 380

His Pro Leu Ser Ile Val Ile Ala Ala Arg Asp Gly Lys Arg Ala Ser
385                 390                 395                 400

Ser Asp Leu Val Ala Ala Thr Ser Ile Gly Tyr Asn Phe His Ala Tyr
                405                 410                 415

Gly Arg Glu Val Glu Pro Val Val Thr Glu Ser Phe Arg Glu Arg Val
            420                 425                 430

Lys Ile Tyr Ala Asp Gly Ile Val Asp His Phe Leu Thr Glu Leu Ala
        435                 440                 445

Lys Lys Phe Gln Gln Asn
    450
```

09-05-2005 20:50:57

<210> 83
<211> 1485
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1462)
<223> FRXA00077

<400> 83
ctaaattgtt ttaacgcgtg aagcagtccc cgcccgattt attcgaggcg gggactttcg 60

ctttccggga taaaaattgc aacgcactac actgagcagt atg aat gat gag aat 115
                                              Met Asn Asp Glu Asn
                                                1   5

att caa agc tcc aac tat cag cca ttc ccg agt ttt gac gat tgg aaa 163
Ile Gln Ser Ser Asn Tyr Gln Pro Phe Pro Ser Phe Asp Asp Trp Lys
                10   15   20

cag atc gag gtg tcg ctc tta gat gtc atc gaa tcc tca cgc cat ttt 211
Gln Ile Glu Val Ser Leu Leu Asp Val Ile Glu Ser Ser Arg His Phe
            25   30   35

```
tct gat ttg aaa gat agc act gat cgt tct gcg tta gat gct gcg cta   259
Ser Asp Leu Lys Asp Ser Thr Asp Arg Ser Ala Leu Asp Ala Ala Leu
         40                  45                  50

gag aga gca aaa aga gct gcc gca gtt gat acc aat gcc ata gaa gga   307
Glu Arg Ala Lys Arg Ala Ala Ala Val Asp Thr Asn Ala Ile Glu Gly
     55                  60                  65

atc ttc caa act gat cgc ggt ttt acc cat aca gtt gca acg cag gta   355
Ile Phe Gln Thr Asp Arg Gly Phe Thr His Thr Val Ala Thr Gln Val
 70                  75                  80                  85

ggg gct tgg gag caa caa atg gcg atg aaa ggc aaa cat gtt aag cct   403
Gly Ala Trp Glu Gln Gln Met Ala Met Lys Gly Lys His Val Lys Pro
                 90                  95                 100

gcg ttt gac gat act cta gaa ggc ttt gag tat gtt ctc gat gca gta   451
Ala Phe Asp Asp Thr Leu Glu Gly Phe Glu Tyr Val Leu Asp Ala Val
            105                 110                 115

act ggt aga act cca atc tct cag caa tgg att aga aat ttg cac gcc   499
Thr Gly Arg Thr Pro Ile Ser Gln Gln Trp Ile Arg Asn Leu His Ala
        120                 125                 130

gtc att ctg cgg agc caa gaa agc cac gag gtt ttt aca gcc gtt gga   547
Val Ile Leu Arg Ser Gln Glu Ser His Glu Val Phe Thr Ala Val Gly
    135                 140                 145

gtc caa aat cag gcg ctt cag aaa ggc gag tat aaa act cag cca aat   595
Val Gln Asn Gln Ala Leu Gln Lys Gly Glu Tyr Lys Thr Gln Pro Asn
150                 155                 160                 165

agt cca cag cgc tca gat gga tct gta cat gca tac gcc cca gtt gaa   643
Ser Pro Gln Arg Ser Asp Gly Ser Val His Ala Tyr Ala Pro Val Glu
                170                 175                 180

gat act cct gct gaa atg gct aga ttt att tca gaa ctt gaa tct aag   691
Asp Thr Pro Ala Glu Met Ala Arg Phe Ile Ser Glu Leu Glu Ser Lys
            185                 190                 195

gaa ttc tta gca gcc gag aag gtt att caa gct gcc tat gcc cac tat   739
Glu Phe Leu Ala Ala Glu Lys Val Ile Gln Ala Ala Tyr Ala His Tyr
        200                 205                 210

gct ttc gta tgt att cat cct ttt gca gat ggg aat gga cga gtt gca   787
Ala Phe Val Cys Ile His Pro Phe Ala Asp Gly Asn Gly Arg Val Ala
    215                 220                 225

cga gcc ttg gct agt gtt ttt cta tac aaa gat cct ggt gtc cct ctc   835
Arg Ala Leu Ala Ser Val Phe Leu Tyr Lys Asp Pro Gly Val Pro Leu
230                 235                 240                 245

gta atc tac caa gat caa cgc aga gat tac atc cat gct cta gaa gca   883
Val Ile Tyr Gln Asp Gln Arg Arg Asp Tyr Ile His Ala Leu Glu Ala
                250                 255                 260

gcg gac aag aat aac ccg ctc ctg ctg att aga ttc ttt gct gaa cga   931
Ala Asp Lys Asn Asn Pro Leu Leu Leu Ile Arg Phe Phe Ala Glu Arg
            265                 270                 275
```

```
gtg acc gat act att aac tct att atc gtt gat ctc act acc ccg atc   979
Val Thr Asp Thr Ile Asn Ser Ile Ile Val Asp Leu Thr Thr Pro Ile
        280                 285                 290

gcg ggt aaa tct ggt tcg gct aag ctt tcg gat gcg cta cgc ccc act   1027
Ala Gly Lys Ser Gly Ser Ala Lys Leu Ser Asp Ala Leu Arg Pro Thr
    295                 300                 305

cgc gta tta cca gaa tta cat gat gct gca cat agg ctc caa gaa agt   1075
Arg Val Leu Pro Glu Leu His Asp Ala Ala His Arg Leu Gln Glu Ser
310                 315                 320                 325

tta ttt aca gaa atc cga tct cga ttg gat gaa gaa gga aaa agg aat   1123
Leu Phe Thr Glu Ile Arg Ser Arg Leu Asp Glu Glu Gly Lys Arg Asn
                330                 335                 340

ggg ttg gag ttt cta ctt caa cgg att ttt atc ggt tcc cca ttc aat   1171
Gly Leu Glu Phe Leu Leu Gln Arg Ile Phe Ile Gly Ser Pro Phe Asn
            345                 350                 355

ctg cca gag ggc tat aac gct ttc cct gat agc tat tgt ctg acc tta   1219
Leu Pro Glu Gly Tyr Asn Ala Phe Pro Asp Ser Tyr Cys Leu Thr Leu
        360                 365                 370

gct ttc aat agc aac tct cca aaa caa atc ttc cac ccg cta tcc ata   1267
Ala Phe Asn Ser Asn Ser Pro Lys Gln Ile Phe His Pro Leu Ser Ile
    375                 380                 385

gta ata gca gct cga gat ggg aaa aga gcg agc agc gac ctc gtg gca   1315
Val Ile Ala Ala Arg Asp Gly Lys Arg Ala Ser Ser Asp Leu Val Ala
390                 395                 400                 405

gct act tct att gga tac aac ttt cac gct tac gga cgt gaa gtc gag   1363
Ala Thr Ser Ile Gly Tyr Asn Phe His Ala Tyr Gly Arg Glu Val Glu
                410                 415                 420

cct gtt gtt act gaa agc ttt cga gaa cgt gtg aaa att tac gcc gac   1411
Pro Val Val Thr Glu Ser Phe Arg Glu Arg Val Lys Ile Tyr Ala Asp
            425                 430                 435

ggg att gta gat cac ttc tta acc gaa ctg gct aaa aag ttt caa cag   1459
Gly Ile Val Asp His Phe Leu Thr Glu Leu Ala Lys Lys Phe Gln Gln
        440                 445                 450

aat taattagcct atctcggctt tcg                                    1485
Asn
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<210> 84
<211> 454
<212> PRT
<213> Corynebacterium glutamicum

<400> 84

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Met Asn Asp Glu Asn Ile Gln Ser Ser Asn Tyr Gln Pro Phe Pro Ser
  1               5                  10                  15

Phe Asp Asp Trp Lys Gln Ile Glu Val Ser Leu Leu Asp Val Ile Glu
            20                  25                  30
```

```
Ser Ser Arg His Phe Ser Asp Leu Lys Asp Ser Thr Asp Arg Ser Ala
         35                  40                  45

Leu Asp Ala Ala Leu Glu Arg Ala Lys Arg Ala Ala Ala Val Asp Thr
     50                  55                  60

Asn Ala Ile Glu Gly Ile Phe Gln Thr Asp Arg Gly Phe Thr His Thr
 65                  70                  75                  80

Val Ala Thr Gln Val Gly Ala Trp Glu Gln Gln Met Ala Met Lys Gly
                 85                  90                  95

Lys His Val Lys Pro Ala Phe Asp Asp Thr Leu Glu Gly Phe Glu Tyr
            100                 105                 110

Val Leu Asp Ala Val Thr Gly Arg Thr Pro Ile Ser Gln Gln Trp Ile
        115                 120                 125

Arg Asn Leu His Ala Val Ile Leu Arg Ser Gln Glu Ser His Glu Val
    130                 135                 140

Phe Thr Ala Val Gly Val Gln Asn Gln Ala Leu Gln Lys Gly Glu Tyr
145                 150                 155                 160

Lys Thr Gln Pro Asn Ser Pro Gln Arg Ser Asp Gly Ser Val His Ala
                165                 170                 175

Tyr Ala Pro Val Glu Asp Thr Pro Ala Glu Met Ala Arg Phe Ile Ser
            180                 185                 190

Glu Leu Glu Ser Lys Glu Phe Leu Ala Ala Glu Lys Val Ile Gln Ala
        195                 200                 205

Ala Tyr Ala His Tyr Ala Phe Val Cys Ile His Pro Phe Ala Asp Gly
    210                 215                 220

Asn Gly Arg Val Ala Arg Ala Leu Ala Ser Val Phe Leu Tyr Lys Asp
225                 230                 235                 240

Pro Gly Val Pro Leu Val Ile Tyr Gln Asp Gln Arg Arg Asp Tyr Ile
                245                 250                 255

His Ala Leu Glu Ala Ala Asp Lys Asn Asn Pro Leu Leu Leu Ile Arg
            260                 265                 270

Phe Phe Ala Glu Arg Val Thr Asp Thr Ile Asn Ser Ile Ile Val Asp
        275                 280                 285

Leu Thr Thr Pro Ile Ala Gly Lys Ser Gly Ser Ala Lys Leu Ser Asp
    290                 295                 300

Ala Leu Arg Pro Thr Arg Val Leu Pro Glu Leu His Asp Ala Ala His
305                 310                 315                 320

Arg Leu Gln Glu Ser Leu Phe Thr Glu Ile Arg Ser Arg Leu Asp Glu
                325                 330                 335

Glu Gly Lys Arg Asn Gly Leu Glu Phe Leu Leu Gln Arg Ile Phe Ile
            340                 345                 350

Gly Ser Pro Phe Asn Leu Pro Glu Gly Tyr Asn Ala Phe Pro Asp Ser
```

```
        355                 360                 365

Tyr Cys Leu Thr Leu Ala Phe Asn Ser Asn Ser Pro Lys Gln Ile Phe
    370                 375                 380

His Pro Leu Ser Ile Val Ile Ala Ala Arg Asp Gly Lys Arg Ala Ser
385                 390                 395                 400

Ser Asp Leu Val Ala Ala Thr Ser Ile Gly Tyr Asn Phe His Ala Tyr
                405                 410                 415

Gly Arg Glu Val Glu Pro Val Val Thr Glu Ser Phe Arg Glu Arg Val
            420                 425                 430

Lys Ile Tyr Ala Asp Gly Ile Val Asp His Phe Leu Thr Glu Leu Ala
        435                 440                 445

Lys Lys Phe Gln Gln Asn
    450
```

5,958,745 5,965,408 5,973,222 5,977,435 5,998,183 6,004,788 6,015,674 6,033,880 6,037,154 6,040,157 6,048,729 6,051,403 6,057,133 6,060,051 6,060,297 6,061,620 6,066,499 6,071,720 6,075,183 6,077,697 6,080,559 6,082,156 6,087,147 6,090,597 6,096,546 6,100,077 6,103,537 6,107,066 6,110,739 6,110,740 6,113,915 6,114,148 6,117,663 6,120,759 6,124,121 6,124,123 6,127,158 6,130,085 6,132,724 6,132,999 6,133,001 6,136,582 6,140,105 6,143,549 6,146,883 6,150,148 6,153,416 6,156,532 6,159,736 6,159,737 6,159,738 6,159,739 6,159,740 6,159,741 6,159,742 6,159,743 6,159,744 6,159,745 6,159,746 6,159,747 6,159,748 6,159,749 6,159,750 6,159,751 6,159,752 6,159,753 6,159,754 6,159,755 6,159,756 6,159,757 6,159,758 6,159,759 6,159,760 6,159,761 6,159,762 6,159,763 6,159,764 6,159,765 6,159,766 6,159,767 6,159,768 6,159,769 6,159,770 6,159,771 6,159,772 6,159,773 6,159,774 6,159,775

```
ctt aac ggc cgt gcg cca cag gct ctg gct acc gca gcg atc ggt gcc   451
Leu Asn Gly Arg Ala Pro Gln Ala Leu Ala Thr Ala Ala Ile Gly Ala
            105                 110                 115

ttc atc ggc ggt atc gtc tcc tcc ttc atc gtg gtc ttc ctc gca cca   499
Phe Ile Gly Gly Ile Val Ser Ser Phe Ile Val Val Phe Leu Ala Pro
        120                 125                 130

acc ctg gcg gaa ctg tcc acc gca ttc ggc ccc gcc gag tac ttc gca   547
Thr Leu Ala Glu Leu Ser Thr Ala Phe Gly Pro Ala Glu Tyr Phe Ala
    135                 140                 145

ctg gca ctc ttc gcg ttc gtc gcc acc tcc tcc gtg gtg tcc gac tcc   595
Leu Ala Leu Phe Ala Phe Val Ala Thr Ser Ser Val Val Ser Asp Ser
150                 155                 160                 165

gtg ttt aag gga ctt gcg tcc ctc att ttc ggc ctc ggc att gcg acc   643
Val Phe Lys Gly Leu Ala Ser Leu Ile Phe Gly Leu Gly Ile Ala Thr
                170                 175                 180

atc ggc atc gat tcg gtc acc ggc atc gag cgc ttc acg ctc ggg gca   691
Ile Gly Ile Asp Ser Val Thr Gly Ile Glu Arg Phe Thr Leu Gly Ala
            185                 190                 195

ccg cag ctt ttc gac gga att tcc ctc gtt act gtt acc gtc gcg att   739
Pro Gln Leu Phe Asp Gly Ile Ser Leu Val Thr Val Thr Val Ala Ile
        200                 205                 210

ttg gca ctg gga gaa gtg ttt tac att gca gcc cgc gca cgc cgt gac   787
Leu Ala Leu Gly Glu Val Phe Tyr Ile Ala Ala Arg Ala Arg Arg Asp
    215                 220                 225

aaa gca aat ctg gag acg cgc tct gca ggc cgt ccg tgg ctt acc gga   835
Lys Ala Asn Leu Glu Thr Arg Ser Ala Gly Arg Pro Trp Leu Thr Gly
230                 235                 240                 245

acg gaa ttc aaa gaa gcc gct cca gcc tgg gca cgc gga acc atc att   883
Thr Glu Phe Lys Glu Ala Ala Pro Ala Trp Ala Arg Gly Thr Ile Ile
                250                 255                 260

ggt ctg cct ttc ggt gtg atc cct gtt ggt gga tct gaa gtt cca acc   931
Gly Leu Pro Phe Gly Val Ile Pro Val Gly Gly Ser Glu Val Pro Thr
            265                 270                 275

ttc ttg gct tac tcc acc gag cgc gca ttg gat aaa cga cgc aaa gat   979
Phe Leu Ala Tyr Ser Thr Glu Arg Ala Leu Asp Lys Arg Arg Lys Asp
        280                 285                 290

ccg cag ttc ggc gat aaa ggt gca atc cga gga ctc gct gct cct gaa   1027
Pro Gln Phe Gly Asp Lys Gly Ala Ile Arg Gly Leu Ala Ala Pro Glu
    295                 300                 305

gct gca ggt aac gcc acc aca ggc atg gcg atg ggc gct ctt ctt gcc   1075
Ala Ala Gly Asn Ala Thr Thr Gly Met Ala Met Gly Ala Leu Leu Ala
310                 315                 320                 325

ctg ggt ctc cca gtc tct gca act gcg gcc atc atg ttg gca gcg ttc   1123
Leu Gly Leu Pro Val Ser Ala Thr Ala Ala Ile Met Leu Ala Ala Phe
                330                 335                 340
```

```
cgc cag tac gga atc cag ccc gga cca cta ctc ttc gat cgc aac cct   1171
Arg Gln Tyr Gly Ile Gln Pro Gly Pro Leu Leu Phe Asp Arg Asn Pro
            345                 350                 355

gaa ctt gtc tgg gca ctt ctt gcc agc ttc ttc atc gcg atg atc gtc   1219
Glu Leu Val Trp Ala Leu Leu Ala Ser Phe Phe Ile Ala Met Ile Val
        360                 365                 370

ctg ctg ttc atc aac ctg ccg ttc gca cag ctg tgg gca aag ctc ctg   1267
Leu Leu Phe Ile Asn Leu Pro Phe Ala Gln Leu Trp Ala Lys Leu Leu
    375                 380                 385

ctc att cca aac cac tac ctc tac tcc ggc atc gca ttg ttc tgt ggc   1315
Leu Ile Pro Asn His Tyr Leu Tyr Ser Gly Ile Ala Leu Phe Cys Gly
390                 395                 400                 405

ctg ggc att tac gcc acc tcc ggc gca gtg ttc gac ctg ctc atg ctg   1363
Leu Gly Ile Tyr Ala Thr Ser Gly Ala Val Phe Asp Leu Leu Met Leu
                410                 415                 420

ctc ggc atc ggt gtc gtg gct ttg atc atg cgt cgc tac ggt tac ccg   1411
Leu Gly Ile Gly Val Val Ala Leu Ile Met Arg Arg Tyr Gly Tyr Pro
            425                 430                 435

ctg gca ccg ctg atg atc ggt atg gtt ctt gga cct ttg gct gaa acc   1459
Leu Ala Pro Leu Met Ile Gly Met Val Leu Gly Pro Leu Ala Glu Thr
        440                 445                 450

tcc ctc cgc gac gca cta ctg tcc tcg gtt ggc gat ttc tcc atc ctc   1507
Ser Leu Arg Asp Ala Leu Leu Ser Ser Val Gly Asp Phe Ser Ile Leu
    455                 460                 465

gtc tcc agc ccc atc acc tgg tct ctc tac gca gtg ctc gcc atc ttc   1555
Val Ser Ser Pro Ile Thr Trp Ser Leu Tyr Ala Val Leu Ala Ile Phe
470                 475                 480                 485

atc gcg gtc agt gtc atc act gca atc cgc ggt cgt cgc aag cac ctg   1603
Ile Ala Val Ser Val Ile Thr Ala Ile Arg Gly Arg Arg Lys His Leu
                490                 495                 500

act tct cag ctc gaa acc atc gac gct taaagtcccc gtatagaaac         1650
Thr Ser Gln Leu Glu Thr Ile Asp Ala
            505                 510

agg                                                              1653
```

<210> 86
<211> 510
<212> PRT
<213> Corynebacterium glutamicum

<400> 86

```
Met Asp Ile Leu Ser Leu Leu Met Glu Gly Phe Ala Gly Ala Leu Thr
  1               5                  10                  15

Pro Met Asn Leu Leu Trp Val Ile Val Gly Cys Leu Leu Gly Thr Ala
             20                  25                  30

Val Gly Val Met Pro Gly Leu Gly Ser Ser Met Ala Val Ala Leu Leu
         35                  40                  45
```

```
Leu Pro Met Thr Phe Ala Leu Asp Pro Thr Ala Ala Phe Ile Met Phe
     50                  55                  60

Ser Gly Val Tyr Phe Gly Gly Leu Phe Gly Asp Ser Thr Met Ala Ile
 65                  70                  75                  80

Leu Met Asn Thr Pro Gly Gln Ala Ser Ala Ile Ala Ser Thr Phe Glu
                 85                  90                  95

Gly His Arg Met Ala Leu Asn Gly Arg Ala Pro Gln Ala Leu Ala Thr
            100                 105                 110

Ala Ala Ile Gly Ala Phe Ile Gly Gly Ile Val Ser Ser Phe Ile Val
        115                 120                 125

Val Phe Leu Ala Pro Thr Leu Ala Glu Leu Ser Thr Ala Phe Gly Pro
    130                 135                 140

Ala Glu Tyr Phe Ala Leu Ala Leu Phe Ala Phe Val Ala Thr Ser Ser
145                 150                 155                 160

Val Val Ser Asp Ser Val Phe Lys Gly Leu Ala Ser Leu Ile Phe Gly
                165                 170                 175

Leu Gly Ile Ala Thr Ile Gly Ile Asp Ser Val Thr Gly Ile Glu Arg
            180                 185                 190

Phe Thr Leu Gly Ala Pro Gln Leu Phe Asp Gly Ile Ser Leu Val Thr
        195                 200                 205

Val Thr Val Ala Ile Leu Ala Leu Gly Glu Val Phe Tyr Ile Ala Ala
    210                 215                 220

Arg Ala Arg Arg Asp Lys Ala Asn Leu Glu Thr Arg Ser Ala Gly Arg
225                 230                 235                 240

Pro Trp Leu Thr Gly Thr Glu Phe Lys Glu Ala Ala Pro Ala Trp Ala
                245                 250                 255

Arg Gly Thr Ile Ile Gly Leu Pro Phe Gly Val Ile Pro Val Gly Gly
            260                 265                 270

Ser Glu Val Pro Thr Phe Leu Ala Tyr Ser Thr Glu Arg Ala Leu Asp
        275                 280                 285

Lys Arg Arg Lys Asp Pro Gln Phe Gly Asp Lys Gly Ala Ile Arg Gly
    290                 295                 300

Leu Ala Ala Pro Glu Ala Ala Gly Asn Ala Thr Thr Gly Met Ala Met
305                 310                 315                 320

Gly Ala Leu Leu Ala Leu Gly Leu Pro Val Ser Ala Thr Ala Ala Ile
                325                 330                 335

Met Leu Ala Ala Phe Arg Gln Tyr Gly Ile Gln Pro Gly Pro Leu Leu
            340                 345                 350

Phe Asp Arg Asn Pro Glu Leu Val Trp Ala Leu Leu Ala Ser Phe Phe
        355                 360                 365
```

```
Ile Ala Met Ile Val Leu Leu Phe Ile Asn Leu Pro Phe Ala Gln Leu
    370                 375                 380

Trp Ala Lys Leu Leu Leu Ile Pro Asn His Tyr Leu Tyr Ser Gly Ile
385                 390                 395                 400

Ala Leu Phe Cys Gly Leu Gly Ile Tyr Ala Thr Ser Gly Ala Val Phe
                405                 410                 415

Asp Leu Leu Met Leu Leu Gly Ile Gly Val Val Ala Leu Ile Met Arg
            420                 425                 430

Arg Tyr Gly Tyr Pro Leu Ala Pro Leu Met Ile Gly Met Val Leu Gly
        435                 440                 445

Pro Leu Ala Glu Thr Ser Leu Arg Asp Ala Leu Leu Ser Ser Val Gly
    450                 455                 460

Asp Phe Ser Ile Leu Val Ser Ser Pro Ile Thr Trp Ser Leu Tyr Ala
465                 470                 475                 480

Val Leu Ala Ile Phe Ile Ala Val Ser Val Ile Thr Ala Ile Arg Gly
                485                 490                 495

Arg Arg Lys His Leu Thr Ser Gln Leu Glu Thr Ile Asp Ala
            500                 505                 510


<210> 87
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> FRXA00080

<400> 87
ttggcagcgt tccgccagta cggaatccag cccggaccac tactcttcga tcgcaaccct 60

gaacttgtct gggcacttct tgccagcttc tttcatcgcg atg atc gtc ctg ctg   115
                                            Met Ile Val Leu Leu
                                              1               5

ttc atc aac ctg ccg ttc gca cag ctg tgg gca aag ctc ctg ctc att   163
Phe Ile Asn Leu Pro Phe Ala Gln Leu Trp Ala Lys Leu Leu Leu Ile
                  10                  15                  20

cca aac cac tac ctc tac tcc ggc atc gca ttg ttc tgt ggc ctg ggc   211
Pro Asn His Tyr Leu Tyr Ser Gly Ile Ala Leu Phe Cys Gly Leu Gly
              25                  30                  35

att tac gcc acc tcc ggc gca gtg ttc gac ctg ctc atg ctg ctc ggc   259
Ile Tyr Ala Thr Ser Gly Ala Val Phe Asp Leu Leu Met Leu Leu Gly
          40                  45                  50

atc ggt gtc gtg gct ttg atc atg cgt cgc tac ggt tac ccg ctg gca   307
Ile Gly Val Val Ala Leu Ile Met Arg Arg Tyr Gly Tyr Pro Leu Ala
     55                  60                  65
```

```
ccg ctg atg atc ggt atg gtt ctt gga cct ttg gct gaa acc tcc ctc   355
Pro Leu Met Ile Gly Met Val Leu Gly Pro Leu Ala Glu Thr Ser Leu
 70                  75                  80                  85

cgc gac gca cta ctg tcc tcg gtt ggc gat ttc tcc atc ctc gtc tcc   403
Arg Asp Ala Leu Leu Ser Ser Val Gly Asp Phe Ser Ile Leu Val Ser
                90                  95                 100

agc ccc atc acc tgg tct ctc tac gca gtg ctc gcc atc ttc atc gcg   451
Ser Pro Ile Thr Trp Ser Leu Tyr Ala Val Leu Ala Ile Phe Ile Ala
            105                 110                 115

gtc agt gtc atc act gca atc cgc ggt cgt cgc aag cac ctg act tct   499
Val Ser Val Ile Thr Ala Ile Arg Gly Arg Arg Lys His Leu Thr Ser
        120                 125                 130

cag ctc gaa acc atc gac gct taaagtcccc gtatagaaac agg             543
Gln Leu Glu Thr Ile Asp Ala
    135                 140
```

<210> 88
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 88

```
Met Ile Val Leu Leu Phe Ile Asn Leu Pro Phe Ala Gln Leu Trp Ala
  1               5                  10                  15

Lys Leu Leu Leu Ile Pro Asn His Tyr Leu Tyr Ser Gly Ile Ala Leu
             20                  25                  30

Phe Cys Gly Leu Gly Ile Tyr Ala Thr Ser Gly Ala Val Phe Asp Leu
         35                  40                  45

Leu Met Leu Leu Gly Ile Gly Val Val Ala Leu Ile Met Arg Arg Tyr
     50                  55                  60

Gly Tyr Pro Leu Ala Pro Leu Met Ile Gly Met Val Leu Gly Pro Leu
 65                  70                  75                  80

Ala Glu Thr Ser Leu Arg Asp Ala Leu Leu Ser Ser Val Gly Asp Phe
                85                  90                  95

Ser Ile Leu Val Ser Ser Pro Ile Thr Trp Ser Leu Tyr Ala Val Leu
            100                 105                 110

Ala Ile Phe Ile Ala Val Ser Val Ile Thr Ala Ile Arg Gly Arg Arg
        115                 120                 125

Lys His Leu Thr Ser Gln Leu Glu Thr Ile Asp Ala
    130                 135                 140
```

<210> 89
<211> 651
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(628)
<223> RXN00087

<400> 89
tcgtcagtca acaaacgttt tcccacccgg aggtctcccc gtgtctaccg aaatccacaa 60

cgccccaccc aaggccccaa cttggcttgg ctgggtgctc atg atc ggc gga ata 115
Met Ile Gly Gly Ile
1 5

atc ggc ctc att ttg tcg gtg atc atc atg gcc gaa aaa ctt gcc atc 163
Ile Gly Leu Ile Leu Ser Val Ile Ile Met Ala Glu Lys Leu Ala Ile
10 15 20

ctc gag gat ccc ggt cac atc acc agc tgc gat ttc aat gca gtc cta 211
Leu Glu Asp Pro Gly His Ile Thr Ser Cys Asp Phe Asn Ala Val Leu
25 30 35

gct tgt ggc gat gtc atg cgt tcc ggc caa gct aac gcg ttc ggc atc 259
Ala Cys Gly Asp Val Met Arg Ser Gly Gln Ala Asn Ala Phe Gly Ile
40 45 50

ccg aat ccg ctc atc ggc atc gcc ggt ttc gcc gct gtc gcc atc atc 307
Pro Asn Pro Leu Ile Gly Ile Ala Gly Phe Ala Ala Val Ala Ile Ile
55 60 65

ggc gcc ggc atc ctc gcg ggc ggc ggg ttc cgc ggt tgg ttc tgg ttc 355
Gly Ala Gly Ile Leu Ala Gly Gly Gly Phe Arg Gly Trp Phe Trp Phe
70 75 80 85

ggc gcc cag gcc gga ctc act ttt gcc atg atg ttc tgc cac tgg ctc 403
Gly Ala Gln Ala Gly Leu Thr Phe Ala Met Met Phe Cys His Trp Leu
90 95 100

gcc tac caa tcc atg tcc gtc atc cgc gcg ctc tgc cct tac tgc atg 451
Ala Tyr Gln Ser Met Ser Val Ile Arg Ala Leu Cys Pro Tyr Cys Met
105 110 115

ggc gtg tgg acc gta tcg atc atc atg ttc gtg ctg gtc act gca tgg 499
Gly Val Trp Thr Val Ser Ile Ile Met Phe Val Leu Val Thr Ala Trp
120 125 130

aat gtg aaa act ttc agc ggc tcc gac agc acg ttc gtc aac gca ctg 547
Asn Val Lys Thr Phe Ser Gly Ser Asp Ser Thr Phe Val Asn Ala Leu
135 140 145

tac aaa tac aag tgg gtc atc gcg atc gtc tgg ctg ctg ctc atc gca 595
Tyr Lys Tyr Lys Trp Val Ile Ala Ile Val Trp Leu Leu Leu Ile Ala
150 155 160 165

gcc gca gct gtg tgg tca ttc cgc tac atg ttc taggcattta aggctttcag 648
Ala Ala Ala Val Trp Ser Phe Arg Tyr Met Phe
170 175

gcc 651

<210> 90
<211> 176
<212> PRT

<213> Corynebacterium glutamicum

<400> 90

```
Met Ile Gly Gly Ile Ile Gly Leu Ile Leu Ser Val Ile Ile Met Ala
  1               5                  10                  15

Glu Lys Leu Ala Ile Leu Glu Asp Pro Gly His Ile Thr Ser Cys Asp
             20                  25                  30

Phe Asn Ala Val Leu Ala Cys Gly Asp Val Met Arg Ser Gly Gln Ala
         35                  40                  45

Asn Ala Phe Gly Ile Pro Asn Pro Leu Ile Gly Ile Ala Gly Phe Ala
     50                  55                  60

Ala Val Ala Ile Ile Gly Ala Gly Ile Leu Ala Gly Gly Gly Phe Arg
 65                  70                  75                  80

Gly Trp Phe Trp Phe Gly Ala Gln Ala Gly Leu Thr Phe Ala Met Met
                 85                  90                  95

Phe Cys His Trp Leu Ala Tyr Gln Ser Met Ser Val Ile Arg Ala Leu
            100                 105                 110

Cys Pro Tyr Cys Met Gly Val Trp Thr Val Ser Ile Ile Met Phe Val
        115                 120                 125

Leu Val Thr Ala Trp Asn Val Lys Thr Phe Ser Gly Ser Asp Ser Thr
    130                 135                 140

Phe Val Asn Ala Leu Tyr Lys Tyr Lys Trp Val Ile Ala Ile Val Trp
145                 150                 155                 160

Leu Leu Leu Ile Ala Ala Ala Ala Val Trp Ser Phe Arg Tyr Met Phe
                165                 170                 175
```

<210> 91
<211> 651
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(628)
<223> FRXA00087

<400> 91

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tcgtcagtca acaaacgttt tcccacccgg aggtctcccc gtgtctaccg aaatccacaa 60

cgccccaccc aaggccccaa cttggcttgg ctgggtgctc atg atc ggc gga ata   115
                                              Met Ile Gly Gly Ile
                                                1               5

atc ggc ctc att ttg tcg gtg atc atc atg gcc gaa aaa ctt gcc atc   163
Ile Gly Leu Ile Leu Ser Val Ile Ile Met Ala Glu Lys Leu Ala Ile
            10                  15                  20
```

```
ctc gag gat ccc ggt cac atc acc agc tgc gat ttc aat gca gtc cta   211
Leu Glu Asp Pro Gly His Ile Thr Ser Cys Asp Phe Asn Ala Val Leu
            25                  30                  35

gct tgt ggc gat gtc atg cgt tcc ggc caa gct aac gcg ttc ggc atc   259
Ala Cys Gly Asp Val Met Arg Ser Gly Gln Ala Asn Ala Phe Gly Ile
        40                  45                  50

ccg aat ccg ctc atc ggc atc gcc ggt ttc gcc gct gtc gcc atc atc   307
Pro Asn Pro Leu Ile Gly Ile Ala Gly Phe Ala Ala Val Ala Ile Ile
    55                  60                  65

ggc gcc ggc atc ctc gcg ggc ggc ggg ttc cgc ggt tgg ttc tgg ttc   355
Gly Ala Gly Ile Leu Ala Gly Gly Gly Phe Arg Gly Trp Phe Trp Phe
70                  75                  80                  85

ggc gcc cag gcc gga ctc act ttt gcc atg atg ttc tgc cac tgg ctc   403
Gly Ala Gln Ala Gly Leu Thr Phe Ala Met Met Phe Cys His Trp Leu
                90                  95                  100

gcc tac caa tcc atg tcc gtc atc cgc gcg ctc tgc cct tac tgc atg   451
Ala Tyr Gln Ser Met Ser Val Ile Arg Ala Leu Cys Pro Tyr Cys Met
            105                 110                 115

ggc gtg tgg acc gta tcg atc atc atg ttc gtg ctg gtc act gca tgg   499
Gly Val Trp Thr Val Ser Ile Ile Met Phe Val Leu Val Thr Ala Trp
        120                 125                 130

aat gtg aaa act ttc agc ggc tcc gac agc acg ttc gtc aac gca ctg   547
Asn Val Lys Thr Phe Ser Gly Ser Asp Ser Thr Phe Val Asn Ala Leu
    135                 140                 145

tac aaa tac aag tgg gtc atc gcg atc gtc tgg ctg ctg ctc atc gca   595
Tyr Lys Tyr Lys Trp Val Ile Ala Ile Val Trp Leu Leu Leu Ile Ala
150                 155                 160                 165

gcc gca gct gtg tgg tca ttc cgc tac atg ttc taggcattta aggctttcag 648
Ala Ala Ala Val Trp Ser Phe Arg Tyr Met Phe
                170                 175

gcc                                                               651
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CORRECTED SHEET (RULE 91)

<210> 92
<211> 176
<212> PRT
<213> Corynebacterium glutamicum

<400> 92

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Met Ile Gly Gly Ile Ile Gly Leu Ile Leu Ser Val Ile Ile Met Ala
  1               5                  10                  15

Glu Lys Leu Ala Ile Leu Glu Asp Pro Gly His Ile Thr Ser Cys Asp
            20                  25                  30

Phe Asn Ala Val Leu Ala Cys Gly Asp Val Met Arg Ser Gly Gln Ala
        35                  40                  45

Asn Ala Phe Gly Ile Pro Asn Pro Leu Ile Gly Ile Ala Gly Phe Ala
    50                  55                  60
```

```
Ala Val Ala Ile Ile Gly Ala Gly Ile Leu Ala Gly Gly Gly Phe Arg
 65                  70                  75                  80

Gly Trp Phe Trp Phe Gly Ala Gln Ala Gly Leu Thr Phe Ala Met Met
                 85                  90                  95

Phe Cys His Trp Leu Ala Tyr Gln Ser Met Ser Val Ile Arg Ala Leu
            100                 105                 110

Cys Pro Tyr Cys Met Gly Val Trp Thr Val Ser Ile Ile Met Phe Val
        115                 120                 125

Leu Val Thr Ala Trp Asn Val Lys Thr Phe Ser Gly Ser Asp Ser Thr
    130                 135                 140

Phe Val Asn Ala Leu Tyr Lys Tyr Lys Trp Val Ile Ala Ile Val Trp
145                 150                 155                 160

Leu Leu Leu Ile Ala Ala Ala Ala Val Trp Ser Phe Arg Tyr Met Phe
                165                 170                 175
```

<210> 93
<211> 426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(403)
<223> RXN00096

<400> 93
ggggaacctg gggtaaaagg agaagtattc attaccccaa taacctacta ggtggggtgg 60

```
acacgcatag tcgacagcca gacgtggcag aatagtgtgc atg act aat gca ggt   115
                                        Met Thr Asn Ala Gly
                                          1               5

gac aac ttc gag atc agg atg cct tct ggc acg gat gac cca ttg tcc   163
Asp Asn Phe Glu Ile Arg Met Pro Ser Gly Thr Asp Asp Pro Leu Ser
                 10                  15                  20

gat gcg gag atc caa aag tat cgc gag gag atc aac cgc ttg gac cgc   211
Asp Ala Glu Ile Gln Lys Tyr Arg Glu Glu Ile Asn Arg Leu Asp Arg
             25                  30                  35

gaa atc ctc gat gcg gtg aaa cgc cgc acg aag att tcc caa acc atc   259
Glu Ile Leu Asp Ala Val Lys Arg Arg Thr Lys Ile Ser Gln Thr Ile
         40                  45                  50

gga aaa aca cgc atg agc tcg ggc gga aca cgt ctc gtg cac acc cga   307
Gly Lys Thr Arg Met Ser Ser Gly Gly Thr Arg Leu Val His Thr Arg
     55                  60                  65

gaa gta gca atc atc aac caa ttc cgt gaa gag atc ggc gag gaa ggc   355
Glu Val Ala Ile Ile Asn Gln Phe Arg Glu Glu Ile Gly Glu Glu Gly
 70                  75                  80                  85
```

```
cct gcc ctc gct gga att ttg ctg cgc atg gga cgc gga aaa ctc gga   403
Pro Ala Leu Ala Gly Ile Leu Leu Arg Met Gly Arg Gly Lys Leu Gly
                 90                  95                  100

taagttatcc acaggtagaa aaa                                       426


<210> 94
<211> 101
<212> PRT
<213> Corynebacterium glutamicum

<400> 94
Met Thr Asn Ala Gly Asp Asn Phe Glu Ile Arg Met Pro Ser Gly Thr
  1               5                  10                  15

Asp Asp Pro Leu Ser Asp Ala Glu Ile Gln Lys Tyr Arg Glu Glu Ile
             20                  25                  30

Asn Arg Leu Asp Arg Glu Ile Leu Asp Ala Val Lys Arg Arg Thr Lys
         35                  40                  45

Ile Ser Gln Thr Ile Gly Lys Thr Arg Met Ser Ser Gly Gly Thr Arg
     50                  55                  60

Leu Val His Thr Arg Glu Val Ala Ile Ile Asn Gln Phe Arg Glu Glu
 65                  70                  75                  80

Ile Gly Glu Glu Gly Pro Ala Leu Ala Gly Ile Leu Leu Arg Met Gly
                 85                  90                  95

Arg Gly Lys Leu Gly
             100


<210> 95
<211> 426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(403)
<223> FRXA00096

<400> 95
ggggaacctg gggtaaaagg agaagtattc attaccccaa taacctacta ggtggggtgg 60

acacgcatag tcgacagcca gacgtggcag aatagtgtgc atg act aat gca ggt   115
                                        Met Thr Asn Ala Gly
                                          1               5

gac aac ttc gag atc agg atg cct tct ggc acg gat gac cca ttg tcc   163
Asp Asn Phe Glu Ile Arg Met Pro Ser Gly Thr Asp Asp Pro Leu Ser
                 10                  15                  20

gat gcg gag atc caa aag tat cgc gag gag atc aac cgc ttg gac cgc   211
Asp Ala Glu Ile Gln Lys Tyr Arg Glu Glu Ile Asn Arg Leu Asp Arg
             25                  30                  35
```

```
gaa atc ctc gat gcg gtg aaa cgc cgc acg aag att tcc caa acc atc   259
Glu Ile Leu Asp Ala Val Lys Arg Arg Thr Lys Ile Ser Gln Thr Ile
         40                  45                  50

gga aaa aca cgc atg agc tcg ggc gga aca cgt ctc gtg cac acc cga   307
Gly Lys Thr Arg Met Ser Ser Gly Gly Thr Arg Leu Val His Thr Arg
     55                  60                  65

gaa gta gca atc atc aac cag ttc cgt gaa gag atc ggc gag gaa ggc   355
Glu Val Ala Ile Ile Asn Gln Phe Arg Glu Glu Ile Gly Glu Glu Gly
 70                  75                  80                  85

cct gcc ctc gct gga att ttg ctg cgc atg gga cgc gga aaa ctc gga   403
Pro Ala Leu Ala Gly Ile Leu Leu Arg Met Gly Arg Gly Lys Leu Gly
                 90                  95                 100

taagttatcc acaggtagaa aaa                                        426
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<210> 96
<211> 101
<212> PRT
<213> Corynebacterium glutamicum

<400> 96

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Met Thr Asn Ala Gly Asp Asn Phe Glu Ile Arg Met Pro Ser Gly Thr
  1               5                  10                  15

Asp Asp Pro Leu Ser Asp Ala Glu Ile Gln Lys Tyr Arg Glu Glu Ile
             20                  25                  30

Asn Arg Leu Asp Arg Glu Ile Leu Asp Ala Val Lys Arg Arg Thr Lys
         35                  40                  45

Ile Ser Gln Thr Ile Gly Lys Thr Arg Met Ser Ser Gly Gly Thr Arg
     50                  55                  60

Leu Val His Thr Arg Glu Val Ala Ile Ile Asn Gln Phe Arg Glu Glu
 65                  70                  75                  80

Ile Gly Glu Glu Gly Pro Ala Leu Ala Gly Ile Leu Leu Arg Met Gly
                 85                  90                  95

Arg Gly Lys Leu Gly
            100
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<210> 97
<211> 1299
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1276)
<223> RXN00097

<400> 97

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tcagggtttt agccgttgat gggcagagtt atccacaggt ttttagcgag ctggtttccg 60

acgaagaaaa tagtggatag gttacagggc agaatcccga atg gag gtg cct tcc   115
```

```
                                                    Met Glu Val Pro Ser
                                                      1               5

ttg ttt acc aac ttc ttc gca gtc aac aac cca gac agt ccg ccc gca   163
Leu Phe Thr Asn Phe Phe Ala Val Asn Asn Pro Asp Ser Pro Pro Ala
                10                  15                  20

cga caa aaa acc aaa ctc aga gaa ctg gaa cac cgc ttc tgg caa gaa   211
Arg Gln Lys Thr Lys Leu Arg Glu Leu Glu His Arg Phe Trp Gln Glu
            25                  30                  35

cac ctg cca ggc gac gac gat gac cat tcc acc gca atc tcc agc ctc   259
His Leu Pro Gly Asp Asp Asp Asp His Ser Thr Ala Ile Ser Ser Leu
        40                  45                  50

gcc atc gtc aca ggt cta aca aaa gcg cag gtc tcc cgc ata tcc atc   307
Ala Ile Val Thr Gly Leu Thr Lys Ala Gln Val Ser Arg Ile Ser Ile
    55                  60                  65

gcg ttt gcc acg ctc gcc gac ttg ccc gaa ctc aaa gcc ctg caa caa   355
Ala Phe Ala Thr Leu Ala Asp Leu Pro Glu Leu Lys Ala Leu Gln Gln
70                  75                  80                  85

aag ctg tac cac ctc gac ctc tcc cga ctg atc acc att agc aac gaa   403
Lys Leu Tyr His Leu Asp Leu Ser Arg Leu Ile Thr Ile Ser Asn Glu
                90                  95                  100

ctc gcc ggc atc aac ccc gac aac ctc gcc ggc gcc gac gca atc ctc   451
Leu Ala Gly Ile Asn Pro Asp Asn Leu Ala Gly Ala Asp Ala Ile Leu
            105                 110                 115

acc gaa tac ctc acc gcc acc agc ccc aac cag att ctg cca agc ccg   499
Thr Glu Tyr Leu Thr Ala Thr Ser Pro Asn Gln Ile Leu Pro Ser Pro
        120                 125                 130

gcg tcc ata gga cgc aag ata aaa gaa ata aga gat ttg ctt gac gac   547
Ala Ser Ile Gly Arg Lys Ile Lys Glu Ile Arg Asp Leu Leu Asp Asp
    135                 140                 145

gca aga gcc acc ggt tcg cgc ggt acc caa gac gac agc tct ttc gga   595
Ala Arg Ala Thr Gly Ser Arg Gly Thr Gln Asp Asp Ser Ser Phe Gly
150                 155                 160                 165

gtg acc ttc tcc cca gac gga acc gcc gaa atc gga gcc tcc gtc gat   643
Val Thr Phe Ser Pro Asp Gly Thr Ala Glu Ile Gly Ala Ser Val Asp
                170                 175                 180

gct gtg gac ggg cac atc atc aac gac gcc gtc acc caa cac gcg aag   691
Ala Val Asp Gly His Ile Ile Asn Asp Ala Val Thr Gln His Ala Lys
            185                 190                 195

aaa aac gac ctc acc tac ggc gaa gct ttc agc gac atc ctt cgg aac   739
Lys Asn Asp Leu Thr Tyr Gly Glu Ala Phe Ser Asp Ile Leu Arg Asn
        200                 205                 210

aat atc caa gtc aag gta gtc ctc aac ttg tac acc gcc aaa gac ctc   787
Asn Ile Gln Val Lys Val Val Leu Asn Leu Tyr Thr Ala Lys Asp Leu
    215                 220                 225

gcc aac gcc cca gtg tgg gcc agc gga atc ggc tgg ttg gat gcc aag   835
Ala Asn Ala Pro Val Trp Ala Ser Gly Ile Gly Trp Leu Asp Ala Lys
```

```
230                 235                 240                 245

act gga aca ttc tgg tca gag aaa gcc aac aaa gaa caa gac atg gat   883
Thr Gly Thr Phe Trp Ser Glu Lys Ala Asn Lys Glu Gln Asp Met Asp
                250                 255                 260

gcg gct gcc aaa atc agc acc gac aaa cac gat cct cca cca gcg ttg   931
Ala Ala Ala Lys Ile Ser Thr Asp Lys His Asp Pro Pro Pro Ala Leu
            265                 270                 275

cgt gac gca ctc att ggt cgt gat ggc acc tgc cga ttc cct ggc tgt   979
Arg Asp Ala Leu Ile Gly Arg Asp Gly Thr Cys Arg Phe Pro Gly Cys
        280                 285                 290

tca gtc cca gcg ctc aaa acc caa gcc gac cac cgc atc ccc tac gaa   1027
Ser Val Pro Ala Leu Lys Thr Gln Ala Asp His Arg Ile Pro Tyr Glu
    295                 300                 305

gaa ggc gga gaa act tgc cta ggc gga atc ggc tgc ctc tgt caa cac   1075
Glu Gly Gly Glu Thr Cys Leu Gly Gly Ile Gly Cys Leu Cys Gln His
310                 315                 320                 325

cac cac aac atg aaa acc gac ggc cga gtc acc tac ctt ctc gat ccc   1123
His His Asn Met Lys Thr Asp Gly Arg Val Thr Tyr Leu Leu Asp Pro
                330                 335                 340

ttc tcc ggc atc atc gtc tgg ctc atg gga gac gga aca tgg gca gtg   1171
Phe Ser Gly Ile Ile Val Trp Leu Met Gly Asp Gly Thr Trp Ala Val
            345                 350                 355

tca gaa ccc aac ggg ccg ctc aat ccc aaa aat gcg aga tgg gcg caa   1219
Ser Glu Pro Asn Gly Pro Leu Asn Pro Lys Asn Ala Arg Trp Ala Gln
        360                 365                 370

aca gtc gcc caa cac cgg gca cgc cac cac aag cgt tgg gtt aag gag   1267
Thr Val Ala Gln His Arg Ala Arg His His Lys Arg Trp Val Lys Glu
    375                 380                 385

gac gcc aag tagccggatg gccacgtcga aaa                            1299
Asp Ala Lys
390
```

<210> 98
<211> 392
<212> PRT
<213> Corynebacterium glutamicum

<400> 98

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Met Glu Val Pro Ser Leu Phe Thr Asn Phe Phe Ala Val Asn Asn Pro
  1               5                  10                  15

Asp Ser Pro Pro Ala Arg Gln Lys Thr Lys Leu Arg Glu Leu Glu His
             20                  25                  30

Arg Phe Trp Gln Glu His Leu Pro Gly Asp Asp Asp His Ser Thr
         35                  40                  45

Ala Ile Ser Ser Leu Ala Ile Val Thr Gly Leu Thr Lys Ala Gln Val
     50                  55                  60
```

```
Ser Arg Ile Ser Ile Ala Phe Ala Thr Leu Ala Asp Leu Pro Glu Leu
 65                  70                  75                  80

Lys Ala Leu Gln Gln Lys Leu Tyr His Leu Asp Leu Ser Arg Leu Ile
                85                  90                  95

Thr Ile Ser Asn Glu Leu Ala Gly Ile Asn Pro Asp Asn Leu Ala Gly
            100                 105                 110

Ala Asp Ala Ile Leu Thr Glu Tyr Leu Thr Ala Thr Ser Pro Asn Gln
        115                 120                 125

Ile Leu Pro Ser Pro Ala Ser Ile Gly Arg Lys Ile Lys Glu Ile Arg
    130                 135                 140

Asp Leu Leu Asp Asp Ala Arg Ala Thr Gly Ser Arg Gly Thr Gln Asp
145                 150                 155                 160

Asp Ser Ser Phe Gly Val Thr Phe Ser Pro Asp Gly Thr Ala Glu Ile
                165                 170                 175

Gly Ala Ser Val Asp Ala Val Asp Gly His Ile Ile Asn Asp Ala Val
            180                 185                 190

Thr Gln His Ala Lys Lys Asn Asp Leu Thr Tyr Gly Glu Ala Phe Ser
        195                 200                 205

Asp Ile Leu Arg Asn Asn Ile Gln Val Lys Val Val Leu Asn Leu Tyr
    210                 215                 220

Thr Ala Lys Asp Leu Ala Asn Ala Pro Val Trp Ala Ser Gly Ile Gly
225                 230                 235                 240

Trp Leu Asp Ala Lys Thr Gly Thr Phe Trp Ser Glu Lys Ala Asn Lys
                245                 250                 255

Glu Gln Asp Met Asp Ala Ala Ala Lys Ile Ser Thr Asp Lys His Asp
            260                 265                 270

Pro Pro Pro Ala Leu Arg Asp Ala Leu Ile Gly Arg Asp Gly Thr Cys
        275                 280                 285

Arg Phe Pro Gly Cys Ser Val Pro Ala Leu Lys Thr Gln Ala Asp His
    290                 295                 300

Arg Ile Pro Tyr Glu Glu Gly Gly Glu Thr Cys Leu Gly Gly Ile Gly
305                 310                 315                 320

Cys Leu Cys Gln His His His Asn Met Lys Thr Asp Gly Arg Val Thr
                325                 330                 335

Tyr Leu Leu Asp Pro Phe Ser Gly Ile Ile Val Trp Leu Met Gly Asp
            340                 345                 350

Gly Thr Trp Ala Val Ser Glu Pro Asn Gly Pro Leu Asn Pro Lys Asn
        355                 360                 365

Ala Arg Trp Ala Gln Thr Val Ala Gln His Arg Ala Arg His His Lys
    370                 375                 380

Arg Trp Val Lys Glu Asp Ala Lys
```

385 390

<210> 99
<211> 1284
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1261)
<223> FRXA00097

<400> 99
ttgatgggca gagttatcca caggttttta gcgagctggt ttccgacgaa gaaaatagtg 60

gataggttac agggcagaat cccgaatgga ggtgccttcc ttg ttt acc aac ttc 115
Leu Phe Thr Asn Phe
1 5

ttc gca gtc aac aac cca gac agt ccg ccc gca cga caa aaa acc aaa 163
Phe Ala Val Asn Asn Pro Asp Ser Pro Pro Ala Arg Gln Lys Thr Lys
10 15 20

ctc aga gaa ctg gaa cac cgc ttc tgg caa gaa cac ctg cca ggc gac 211
Leu Arg Glu Leu Glu His Arg Phe Trp Gln Glu His Leu Pro Gly Asp
25 30 35

gac gat gac cat tcc acc gca atc tcc agc ctc gcc atc gtc aca ggt 259
Asp Asp Asp His Ser Thr Ala Ile Ser Ser Leu Ala Ile Val Thr Gly
40 45 50

cta aca aaa gcg cag gtc tcc cgc ata tcc atc gcg ttt gcc acg ctc 307
Leu Thr Lys Ala Gln Val Ser Arg Ile Ser Ile Ala Phe Ala Thr Leu
55 60 65

gcc gac ttg ccc gaa ctc aaa gcc ctg caa caa aag ctg tac cac ctc 355
Ala Asp Leu Pro Glu Leu Lys Ala Leu Gln Gln Lys Leu Tyr His Leu
70 75 80 85

gac ctc tcc cga ctg atc acc att agc aac gaa ctc gcc ggc atc aac 403
Asp Leu Ser Arg Leu Ile Thr Ile Ser Asn Glu Leu Ala Gly Ile Asn
90 95 100

ccc gac aac ctc gcc ggc gcc gac gca atc ctc acc gaa tac ctc acc 451
Pro Asp Asn Leu Ala Gly Ala Asp Ala Ile Leu Thr Glu Tyr Leu Thr
105 110 115

gcc acc agc ccc aac cag att ctg cca agc ccg gcg tcc ata gga cgc 499
Ala Thr Ser Pro Asn Gln Ile Leu Pro Ser Pro Ala Ser Ile Gly Arg
120 125 130

aag ata aaa gaa ata aga gat ttg ctt gac gac gca aga gcc acc ggt 547
Lys Ile Lys Glu Ile Arg Asp Leu Leu Asp Asp Ala Arg Ala Thr Gly
135 140 145

tcg cgc ggt acc caa gac gac agc tct ttc gga gtg acc ttc tcc cca 595
Ser Arg Gly Thr Gln Asp Asp Ser Ser Phe Gly Val Thr Phe Ser Pro
150 155 160 165

gac gga acc gcc gaa atc gga gcc tcc gtc gat gct gtg gac ggg cac 643

```
Asp Gly Thr Ala Glu Ile Gly Ala Ser Val Asp Ala Val Asp Gly His
                170                 175                 180

atc atc aac gac gcc gtc acc caa cac gcg aag aaa aac gac ctc acc   691
Ile Ile Asn Asp Ala Val Thr Gln His Ala Lys Lys Asn Asp Leu Thr
            185                 190                 195

tac ggc gaa gct ttc agc gac atc ctt cgg aac aat atc caa gtc aag   739
Tyr Gly Glu Ala Phe Ser Asp Ile Leu Arg Asn Asn Ile Gln Val Lys
        200                 205                 210

gta gtc ctc aac ttg tac acc gcc aaa gac ctc gcc aac gcc cca gtg   787
Val Val Leu Asn Leu Tyr Thr Ala Lys Asp Leu Ala Asn Ala Pro Val
    215                 220                 225

tgg gcc agc gga atc ggc tgg ttg gat gcc aag act gga aca ttc tgg   835
Trp Ala Ser Gly Ile Gly Trp Leu Asp Ala Lys Thr Gly Thr Phe Trp
230                 235                 240                 245

tca gag aaa gcc aac aaa gaa caa gac atg gat gcg gct gcc aaa atc   883
Ser Glu Lys Ala Asn Lys Glu Gln Asp Met Asp Ala Ala Ala Lys Ile
                250                 255                 260

agc acc gac aaa cac gat cct cca cca gcg ttg cgt gac gca ctc att   931
Ser Thr Asp Lys His Asp Pro Pro Pro Ala Leu Arg Asp Ala Leu Ile
            265                 270                 275

ggt cgt gat ggc acc tgc cga ttc cct ggc tgt tca gtc cca gcg ctc   979
Gly Arg Asp Gly Thr Cys Arg Phe Pro Gly Cys Ser Val Pro Ala Leu
        280                 285                 290

aaa acc caa gcc gac cac cgc atc ccc tac gaa gaa ggc gga gaa act   1027
Lys Thr Gln Ala Asp His Arg Ile Pro Tyr Glu Glu Gly Gly Glu Thr
    295                 300                 305

tgc cta ggc gga atc ggc tgc ctc tgt caa cac cac cac aac atg aaa   1075
Cys Leu Gly Gly Ile Gly Cys Leu Cys Gln His His His Asn Met Lys
310                 315                 320                 325

acc gac ggc cga gtc acc tac ctt ctc gat ccc ttc tcc ggc atc atc   1123
Thr Asp Gly Arg Val Thr Tyr Leu Leu Asp Pro Phe Ser Gly Ile Ile
                330                 335                 340

gtc tgg ctc atg gga gac gga aca tgg gca gtg tca gaa ccc aac ggg   1171
Val Trp Leu Met Gly Asp Gly Thr Trp Ala Val Ser Glu Pro Asn Gly
            345                 350                 355

ccg ctc aat ccc aaa aat gcg aga tgg gcg caa aca gtc gcc caa cac   1219
Pro Leu Asn Pro Lys Asn Ala Arg Trp Ala Gln Thr Val Ala Gln His
        360                 365                 370

cgg gca cgc cac cac aag cgt tgg gtt aag gag gac gcc aag           1261
Arg Ala Arg His His Lys Arg Trp Val Lys Glu Asp Ala Lys
    375                 380                 385

tagccggatg gccacgtcga aaa                                        1284
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<210> 100
<211> 387
<212> PRT

<213> Corynebacterium glutamicum

<400> 100

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Leu Phe Thr Asn Phe Phe Ala Val Asn Asn Pro Asp Ser Pro Pro Ala
 1               5                  10                  15

Arg Gln Lys Thr Lys Leu Arg Glu Leu Glu His Arg Phe Trp Gln Glu
            20                  25                  30

His Leu Pro Gly Asp Asp Asp Asp His Ser Thr Ala Ile Ser Ser Leu
        35                  40                  45

Ala Ile Val Thr Gly Leu Thr Lys Ala Gln Val Ser Arg Ile Ser Ile
    50                  55                  60

Ala Phe Ala Thr Leu Ala Asp Leu Pro Glu Leu Lys Ala Leu Gln Gln
65                  70                  75                  80

Lys Leu Tyr His Leu Asp Leu Ser Arg Leu Ile Thr Ile Ser Asn Glu
                85                  90                  95

Leu Ala Gly Ile Asn Pro Asp Asn Leu Ala Gly Ala Asp Ala Ile Leu
            100                 105                 110

Thr Glu Tyr Leu Thr Ala Thr Ser Pro Asn Gln Ile Leu Pro Ser Pro
        115                 120                 125

Ala Ser Ile Gly Arg Lys Ile Lys Glu Ile Arg Asp Leu Leu Asp Asp
    130                 135                 140

Ala Arg Ala Thr Gly Ser Arg Gly Thr Gln Asp Asp Ser Ser Phe Gly
145                 150                 155                 160

Val Thr Phe Ser Pro Asp Gly Thr Ala Glu Ile Gly Ala Ser Val Asp
                165                 170                 175

Ala Val Asp Gly His Ile Ile Asn Asp Ala Val Thr Gln His Ala Lys
            180                 185                 190

Lys Asn Asp Leu Thr Tyr Gly Glu Ala Phe Ser Asp Ile Leu Arg Asn
        195                 200                 205

Asn Ile Gln Val Lys Val Val Leu Asn Leu Tyr Thr Ala Lys Asp Leu
    210                 215                 220

Ala Asn Ala Pro Val Trp Ala Ser Gly Ile Gly Trp Leu Asp Ala Lys
225                 230                 235                 240

Thr Gly Thr Phe Trp Ser Glu Lys Ala Asn Lys Glu Gln Asp Met Asp
                245                 250                 255

Ala Ala Ala Lys Ile Ser Thr Asp Lys His Asp Pro Pro Pro Ala Leu
            260                 265                 270

Arg Asp Ala Leu Ile Gly Arg Asp Gly Thr Cys Arg Phe Pro Gly Cys
        275                 280                 285

Ser Val Pro Ala Leu Lys Thr Gln Ala Asp His Arg Ile Pro Tyr Glu
    290                 295                 300

Glu Gly Gly Glu Thr Cys Leu Gly Gly Ile Gly Cys Leu Cys Gln His
```

```
305                 310                 315                 320

His His Asn Met Lys Thr Asp Gly Arg Val Thr Tyr Leu Leu Asp Pro
                325                 330                 335

Phe Ser Gly Ile Ile Val Trp Leu Met Gly Asp Gly Thr Trp Ala Val
            340                 345                 350

Ser Glu Pro Asn Gly Pro Leu Asn Pro Lys Asn Ala Arg Trp Ala Gln
        355                 360                 365

Thr Val Ala Gln His Arg Ala Arg His His Lys Arg Trp Val Lys Glu
    370                 375                 380

Asp Ala Lys
385
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<210> 101
<211> 612
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(589)
<223> RXN00114

<400> 101

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tgcattccct aacgggaatg cagctttttg tgttcctagt gcaaatcgaa atctcatgtg 60

atttacttaa aacctaatta aatctactat cggagatctc atg aaa ctt ctc aag   115
                                              Met Lys Leu Leu Lys
                                                1               5

ttt gct gca gca gga acc ttc gca cta gcc ctg gct ggc tgc aca cag   163
Phe Ala Ala Ala Gly Thr Phe Ala Leu Ala Leu Ala Gly Cys Thr Gln
                10                  15                  20

act gag tct ctc gta gca aca atc gaa tct gca acc tct gca gca cag   211
Thr Glu Ser Leu Val Ala Thr Ile Glu Ser Ala Thr Ser Ala Ala Gln
            25                  30                  35

gca tcc gga aac gac gta gaa gga gac caa acc tcc gcg ttc gaa ctc   259
Ala Ser Gly Asn Asp Val Glu Gly Asp Gln Thr Ser Ala Phe Glu Leu
        40                  45                  50

tcc gtt ggc gaa tgc ttc aac gac acc tac gaa gaa gaa atc tcc gaa   307
Ser Val Gly Glu Cys Phe Asn Asp Thr Tyr Glu Glu Glu Ile Ser Glu
    55                  60                  65

gta ccc atc gtc gac tgc gca gaa cct cac gac aac gag atc tac tac   355
Val Pro Ile Val Asp Cys Ala Glu Pro His Asp Asn Glu Ile Tyr Tyr
70                  75                  80                  85

ctc tac gac atc gaa ggc gac gac ttc cca acc gac atc acc acc aca   403
Leu Tyr Asp Ile Glu Gly Asp Asp Phe Pro Thr Asp Ile Thr Thr Thr
                90                  95                  100

ggc tac gaa ggc tgc ctc cca aca ttt gaa ggc ttc gta gga gct cct   451
Gly Tyr Glu Gly Cys Leu Pro Thr Phe Glu Gly Phe Val Gly Ala Pro
```

```
            105                 110                 115

tac gaa acc tcc atc tac gag gtc tac cca atg acc cca acc ttt ggc   499
Tyr Glu Thr Ser Ile Tyr Glu Val Tyr Pro Met Thr Pro Thr Phe Gly
        120                 125                 130

tcc tgg aca aac ggc gac cgc gag gta gtg tgc tcc gtg tac ttg gcc   547
Ser Trp Thr Asn Gly Asp Arg Glu Val Val Cys Ser Val Tyr Leu Ala
    135                 140                 145

acc ggt gag cag atg acc gga acc gca gca gga acc gcg cag           589
Thr Gly Glu Gln Met Thr Gly Thr Ala Ala Gly Thr Ala Gln
150                 155                 160

tagattttgg atagggaatt ttg                                        612


<210> 102
<211> 163
<212> PRT
<213> Corynebacterium glutamicum

<400> 102
Met Lys Leu Leu Lys Phe Ala Ala Ala Gly Thr Phe Ala Leu Ala Leu
  1               5                  10                  15

Ala Gly Cys Thr Gln Thr Glu Ser Leu Val Ala Thr Ile Glu Ser Ala
             20                  25                  30

Thr Ser Ala Ala Gln Ala Ser Gly Asn Asp Val Glu Gly Asp Gln Thr
         35                  40                  45

Ser Ala Phe Glu Leu Ser Val Gly Glu Cys Phe Asn Asp Thr Tyr Glu
     50                  55                  60

Glu Glu Ile Ser Glu Val Pro Ile Val Asp Cys Ala Glu Pro His Asp
 65                  70                  75                  80

Asn Glu Ile Tyr Tyr Leu Tyr Asp Ile Glu Gly Asp Asp Phe Pro Thr
                 85                  90                  95

Asp Ile Thr Thr Thr Gly Tyr Glu Gly Cys Leu Pro Thr Phe Glu Gly
            100                 105                 110

Phe Val Gly Ala Pro Tyr Glu Thr Ser Ile Tyr Glu Val Tyr Pro Met
        115                 120                 125

Thr Pro Thr Phe Gly Ser Trp Thr Asn Gly Asp Arg Glu Val Val Cys
    130                 135                 140

Ser Val Tyr Leu Ala Thr Gly Glu Gln Met Thr Gly Thr Ala Ala Gly
145                 150                 155                 160

Thr Ala Gln


<210> 103
<211> 612
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(589)
<223> FRXA00114

<400> 103
tgcattccct aacgggaatg cagctttttg tgttcctagt gcaaatcgaa atctcatgtg 60

atttacttaa aacctaatta aatctactat cggagatctc atg aaa ctt ctc aag 115
Met Lys Leu Leu Lys
1 5

ttt gct gca gca gga acc ttc gca cta gcc ctg gct ggc tgc aca cag 163
Phe Ala Ala Ala Gly Thr Phe Ala Leu Ala Leu Ala Gly Cys Thr Gln
10 15 20

act gag tct ctc gta gca aca atc gaa tct gca acc tct gca gca cag 211
Thr Glu Ser Leu Val Ala Thr Ile Glu Ser Ala Thr Ser Ala Ala Gln
25 30 35

gca tcc gga aac gac gta gaa gga gac caa acc tcc gcg ttc gaa ctc 259
Ala Ser Gly Asn Asp Val Glu Gly Asp Gln Thr Ser Ala Phe Glu Leu
40 45 50

tcc gtt ggc gaa tgc ttc aac gac acc tac gaa gaa gaa atc tcc gaa 307
Ser Val Gly Glu Cys Phe Asn Asp Thr Tyr Glu Glu Glu Ile Ser Glu
55 60 65

gta ccc atc gtc gac tgc gca gaa cct cac gac aac gag atc tac tac 355
Val Pro Ile Val Asp Cys Ala Glu Pro His Asp Asn Glu Ile Tyr Tyr
70 75 80 85

ctc tac gac atc gaa ggc gac gac ttc cca acc gac atc acc acc aca 403
Leu Tyr Asp Ile Glu Gly Asp Asp Phe Pro Thr Asp Ile Thr Thr Thr
90 95 100

ggc tac gaa ggc tgc ctc cca aca ttt gaa ggc ttc gta gga gct cct 451
Gly Tyr Glu Gly Cys Leu Pro Thr Phe Glu Gly Phe Val Gly Ala Pro
105 110 115

tac gaa acc tcc atc tac gag gtc tac cca atg acc cca acc ttt ggc 499
Tyr Glu Thr Ser Ile Tyr Glu Val Tyr Pro Met Thr Pro Thr Phe Gly
120 125 130

tcc tgg aca aac ggc gac cgc gag gta gtg tgc tcc gtg tac ttg gcc 547
Ser Trp Thr Asn Gly Asp Arg Glu Val Val Cys Ser Val Tyr Leu Ala
135 140 145

acc ggt gag cag atg acc gga acc gca gca gga acc gcg cag 589
Thr Gly Glu Gln Met Thr Gly Thr Ala Ala Gly Thr Ala Gln
150 155 160

tagattttgg atagggaatt ttg 612

<210> 104
<211> 163
<212> PRT
<213> Corynebacterium glutamicum

<400> 104
Met Lys Leu Leu Lys Phe Ala Ala Ala Gly Thr Phe Ala Leu Ala Leu
1 5 10 15

Ala Gly Cys Thr Gln Thr Glu Ser Leu Val Ala Thr Ile Glu Ser Ala
20 25 30

Thr Ser Ala Ala Gln Ala Ser Gly Asn Asp Val Glu Gly Asp Gln Thr
35 40 45

Ser Ala Phe Glu Leu Ser Val Gly Glu Cys Phe Asn Asp Thr Tyr Glu
50 55 60

Glu Glu Ile Ser Glu Val Pro Ile Val Asp Cys Ala Glu Pro His Asp
65 70 75 80

Asn Glu Ile Tyr Tyr Leu Tyr Asp Ile Glu Gly Asp Asp Phe Pro Thr
85 90 95

Asp Ile Thr Thr Thr Gly Tyr Glu Gly Cys Leu Pro Thr Phe Glu Gly
100 105 110

Phe Val Gly Ala Pro Tyr Glu Thr Ser Ile Tyr Glu Val Tyr Pro Met
115 120 125

Thr Pro Thr Phe Gly Ser Trp Thr Asn Gly Asp Arg Glu Val Val Cys
130 135 140

Ser Val Tyr Leu Ala Thr Gly Glu Gln Met Thr Gly Thr Ala Ala Gly
145 150 155 160

Thr Ala Gln

<210> 105
<211> 963
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(940)
<223> RXN00120

<400> 105
acaaactctt aatttaatga gacgtaagta gttgatagtt aggggaaata ctcccaaatc 60

ctcacaggaa acgctctgaa ttctttcaaa aaaatgtttc atg ctt att ggc atg 115
Met Leu Ile Gly Met
1 5

agc aat caa aca gtc aat caa gca gtg tcg tca ggg gtg aaa gca tcc 163
Ser Asn Gln Thr Val Asn Gln Ala Val Ser Ser Gly Val Lys Ala Ser
10 15 20

ccg cac agg ttc aat cgt ttt gaa atc aaa tac ttg att aca gag caa 211
Pro His Arg Phe Asn Arg Phe Glu Ile Lys Tyr Leu Ile Thr Glu Gln
25 30 35

gat gta cct gca ctc cgc gag cag ttg gca acg agg atg agc acg gat 259

```
Asp Val Pro Ala Leu Arg Glu Gln Leu Ala Thr Arg Met Ser Thr Asp
         40                  45                  50

ccg ctt tcc cca ccc gga ggc tac cga gtg gaa tcc ctt tac ttc gat   307
Pro Leu Ser Pro Pro Gly Gly Tyr Arg Val Glu Ser Leu Tyr Phe Asp
     55                  60                  65

tca gcc gat tta cgg tgc tac acc gaa aag atc gag ggt ctg aaa ttc   355
Ser Ala Asp Leu Arg Cys Tyr Thr Glu Lys Ile Glu Gly Leu Lys Phe
 70                  75                  80                  85

cga agg aaa cta cgg atc cgt acc tac ggt gat gga gtg ctc act cca   403
Arg Arg Lys Leu Arg Ile Arg Thr Tyr Gly Asp Gly Val Leu Thr Pro
             90                  95                 100

gaa tcc acc gtg tcg gta gag atc aag cag cgg gtt aac aaa gta act   451
Glu Ser Thr Val Ser Val Glu Ile Lys Gln Arg Val Asn Lys Val Thr
        105                 110                 115

caa aag cgt cgg ctg gat ttg ccc ttt ata tat gcg ctc gcc ctg ggc   499
Gln Lys Arg Arg Leu Asp Leu Pro Phe Ile Tyr Ala Leu Ala Leu Gly
    120                 125                 130

gat agc acg ggc gcc gcg gta ggc gag cag gtg gac gtc gag aag ctt   547
Asp Ser Thr Gly Ala Ala Val Gly Glu Gln Val Asp Val Glu Lys Leu
135                 140                 145

ctt gaa atc tct ccg gaa aac cag cac gct ttg att cac gaa atg gcg   595
Leu Glu Ile Ser Pro Glu Asn Gln His Ala Leu Ile His Glu Met Ala
150                 155                 160                 165

tcg ttt gct aaa aat tat cgg ctg cga ccc atc gcc acc acg aag tat   643
Ser Phe Ala Lys Asn Tyr Arg Leu Arg Pro Ile Ala Thr Thr Lys Tyr
                170                 175                 180

cac cgc gag gca ttc gtc ggc gct gat gcg gag gaa agt tcg cga gtc   691
His Arg Glu Ala Phe Val Gly Ala Asp Ala Glu Glu Ser Ser Arg Val
        185                 190                 195

acc att gac cac ggt gtt tca ggc cgt gat cgt gat ttt ctg ctt ggc   739
Thr Ile Asp His Gly Val Ser Gly Arg Asp Arg Asp Phe Leu Leu Gly
    200                 205                 210

caa gac ctt gaa gac cgc cca acg gtg gcg caa gga ttg gca gtc gtg   787
Gln Asp Leu Glu Asp Arg Pro Thr Val Ala Gln Gly Leu Ala Val Val
215                 220                 225

gaa atc aaa tgc gat gaa cgc gtg ccg ttt tgg ctc act gat atg act   835
Glu Ile Lys Cys Asp Glu Arg Val Pro Phe Trp Leu Thr Asp Met Thr
230                 235                 240                 245

gct caa ctg gaa atg tcc gtg att cgg atg tcc aaa tac tgc gaa acc   883
Ala Gln Leu Glu Met Ser Val Ile Arg Met Ser Lys Tyr Cys Glu Thr
                250                 255                 260

atc gaa gcg ttt cac aac cgt ccg gca tca gct ttc ggc gct gtc gac   931
Ile Glu Ala Phe His Asn Arg Pro Ala Ser Ala Phe Gly Ala Val Asp
        265                 270                 275

ccc atc ttc taaacaagaa aggcccctcc aat                            963
Pro Ile Phe
```

280

<210> 106
<211> 280
<212> PRT
<213> Corynebacterium glutamicum

<400> 106

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Met Leu Ile Gly Met Ser Asn Gln Thr Val Asn Gln Ala Val Ser Ser
 1               5                  10                  15

Gly Val Lys Ala Ser Pro His Arg Phe Asn Arg Phe Glu Ile Lys Tyr
            20                  25                  30

Leu Ile Thr Glu Gln Asp Val Pro Ala Leu Arg Glu Gln Leu Ala Thr
        35                  40                  45

Arg Met Ser Thr Asp Pro Leu Ser Pro Pro Gly Gly Tyr Arg Val Glu
    50                  55                  60

Ser Leu Tyr Phe Asp Ser Ala Asp Leu Arg Cys Tyr Thr Glu Lys Ile
65                  70                  75                  80

Glu Gly Leu Lys Phe Arg Arg Lys Leu Arg Ile Arg Thr Tyr Gly Asp
                85                  90                  95

Gly Val Leu Thr Pro Glu Ser Thr Val Ser Val Glu Ile Lys Gln Arg
            100                 105                 110

Val Asn Lys Val Thr Gln Lys Arg Arg Leu Asp Leu Pro Phe Ile Tyr
        115                 120                 125

Ala Leu Ala Leu Gly Asp Ser Thr Gly Ala Ala Val Gly Glu Gln Val
    130                 135                 140

Asp Val Glu Lys Leu Leu Glu Ile Ser Pro Glu Asn Gln His Ala Leu
145                 150                 155                 160

Ile His Glu Met Ala Ser Phe Ala Lys Asn Tyr Arg Leu Arg Pro Ile
                165                 170                 175

Ala Thr Thr Lys Tyr His Arg Glu Ala Phe Val Gly Ala Asp Ala Glu
            180                 185                 190

Glu Ser Ser Arg Val Thr Ile Asp His Gly Val Ser Gly Arg Asp Arg
        195                 200                 205

Asp Phe Leu Leu Gly Gln Asp Leu Glu Asp Arg Pro Thr Val Ala Gln
    210                 215                 220

Gly Leu Ala Val Val Glu Ile Lys Cys Asp Glu Arg Val Pro Phe Trp
225                 230                 235                 240

Leu Thr Asp Met Thr Ala Gln Leu Glu Met Ser Val Ile Arg Met Ser
                245                 250                 255

Lys Tyr Cys Glu Thr Ile Glu Ala Phe His Asn Arg Pro Ala Ser Ala
            260                 265                 270

Phe Gly Ala Val Asp Pro Ile Phe
```

275 280

<210> 107
<211> 777
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(754)
<223> FRXA00120

<400> 107
aatcaaatac ttgattacag agcaagatgt acctgcactc cgcgagcagt tggcaacgag 60

gatgagcacg gatccgcttt ccccacccgg aggctaccga gtg gaa tcc ctt tac 115
Val Glu Ser Leu Tyr
1 5

ttc gat tca gcc gat tta cgg tgc tac acc gaa aag atc gag ggt ctg 163
Phe Asp Ser Ala Asp Leu Arg Cys Tyr Thr Glu Lys Ile Glu Gly Leu
10 15 20

aaa ttc cga agg aaa cta cgg atc cgt acc tac ggt gat gga gtg ctc 211
Lys Phe Arg Arg Lys Leu Arg Ile Arg Thr Tyr Gly Asp Gly Val Leu
25 30 35

act cca gaa tcc acc gtg tcg gta gag atc aag cag cgg gtt aac aaa 259
Thr Pro Glu Ser Thr Val Ser Val Glu Ile Lys Gln Arg Val Asn Lys
40 45 50

gta act caa aag cgt cgg ctg gat ttg ccc ttt ata tat gcg ctc gcc 307
Val Thr Gln Lys Arg Arg Leu Asp Leu Pro Phe Ile Tyr Ala Leu Ala
55 60 65

ctg ggc gat agc acg ggc gcc gcg gta ggc gag cag gtg gac gtc gag 355
Leu Gly Asp Ser Thr Gly Ala Ala Val Gly Glu Gln Val Asp Val Glu
70 75 80 85

aag ctt ctt gaa atc tct ccg gaa aac cag cac gct ttg att cac gaa 403
Lys Leu Leu Glu Ile Ser Pro Glu Asn Gln His Ala Leu Ile His Glu
90 95 100

atg gcg tcg ttt gct aaa aat tat cgg ctg cga ccc atc gcc acc acg 451
Met Ala Ser Phe Ala Lys Asn Tyr Arg Leu Arg Pro Ile Ala Thr Thr
105 110 115

aag tat cac cgc gag gca ttc gtc ggc gct gat gcg gag gaa agt tcg 499
Lys Tyr His Arg Glu Ala Phe Val Gly Ala Asp Ala Glu Glu Ser Ser
120 125 130

cga gtc acc att gac cac ggt gtt tca ggc cgt gat cgt gat ttt ctg 547
Arg Val Thr Ile Asp His Gly Val Ser Gly Arg Asp Arg Asp Phe Leu
135 140 145

ctt ggc caa gac ctt gaa gac cgc cca acg gtg gcg caa gga ttg gca 595
Leu Gly Gln Asp Leu Glu Asp Arg Pro Thr Val Ala Gln Gly Leu Ala
150 155 160 165

gtc gtg gaa atc aaa tgc gat gaa cgc gtg ccg ttt tgg ctc act gat 643

```
Val Val Glu Ile Lys Cys Asp Glu Arg Val Pro Phe Trp Leu Thr Asp
                170                 175                 180

atg act gct caa ctg gaa atg tcc gtg att cgg atg tcc aaa tac tgc   691
Met Thr Ala Gln Leu Glu Met Ser Val Ile Arg Met Ser Lys Tyr Cys
            185                 190                 195

gaa acc atc gaa gcg ttt cac aac cgt ccg gca tca gct ttc ggc gct   739
Glu Thr Ile Glu Ala Phe His Asn Arg Pro Ala Ser Ala Phe Gly Ala
        200                 205                 210

gtc gac ccc atc ttc taaacaagaa aggcccctcc aat                    777
Val Asp Pro Ile Phe
    215


<210> 108
<211> 218
<212> PRT
<213> Corynebacterium glutamicum

<400> 108
Val Glu Ser Leu Tyr Phe Asp Ser Ala Asp Leu Arg Cys Tyr Thr Glu
  1               5                  10                  15

Lys Ile Glu Gly Leu Lys Phe Arg Arg Lys Leu Arg Ile Arg Thr Tyr
             20                  25                  30

Gly Asp Gly Val Leu Thr Pro Glu Ser Thr Val Ser Val Glu Ile Lys
         35                  40                  45

Gln Arg Val Asn Lys Val Thr Gln Lys Arg Arg Leu Asp Leu Pro Phe
     50                  55                  60

Ile Tyr Ala Leu Ala Leu Gly Asp Ser Thr Gly Ala Ala Val Gly Glu
 65                  70                  75                  80

Gln Val Asp Val Glu Lys Leu Leu Glu Ile Ser Pro Glu Asn Gln His
                 85                  90                  95

Ala Leu Ile His Glu Met Ala Ser Phe Ala Lys Asn Tyr Arg Leu Arg
            100                 105                 110

Pro Ile Ala Thr Thr Lys Tyr His Arg Glu Ala Phe Val Gly Ala Asp
        115                 120                 125

Ala Glu Glu Ser Ser Arg Val Thr Ile Asp His Gly Val Ser Gly Arg
    130                 135                 140

Asp Arg Asp Phe Leu Leu Gly Gln Asp Leu Glu Asp Arg Pro Thr Val
145                 150                 155                 160

Ala Gln Gly Leu Ala Val Val Glu Ile Lys Cys Asp Glu Arg Val Pro
                165                 170                 175

Phe Trp Leu Thr Asp Met Thr Ala Gln Leu Glu Met Ser Val Ile Arg
            180                 185                 190

Met Ser Lys Tyr Cys Glu Thr Ile Glu Ala Phe His Asn Arg Pro Ala
        195                 200                 205
```

```
Ser Ala Phe Gly Ala Val Asp Pro Ile Phe
    210                 215


<210> 109
<211> 1827
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1804)
<223> RXN00128

<400> 109
ccattttccg tttggtcttg cctaaagaac cgcatggaaa ttatcgtgaa gcaccgatcc 60

cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg   115
                                            Val Ser Lys Ile Ser
                                              1               5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg   163
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
                 10                  15                  20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc   211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
             25                  30                  35

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg   259
Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro
         40                  45                  50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg   307
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala
     55                  60                  65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg   355
Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly
 70                  75                  80                  85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc   403
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg
                 90                  95                 100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att   451
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile
            105                 110                 115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat   499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr
        120                 125                 130

cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa   547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu
    135                 140                 145

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag   595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu
150                 155                 160                 165
```

```
aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt   643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe
                170                 175                 180

gat cct tct ggc cag gtg ttg gtg ggg gat cgg cgt tgg ttg ttc aat   691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn
            185                 190                 195

gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt   739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly
        200                 205                 210

cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat   787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp
    215                 220                 225

gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg   835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu
230                 235                 240                 245

gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg   883
Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val
                250                 255                 260

tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct   931
Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala
            265                 270                 275

gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac   979
Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp
        280                 285                 290

ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg   1027
Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu
    295                 300                 305

ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg   1075
Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val
310                 315                 320                 325

agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg   1123
Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala
                330                 335                 340

att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac   1171
Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn
            345                 350                 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg   1219
Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala
        360                 365                 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt   1267
Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser
    375                 380                 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga   1315
Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg
390                 395                 400                 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg   1363
```

```
Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu
                410                 415                 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act   1411
Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr
            425                 430                 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc   1459
Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val
        440                 445                 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag   1507
Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
    455                 460                 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca   1555
Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
470                 475                 480                 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg   1603
Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
                490                 495                 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat   1651
Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
            505                 510                 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac   1699
Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
        520                 525                 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat   1747
Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
    535                 540                 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg   1795
Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
550                 555                 560                 565

gtt gcg tac tgatggagct gttcttcccg cgc                            1827
Val Ala Tyr
```

<210> 110
<211> 568
<212> PRT
<213> Corynebacterium glutamicum

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<400> 110
Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
  1               5                  10                  15

Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
             20                  25                  30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
         35                  40                  45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
     50                  55                  60
```

```
Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
 65                  70                  75                  80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
                 85                  90                  95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
            100                 105                 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
        115                 120                 125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
    130                 135                 140

Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
145                 150                 155                 160

Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
                165                 170                 175

Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
            180                 185                 190

Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
        195                 200                 205

Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
    210                 215                 220

Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
225                 230                 235                 240

Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
                245                 250                 255

Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
            260                 265                 270

Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
        275                 280                 285

Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
    290                 295                 300

Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
305                 310                 315                 320

Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
                325                 330                 335

Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
            340                 345                 350

Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
        355                 360                 365

Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
    370                 375                 380
```

```
Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
385                 390                 395                 400

Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
                405                 410                 415

Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
            420                 425                 430

Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
        435                 440                 445

Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
    450                 455                 460

Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
465                 470                 475                 480

Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
                485                 490                 495

Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
            500                 505                 510

Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
        515                 520                 525

Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro
    530                 535                 540

Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
545                 550                 555                 560

Arg Ala Ala Pro Val Val Ala Tyr
                565
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<210> 111
<211> 1827
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1804)
<223> FRXA00128

<400> 111
ccatttccg tttggtcttg cctaaagaac cgcatggaaa ttatcgtgaa gcaccgatcc 60

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cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg   115
                                              Val Ser Lys Ile Ser
                                                1               5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg   163
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
                  10                  15                  20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc   211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
              25                  30                  35
```

```
tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg   259
Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro
         40                  45                  50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg   307
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala
     55                  60                  65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg   355
Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly
 70                  75                  80                  85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc   403
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg
                 90                  95                 100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att   451
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile
            105                 110                 115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat   499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr
        120                 125                 130

cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa   547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu
    135                 140                 145

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag   595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu
150                 155                 160                 165

aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt   643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe
                170                 175                 180

gat cct tct ggc cag gtg ttg gtg ggg gat cgg cgt tgg ttg ttc aat   691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn
            185                 190                 195

gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt   739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly
        200                 205                 210

cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat   787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp
    215                 220                 225

gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg   835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu
230                 235                 240                 245

gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg   883
Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val
                250                 255                 260

tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct   931
Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala
            265                 270                 275
```

```
gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac   979
Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp
        280                 285                 290

ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg   1027
Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu
    295                 300                 305

ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg   1075
Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val
310                 315                 320                 325

agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg   1123
Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala
                330                 335                 340

att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac   1171
Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn
            345                 350                 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg   1219
Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala
        360                 365                 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt   1267
Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser
    375                 380                 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga   1315
Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg
390                 395                 400                 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg   1363
Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu
                410                 415                 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act   1411
Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr
            425                 430                 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc   1459
Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val
        440                 445                 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag   1507
Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
    455                 460                 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca   1555
Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
470                 475                 480                 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg   1603
Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
                490                 495                 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat   1651
Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
            505                 510                 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac   1699
```

```
Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
        520                 525                 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat   1747
Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
    535                 540                 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg   1795
Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
550                 555                 560                 565

gtt gcg tac tgatggagct gttcttcccg cgc                             1827
Val Ala Tyr
```

<210> 112
<211> 568
<212> PRT
<213> Corynebacterium glutamicum

<400> 112

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Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
  1               5                  10                  15

Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
             20                  25                  30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
         35                  40                  45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
     50                  55                  60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
 65                  70                  75                  80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
                 85                  90                  95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
            100                 105                 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
        115                 120                 125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
    130                 135                 140

Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
145                 150                 155                 160

Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
                165                 170                 175

Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
            180                 185                 190

Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
        195                 200                 205
```

```
Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
    210                 215                 220

Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
225                 230                 235                 240

Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
                245                 250                 255

Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
            260                 265                 270

Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
        275                 280                 285

Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
    290                 295                 300

Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
305                 310                 315                 320

Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
                325                 330                 335

Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
            340                 345                 350

Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
        355                 360                 365

Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
    370                 375                 380

Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
385                 390                 395                 400

Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
                405                 410                 415

Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
            420                 425                 430

Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
        435                 440                 445

Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
    450                 455                 460

Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
465                 470                 475                 480

Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
                485                 490                 495

Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
            500                 505                 510

Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
        515                 520                 525

Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro
```

```
    530                 535                 540

Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
545                 550                 555                 560

Arg Ala Ala Pro Val Val Ala Tyr
                565

<210> 113
<211> 966
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(943)
<223> RXN00154

<400> 113
tagccagacg gcagtatttt gaagcggtga ataaacgttt gctcgaattt ccatagtgtt 60

agggaagtgt agtgcagtgc tttgactagg gtggtgagct atg agt ttt tca gac   115
                                              Met Ser Phe Ser Asp
                                                1               5

ccc tat gca ggc aat att ttt ggt gga cac tcc cgc aac aag cag ccg   163
Pro Tyr Ala Gly Asn Ile Phe Gly Gly His Ser Arg Asn Lys Gln Pro
                  10                  15                  20

gag tat ccc gat gtg ccc gca aaa cca ggc ctt gtg gtg gaa gtt cgt   211
Glu Tyr Pro Asp Val Pro Ala Lys Pro Gly Leu Val Val Glu Val Arg
             25                  30                  35

gga gat ggc ttc gtc ggc gct gtg acc ggt ttt gaa cgc acc tac gat   259
Gly Asp Gly Phe Val Gly Ala Val Thr Gly Phe Glu Arg Thr Tyr Asp
         40                  45                  50

ggt gat ttt gtg cgt ctc gag gac cgc cgc gga cgc gat gcg ctg tac   307
Gly Asp Phe Val Arg Leu Glu Asp Arg Arg Gly Arg Asp Ala Leu Tyr
     55                  60                  65

aag ctg cgc aag ggt gcg ttc atg att gat ggg cag atc gtt aac ctc   355
Lys Leu Arg Lys Gly Ala Phe Met Ile Asp Gly Gln Ile Val Asn Leu
 70                  75                  80                  85

acc cgt ttc gtg gaa aaa caa gca cca cgt aaa tct aat tct ggt tcc   403
Thr Arg Phe Val Glu Lys Gln Ala Pro Arg Lys Ser Asn Ser Gly Ser
                 90                  95                 100

agg cgt gta gaa aac gcg caa gca aag gtc gcg gcg ccg tca cgc atc   451
Arg Arg Val Glu Asn Ala Gln Ala Lys Val Ala Ala Pro Ser Arg Ile
            105                 110                 115

tgg gta gaa ggc atc cat gac gcc gcc atc gtg gag aaa gtg tgg gga   499
Trp Val Glu Gly Ile His Asp Ala Ala Ile Val Glu Lys Val Trp Gly
        120                 125                 130

cac gac ctt cgc gtt gag ggc gtc gtg gtg gag tac ctg gaa ggt cta   547
His Asp Leu Arg Val Glu Gly Val Val Val Glu Tyr Leu Glu Gly Leu
    135                 140                 145
```

```
gac aac ctg gag gaa cgt ctc gcg gaa ttt cag cct ggg cct gga cga   595
Asp Asn Leu Glu Glu Arg Leu Ala Glu Phe Gln Pro Gly Pro Gly Arg
150                 155                 160                 165

cgc atc gga gtg ctc gct gat cac ctt gtt gag gga tct aaa gaa act   643
Arg Ile Gly Val Leu Ala Asp His Leu Val Glu Gly Ser Lys Glu Thr
                170                 175                 180

cgg atg act aaa tca cta ccc gcg gat gtc gct gtc acc ggc cac ccc   691
Arg Met Thr Lys Ser Leu Pro Ala Asp Val Ala Val Thr Gly His Pro
            185                 190                 195

tac atc gat att tgg gct gct gtg aaa cca gag cgt ttg ggg ctt aag   739
Tyr Ile Asp Ile Trp Ala Ala Val Lys Pro Glu Arg Leu Gly Leu Lys
        200                 205                 210

gcg tgg cct gag gtg cca tac ggg gag gat tgg aaa acc ggc atc tgc   787
Ala Trp Pro Glu Val Pro Tyr Gly Glu Asp Trp Lys Thr Gly Ile Cys
    215                 220                 225

aaa cga gtt ggc tgg tca gac ccc aaa gaa ggc tgg cac cgt gtg tat   835
Lys Arg Val Gly Trp Ser Asp Pro Lys Glu Gly Trp His Arg Val Tyr
230                 235                 240                 245

aac gcc gtg aat tcc ttc cgc gat ttg gac tac acc cta att ggg gca   883
Asn Ala Val Asn Ser Phe Arg Asp Leu Asp Tyr Thr Leu Ile Gly Ala
                250                 255                 260

gtg gaa cgt ttg gtg gat ttt gtg acc aac ctc gat ttg agt aaa gag   931
Val Glu Arg Leu Val Asp Phe Val Thr Asn Leu Asp Leu Ser Lys Glu
            265                 270                 275

gac gtc ctc gcc tgatttttcg ggtgtgtttt tgc                        966
Asp Val Leu Ala
        280
```

20050208.0000

<210> 114
<211> 281
<212> PRT
<213> Corynebacterium glutamicum

<400> 114

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Met Ser Phe Ser Asp Pro Tyr Ala Gly Asn Ile Phe Gly Gly His Ser
  1               5                  10                  15

Arg Asn Lys Gln Pro Glu Tyr Pro Asp Val Pro Ala Lys Pro Gly Leu
             20                  25                  30

Val Val Glu Val Arg Gly Asp Gly Phe Val Gly Ala Val Thr Gly Phe
         35                  40                  45

Glu Arg Thr Tyr Asp Gly Asp Phe Val Arg Leu Glu Asp Arg Arg Gly
     50                  55                  60

Arg Asp Ala Leu Tyr Lys Leu Arg Lys Gly Ala Phe Met Ile Asp Gly
 65                  70                  75                  80

Gln Ile Val Asn Leu Thr Arg Phe Val Glu Lys Gln Ala Pro Arg Lys
                 85                  90                  95
```

```
Ser Asn Ser Gly Ser Arg Arg Val Glu Asn Ala Gln Ala Lys Val Ala
           100                 105                 110

Ala Pro Ser Arg Ile Trp Val Glu Gly Ile His Asp Ala Ala Ile Val
       115                 120                 125

Glu Lys Val Trp Gly His Asp Leu Arg Val Glu Gly Val Val Val Glu
   130                 135                 140

Tyr Leu Glu Gly Leu Asp Asn Leu Glu Glu Arg Leu Ala Glu Phe Gln
145                 150                 155                 160

Pro Gly Pro Gly Arg Arg Ile Gly Val Leu Ala Asp His Leu Val Glu
               165                 170                 175

Gly Ser Lys Glu Thr Arg Met Thr Lys Ser Leu Pro Ala Asp Val Ala
           180                 185                 190

Val Thr Gly His Pro Tyr Ile Asp Ile Trp Ala Ala Val Lys Pro Glu
       195                 200                 205

Arg Leu Gly Leu Lys Ala Trp Pro Glu Val Pro Tyr Gly Glu Asp Trp
   210                 215                 220

Lys Thr Gly Ile Cys Lys Arg Val Gly Trp Ser Asp Pro Lys Glu Gly
225                 230                 235                 240

Trp His Arg Val Tyr Asn Ala Val Asn Ser Phe Arg Asp Leu Asp Tyr
               245                 250                 255

Thr Leu Ile Gly Ala Val Glu Arg Leu Val Asp Phe Val Thr Asn Leu
           260                 265                 270

Asp Leu Ser Lys Glu Asp Val Leu Ala
       275                 280


<210> 115
<211> 966
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(943)
<223> FRXA00154

<400> 115
tagccagacg gcagtatttt gaagcggtga ataaacgttt gctcgaattt ccatagtgtt 60

agggaagtgt agtgcagtgc tttgactagg gtggtgagct atg agt ttt tca gac   115
                                              Met Ser Phe Ser Asp
                                                1               5

ccc tat gca ggc aat att ttt ggt gga cac tcc cgc aac aag cag ccg   163
Pro Tyr Ala Gly Asn Ile Phe Gly Gly His Ser Arg Asn Lys Gln Pro
                 10                  15                  20

gag tat ccc gat gtg ccc gca aaa cca ggc ctt gtg gtg gaa gtt cgt   211
Glu Tyr Pro Asp Val Pro Ala Lys Pro Gly Leu Val Val Glu Val Arg
```

```
                25                  30                  35

gga gat ggc ttc gtc ggc gct gtg acc ggt ttt gaa cgc acc tac gat   259
Gly Asp Gly Phe Val Gly Ala Val Thr Gly Phe Glu Arg Thr Tyr Asp
         40                  45                  50

ggt gat ttt gtg cgt ctc gag gac cgc cgc gga cgc gat gcg ctg tac   307
Gly Asp Phe Val Arg Leu Glu Asp Arg Arg Gly Arg Asp Ala Leu Tyr
     55                  60                  65

aag ctg cgc aag ggt gcg ttc atg att gat ggg cag atc gtt aac ctc   355
Lys Leu Arg Lys Gly Ala Phe Met Ile Asp Gly Gln Ile Val Asn Leu
 70                  75                  80                  85

acc cgt ttc gtg gaa aaa caa gca cca cgt aaa tct aat tct ggt tcc   403
Thr Arg Phe Val Glu Lys Gln Ala Pro Arg Lys Ser Asn Ser Gly Ser
                 90                  95                 100

agg cgt gta gaa aac gcg caa gca aag gtc gcg gcg ccg tca cgc atc   451
Arg Arg Val Glu Asn Ala Gln Ala Lys Val Ala Ala Pro Ser Arg Ile
            105                 110                 115

tgg gta gaa ggc atc cat gac gcc gcc atc gtg gag aaa gtg tgg gga   499
Trp Val Glu Gly Ile His Asp Ala Ala Ile Val Glu Lys Val Trp Gly
        120                 125                 130

cac gac ctt cgc gtt gag ggc gtc gtg gtg gag tac ctg gaa ggt cta   547
His Asp Leu Arg Val Glu Gly Val Val Val Glu Tyr Leu Glu Gly Leu
    135                 140                 145

gac aac ctg gag gaa cgt ctc gcg gaa ttt cag cct ggg cct gga cga   595
Asp Asn Leu Glu Glu Arg Leu Ala Glu Phe Gln Pro Gly Pro Gly Arg
150                 155                 160                 165

cgc atc gga gtg ctc gct gat cac ctt gtt gag gga tct aaa gaa act   643
Arg Ile Gly Val Leu Ala Asp His Leu Val Glu Gly Ser Lys Glu Thr
                170                 175                 180

cgg atg act aaa tca cta ccc gcg gat gtc gct gtc acc ggc cac ccc   691
Arg Met Thr Lys Ser Leu Pro Ala Asp Val Ala Val Thr Gly His Pro
            185                 190                 195

tac atc gat att tgg gct gct gtg aaa cca gag cgt ttg ggg ctt aag   739
Tyr Ile Asp Ile Trp Ala Ala Val Lys Pro Glu Arg Leu Gly Leu Lys
        200                 205                 210

gcg tgg cct gag gtg cca tac ggg gag gat tgg aaa acc ggc atc tgc   787
Ala Trp Pro Glu Val Pro Tyr Gly Glu Asp Trp Lys Thr Gly Ile Cys
    215                 220                 225

aaa cga gtt ggc tgg tca gac ccc aaa gaa ggc tgg cac cgt gtg tat   835
Lys Arg Val Gly Trp Ser Asp Pro Lys Glu Gly Trp His Arg Val Tyr
230                 235                 240                 245

aac gcc gtg aat tcc ttc cgc gat ttg gac tac acc cta att ggg gca   883
Asn Ala Val Asn Ser Phe Arg Asp Leu Asp Tyr Thr Leu Ile Gly Ala
                250                 255                 260

gtg gaa cgt ttg gtg gat ttt gtg acc aac ctc gat ttg agt aaa gag   931
Val Glu Arg Leu Val Asp Phe Val Thr Asn Leu Asp Leu Ser Lys Glu
            265                 270                 275
```

gac gtc ctc gcc tgatttttcg ggtgtgtttt tgc 966
Asp Val Leu Ala
280

<210> 116
<211> 281
<212> PRT
<213> Corynebacterium glutamicum

<400> 116
Met Ser Phe Ser Asp Pro Tyr Ala Gly Asn Ile Phe Gly Gly His Ser
1 5 10 15

Arg Asn Lys Gln Pro Glu Tyr Pro Asp Val Pro Ala Lys Pro Gly Leu
20 25 30

Val Val Glu Val Arg Gly Asp Gly Phe Val Gly Ala Val Thr Gly Phe
35 40 45

Glu Arg Thr Tyr Asp Gly Asp Phe Val Arg Leu Glu Asp Arg Arg Gly
50 55 60

Arg Asp Ala Leu Tyr Lys Leu Arg Lys Gly Ala Phe Met Ile Asp Gly
65 70 75 80

Gln Ile Val Asn Leu Thr Arg Phe Val Glu Lys Gln Ala Pro Arg Lys
85 90 95

Ser Asn Ser Gly Ser Arg Arg Val Glu Asn Ala Gln Ala Lys Val Ala
100 105 110

Ala Pro Ser Arg Ile Trp Val Glu Gly Ile His Asp Ala Ala Ile Val
115 120 125

Glu Lys Val Trp Gly His Asp Leu Arg Val Glu Gly Val Val Val Glu
130 135 140

Tyr Leu Glu Gly Leu Asp Asn Leu Glu Glu Arg Leu Ala Glu Phe Gln
145 150 155 160

Pro Gly Pro Gly Arg Arg Ile Gly Val Leu Ala Asp His Leu Val Glu
165 170 175

Gly Ser Lys Glu Thr Arg Met Thr Lys Ser Leu Pro Ala Asp Val Ala
180 185 190

Val Thr Gly His Pro Tyr Ile Asp Ile Trp Ala Ala Val Lys Pro Glu
195 200 205

Arg Leu Gly Leu Lys Ala Trp Pro Glu Val Pro Tyr Gly Glu Asp Trp
210 215 220

Lys Thr Gly Ile Cys Lys Arg Val Gly Trp Ser Asp Pro Lys Glu Gly
225 230 235 240

Trp His Arg Val Tyr Asn Ala Val Asn Ser Phe Arg Asp Leu Asp Tyr
245 250 255

Thr Leu Ile Gly Ala Val Glu Arg Leu Val Asp Phe Val Thr Asn Leu

```
            260                 265                 270

Asp Leu Ser Lys Glu Asp Val Leu Ala
        275                 280


<210> 117
<211> 477
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(454)
<223> RXN00162

<400> 117
ggagacgtcg aaaagcataa acctggaact tttccgggcc cgcgcccgac tgctttgctg 60

aagccctatc ccgctatttt atttttgaag gaagagttgc gtg tct acc acc acc   115
                                            Val Ser Thr Thr Thr
                                              1               5

cca atc cac cct gag cgc aag aaa cgc gtt cgt cag gcc ctc acc atg   163
Pro Ile His Pro Glu Arg Lys Lys Arg Val Arg Gln Ala Leu Thr Met
                 10                  15                  20

ttc tcc atc gct gcg tgg gtg act ggt gtg ttt ttg ctg gcg ctg gtg   211
Phe Ser Ile Ala Ala Trp Val Thr Gly Val Phe Leu Leu Ala Leu Val
             25                  30                  35

gcg gag atg atc atg aag tac ata att ggc atg gat ctt cct gag tgg   259
Ala Glu Met Ile Met Lys Tyr Ile Ile Gly Met Asp Leu Pro Glu Trp
         40                  45                  50

gca cga ttc gtt ccg att gca cat gga tgg gtt tac att gtt ttc ttg   307
Ala Arg Phe Val Pro Ile Ala His Gly Trp Val Tyr Ile Val Phe Leu
     55                  60                  65

atg acc acc ctg aac ctg ggt ctg aag gcg cgt tgg aat ccg act cgt   355
Met Thr Thr Leu Asn Leu Gly Leu Lys Ala Arg Trp Asn Pro Thr Arg
 70                  75                  80                  85

tgg gtg acc acc gct atc gca ggt gtg gtt ccg ctg ctg tcg ttt ttt   403
Trp Val Thr Thr Ala Ile Ala Gly Val Val Pro Leu Leu Ser Phe Phe
                 90                  95                 100

gtt gag cac aac cgc cgc aag gaa gtt act cag aca ttc cag ctg aac   451
Val Glu His Asn Arg Arg Lys Glu Val Thr Gln Thr Phe Gln Leu Asn
            105                 110                 115

tca tagttaaata cacaaaaacc tcc                                    477
Ser


<210> 118
<211> 118
<212> PRT
<213> Corynebacterium glutamicum
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<400> 118
Val Ser Thr Thr Thr Pro Ile His Pro Glu Arg Lys Lys Arg Val Arg
1 5 10 15

Gln Ala Leu Thr Met Phe Ser Ile Ala Ala Trp Val Thr Gly Val Phe
20 25 30

Leu Leu Ala Leu Val Ala Glu Met Ile Met Lys Tyr Ile Ile Gly Met
35 40 45

Asp Leu Pro Glu Trp Ala Arg Phe Val Pro Ile Ala His Gly Trp Val
50 55 60

Tyr Ile Val Phe Leu Met Thr Thr Leu Asn Leu Gly Leu Lys Ala Arg
65 70 75 80

Trp Asn Pro Thr Arg Trp Val Thr Thr Ala Ile Ala Gly Val Val Pro
85 90 95

Leu Leu Ser Phe Phe Val Glu His Asn Arg Arg Lys Glu Val Thr Gln
100 105 110

Thr Phe Gln Leu Asn Ser
115

<210> 119
<211> 477
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(454)
<223> FRXA00162

<400> 119
ggagacgtcg aaaagcataa acctggaact tttccgggcc cgcgcccgac tgctttgctg 60

aagccctatc ccgctatttt atttttgaag gaagagttgc gtg tct acc acc acc 115
Val Ser Thr Thr Thr
1 5

cca atc cac cct gag cgc aag aaa cgc gtt cgt cag gcc ctc acc atg 163
Pro Ile His Pro Glu Arg Lys Lys Arg Val Arg Gln Ala Leu Thr Met
10 15 20

ttc tcc atc gct gcg tgg gtg act ggt gtg ttt ttg ctg gcg ctg gtg 211
Phe Ser Ile Ala Ala Trp Val Thr Gly Val Phe Leu Leu Ala Leu Val
25 30 35

gcg gag atg atc atg aag tac ata att ggc atg gat ctt cct gag tgg 259
Ala Glu Met Ile Met Lys Tyr Ile Ile Gly Met Asp Leu Pro Glu Trp
40 45 50

gca cga ttc gtt ccg att gca cat gga tgg gtt tac att gtt ttc ttg 307
Ala Arg Phe Val Pro Ile Ala His Gly Trp Val Tyr Ile Val Phe Leu
55 60 65

atg acc acc ctg aac ctg ggt ctg aag gcg cgt tgg aat ccg act cgt 355
Met Thr Thr Leu Asn Leu Gly Leu Lys Ala Arg Trp Asn Pro Thr Arg

```
 70                  75                  80                  85

tgg gtg acc acc gct atc gca ggt gtg gtt ccg ctg ctg tcg ttt ttt   403
Trp Val Thr Thr Ala Ile Ala Gly Val Val Pro Leu Leu Ser Phe Phe
                 90                  95                 100

gtt gag cac aac cgc cgc aag gaa gtt act cag aca ttc cag ctg aac   451
Val Glu His Asn Arg Arg Lys Glu Val Thr Gln Thr Phe Gln Leu Asn
            105                 110                 115

tca tagttaaata cacaaaaacc tcc                                    477
Ser
```

<210> 120
<211> 118
<212> PRT
<213> Corynebacterium glutamicum

<400> 120

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Val Ser Thr Thr Thr Pro Ile His Pro Glu Arg Lys Lys Arg Val Arg
  1               5                  10                  15

Gln Ala Leu Thr Met Phe Ser Ile Ala Ala Trp Val Thr Gly Val Phe
             20                  25                  30

Leu Leu Ala Leu Val Ala Glu Met Ile Met Lys Tyr Ile Ile Gly Met
         35                  40                  45

Asp Leu Pro Glu Trp Ala Arg Phe Val Pro Ile Ala His Gly Trp Val
     50                  55                  60

Tyr Ile Val Phe Leu Met Thr Thr Leu Asn Leu Gly Leu Lys Ala Arg
 65                  70                  75                  80

Trp Asn Pro Thr Arg Trp Val Thr Thr Ala Ile Ala Gly Val Val Pro
                 85                  90                  95

Leu Leu Ser Phe Phe Val Glu His Asn Arg Arg Lys Glu Val Thr Gln
            100                 105                 110

Thr Phe Gln Leu Asn Ser
        115
```

<210> 121
<211> 621
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(598)
<223> RXN00167

<400> 121

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ccgacaatcc agtggaactt ccctatcgct gtgatgcatt tttactttca cgttccggta 60

ccctggcagg cagatcttcc aatctttagg agccctcgcc atg tac ctg ttg aat   115
                                               Met Tyr Leu Leu Asn
```

```
                                                    1               5

cca cca gtc act gaa ccc gag atc ctc act gtc aac gag att ccg acc   163
Pro Pro Val Thr Glu Pro Glu Ile Leu Thr Val Asn Glu Ile Pro Thr
                10                  15                  20

gtc gtc gct gtc ttt gac aac cac ccc atg aac gac atg ccc gca gca   211
Val Val Ala Val Phe Asp Asn His Pro Met Asn Asp Met Pro Ala Ala
            25                  30                  35

ttc gat caa acc tac caa gtg ctc ttc ccc acc ttg ggt gcc aag ggc   259
Phe Asp Gln Thr Tyr Gln Val Leu Phe Pro Thr Leu Gly Ala Lys Gly
        40                  45                  50

atc gcg cca att ggc ccc gga ttt gct ctg tac acc tcc gaa cca act   307
Ile Ala Pro Ile Gly Pro Gly Phe Ala Leu Tyr Thr Ser Glu Pro Thr
    55                  60                  65

gac acc gtc agc ttt gaa gtg ggc atc cca gtc agc caa cca ctt gag   355
Asp Thr Val Ser Phe Glu Val Gly Ile Pro Val Ser Gln Pro Leu Glu
70                  75                  80                  85

gga gat gtt tca gcc gcc agc ggc atc gtg ctg aaa aac tca gtg gtc   403
Gly Asp Val Ser Ala Ala Ser Gly Ile Val Leu Lys Asn Ser Val Val
                90                  95                  100

cct gcc gga aaa att gcg cga atc agc cac atc ggc tca ttc gac gga   451
Pro Ala Gly Lys Ile Ala Arg Ile Ser His Ile Gly Ser Phe Asp Gly
            105                 110                 115

ctg agc caa gca tgg ggt tca ttc gtg gaa gct ctt gaa tct gca ggc   499
Leu Ser Gln Ala Trp Gly Ser Phe Val Glu Ala Leu Glu Ser Ala Gly
        120                 125                 130

cat gag atc gat atg ccg tgt tgg gag gta tat gtc acc gag cct tcc   547
His Glu Ile Asp Met Pro Cys Trp Glu Val Tyr Val Thr Glu Pro Ser
    135                 140                 145

ccc gac atg gat ccc gca aca ctc caa act gat cta tac gtc ctg ttg   595
Pro Asp Met Asp Pro Ala Thr Leu Gln Thr Asp Leu Tyr Val Leu Leu
150                 155                 160                 165

aag tagagaagct ttctggtcaa gtt                                    621
Lys
```

<210> 122
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

<400> 122

```
Met Tyr Leu Leu Asn Pro Pro Val Thr Glu Pro Glu Ile Leu Thr Val
  1               5                  10                  15

Asn Glu Ile Pro Thr Val Val Ala Val Phe Asp Asn His Pro Met Asn
            20                  25                  30

Asp Met Pro Ala Ala Phe Asp Gln Thr Tyr Gln Val Leu Phe Pro Thr
        35                  40                  45
```

```
Leu Gly Ala Lys Gly Ile Ala Pro Ile Gly Pro Gly Phe Ala Leu Tyr
     50                  55                  60

Thr Ser Glu Pro Thr Asp Thr Val Ser Phe Glu Val Gly Ile Pro Val
 65                  70                  75                  80

Ser Gln Pro Leu Glu Gly Asp Val Ser Ala Ala Ser Gly Ile Val Leu
                 85                  90                  95

Lys Asn Ser Val Val Pro Ala Gly Lys Ile Ala Arg Ile Ser His Ile
            100                 105                 110

Gly Ser Phe Asp Gly Leu Ser Gln Ala Trp Gly Ser Phe Val Glu Ala
        115                 120                 125

Leu Glu Ser Ala Gly His Glu Ile Asp Met Pro Cys Trp Glu Val Tyr
    130                 135                 140

Val Thr Glu Pro Ser Pro Asp Met Asp Pro Ala Thr Leu Gln Thr Asp
145                 150                 155                 160

Leu Tyr Val Leu Leu Lys
                165
```

<210> 123
<211> 361
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(361)
<223> FRXA00167

<400> 123

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ccgacaatcc agtggaactt ccctatcgct gtgatgcatt tttactttca cgttccggta 60

ccctggcagg cagatcttcc aatctttagg agccctcgcc atg tac ctg ttg aat   115
                                            Met Tyr Leu Leu Asn
                                              1               5

cca cca gtc act gaa ccc gag atc ctc act gtc aac gag att ccg acc   163
Pro Pro Val Thr Glu Pro Glu Ile Leu Thr Val Asn Glu Ile Pro Thr
                 10                  15                  20

gtc gtc gct gtc ttt gac aac cac ccc atg aac gac atg ccc gca gca   211
Val Val Ala Val Phe Asp Asn His Pro Met Asn Asp Met Pro Ala Ala
             25                  30                  35

ttc gat caa acc tac caa gtg ctc ttc ccc acc ttg ggt gcc aag ggc   259
Phe Asp Gln Thr Tyr Gln Val Leu Phe Pro Thr Leu Gly Ala Lys Gly
         40                  45                  50

atc gcg cca att ggc ccc gga ttt gct ctg tac acc tcc gaa cca act   307
Ile Ala Pro Ile Gly Pro Gly Phe Ala Leu Tyr Thr Ser Glu Pro Thr
     55                  60                  65

gac acc gtc agc ttt gaa gtg ggc atg cca gtc agc caa cca ctt gag   355
Asp Thr Val Ser Phe Glu Val Gly Met Pro Val Ser Gln Pro Leu Glu
```

```
 70                  75                  80                  85

gga gag                                                          361
Gly Glu


<210> 124
<211> 87
<212> PRT
<213> Corynebacterium glutamicum

<400> 124
Met Tyr Leu Leu Asn Pro Pro Val Thr Glu Pro Glu Ile Leu Thr Val
  1               5                  10                  15

Asn Glu Ile Pro Thr Val Val Ala Val Phe Asp Asn His Pro Met Asn
             20                  25                  30

Asp Met Pro Ala Ala Phe Asp Gln Thr Tyr Gln Val Leu Phe Pro Thr
         35                  40                  45

Leu Gly Ala Lys Gly Ile Ala Pro Ile Gly Pro Gly Phe Ala Leu Tyr
     50                  55                  60

Thr Ser Glu Pro Thr Asp Thr Val Ser Phe Glu Val Gly Met Pro Val
 65                  70                  75                  80

Ser Gln Pro Leu Glu Gly Glu
                85


<210> 125
<211> 281
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(258)
<223> RXN00171

<400> 125
aaa gat cag cag aag cag att cat aac ttg gca gct gag gta aag cgt   48
Lys Asp Gln Gln Lys Gln Ile His Asn Leu Ala Ala Glu Val Lys Arg
  1               5                  10                  15

ctt cgt gag cgt gac gat gca cga gat cag cag cta gga gtg ctt aat   96
Leu Arg Glu Arg Asp Asp Ala Arg Asp Gln Gln Leu Gly Val Leu Asn
             20                  25                  30

gaa gcc atg ttt tca cta cta gga gat gga ctt gac cgt ttt cgt gaa   144
Glu Ala Met Phe Ser Leu Leu Gly Asp Gly Leu Asp Arg Phe Arg Glu
         35                  40                  45

tct ggc gat gag gca tcc ttc aat gct gca ttg aac tat cag gca gtg   192
Ser Gly Asp Glu Ala Ser Phe Asn Ala Ala Leu Asn Tyr Gln Ala Val
     50                  55                  60

gtg gca cca gaa atg ttt aag acc gtg tat ggt gtc gat ccg tct acc   240
Val Ala Pro Glu Met Phe Lys Thr Val Tyr Gly Val Asp Pro Ser Thr
```

```
 65                  70                  75                  80

gga gag cct att ccc act taaagtacaa cacagtcttt tca                 281
Gly Glu Pro Ile Pro Thr
                 85


<210> 126
<211> 86
<212> PRT
<213> Corynebacterium glutamicum

<400> 126
Lys Asp Gln Gln Lys Gln Ile His Asn Leu Ala Ala Glu Val Lys Arg
  1               5                  10                  15

Leu Arg Glu Arg Asp Asp Ala Arg Asp Gln Gln Leu Gly Val Leu Asn
             20                  25                  30

Glu Ala Met Phe Ser Leu Leu Gly Asp Gly Leu Asp Arg Phe Arg Glu
         35                  40                  45

Ser Gly Asp Glu Ala Ser Phe Asn Ala Ala Leu Asn Tyr Gln Ala Val
     50                  55                  60

Val Ala Pro Glu Met Phe Lys Thr Val Tyr Gly Val Asp Pro Ser Thr
 65                  70                  75                  80

Gly Glu Pro Ile Pro Thr
                 85


<210> 127
<211> 354
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(331)
<223> FRXA00171

<400> 127
cgattaaggt aggggcctta aaaaggggaa taaagaatat tgggcccaga cgaaaactgc 60

tggcgagatc atcaaagatc agcagaagca gattcataac ttg gca gct gag gta   115
                                            Leu Ala Ala Glu Val
                                              1               5

aag cgt ctt cgt gag cgt gac gat gca cga gat cag cag cta gga gtg   163
Lys Arg Leu Arg Glu Arg Asp Asp Ala Arg Asp Gln Gln Leu Gly Val
                 10                  15                  20

ctt aat gaa gcc atg ttt tca cta cta gga gat gga ctt gac cgt ttt   211
Leu Asn Glu Ala Met Phe Ser Leu Leu Gly Asp Gly Leu Asp Arg Phe
             25                  30                  35

cgt gaa tct ggc gat gag gca tcc ttc aat gct gca ttg aac tat cag   259
Arg Glu Ser Gly Asp Glu Ala Ser Phe Asn Ala Ala Leu Asn Tyr Gln
         40                  45                  50
```

```
gca gtg gtg gca cca gaa atg ttt aag acc gtg tat ggt gtc gat ccg   307
Ala Val Val Ala Pro Glu Met Phe Lys Thr Val Tyr Gly Val Asp Pro
     55                  60                  65

tct acc gga gag cct att ccc act taaagtacaa cacagtcttt tca        354
Ser Thr Gly Glu Pro Ile Pro Thr
 70                  75


<210> 128
<211> 77
<212> PRT
<213> Corynebacterium glutamicum

<400> 128
Leu Ala Ala Glu Val Lys Arg Leu Arg Glu Arg Asp Asp Ala Arg Asp
  1               5                  10                  15

Gln Gln Leu Gly Val Leu Asn Glu Ala Met Phe Ser Leu Leu Gly Asp
             20                  25                  30

Gly Leu Asp Arg Phe Arg Glu Ser Gly Asp Glu Ala Ser Phe Asn Ala
         35                  40                  45

Ala Leu Asn Tyr Gln Ala Val Val Ala Pro Glu Met Phe Lys Thr Val
     50                  55                  60

Tyr Gly Val Asp Pro Ser Thr Gly Glu Pro Ile Pro Thr
 65                  70                  75


<210> 129
<211> 564
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(541)
<223> RXN00194

<400> 129
aaatatgaga acatagtgag agttaaacca agttctgtag gtgcttgttg cagcgggcgc 60

gaaggcgtac cactgcaact tgcgaataaa ggagtaaaac gtg gct ggt tcc tcc   115
                                            Val Ala Gly Ser Ser
                                              1               5

cac acg att gag cct gag atc tac cgc ggt gta tcc acc ctt gat gag   163
His Thr Ile Glu Pro Glu Ile Tyr Arg Gly Val Ser Thr Leu Asp Glu
                 10                  15                  20

cct tcg gct gca tgg gga tgg cac ggt ctc aag cgc aac acc atc caa   211
Pro Ser Ala Ala Trp Gly Trp His Gly Leu Lys Arg Asn Thr Ile Gln
             25                  30                  35

ctc gct ggc tgg att tcc gtt ctg ttc atg ctt gga tac aac ttc ggt   259
Leu Ala Gly Trp Ile Ser Val Leu Phe Met Leu Gly Tyr Asn Phe Gly
         40                  45                  50

aac cac aag ggc cac gtt gaa acc atc tgg ctt ctc gtc atc acc gcc   307
```

```
Asn His Lys Gly His Val Glu Thr Ile Trp Leu Leu Val Ile Thr Ala
     55                  60                  65

ctt ctg gtc atc ggc ctg ctg atc cac ctg ttc gag cca aag ctc ttc   355
Leu Leu Val Ile Gly Leu Leu Ile His Leu Phe Glu Pro Lys Leu Phe
 70                  75                  80                  85

cag gtt cgc acc atc act tcc cgc aac aag cct gtc ggc cac gtc gag   403
Gln Val Arg Thr Ile Thr Ser Arg Asn Lys Pro Val Gly His Val Glu
                 90                  95                 100

cca gac tgg acc tac gac cag gca acc ctc acc ggc acc tgg ggt aac   451
Pro Asp Trp Thr Tyr Asp Gln Ala Thr Leu Thr Gly Thr Trp Gly Asn
            105                 110                 115

ctc act gac tcc cag ctt cgc tcc gtc aac atc gag cca agc cgt gtc   499
Leu Thr Asp Ser Gln Leu Arg Ser Val Asn Ile Glu Pro Ser Arg Val
        120                 125                 130

gct cac ctg cgt gct gca gat tct gcg aaa gaa cta gac aac           541
Ala His Leu Arg Ala Ala Asp Ser Ala Lys Glu Leu Asp Asn
    135                 140                 145

tagtttttta aaaagaaaat gcg                                        564


<210> 130
<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 130
Val Ala Gly Ser Ser His Thr Ile Glu Pro Glu Ile Tyr Arg Gly Val
  1               5                  10                  15

Ser Thr Leu Asp Glu Pro Ser Ala Ala Trp Gly Trp His Gly Leu Lys
             20                  25                  30

Arg Asn Thr Ile Gln Leu Ala Gly Trp Ile Ser Val Leu Phe Met Leu
         35                  40                  45

Gly Tyr Asn Phe Gly Asn His Lys Gly His Val Glu Thr Ile Trp Leu
     50                  55                  60

Leu Val Ile Thr Ala Leu Leu Val Ile Gly Leu Leu Ile His Leu Phe
 65                  70                  75                  80

Glu Pro Lys Leu Phe Gln Val Arg Thr Ile Thr Ser Arg Asn Lys Pro
                 85                  90                  95

Val Gly His Val Glu Pro Asp Trp Thr Tyr Asp Gln Ala Thr Leu Thr
            100                 105                 110

Gly Thr Trp Gly Asn Leu Thr Asp Ser Gln Leu Arg Ser Val Asn Ile
        115                 120                 125

Glu Pro Ser Arg Val Ala His Leu Arg Ala Ala Asp Ser Ala Lys Glu
    130                 135                 140

Leu Asp Asn
145
```

<210> 131
<211> 385
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> FRXA00194

<400> 131
aaatatgaga acatagtgag agttaaacca agttctgtag gtgcttgttg cagcgggcgc 60

gaaggcgtac cactgcaact tgcgaataaa ggagtaaaac gtg gct ggt tcc tcc 115
Val Ala Gly Ser Ser
1 5

cac acg att gag cct gag atc tac cgc ggt gta tcc acc ctt gat gag 163
His Thr Ile Glu Pro Glu Ile Tyr Arg Gly Val Ser Thr Leu Asp Glu
10 15 20

cct tcg gct gca tgg gga tgg cac ggt ctc aag cgc aac acc atc caa 211
Pro Ser Ala Ala Trp Gly Trp His Gly Leu Lys Arg Asn Thr Ile Gln
25 30 35

ctc gct ggc tgg att tcc gtt ctg ttc atg ctt gga tac aac ttc ggt 259
Leu Ala Gly Trp Ile Ser Val Leu Phe Met Leu Gly Tyr Asn Phe Gly
40 45 50

aac cac aag ggc cac gtt gaa acc atc tgg ctt ctc gtc atc acc gcc 307
Asn His Lys Gly His Val Glu Thr Ile Trp Leu Leu Val Ile Thr Ala
55 60 65

ctt ctg gtc atc ggc ctg ctg atc cac ctg ttc gag cca aaa gct ctt 355
Leu Leu Val Ile Gly Leu Leu Ile His Leu Phe Glu Pro Lys Ala Leu
70 75 80 85

cca ggt tcg cac cat cac ttc tcg caa caa 385
Pro Gly Ser His His His Phe Ser Gln Gln
90 95

<210> 132
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 132
Val Ala Gly Ser Ser His Thr Ile Glu Pro Glu Ile Tyr Arg Gly Val
1 5 10 15

Ser Thr Leu Asp Glu Pro Ser Ala Ala Trp Gly Trp His Gly Leu Lys
20 25 30

Arg Asn Thr Ile Gln Leu Ala Gly Trp Ile Ser Val Leu Phe Met Leu
35 40 45

Gly Tyr Asn Phe Gly Asn His Lys Gly His Val Glu Thr Ile Trp Leu
50 55 60

```
Leu Val Ile Thr Ala Leu Leu Val Ile Gly Leu Leu Ile His Leu Phe
 65                  70                  75                  80

Glu Pro Lys Ala Leu Pro Gly Ser His His His Phe Ser Gln Gln
                 85                  90                  95


<210> 133
<211> 1335
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1312)
<223> RXN00197

<400> 133
gtcgatgata ttttggcaac cgaatctgag gcacgcgcgc gtgcgaatgc tttgatcaac 60

cggttggcaa ccaacttgta agctaaggag cttccgcctc gtg gca gcc tat ctt   115
                                            Val Ala Ala Tyr Leu
                                              1               5

ctt ggt gtc gta tta ttt ttc ctc ggc atc gca gta acc atc gcg ctt   163
Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala Val Thr Ile Ala Leu
                10                  15                  20

cac gag tgg ggg cac ttc atc aca gcg cgc att ttc gga atg aaa gtg   211
His Glu Trp Gly His Phe Ile Thr Ala Arg Ile Phe Gly Met Lys Val
            25                  30                  35

cgg cgt ttc ttc atc ggt ttc ggc ccg acg gtg ttt gcc aaa aga cgc   259
Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val Phe Ala Lys Arg Arg
        40                  45                  50

ggc gaa acc gtg tac ggc ctt aaa gcg att ccg gtc ggc ggt ttt tgt   307
Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro Val Gly Gly Phe Cys
    55                  60                  65

gac atc gcg ggg atg act gcc caa gat gaa ctt gat ccg gaa gac ctg   355
Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu Asp Pro Glu Asp Leu
70                  75                  80                  85

ccg cgc gcc atg tat cta aag ccc tgg tgg cag cgc ata att gtg ctt   403
Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln Arg Ile Ile Val Leu
                90                  95                  100

tcc ggc ggc gtg atc atg aat ctg atc gtc ggc ttt ttg gtg ctt tac   451
Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly Phe Leu Val Leu Tyr
            105                 110                 115

ggc gtg gcg gtg agc tcc gga atc ccg aat ccg gat gtg gat acc acc   499
Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro Asp Val Asp Thr Thr
        120                 125                 130

gcg aca gtc gac acc gtt cag tgc gtg ccg gaa acc caa att tcc gca   547
Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu Thr Gln Ile Ser Ala
    135                 140                 145
```

```
act gaa ctg tcc tcc tgc gta ggt tca ggc cca gcg ggc gac gcc ggc   595
Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro Ala Gly Asp Ala Gly
150                 155                 160                 165

att gag cac ggc gat aag att ttg gcc gtc aac ggc caa gag atg gca   643
Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn Gly Gln Glu Met Ala
                170                 175                 180

agc ttc acc gcc atc cgc gat gcg atc ctc gag ctc cca ggc gaa acg   691
Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu Leu Pro Gly Glu Thr
            185                 190                 195

gca acg ctg acg att gaa cgg gag gga acg ctt ttc gac gtc gac ctc   739
Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu Phe Asp Val Asp Leu
        200                 205                 210

cag gtt gcc tct gtc acc cgt ctc gcc tct gac ggt tca gaa att acc   787
Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp Gly Ser Glu Ile Thr
    215                 220                 225

gtc ggc gcg gtg ggc atg tcg agc ctt cca ccg acc gat gtg tac aaa   835
Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro Thr Asp Val Tyr Lys
230                 235                 240                 245

aaa tac ggc cca atc gag ggt gtg gga gca act gca cgt ttc acc ggc   883
Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr Ala Arg Phe Thr Gly
                250                 255                 260

gac atg atc agc gcc acg tgg gat ggc ctc aaa gcc ttc ccg gcg aaa   931
Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys Ala Phe Pro Ala Lys
            265                 270                 275

atc cca ggg gtc gtc gca tcc atc ttc ggt gca gaa cga gat gta gaa   979
Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala Glu Arg Asp Val Glu
        280                 285                 290

agc ccc atg agt gtg gtg ggc gcc gta cgc atc ggc ggc gaa ttt gtc   1027
Ser Pro Met Ser Val Val Gly Ala Val Arg Ile Gly Gly Glu Phe Val
    295                 300                 305

gaa cgt tcc atg tgg gac atg ttc atg atg atg ctg gcc agc ctg aac   1075
Glu Arg Ser Met Trp Asp Met Phe Met Met Met Leu Ala Ser Leu Asn
310                 315                 320                 325

ttc ttc ctc gcg ctg ttt aac ctc gtg ccg ctg cca cca ctt gat ggc   1123
Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu Pro Pro Leu Asp Gly
                330                 335                 340

gga cac att gcc gtg gtg atc tat gaa aaa atc cgc gac ttc ttc cgc   1171
Gly His Ile Ala Val Val Ile Tyr Glu Lys Ile Arg Asp Phe Phe Arg
            345                 350                 355

aaa ctg cgc gga aaa cca gcg ggc ggc cca gcg gat tac acc aaa cta   1219
Lys Leu Arg Gly Lys Pro Ala Gly Gly Pro Ala Asp Tyr Thr Lys Leu
        360                 365                 370

atg ccc gtc acc gta gct gtc gca gcc ttg ctg atg aca gtg gga ggc   1267
Met Pro Val Thr Val Ala Val Ala Ala Leu Leu Met Thr Val Gly Gly
    375                 380                 385

ctg gtc att gtc gcc gat gtg gtc aat ccc atc cga ctc ttt ggc       1312
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```
Leu Val Ile Val Ala Asp Val Val Asn Pro Ile Arg Leu Phe Gly
390                 395                 400

taacgatacg gaattgaact gcc                                          1335


<210> 134
<211> 404
<212> PRT
<213> Corynebacterium glutamicum

<400> 134
Val Ala Ala Tyr Leu Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala
  1               5                  10                  15

Val Thr Ile Ala Leu His Glu Trp Gly His Phe Ile Thr Ala Arg Ile
             20                  25                  30

Phe Gly Met Lys Val Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val
         35                  40                  45

Phe Ala Lys Arg Arg Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro
     50                  55                  60

Val Gly Gly Phe Cys Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu
 65                  70                  75                  80

Asp Pro Glu Asp Leu Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln
                 85                  90                  95

Arg Ile Ile Val Leu Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly
            100                 105                 110

Phe Leu Val Leu Tyr Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro
        115                 120                 125

Asp Val Asp Thr Thr Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu
    130                 135                 140

Thr Gln Ile Ser Ala Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro
145                 150                 155                 160

Ala Gly Asp Ala Gly Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn
                165                 170                 175

Gly Gln Glu Met Ala Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu
            180                 185                 190

Leu Pro Gly Glu Thr Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu
        195                 200                 205

Phe Asp Val Asp Leu Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp
    210                 215                 220

Gly Ser Glu Ile Thr Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro
225                 230                 235                 240

Thr Asp Val Tyr Lys Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr
                245                 250                 255

Ala Arg Phe Thr Gly Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys
```

```
            260                 265                 270

Ala Phe Pro Ala Lys Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala
        275                 280                 285

Glu Arg Asp Val Glu Ser Pro Met Ser Val Val Gly Ala Val Arg Ile
    290                 295                 300

Gly Gly Glu Phe Val Glu Arg Ser Met Trp Asp Met Phe Met Met Met
305                 310                 315                 320

Leu Ala Ser Leu Asn Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu
                325                 330                 335

Pro Pro Leu Asp Gly Gly His Ile Ala Val Val Ile Tyr Glu Lys Ile
            340                 345                 350

Arg Asp Phe Phe Arg Lys Leu Arg Gly Lys Pro Ala Gly Gly Pro Ala
        355                 360                 365

Asp Tyr Thr Lys Leu Met Pro Val Thr Val Ala Val Ala Ala Leu Leu
    370                 375                 380

Met Thr Val Gly Gly Leu Val Ile Val Ala Asp Val Val Asn Pro Ile
385                 390                 395                 400

Arg Leu Phe Gly
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<210> 135
<211> 1111
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1111)
<223> FRXA00197

<400> 135

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gtcgatgata ttttggcaac cgaatctgag gcacgcgcgc gtgcgaatgc tttgatcaac 60

cggttggcaa ccaacttgta agctaaggag cttccgcctc gtg gca gcc tat ctt   115
                                              Val Ala Ala Tyr Leu
                                                1               5

ctt ggt gtc gta tta ttt ttc ctc ggc atc gca gta acc atc gcg ctt   163
Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala Val Thr Ile Ala Leu
                  10                  15                  20

cac gag tgg ggg cac ttc atc aca gcg cgc att ttc gga atg aaa gtg   211
His Glu Trp Gly His Phe Ile Thr Ala Arg Ile Phe Gly Met Lys Val
              25                  30                  35

cgg cgt ttc ttc atc ggt ttc ggc ccg acg gtg ttt gcc aaa aga cgc   259
Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val Phe Ala Lys Arg Arg
          40                  45                  50

ggc gaa acc gtg tac ggc ctt aaa gcg att ccg gtc ggc ggt ttt tgt   307
Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro Val Gly Gly Phe Cys
```

```
     55                  60                  65

gac atc gcg ggg atg act gcc caa gat gaa ctt gat ccg gaa gac ctg   355
Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu Asp Pro Glu Asp Leu
 70                  75                  80                  85

ccg cgc gcc atg tat cta aag ccc tgg tgg cag cgc ata att gtg ctt   403
Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln Arg Ile Ile Val Leu
                 90                  95                 100

tcc ggc ggc gtg atc atg aat ctg atc gtc ggc ttt ttg gtg ctt tac   451
Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly Phe Leu Val Leu Tyr
            105                 110                 115

ggc gtg gcg gtg agc tcc gga atc ccg aat ccg gat gtg gat acc acc   499
Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro Asp Val Asp Thr Thr
        120                 125                 130

gcg aca gtc gac acc gtt cag tgc gtg ccg gaa acc caa att tcc gca   547
Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu Thr Gln Ile Ser Ala
    135                 140                 145

act gaa ctg tcc tcc tgc gta ggt tca ggc cca gcg ggc gac gcc ggc   595
Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro Ala Gly Asp Ala Gly
150                 155                 160                 165

att gag cac ggc gat aag att ttg gcc gtc aac ggc caa gag atg gca   643
Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn Gly Gln Glu Met Ala
                170                 175                 180

agc ttc acc gcc atc cgc gat gcg atc ctc gag ctc cca ggc gaa acg   691
Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu Leu Pro Gly Glu Thr
            185                 190                 195

gca acg ctg acg att gaa cgg gag gga acg ctt ttc gac gtc gac ctc   739
Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu Phe Asp Val Asp Leu
        200                 205                 210

cag gtt gcc tct gtc acc cgt ctc gcc tct gac ggt tca gaa att acc   787
Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp Gly Ser Glu Ile Thr
    215                 220                 225

gtc ggc gcg gtg ggc atg tcg agc ctt cca ccg acc gat gtg tac aaa   835
Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro Thr Asp Val Tyr Lys
230                 235                 240                 245

aaa tac ggc cca atc gag ggt gtg gga gca act gca cgt ttc acc ggc   883
Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr Ala Arg Phe Thr Gly
                250                 255                 260

gac atg atc agc gcc acg tgg gat ggc ctc aaa gcc ttc ccg gcg aaa   931
Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys Ala Phe Pro Ala Lys
            265                 270                 275

atc cca ggg gtc gtc gca tcc atc ttc ggt gca gaa cga gat gta gaa   979
Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala Glu Arg Asp Val Glu
        280                 285                 290

agc ccc atg agt gtg gtg ggc gcg tca cgc atc ggc ggc gaa ttt gtc  1027
Ser Pro Met Ser Val Val Gly Ala Ser Arg Ile Gly Gly Glu Phe Val
    295                 300                 305
```

```
gaa cgt tcc atg tgg gac atg ttc atg atg atg ctg gcc agc ctg aac   1075
Glu Arg Ser Met Trp Asp Met Phe Met Met Met Leu Ala Ser Leu Asn
310                 315                 320                 325

ttc ttc ctc gcg ctg ttt aac ctc gtg ccg ctg cca                   1111
Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu Pro
                330                 335
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<210> 136
<211> 337
<212> PRT
<213> Corynebacterium glutamicum

<400> 136

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Val Ala Ala Tyr Leu Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala
  1               5                  10                  15

Val Thr Ile Ala Leu His Glu Trp Gly His Phe Ile Thr Ala Arg Ile
             20                  25                  30

Phe Gly Met Lys Val Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val
         35                  40                  45

Phe Ala Lys Arg Arg Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro
     50                  55                  60

Val Gly Gly Phe Cys Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu
 65                  70                  75                  80

Asp Pro Glu Asp Leu Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln
                 85                  90                  95

Arg Ile Ile Val Leu Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly
            100                 105                 110

Phe Leu Val Leu Tyr Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro
        115                 120                 125

Asp Val Asp Thr Thr Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu
    130                 135                 140

Thr Gln Ile Ser Ala Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro
145                 150                 155                 160

Ala Gly Asp Ala Gly Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn
                165                 170                 175

Gly Gln Glu Met Ala Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu
            180                 185                 190

Leu Pro Gly Glu Thr Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu
        195                 200                 205

Phe Asp Val Asp Leu Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp
    210                 215                 220

Gly Ser Glu Ile Thr Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro
225                 230                 235                 240
```

```
Thr Asp Val Tyr Lys Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr
                245                 250                 255

Ala Arg Phe Thr Gly Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys
            260                 265                 270

Ala Phe Pro Ala Lys Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala
        275                 280                 285

Glu Arg Asp Val Glu Ser Pro Met Ser Val Val Gly Ala Ser Arg Ile
    290                 295                 300

Gly Gly Glu Phe Val Glu Arg Ser Met Trp Asp Met Phe Met Met Met
305                 310                 315                 320

Leu Ala Ser Leu Asn Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu
                325                 330                 335

Pro
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<210> 137
<211> 1113
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1090)
<223> RXN00216

<400> 137

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gtgttgctcg cggccaggca gcagtgctgt acctgcctga cgcggatggt gacatcgttc 60

ttggatcagg caccatctgc cacacggagt cttaagaaaa ttg ggc gct tat ggt   115
                                              Leu Gly Ala Tyr Gly
                                                1               5

tta ggt gag ctt cct gga aaa tcc gcc gcg gaa gcc gcc gac att att   163
Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu Ala Ala Asp Ile Ile
                  10                  15                  20

cag ggt gaa acg ggc gat ctt ctc cat att cct cag ctt ccg gcg cga   211
Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg
              25                  30                  35

ggt ttg ggt gct gat ctg atc ggt cga acc gtc ggt ctg ctg gac atg   259
Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val Gly Leu Leu Asp Met
          40                  45                  50

atc aac gtt gat cgc ggg gcc cga tct tgg gtg atg agc aca cgc ccc   307
Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val Met Ser Thr Arg Pro
      55                  60                  65

agc aga ttg acg cac ctg acc ggc gat ttc ctt gac atg gat ttg gat   355
Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu Asp Met Asp Leu Asp
  70                  75                  80                  85

gcg tgc gag gaa acc tgg gga acg ggc gtc gac aag cta aaa atc caa   403
Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp Lys Leu Lys Ile Gln
```

```
                    90                  95                 100

gtt gct ggt ccc tgg act tta ggt gcg cgc att gag ttg gcc aat ggc   451
Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile Glu Leu Ala Asn Gly
            105                 110                 115

cat cgc gtt ttg tct gat cgc ggt gcg atg cgt gat ctc acg cag gcg   499
His Arg Val Leu Ser Asp Arg Gly Ala Met Arg Asp Leu Thr Gln Ala
        120                 125                 130

ctg atc gcc ggc atc gat gcg cat gca cgc aag gtt gct ggg cga ttt   547
Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys Val Ala Gly Arg Phe
    135                 140                 145

cgc gcc gaa gtg cag gtg caa att gat gag ccg gag ctg aaa tcg ctt   595
Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro Glu Leu Lys Ser Leu
150                 155                 160                 165

atc gac ggc tcc ctc cct ggc act tcc acc ttt gac att att cct gcg   643
Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe Asp Ile Ile Pro Ala
                170                 175                 180

gtg aat gtc gct gat gcc agt gaa cgt ttg cag cag gtc ttt agc tcg   691
Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln Gln Val Phe Ser Ser
            185                 190                 195

att gag ggg ccg aca tat ctc aac ctc acc ggc cag att cct act tgg   739
Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly Gln Ile Pro Thr Trp
        200                 205                 210

gat gtg gct cgg ggt gcg ggc gcc gat act gtg cag att tcc atg gat   787
Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val Gln Ile Ser Met Asp
    215                 220                 225

caa gtc cgt gga aat gaa cat ttg gat ggt ttt ggt gaa acc atc acc   835
Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe Gly Glu Thr Ile Thr
230                 235                 240                 245

agt gga att cgt ctt ggt ttg ggc att acg aca gga aaa gat gtc gta   883
Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr Gly Lys Asp Val Val
                250                 255                 260

gat gaa ctg ctc gag cga ccg cgg caa aag gcc gtt gag gta gca cgc   931
Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala Val Glu Val Ala Arg
            265                 270                 275

ttt ttt gat cgt tta ggt gtg ggc cga aac tat ctc gtg gat gct gtt   979
Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val
        280                 285                 290

gat att cat ccg ggt gag gat ttg gtg cag ggg acc atc acc gag gcc  1027
Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly Thr Ile Thr Glu Ala
    295                 300                 305

gcg cag gct tat cgc atg gcc cgg gtg atg tcg gag atg ttg tcg aag  1075
Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys
310                 315                 320                 325

gat tca tgc gac ctt taaggcttta ccggcgctgg gtg                   1113
Asp Ser Cys Asp Leu
                330
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<210> 138
<211> 330
<212> PRT
<213> Corynebacterium glutamicum

<400> 138

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Leu Gly Ala Tyr Gly Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu
  1               5                  10                  15

Ala Ala Asp Ile Ile Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro
             20                  25                  30

Gln Leu Pro Ala Arg Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val
         35                  40                  45

Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val
     50                  55                  60

Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu
 65                  70                  75                  80

Asp Met Asp Leu Asp Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp
                 85                  90                  95

Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile
            100                 105                 110

Glu Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg
        115                 120                 125

Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys
    130                 135                 140

Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro
145                 150                 155                 160

Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe
                165                 170                 175

Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln
            180                 185                 190

Gln Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly
        195                 200                 205

Gln Ile Pro Thr Trp Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val
    210                 215                 220

Gln Ile Ser Met Asp Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe
225                 230                 235                 240

Gly Glu Thr Ile Thr Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr
                245                 250                 255

Gly Lys Asp Val Val Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala
            260                 265                 270

Val Glu Val Ala Arg Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr
        275                 280                 285
```

```
Leu Val Asp Ala Val Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly
    290                 295                 300

Thr Ile Thr Glu Ala Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser
305                 310                 315                 320

Glu Met Leu Ser Lys Asp Ser Cys Asp Leu
                325                 330


<210> 139
<211> 1269
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1246)
<223> RXN00222

<400> 139
agggaaaaac taccgtccgc ctggacaaag tcatcgatgt actccgcgtc cttggactcg 60

agctttctgt tggaattcac gatcccctca aggttaatca atg acc ccc act gcc   115
                                            Met Thr Pro Thr Ala
                                              1               5

gat atc tgg ttt aaa gat act ttg gct gct cat ttc aca cgc gac ggc   163
Asp Ile Trp Phe Lys Asp Thr Leu Ala Ala His Phe Thr Arg Asp Gly
                 10                  15                  20

gac cag acc aca ttc tcc tac aca gct gat tac gca ggt cca ccg att   211
Asp Gln Thr Thr Phe Ser Tyr Thr Ala Asp Tyr Ala Gly Pro Pro Ile
             25                  30                  35

gcc acg tcc ctg ccc atc aat tct gaa ccc gtg att acg cgc tct gga   259
Ala Thr Ser Leu Pro Ile Asn Ser Glu Pro Val Ile Thr Arg Ser Gly
         40                  45                  50

gcg atc cca cca ttt ttc gcg gga tta ctc ccc gaa ggt cgt cgc tta   307
Ala Ile Pro Pro Phe Phe Ala Gly Leu Leu Pro Glu Gly Arg Arg Leu
     55                  60                  65

agt tca ctc cgg aga aac att aaa gcc tct gcc gat gat gaa ctt tca   355
Ser Ser Leu Arg Arg Asn Ile Lys Ala Ser Ala Asp Asp Glu Leu Ser
 70                  75                  80                  85

ctc ctt cta gca gtg gga gct gat cct gtt ggt gca gtc gct atc ttc   403
Leu Leu Leu Ala Val Gly Ala Asp Pro Val Gly Ala Val Ala Ile Phe
                 90                  95                 100

ccc cat ggt gaa aat aca caa cct gca cca ccc aca gtt gat ttt gac   451
Pro His Gly Glu Asn Thr Gln Pro Ala Pro Pro Thr Val Asp Phe Asp
            105                 110                 115

gat gaa ctt gat ttc tcg gct gca cta acc gag tcc ggg att gcg gat   499
Asp Glu Leu Asp Phe Ser Ala Ala Leu Thr Glu Ser Gly Ile Ala Asp
        120                 125                 130

ccc gtt gca ctg gcc ggt gtc caa gac aaa gcc tct gca cgc acc atc   547
```

```
Pro Val Ala Leu Ala Gly Val Gln Asp Lys Ala Ser Ala Arg Thr Ile
    135                 140                 145

gcg gtc ccc gtt gca agc gat gcc atc ttg aaa ctc tcc ccg cct gaa   595
Ala Val Pro Val Ala Ser Asp Ala Ile Leu Lys Leu Ser Pro Pro Glu
150                 155                 160                 165

tac cct tac ttg gtg gaa aac gaa gca gct tgt tac cag ttg ctg acc   643
Tyr Pro Tyr Leu Val Glu Asn Glu Ala Ala Cys Tyr Gln Leu Leu Thr
                170                 175                 180

aaa aat aag ctt cgc att gaa ctg tcc aaa gta gaa gtt ctc cat gac   691
Lys Asn Lys Leu Arg Ile Glu Leu Ser Lys Val Glu Val Leu His Asp
            185                 190                 195

aaa cac ggc agg tcc gga ctc tta gtt cac cgc ttt gac cgc aca ccc   739
Lys His Gly Arg Ser Gly Leu Leu Val His Arg Phe Asp Arg Thr Pro
        200                 205                 210

aaa ggc aaa atc ccc gtc gag gat gca gga cag gtc ttg gga atc tgg   787
Lys Gly Lys Ile Pro Val Glu Asp Ala Gly Gln Val Leu Gly Ile Trp
    215                 220                 225

cct gca gat aaa tac tta gtg agc tac gag gac atc gca caa gcc ctc   835
Pro Ala Asp Lys Tyr Leu Val Ser Tyr Glu Asp Ile Ala Gln Ala Leu
230                 235                 240                 245

act aaa gtg tgc gcc tcc ccc atc ttg gcg atg cgc aat ctc gcc ttc   883
Thr Lys Val Cys Ala Ser Pro Ile Leu Ala Met Arg Asn Leu Ala Phe
                250                 255                 260

caa atc gca gtc gcg tgg ctc agc ggc aat ggt gat ctt cat gcc aag   931
Gln Ile Ala Val Ala Trp Leu Ser Gly Asn Gly Asp Leu His Ala Lys
            265                 270                 275

aac atc tcc att atc aac aaa ggc cgc gga ttt gag atc agc ccc atc   979
Asn Ile Ser Ile Ile Asn Lys Gly Arg Gly Phe Glu Ile Ser Pro Ile
        280                 285                 290

tat gac atc cct gcc acc gca gta tat ggc gac acc acg atg gca tta   1027
Tyr Asp Ile Pro Ala Thr Ala Val Tyr Gly Asp Thr Thr Met Ala Leu
    295                 300                 305

gaa atc cag gga tcc aaa aag gat ctc agc caa aag aaa ttc cta aaa   1075
Glu Ile Gln Gly Ser Lys Lys Asp Leu Ser Gln Lys Lys Phe Leu Lys
310                 315                 320                 325

ttc tgt aca tcc atc gga cta cca gaa aaa aca gcc atg tcg gtt gcg   1123
Phe Cys Thr Ser Ile Gly Leu Pro Glu Lys Thr Ala Met Ser Val Ala
                330                 335                 340

aac gct gca ctg ttg gca aca gaa aat gcc gca gag aca att ctt gct   1171
Asn Ala Ala Leu Leu Ala Thr Glu Asn Ala Ala Glu Thr Ile Leu Ala
            345                 350                 355

tcg gga aat ttt gat aca cgg atg aat cga gat ctg gcc agg gtt ctc   1219
Ser Gly Asn Phe Asp Thr Arg Met Asn Arg Asp Leu Ala Arg Val Leu
        360                 365                 370

aaa cat cga cga agc gca tgg gga gct taattcgcct gtttaagagg         1266
Lys His Arg Arg Ser Ala Trp Gly Ala
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375 380

tcg 1269

<210> 140
<211> 382
<212> PRT
<213> Corynebacterium glutamicum

<400> 140

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Met Thr Pro Thr Ala Asp Ile Trp Phe Lys Asp Thr Leu Ala Ala His
  1               5                  10                  15

Phe Thr Arg Asp Gly Asp Gln Thr Thr Phe Ser Tyr Thr Ala Asp Tyr
             20                  25                  30

Ala Gly Pro Pro Ile Ala Thr Ser Leu Pro Ile Asn Ser Glu Pro Val
         35                  40                  45

Ile Thr Arg Ser Gly Ala Ile Pro Pro Phe Phe Ala Gly Leu Leu Pro
     50                  55                  60

Glu Gly Arg Arg Leu Ser Ser Leu Arg Arg Asn Ile Lys Ala Ser Ala
 65                  70                  75                  80

Asp Asp Glu Leu Ser Leu Leu Leu Ala Val Gly Ala Asp Pro Val Gly
                 85                  90                  95

Ala Val Ala Ile Phe Pro His Gly Glu Asn Thr Gln Pro Ala Pro Pro
            100                 105                 110

Thr Val Asp Phe Asp Asp Glu Leu Asp Phe Ser Ala Ala Leu Thr Glu
        115                 120                 125

Ser Gly Ile Ala Asp Pro Val Ala Leu Ala Gly Val Gln Asp Lys Ala
    130                 135                 140

Ser Ala Arg Thr Ile Ala Val Pro Val Ala Ser Asp Ala Ile Leu Lys
145                 150                 155                 160

Leu Ser Pro Pro Glu Tyr Pro Tyr Leu Val Glu Asn Glu Ala Ala Cys
                165                 170                 175

Tyr Gln Leu Leu Thr Lys Asn Lys Leu Arg Ile Glu Leu Ser Lys Val
            180                 185                 190

Glu Val Leu His Asp Lys His Gly Arg Ser Gly Leu Leu Val His Arg
        195                 200                 205

Phe Asp Arg Thr Pro Lys Gly Lys Ile Pro Val Glu Asp Ala Gly Gln
    210                 215                 220

Val Leu Gly Ile Trp Pro Ala Asp Lys Tyr Leu Val Ser Tyr Glu Asp
225                 230                 235                 240

Ile Ala Gln Ala Leu Thr Lys Val Cys Ala Ser Pro Ile Leu Ala Met
                245                 250                 255

Arg Asn Leu Ala Phe Gln Ile Ala Val Ala Trp Leu Ser Gly Asn Gly
            260                 265                 270
```

```
Asp Leu His Ala Lys Asn Ile Ser Ile Ile Asn Lys Gly Arg Gly Phe
        275                 280                 285

Glu Ile Ser Pro Ile Tyr Asp Ile Pro Ala Thr Ala Val Tyr Gly Asp
    290                 295                 300

Thr Thr Met Ala Leu Glu Ile Gln Gly Ser Lys Lys Asp Leu Ser Gln
305                 310                 315                 320

Lys Lys Phe Leu Lys Phe Cys Thr Ser Ile Gly Leu Pro Glu Lys Thr
                325                 330                 335

Ala Met Ser Val Ala Asn Ala Ala Leu Leu Ala Thr Glu Asn Ala Ala
            340                 345                 350

Glu Thr Ile Leu Ala Ser Gly Asn Phe Asp Thr Arg Met Asn Arg Asp
        355                 360                 365

Leu Ala Arg Val Leu Lys His Arg Arg Ser Ala Trp Gly Ala
    370                 375                 380
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CONFIDENTIAL

<210> 141
<211> 1269
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1246)
<223> FRXA00222

<400> 141

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agggaaaaac taccgtccgc ctggacaaag tcatcgatgt actccgcgtc cttggactcg 60

agctttctgt tggaattcac gatcccctca aggttaatca atg acc ccc act gcc   115
                                            Met Thr Pro Thr Ala
                                              1               5

gat atc tgg ttt aaa gat act ttg gct gct cat ttc aca cgc gac ggc   163
Asp Ile Trp Phe Lys Asp Thr Leu Ala Ala His Phe Thr Arg Asp Gly
                  10                  15                  20

gac cag acc aca ttc tcc tac aca gct gat tac gca ggt cca ccg att   211
Asp Gln Thr Thr Phe Ser Tyr Thr Ala Asp Tyr Ala Gly Pro Pro Ile
             25                  30                  35

gcc acg tcc ctg ccc atc aat tct gaa ccc gtg att acg cgc tct gga   259
Ala Thr Ser Leu Pro Ile Asn Ser Glu Pro Val Ile Thr Arg Ser Gly
         40                  45                  50

gcg atc cca cca ttt ttc gcg gga tta ctc ccc gaa ggt cgt cgc tta   307
Ala Ile Pro Pro Phe Phe Ala Gly Leu Leu Pro Glu Gly Arg Arg Leu
     55                  60                  65

agt tca ctc cgg aga aac att aaa gcc tct gcc gat gat gaa ctt tca   355
Ser Ser Leu Arg Arg Asn Ile Lys Ala Ser Ala Asp Asp Glu Leu Ser
 70                  75                  80                  85

ctc ctt cta gca gtg gga gct gat cct gtt ggt gca gtc gct atc ttc   403
```

```
Leu Leu Leu Ala Val Gly Ala Asp Pro Val Gly Ala Val Ala Ile Phe
                 90                  95                 100

ccc cat ggt gaa aat aca caa cct gca cca ccc aca gtt gat ttt gac   451
Pro His Gly Glu Asn Thr Gln Pro Ala Pro Pro Thr Val Asp Phe Asp
            105                 110                 115

gat gaa ctt gat ttc tcg gct gca cta acc gag tcc ggg att gcg gat   499
Asp Glu Leu Asp Phe Ser Ala Ala Leu Thr Glu Ser Gly Ile Ala Asp
        120                 125                 130

ccc gtt gca ctg gcc ggt gtc caa gac aaa gcc tct gca cgc acc atc   547
Pro Val Ala Leu Ala Gly Val Gln Asp Lys Ala Ser Ala Arg Thr Ile
    135                 140                 145

gcg gtc ccc gtt gca agc gat gcc atc ttg aaa ctc tcc ccg cct gaa   595
Ala Val Pro Val Ala Ser Asp Ala Ile Leu Lys Leu Ser Pro Pro Glu
150                 155                 160                 165

tac cct tac ttg gtg gaa aac gaa gca gct tgt tac cag ttg ctg acc   643
Tyr Pro Tyr Leu Val Glu Asn Glu Ala Ala Cys Tyr Gln Leu Leu Thr
                170                 175                 180

aaa aat aag ctt cgc att gaa ctg tcc aaa gta gaa gtt ctc cat gac   691
Lys Asn Lys Leu Arg Ile Glu Leu Ser Lys Val Glu Val Leu His Asp
            185                 190                 195

aaa cac ggc agg tcc gga ctc tta gtt cac cgc ttt gac cgc aca ccc   739
Lys His Gly Arg Ser Gly Leu Leu Val His Arg Phe Asp Arg Thr Pro
        200                 205                 210

aaa ggc aaa atc ccc gtc gag gat gca gga cag gtc ttg gga atc tgg   787
Lys Gly Lys Ile Pro Val Glu Asp Ala Gly Gln Val Leu Gly Ile Trp
    215                 220                 225

cct gca gat aaa tac tta gtg agc tac gag gac atc gca caa gcc ctc   835
Pro Ala Asp Lys Tyr Leu Val Ser Tyr Glu Asp Ile Ala Gln Ala Leu
230                 235                 240                 245

act aaa gtg tgc gcc tcc ccc atc ttg gcg atg cgc aat ctc gcc ttc   883
Thr Lys Val Cys Ala Ser Pro Ile Leu Ala Met Arg Asn Leu Ala Phe
                250                 255                 260

caa atc gca gtc gcg tgg ctc agc ggc aat ggt gat ctt cat gcc aag   931
Gln Ile Ala Val Ala Trp Leu Ser Gly Asn Gly Asp Leu His Ala Lys
            265                 270                 275

aac atc tcc att atc aac aaa ggc cgc gga ttt gag atc agc ccc atc   979
Asn Ile Ser Ile Ile Asn Lys Gly Arg Gly Phe Glu Ile Ser Pro Ile
        280                 285                 290

tat gac atc cct gcc acc gca gta tat ggc gac acc acg atg gca tta   1027
Tyr Asp Ile Pro Ala Thr Ala Val Tyr Gly Asp Thr Thr Met Ala Leu
    295                 300                 305

gaa atc cag gga tcc aaa aag gat ctc agc caa aag aaa ttc cta aaa   1075
Glu Ile Gln Gly Ser Lys Lys Asp Leu Ser Gln Lys Lys Phe Leu Lys
310                 315                 320                 325

ttc tgt aca tcc atc gga cta cca gaa aaa aca gcc atg tcg gtt gcg   1123
Phe Cys Thr Ser Ile Gly Leu Pro Glu Lys Thr Ala Met Ser Val Ala
```

```
                330                 335                 340

aac gct gca ctg ttg gca aca gaa aat gcc gca gag aca att ctt gct   1171
Asn Ala Ala Leu Leu Ala Thr Glu Asn Ala Ala Glu Thr Ile Leu Ala
            345                 350                 355

tcg gga aat ttt gat aca cgg atg aat cga gat ctg gcc agg gtt ctc   1219
Ser Gly Asn Phe Asp Thr Arg Met Asn Arg Asp Leu Ala Arg Val Leu
        360                 365                 370

aaa cat cga cga agc gca tgg gga gct taattcgcct gtttaagagg         1266
Lys His Arg Arg Ser Ala Trp Gly Ala
    375                 380

tcg                                                               1269
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<210> 142
<211> 382
<212> PRT
<213> Corynebacterium glutamicum

<400> 142

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Met Thr Pro Thr Ala Asp Ile Trp Phe Lys Asp Thr Leu Ala Ala His
  1               5                  10                  15

Phe Thr Arg Asp Gly Asp Gln Thr Thr Phe Ser Tyr Thr Ala Asp Tyr
             20                  25                  30

Ala Gly Pro Pro Ile Ala Thr Ser Leu Pro Ile Asn Ser Glu Pro Val
         35                  40                  45

Ile Thr Arg Ser Gly Ala Ile Pro Pro Phe Phe Ala Gly Leu Leu Pro
     50                  55                  60

Glu Gly Arg Arg Leu Ser Ser Leu Arg Arg Asn Ile Lys Ala Ser Ala
 65                  70                  75                  80

Asp Asp Glu Leu Ser Leu Leu Leu Ala Val Gly Ala Asp Pro Val Gly
                 85                  90                  95

Ala Val Ala Ile Phe Pro His Gly Glu Asn Thr Gln Pro Ala Pro Pro
            100                 105                 110

Thr Val Asp Phe Asp Asp Glu Leu Asp Phe Ser Ala Ala Leu Thr Glu
        115                 120                 125

Ser Gly Ile Ala Asp Pro Val Ala Leu Ala Gly Val Gln Asp Lys Ala
    130                 135                 140

Ser Ala Arg Thr Ile Ala Val Pro Val Ala Ser Asp Ala Ile Leu Lys
145                 150                 155                 160

Leu Ser Pro Pro Glu Tyr Pro Tyr Leu Val Glu Asn Glu Ala Ala Cys
                165                 170                 175

Tyr Gln Leu Leu Thr Lys Asn Lys Leu Arg Ile Glu Leu Ser Lys Val
            180                 185                 190

Glu Val Leu His Asp Lys His Gly Arg Ser Gly Leu Leu Val His Arg
        195                 200                 205
```

```
Phe Asp Arg Thr Pro Lys Gly Lys Ile Pro Val Glu Asp Ala Gly Gln
    210                 215                 220

Val Leu Gly Ile Trp Pro Ala Asp Lys Tyr Leu Val Ser Tyr Glu Asp
225                 230                 235                 240

Ile Ala Gln Ala Leu Thr Lys Val Cys Ala Ser Pro Ile Leu Ala Met
                245                 250                 255

Arg Asn Leu Ala Phe Gln Ile Ala Val Ala Trp Leu Ser Gly Asn Gly
            260                 265                 270

Asp Leu His Ala Lys Asn Ile Ser Ile Ile Asn Lys Gly Arg Gly Phe
        275                 280                 285

Glu Ile Ser Pro Ile Tyr Asp Ile Pro Ala Thr Ala Val Tyr Gly Asp
    290                 295                 300

Thr Thr Met Ala Leu Glu Ile Gln Gly Ser Lys Lys Asp Leu Ser Gln
305                 310                 315                 320

Lys Lys Phe Leu Lys Phe Cys Thr Ser Ile Gly Leu Pro Glu Lys Thr
                325                 330                 335

Ala Met Ser Val Ala Asn Ala Ala Leu Leu Ala Thr Glu Asn Ala Ala
            340                 345                 350

Glu Thr Ile Leu Ala Ser Gly Asn Phe Asp Thr Arg Met Asn Arg Asp
        355                 360                 365

Leu Ala Arg Val Leu Lys His Arg Arg Ser Ala Trp Gly Ala
    370                 375                 380


<210> 143
<211> 633
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(610)
<223> RXN00232

<400> 143
gctgaaaaaa ctcccatttg gacaatgaac acttgtcaaa atgggagttt tggattttcg 60

caccaccggc agcactcgaa aacgtgttta tacttgaact atg aac gac agg gct   115
                                          Met Asn Asp Arg Ala
                                            1               5

cac caa cga ata ggc gac atc gag cga tcc caa gcc ctc gac cga ctt   163
His Gln Arg Ile Gly Asp Ile Glu Arg Ser Gln Ala Leu Asp Arg Leu
                10                  15                  20

ggg tca tat ttt gca gac gga tac ctc gac atc gac gaa ttc gat acc   211
Gly Ser Tyr Phe Ala Asp Gly Tyr Leu Asp Ile Asp Glu Phe Asp Thr
            25                  30                  35

cga acc ggc gcc gca gca atc gca cgc aca gcc ggt gaa ata gat gtc   259
```

```
Arg Thr Gly Ala Ala Ala Ile Ala Arg Thr Ala Gly Glu Ile Asp Val
          40                  45                  50

ttg ttc aca gat ctt ccc gaa caa cag gca agc acc gcc gtg aca ccc   307
Leu Phe Thr Asp Leu Pro Glu Gln Gln Ala Ser Thr Ala Val Thr Pro
     55                  60                  65

gtg caa gac gat acc gag aaa gaa tta gac ctg gtc cta cag cga gga   355
Val Gln Asp Asp Thr Glu Lys Glu Leu Asp Leu Val Leu Gln Arg Gly
 70                  75                  80                  85

aag aag ctc aag cag atc gac tcc gcc att tgg gct gtc gtg atg gtc   403
Lys Lys Leu Lys Gln Ile Asp Ser Ala Ile Trp Ala Val Val Met Val
                 90                  95                 100

tcg ttc ttc cta ggc ttg ttt gtt ttc aac gtg cca tat ttc tgg gtt   451
Ser Phe Phe Leu Gly Leu Phe Val Phe Asn Val Pro Tyr Phe Trp Val
            105                 110                 115

gtg ttc atc ctt ggc gga gcg gcc tcc gcg ggt gcg cga ttc ttg ctc   499
Val Phe Ile Leu Gly Gly Ala Ala Ser Ala Gly Ala Arg Phe Leu Leu
        120                 125                 130

aaa gta gat gac gcc gat gaa aaa ctc ttt gag gaa ctc cac agc aag   547
Lys Val Asp Asp Ala Asp Glu Lys Leu Phe Glu Glu Leu His Ser Lys
    135                 140                 145

gaa caa agc gaa cgc gaa gca cgc cta cgc att gcg gca caa cgt cga   595
Glu Gln Ser Glu Arg Glu Ala Arg Leu Arg Ile Ala Ala Gln Arg Arg
150                 155                 160                 165

cgc gag ttg gaa caa tagccacaaa agctatcaag ccc                    633
Arg Glu Leu Glu Gln
                170
```

<210> 144
<211> 170
<212> PRT
<213> Corynebacterium glutamicum

<400> 144

```
Met Asn Asp Arg Ala His Gln Arg Ile Gly Asp Ile Glu Arg Ser Gln
  1               5                  10                  15

Ala Leu Asp Arg Leu Gly Ser Tyr Phe Ala Asp Gly Tyr Leu Asp Ile
             20                  25                  30

Asp Glu Phe Asp Thr Arg Thr Gly Ala Ala Ala Ile Ala Arg Thr Ala
         35                  40                  45

Gly Glu Ile Asp Val Leu Phe Thr Asp Leu Pro Glu Gln Gln Ala Ser
     50                  55                  60

Thr Ala Val Thr Pro Val Gln Asp Asp Thr Glu Lys Glu Leu Asp Leu
 65                  70                  75                  80

Val Leu Gln Arg Gly Lys Lys Leu Lys Gln Ile Asp Ser Ala Ile Trp
                 85                  90                  95

Ala Val Val Met Val Ser Phe Phe Leu Gly Leu Phe Val Phe Asn Val
```

```
            100                 105                 110

Pro Tyr Phe Trp Val Val Phe Ile Leu Gly Gly Ala Ala Ser Ala Gly
        115                 120                 125

Ala Arg Phe Leu Leu Lys Val Asp Asp Ala Asp Glu Lys Leu Phe Glu
    130                 135                 140

Glu Leu His Ser Lys Glu Gln Ser Glu Arg Glu Ala Arg Leu Arg Ile
145                 150                 155                 160

Ala Ala Gln Arg Arg Arg Glu Leu Glu Gln
                165                 170


<210> 145
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(610)
<223> FRXA00232

<400> 145
gctgaaaaaa ctcccatttg gacaatgaac acttgtcaaa atgggagttt tggattttcg 60

caccaccggc agcactcgaa aacgtgttta tacttgaact atg aac gac agg gct   115
                                            Met Asn Asp Arg Ala
                                              1               5

cac caa cga ata ggc gac atc gag cga tcc caa gcc ctc gac cga ctt   163
His Gln Arg Ile Gly Asp Ile Glu Arg Ser Gln Ala Leu Asp Arg Leu
                10                  15                  20

ggg tca tat ttt gca gac gga tac ctc gac atc gac gaa ttc gat acc   211
Gly Ser Tyr Phe Ala Asp Gly Tyr Leu Asp Ile Asp Glu Phe Asp Thr
            25                  30                  35

cga acc ggc gcc gca gca atc gca cgc aca gcc ggt gaa ata gat gtc   259
Arg Thr Gly Ala Ala Ala Ile Ala Arg Thr Ala Gly Glu Ile Asp Val
        40                  45                  50

ttg ttc aca gat ctt ccc gaa caa cag gca agc acc gcc gtg aca ccc   307
Leu Phe Thr Asp Leu Pro Glu Gln Gln Ala Ser Thr Ala Val Thr Pro
    55                  60                  65

gtg caa gac gat acc gag aaa gaa tta gac ctg gtc cta cag cga gga   355
Val Gln Asp Asp Thr Glu Lys Glu Leu Asp Leu Val Leu Gln Arg Gly
70                  75                  80                  85

aag aag ctc aag cag atc gac tcc gcc att tgg gct gtc gtg atg gtc   403
Lys Lys Leu Lys Gln Ile Asp Ser Ala Ile Trp Ala Val Val Met Val
                90                  95                  100

tcg ttc ttc cta ggc ttg ttt gtt ttc aac gtg cca tat ttc tgg gtt   451
Ser Phe Phe Leu Gly Leu Phe Val Phe Asn Val Pro Tyr Phe Trp Val
            105                 110                 115

gtg ttc atc ctt ggc gga gcg gcc tcc gcg ggt gcg cga ttc ttg ctc   499
```

```
Val Phe Ile Leu Gly Gly Ala Ala Ser Ala Gly Ala Arg Phe Leu Leu
        120                 125                 130

aaa gta gat gac gcc gat gaa aaa ctc ttt gag gaa ctc cac agc aag   547
Lys Val Asp Asp Ala Asp Glu Lys Leu Phe Glu Glu Leu His Ser Lys
    135                 140                 145

gaa caa agc gaa cgc gaa gca cgc cta cgc att gcg gca caa cgt cga   595
Glu Gln Ser Glu Arg Glu Ala Arg Leu Arg Ile Ala Ala Gln Arg Arg
150                 155                 160                 165

cgc gag ttg gaa caa tagccacaaa agctatc                           627
Arg Glu Leu Glu Gln
                170
```

<210> 146
<211> 170
<212> PRT
<213> Corynebacterium glutamicum

<400> 146

```
Met Asn Asp Arg Ala His Gln Arg Ile Gly Asp Ile Glu Arg Ser Gln
  1               5                  10                  15

Ala Leu Asp Arg Leu Gly Ser Tyr Phe Ala Asp Gly Tyr Leu Asp Ile
             20                  25                  30

Asp Glu Phe Asp Thr Arg Thr Gly Ala Ala Ala Ile Ala Arg Thr Ala
         35                  40                  45

Gly Glu Ile Asp Val Leu Phe Thr Asp Leu Pro Glu Gln Gln Ala Ser
     50                  55                  60

Thr Ala Val Thr Pro Val Gln Asp Asp Thr Glu Lys Glu Leu Asp Leu
 65                  70                  75                  80

Val Leu Gln Arg Gly Lys Lys Leu Lys Gln Ile Asp Ser Ala Ile Trp
                 85                  90                  95

Ala Val Val Met Val Ser Phe Phe Leu Gly Leu Phe Val Phe Asn Val
            100                 105                 110

Pro Tyr Phe Trp Val Val Phe Ile Leu Gly Gly Ala Ala Ser Ala Gly
        115                 120                 125

Ala Arg Phe Leu Leu Lys Val Asp Asp Ala Asp Glu Lys Leu Phe Glu
    130                 135                 140

Glu Leu His Ser Lys Glu Gln Ser Glu Arg Glu Ala Arg Leu Arg Ile
145                 150                 155                 160

Ala Ala Gln Arg Arg Arg Glu Leu Glu Gln
                165                 170
```

<210> 147
<211> 849
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(826)
<223> RXN00236

<400> 147
aatgcgagag ttctaaaacg agccggtaac atcgaccccc atgagttcag gggttagaaa 60

agcaatggga tttggatgcg gttcggtttt ggccgtcatc atg gtg atc tca ttt 115
Met Val Ile Ser Phe
1 5

gtt gga tgg gcg ctc agc ttc atg gat gga acg gca cct att cgc caa 163
Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr Ala Pro Ile Arg Gln
10 15 20

ctc cag caa atc cct gaa gat gtt ccg ccg gcg cgt ggt gta gaa gtt 211
Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala Arg Gly Val Glu Val
25 30 35

ccg caa att gat aca gag gca gat gga cgc aca tcc aac cat ttg cgt 259
Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr Ser Asn His Leu Arg
40 45 50

ttt tgg gcg gaa cca att gct caa gat act ggt gtg tcc gct caa gcg 307
Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly Val Ser Ala Gln Ala
55 60 65

att gcg gct tat gga aac gca gag ctc atc gcg agt act gcg tgg cct 355
Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala Ser Thr Ala Trp Pro
70 75 80 85

ggc tgc aat ctg ggg tgg aat acc ttg gca ggt atc ggc cag gtg gaa 403
Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly Ile Gly Gln Val Glu
90 95 100

acc cgt cac ggt acc tac aac ggc aaa atg ttc ggg ggc agt tcc ctg 451
Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe Gly Gly Ser Ser Leu
105 110 115

gat gaa aat gga gtt gca acc cct cca atc atc ggc gtt cca ctt gat 499
Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile Gly Val Pro Leu Asp
120 125 130

ggt tca ccg ggg ttt gcg gaa att ccc gac act gat ggt ggg gaa tta 547
Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr Asp Gly Gly Glu Leu
135 140 145

gat ggc gat act gaa tat gat cgc gcg gta ggt ccc atg cag ttc att 595
Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly Pro Met Gln Phe Ile
150 155 160 165

ccg gaa acg tgg cga ctt atg gga ttg gat gca aac ggt gat ggg gta 643
Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala Asn Gly Asp Gly Val
170 175 180

gcg gac ccc aac caa att gat gac gca gca ttg agt gcc gca aac ctg 691
Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu Ser Ala Ala Asn Leu
185 190 195

ttg tgt tcc aac gat cgt gac ttg tcc act cct gaa gga tgg acc gca 739

```
Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro Glu Gly Trp Thr Ala
        200                 205                 210

gct gtt cat tct tac aac atg tct aat cag tat ttg atg gac gtt cga   787
Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr Leu Met Asp Val Arg
    215                 220                 225

gat gct gcc gcg tcc tac gct tta cga cag ccg gcg atc taaaacttaa   836
Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro Ala Ile
230                 235                 240

caagcgcaac ccc                                                  849


<210> 148
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

<400> 148
Met Val Ile Ser Phe Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr
  1               5                  10                  15

Ala Pro Ile Arg Gln Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala
             20                  25                  30

Arg Gly Val Glu Val Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr
         35                  40                  45

Ser Asn His Leu Arg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly
     50                  55                  60

Val Ser Ala Gln Ala Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala
 65                  70                  75                  80

Ser Thr Ala Trp Pro Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly
                 85                  90                  95

Ile Gly Gln Val Glu Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe
            100                 105                 110

Gly Gly Ser Ser Leu Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile
        115                 120                 125

Gly Val Pro Leu Asp Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr
    130                 135                 140

Asp Gly Gly Glu Leu Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly
145                 150                 155                 160

Pro Met Gln Phe Ile Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala
                165                 170                 175

Asn Gly Asp Gly Val Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu
            180                 185                 190

Ser Ala Ala Asn Leu Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro
        195                 200                 205

Glu Gly Trp Thr Ala Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr
    210                 215                 220
```

```
Leu Met Asp Val Arg Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro
225                 230                 235                 240

Ala Ile
```

<210> 149
<211> 849
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(826)
<223> FRXA00236

<400> 149

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aatgcgagag ttctaaaacg agccggtaac atcgaccccc atgagttcag gggttagaaa 60

agcaatggga tttggatgcg gttcggtttt ggccgtcatc atg gtg atc tca ttt   115
                                              Met Val Ile Ser Phe
                                                1               5

gtt gga tgg gcg ctc agc ttc atg gat gga acg gca cct att cgc caa   163
Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr Ala Pro Ile Arg Gln
                  10                  15                  20

ctc cag caa atc cct gaa gat gtt ccg ccg gcg cgt ggt gta gaa gtt   211
Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala Arg Gly Val Glu Val
              25                  30                  35

ccg caa att gat aca gag gca gat gga cgc aca tcc aac cat ttg cgt   259
Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr Ser Asn His Leu Arg
          40                  45                  50

ttt tgg gcg gaa cca att gct caa gat act ggt gtg tcc gct caa gcg   307
Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly Val Ser Ala Gln Ala
      55                  60                  65

att gcg gct tat gga aac gca gag ctc atc gcg agt act gcg tgg cct   355
Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala Ser Thr Ala Trp Pro
  70                  75                  80                  85

ggc tgc aat ctg ggg tgg aat acc ttg gca ggt atc ggc cag gtg gaa   403
Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly Ile Gly Gln Val Glu
                  90                  95                 100

acc cgt cac ggt acc tac aac ggc aaa atg ttc ggg ggc agt tcc ctg   451
Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe Gly Gly Ser Ser Leu
             105                 110                 115

gat gaa aat gga gtt gca acc cct cca atc atc ggc gtt cca ctt gat   499
Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile Gly Val Pro Leu Asp
         120                 125                 130

ggt tca ccg ggg ttt gcg gaa att ccc gac act gat ggt ggg gaa tta   547
Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr Asp Gly Gly Glu Leu
     135                 140                 145
```

```
gat ggc gat act gaa tat gat cgc gcg gta ggt ccc atg cag ttc att   595
Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly Pro Met Gln Phe Ile
150                 155                 160                 165

ccg gaa acg tgg cga ctt atg gga ttg gat gca aac ggt gat ggg gta   643
Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala Asn Gly Asp Gly Val
                170                 175                 180

gcg gac ccc aac caa att gat gac gca gca ttg agt gcc gca aac ctg   691
Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu Ser Ala Ala Asn Leu
            185                 190                 195

ttg tgt tcc aac gat cgt gac ttg tcc act cct gaa gga tgg acc gca   739
Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro Glu Gly Trp Thr Ala
        200                 205                 210

gct gtt cat tct tac aac atg tct aat cag tat ttg atg gac gtt cga   787
Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr Leu Met Asp Val Arg
    215                 220                 225

gat gct gcc gcg tcc tac gct tta cga cag ccg gcg atc taaaacttaa   836
Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro Ala Ile
230                 235                 240

caagcgcaac ccc                                                  849
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<210> 150
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

<400> 150

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Met Val Ile Ser Phe Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr
  1               5                  10                  15

Ala Pro Ile Arg Gln Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala
             20                  25                  30

Arg Gly Val Glu Val Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr
         35                  40                  45

Ser Asn His Leu Arg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly
     50                  55                  60

Val Ser Ala Gln Ala Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala
 65                  70                  75                  80

Ser Thr Ala Trp Pro Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly
                 85                  90                  95

Ile Gly Gln Val Glu Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe
            100                 105                 110

Gly Gly Ser Ser Leu Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile
        115                 120                 125

Gly Val Pro Leu Asp Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr
    130                 135                 140

Asp Gly Gly Glu Leu Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly
```

```
145                 150                 155                 160

Pro Met Gln Phe Ile Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala
                165                 170                 175

Asn Gly Asp Gly Val Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu
            180                 185                 190

Ser Ala Ala Asn Leu Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro
        195                 200                 205

Glu Gly Trp Thr Ala Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr
    210                 215                 220

Leu Met Asp Val Arg Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro
225                 230                 235                 240

Ala Ile
```

20050170000

<210> 151
<211> 1401
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1378)
<223> RXN00242

<400> 151

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ggatcactat cgctttaaac accgaaacct tcctgctagt tcaccaagat ttttaagttt 60

taccgcaatt tcttgagagc tttgggagga taatggcggt gtg aat gaa tgg cga   115
                                          Val Asn Glu Trp Arg
                                            1               5

aca gtc tcg ctt gta gat tcc acg gcg ctg acc gtg atc atc agt gtg   163
Thr Val Ser Leu Val Asp Ser Thr Ala Leu Thr Val Ile Ile Ser Val
                10                  15                  20

gcc gtg ttt act tct gct gtg gct ctg ctc gga gtt gtg aaa aag cgc   211
Ala Val Phe Thr Ser Ala Val Ala Leu Leu Gly Val Val Lys Lys Arg
            25                  30                  35

tct cgg tgg cgg gtt ctc gga gct ctc atc tcc tca gca gtt ctc acc   259
Ser Arg Trp Arg Val Leu Gly Ala Leu Ile Ser Ser Ala Val Leu Thr
        40                  45                  50

agt ggc gca tgg gtg gtt att gaa aag ctg tgg aag cct ttc ccc gac   307
Ser Gly Ala Trp Val Val Ile Glu Lys Leu Trp Lys Pro Phe Pro Asp
    55                  60                  65

ccc aat ccg tgg acc atc tat ctt tcc gct ggt ttg gcg gtt ttt cct   355
Pro Asn Pro Trp Thr Ile Tyr Leu Ser Ala Gly Leu Ala Val Phe Pro
70                  75                  80                  85

ctg ttg agc atc ttg ttc cgc act ggt cgt aca aga ata ctg atg gct   403
Leu Leu Ser Ile Leu Phe Arg Thr Gly Arg Thr Arg Ile Leu Met Ala
                90                  95                  100
```

```
aca ctc acc gtg att gca ctg gtt aat acg gcc gca gtc atc aat gtc   451
Thr Leu Thr Val Ile Ala Leu Val Asn Thr Ala Ala Val Ile Asn Val
            105                 110                 115

atc tac cag cca tac ccg acg ttg ggt tct ttc aat ccc gtg cca acg   499
Ile Tyr Gln Pro Tyr Pro Thr Leu Gly Ser Phe Asn Pro Val Pro Thr
        120                 125                 130

gct gtg tcc atg tcg tat gca gat ttt gaa tct cag acc act gcc ccg   547
Ala Val Ser Met Ser Tyr Ala Asp Phe Glu Ser Gln Thr Thr Ala Pro
    135                 140                 145

acg atg gat gac cgt gaa gtc ggt gcc ctt gtg cag gtg ccg cta gct   595
Thr Met Asp Asp Arg Glu Val Gly Ala Leu Val Gln Val Pro Leu Ala
150                 155                 160                 165

gga aca aca gat gat tcc acc tcc ggc ttt gat gcg cgc gat gcc tac   643
Gly Thr Thr Asp Asp Ser Thr Ser Gly Phe Asp Ala Arg Asp Ala Tyr
                170                 175                 180

gcc tat att ccg cct gcg tat tgg gat aat cct tcc cta caa ctg cca   691
Ala Tyr Ile Pro Pro Ala Tyr Trp Asp Asn Pro Ser Leu Gln Leu Pro
            185                 190                 195

gtt ttg gtt ctc atg ccc gga aac ccc ggc cag cca gat cag tgg ttt   739
Val Leu Val Leu Met Pro Gly Asn Pro Gly Gln Pro Asp Gln Trp Phe
        200                 205                 210

agc agt gga aat gcc gat caa aca gca gat aat ttc caa gca acc cac   787
Ser Ser Gly Asn Ala Asp Gln Thr Ala Asp Asn Phe Gln Ala Thr His
    215                 220                 225

gat ggc atc agc ccc att gtc atc agc gtg gat ggc aca gga tca ttc   835
Asp Gly Ile Ser Pro Ile Val Ile Ser Val Asp Gly Thr Gly Ser Phe
230                 235                 240                 245

agc gga aac cct gct tgc gtg gat tct gat gcc caa agc gtg atg aca   883
Ser Gly Asn Pro Ala Cys Val Asp Ser Asp Ala Gln Ser Val Met Thr
                250                 255                 260

tat cta tcc cac gat gtc ccc atg ttg atc aaa cag aaa ttc cga gtc   931
Tyr Leu Ser His Asp Val Pro Met Leu Ile Lys Gln Lys Phe Arg Val
            265                 270                 275

aat cag gat cag cgc acc tgg aca att ggt ggt tta agt tac ggc ggc   979
Asn Gln Asp Gln Arg Thr Trp Thr Ile Gly Gly Leu Ser Tyr Gly Gly
        280                 285                 290

acc tgt gct ttg cag atc atg acc aat cac ccc gaa gcg tat ggt tct   1027
Thr Cys Ala Leu Gln Ile Met Thr Asn His Pro Glu Ala Tyr Gly Ser
    295                 300                 305

ttc ctt gac ttc tcg ggc cag gaa gaa cca aca ctt ggc aca cgc cag   1075
Phe Leu Asp Phe Ser Gly Gln Glu Glu Pro Thr Leu Gly Thr Arg Gln
310                 315                 320                 325

caa act gtt gat cag ctt ttc ggc ggc gat gaa gac gca ttc aaa gcc   1123
Gln Thr Val Asp Gln Leu Phe Gly Gly Asp Glu Asp Ala Phe Lys Ala
                330                 335                 340
```

```
gtt aat ccg gaa gat ctg ctc aat caa gca atc agc tca gga gcg cat   1171
Val Asn Pro Glu Asp Leu Leu Asn Gln Ala Ile Ser Ser Gly Ala His
            345                 350                 355

acc tac agc ggg att tcg ggc agg ttt att gct ggt agc aac gat aaa   1219
Thr Tyr Ser Gly Ile Ser Gly Arg Phe Ile Ala Gly Ser Asn Asp Lys
        360                 365                 370

agt gca gtg agc gcg ctg tct cat ctt gat aat ttg agc aat cag gcg   1267
Ser Ala Val Ser Ala Leu Ser His Leu Asp Asn Leu Ser Asn Gln Ala
    375                 380                 385

ggc atg tcc acc acc ttt gat acc gtg gcc ggt gga cat tcc ttc cag   1315
Gly Met Ser Thr Thr Phe Asp Thr Val Ala Gly Gly His Ser Phe Gln
390                 395                 400                 405

gtg tgg cgc gtg gct tta gcg aat act ttt gat tgg gtt gcc aag cgc   1363
Val Trp Arg Val Ala Leu Ala Asn Thr Phe Asp Trp Val Ala Lys Arg
                410                 415                 420

ggc gga ttg cag gtt taacaatgaa agacgcttca cag                    1401
Gly Gly Leu Gln Val
            425
```

<210> 152
<211> 426
<212> PRT
<213> Corynebacterium glutamicum

<400> 152

```
Val Asn Glu Trp Arg Thr Val Ser Leu Val Asp Ser Thr Ala Leu Thr
  1               5                  10                  15

Val Ile Ile Ser Val Ala Val Phe Thr Ser Ala Val Ala Leu Leu Gly
             20                  25                  30

Val Val Lys Lys Arg Ser Arg Trp Arg Val Leu Gly Ala Leu Ile Ser
         35                  40                  45

Ser Ala Val Leu Thr Ser Gly Ala Trp Val Val Ile Glu Lys Leu Trp
     50                  55                  60

Lys Pro Phe Pro Asp Pro Asn Pro Trp Thr Ile Tyr Leu Ser Ala Gly
 65                  70                  75                  80

Leu Ala Val Phe Pro Leu Leu Ser Ile Leu Phe Arg Thr Gly Arg Thr
                85                  90                  95

Arg Ile Leu Met Ala Thr Leu Thr Val Ile Ala Leu Val Asn Thr Ala
            100                 105                 110

Ala Val Ile Asn Val Ile Tyr Gln Pro Tyr Pro Thr Leu Gly Ser Phe
        115                 120                 125

Asn Pro Val Pro Thr Ala Val Ser Met Ser Tyr Ala Asp Phe Glu Ser
    130                 135                 140

Gln Thr Thr Ala Pro Thr Met Asp Asp Arg Glu Val Gly Ala Leu Val
145                 150                 155                 160
```

```
Gln Val Pro Leu Ala Gly Thr Thr Asp Asp Ser Thr Ser Gly Phe Asp
                165                 170                 175

Ala Arg Asp Ala Tyr Ala Tyr Ile Pro Pro Ala Tyr Trp Asp Asn Pro
            180                 185                 190

Ser Leu Gln Leu Pro Val Leu Val Leu Met Pro Gly Asn Pro Gly Gln
        195                 200                 205

Pro Asp Gln Trp Phe Ser Ser Gly Asn Ala Asp Gln Thr Ala Asp Asn
    210                 215                 220

Phe Gln Ala Thr His Asp Gly Ile Ser Pro Ile Val Ile Ser Val Asp
225                 230                 235                 240

Gly Thr Gly Ser Phe Ser Gly Asn Pro Ala Cys Val Asp Ser Asp Ala
                245                 250                 255

Gln Ser Val Met Thr Tyr Leu Ser His Asp Val Pro Met Leu Ile Lys
            260                 265                 270

Gln Lys Phe Arg Val Asn Gln Asp Gln Arg Thr Trp Thr Ile Gly Gly
        275                 280                 285

Leu Ser Tyr Gly Gly Thr Cys Ala Leu Gln Ile Met Thr Asn His Pro
    290                 295                 300

Glu Ala Tyr Gly Ser Phe Leu Asp Phe Ser Gly Gln Glu Glu Pro Thr
305                 310                 315                 320

Leu Gly Thr Arg Gln Gln Thr Val Asp Gln Leu Phe Gly Gly Asp Glu
                325                 330                 335

Asp Ala Phe Lys Ala Val Asn Pro Glu Asp Leu Leu Asn Gln Ala Ile
            340                 345                 350

Ser Ser Gly Ala His Thr Tyr Ser Gly Ile Ser Gly Arg Phe Ile Ala
        355                 360                 365

Gly Ser Asn Asp Lys Ser Ala Val Ser Ala Leu Ser His Leu Asp Asn
    370                 375                 380

Leu Ser Asn Gln Ala Gly Met Ser Thr Thr Phe Asp Thr Val Ala Gly
385                 390                 395                 400

Gly His Ser Phe Gln Val Trp Arg Val Ala Leu Ala Asn Thr Phe Asp
                405                 410                 415

Trp Val Ala Lys Arg Gly Gly Leu Gln Val
            420                 425
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<210> 153
<211> 1303
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1303)
<223> FRXA00242

<400> 153
ggatcactat cgctttaaac accgaaacct tcctgctagt tcaccaagat ttttaagttt 60

taccgcaatt tcttgagagc tttgggagga taatggcggt gtg aat gaa tgg cga 115
Val Asn Glu Trp Arg
1 5

aca gtc tcg ctt gta gat tcc acg gcg ctg acc gtg atc atc agt gtg 163
Thr Val Ser Leu Val Asp Ser Thr Ala Leu Thr Val Ile Ile Ser Val
10 15 20

gcc gtg ttt act tct gct gtg gct ctg ctc gga gtt gtg aaa aag cgc 211
Ala Val Phe Thr Ser Ala Val Ala Leu Leu Gly Val Val Lys Lys Arg
25 30 35

tct cgg tgg cgg gtt ctc gga gct ctc atc tcc tca gca gtt ctc acc 259
Ser Arg Trp Arg Val Leu Gly Ala Leu Ile Ser Ser Ala Val Leu Thr
40 45 50

agt ggc gca tgg gtg gtt att gaa aag ctg tgg aag cct ttc ccc gac 307
Ser Gly Ala Trp Val Val Ile Glu Lys Leu Trp Lys Pro Phe Pro Asp
55 60 65

ccc aat ccg tgg acc atc tat ctt tcc gct ggt ttg gcg gtt ttt cct 355
Pro Asn Pro Trp Thr Ile Tyr Leu Ser Ala Gly Leu Ala Val Phe Pro
70 75 80 85

ctg ttg agc atc ttg ttc cgc act ggt cgt aca aga ata ctg atg gct 403
Leu Leu Ser Ile Leu Phe Arg Thr Gly Arg Thr Arg Ile Leu Met Ala
90 95 100

aca ctc acc gtg att gca ctg gtt aat acg gcc gca gtc atc aat gtc 451
Thr Leu Thr Val Ile Ala Leu Val Asn Thr Ala Ala Val Ile Asn Val
105 110 115

atc tac cag cca tac ccg acg ttg ggt tct ttc aat ccc gtg cca acg 499
Ile Tyr Gln Pro Tyr Pro Thr Leu Gly Ser Phe Asn Pro Val Pro Thr
120 125 130

gct gtg tcc atg tcg tat gca gat ttt gaa tct cag acc act gcc ccg 547
Ala Val Ser Met Ser Tyr Ala Asp Phe Glu Ser Gln Thr Thr Ala Pro
135 140 145

acg atg gat gac cgt gaa gtc ggt gcc ctt gtg cag gtg ccg cta gct 595
Thr Met Asp Asp Arg Glu Val Gly Ala Leu Val Gln Val Pro Leu Ala
150 155 160 165

gga aca aca gat gat tcc acc tcc ggc ttt gat gcg cgc gat gcc tac 643
Gly Thr Thr Asp Asp Ser Thr Ser Gly Phe Asp Ala Arg Asp Ala Tyr
170 175 180

gcc tat att ccg cct gcg tat tgg gat aat cct tcc cta caa ctg cca 691
Ala Tyr Ile Pro Pro Ala Tyr Trp Asp Asn Pro Ser Leu Gln Leu Pro
185 190 195

gtt ttg gtt ctc atg ccc gga aac ccc ggc cag cca gat cag tgg ttt 739
Val Leu Val Leu Met Pro Gly Asn Pro Gly Gln Pro Asp Gln Trp Phe
200 205 210

agc agt gga aat gcc gat caa aca gca gat aat ttc caa gca acc cac 787

```
Ser Ser Gly Asn Ala Asp Gln Thr Ala Asp Asn Phe Gln Ala Thr His
    215                 220                 225

gat ggc atc agc ccc att gtc atc agc gtg gat ggc aca gga tca ttc   835
Asp Gly Ile Ser Pro Ile Val Ile Ser Val Asp Gly Thr Gly Ser Phe
230                 235                 240                 245

agc gga aac cct gct tgc gtg gat tct gat gcc caa agc gtg atg aca   883
Ser Gly Asn Pro Ala Cys Val Asp Ser Asp Ala Gln Ser Val Met Thr
                250                 255                 260

tat cta tcc cac gat gtc ccc atg ttg atc aaa cag aaa ttc cga gtc   931
Tyr Leu Ser His Asp Val Pro Met Leu Ile Lys Gln Lys Phe Arg Val
            265                 270                 275

aat cag gat cag cgc acc tgg aca att ggt ggt tta agt tac ggc ggc   979
Asn Gln Asp Gln Arg Thr Trp Thr Ile Gly Gly Leu Ser Tyr Gly Gly
        280                 285                 290

acc tgt gct ttg cag atc atg acc aat cac ccc gaa gcg tat ggt tct   1027
Thr Cys Ala Leu Gln Ile Met Thr Asn His Pro Glu Ala Tyr Gly Ser
    295                 300                 305

ttc ctt gac ttc tcg ggc cag gaa gaa cca aca ctt ggc aca cgc cag   1075
Phe Leu Asp Phe Ser Gly Gln Glu Glu Pro Thr Leu Gly Thr Arg Gln
310                 315                 320                 325

caa act gtt gat cag ctt ttc ggc ggc gat gaa gac gca ttc aaa gcc   1123
Gln Thr Val Asp Gln Leu Phe Gly Gly Asp Glu Asp Ala Phe Lys Ala
                330                 335                 340

gtt aat ccg gaa gat ctg ctc aat caa gca atc agc tca gga gcg cat   1171
Val Asn Pro Glu Asp Leu Leu Asn Gln Ala Ile Ser Ser Gly Ala His
            345                 350                 355

acc tac agc ggg att tcg ggc agg ttt att gct ggt agc aac gat aaa   1219
Thr Tyr Ser Gly Ile Ser Gly Arg Phe Ile Ala Gly Ser Asn Asp Lys
        360                 365                 370

agt gca gtg agc gcg ctg tct cat ctt gat aat ttg agc aat cag gcg   1267
Ser Ala Val Ser Ala Leu Ser His Leu Asp Asn Leu Ser Asn Gln Ala
    375                 380                 385

ggc atg tcc acc acc ttt gat acc gtg gcc ggt gga                  1303
Gly Met Ser Thr Thr Phe Asp Thr Val Ala Gly Gly
390                 395                 400
```

<210> 154
<211> 401
<212> PRT
<213> Corynebacterium glutamicum

<400> 154

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Val Asn Glu Trp Arg Thr Val Ser Leu Val Asp Ser Thr Ala Leu Thr
  1               5                  10                  15

Val Ile Ile Ser Val Ala Val Phe Thr Ser Ala Val Ala Leu Leu Gly
            20                  25                  30

Val Val Lys Lys Arg Ser Arg Trp Arg Val Leu Gly Ala Leu Ile Ser
```

```
          35                  40                  45

Ser Ala Val Leu Thr Ser Gly Ala Trp Val Val Ile Glu Lys Leu Trp
     50                  55                  60

Lys Pro Phe Pro Asp Pro Asn Pro Trp Thr Ile Tyr Leu Ser Ala Gly
 65                  70                  75                  80

Leu Ala Val Phe Pro Leu Leu Ser Ile Leu Phe Arg Thr Gly Arg Thr
                 85                  90                  95

Arg Ile Leu Met Ala Thr Leu Thr Val Ile Ala Leu Val Asn Thr Ala
            100                 105                 110

Ala Val Ile Asn Val Ile Tyr Gln Pro Tyr Pro Thr Leu Gly Ser Phe
        115                 120                 125

Asn Pro Val Pro Thr Ala Val Ser Met Ser Tyr Ala Asp Phe Glu Ser
    130                 135                 140

Gln Thr Thr Ala Pro Thr Met Asp Asp Arg Glu Val Gly Ala Leu Val
145                 150                 155                 160

Gln Val Pro Leu Ala Gly Thr Thr Asp Asp Ser Thr Ser Gly Phe Asp
                165                 170                 175

Ala Arg Asp Ala Tyr Ala Tyr Ile Pro Pro Ala Tyr Trp Asp Asn Pro
            180                 185                 190

Ser Leu Gln Leu Pro Val Leu Val Leu Met Pro Gly Asn Pro Gly Gln
        195                 200                 205

Pro Asp Gln Trp Phe Ser Ser Gly Asn Ala Asp Gln Thr Ala Asp Asn
    210                 215                 220

Phe Gln Ala Thr His Asp Gly Ile Ser Pro Ile Val Ile Ser Val Asp
225                 230                 235                 240

Gly Thr Gly Ser Phe Ser Gly Asn Pro Ala Cys Val Asp Ser Asp Ala
                245                 250                 255

Gln Ser Val Met Thr Tyr Leu Ser His Asp Val Pro Met Leu Ile Lys
            260                 265                 270

Gln Lys Phe Arg Val Asn Gln Asp Gln Arg Thr Trp Thr Ile Gly Gly
        275                 280                 285

Leu Ser Tyr Gly Gly Thr Cys Ala Leu Gln Ile Met Thr Asn His Pro
    290                 295                 300

Glu Ala Tyr Gly Ser Phe Leu Asp Phe Ser Gly Gln Glu Glu Pro Thr
305                 310                 315                 320

Leu Gly Thr Arg Gln Gln Thr Val Asp Gln Leu Phe Gly Gly Asp Glu
                325                 330                 335

Asp Ala Phe Lys Ala Val Asn Pro Glu Asp Leu Leu Asn Gln Ala Ile
            340                 345                 350

Ser Ser Gly Ala His Thr Tyr Ser Gly Ile Ser Gly Arg Phe Ile Ala
        355                 360                 365
```

```
Gly Ser Asn Asp Lys Ser Ala Val Ser Ala Leu Ser His Leu Asp Asn
    370                 375                 380

Leu Ser Asn Gln Ala Gly Met Ser Thr Thr Phe Asp Thr Val Ala Gly
385                 390                 395                 400

Gly
```

<210> 155
<211> 1050
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1027)
<223> RXN00247

<400> 155

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aacccctaac tactgacctc gcaccacttg ttgcagcccg ttaccacgct gcattgagcg 60

cactgctggc acatatctaa gaccgctaag gaaatcagct atg cag aca tta atc   115
                                              Met Gln Thr Leu Ile
                                                1               5

ttt atc gcc att gca ggc gtc gca gca cag ctt gtt gat ggc ggc ctc   163
Phe Ile Ala Ile Ala Gly Val Ala Ala Gln Leu Val Asp Gly Gly Leu
                  10                  15                  20

ggc atg ggg ttc ggc gtc acc tca acc acc atc ctc atc atg ctc gca   211
Gly Met Gly Phe Gly Val Thr Ser Thr Thr Ile Leu Ile Met Leu Ala
              25                  30                  35

ggt tta ggc cct gcg cag gca tcc gcc gtc gtg cac acc gca gag gtt   259
Gly Leu Gly Pro Ala Gln Ala Ser Ala Val Val His Thr Ala Glu Val
          40                  45                  50

gga acc acc tta gtt tct ggt tta agc cac tgg aaa ttt ggc aac gtg   307
Gly Thr Thr Leu Val Ser Gly Leu Ser His Trp Lys Phe Gly Asn Val
      55                  60                  65

gat tgg aaa gta gtt gtc cgg ctc ggt atc ccc ggc gct atc ggc gca   355
Asp Trp Lys Val Val Val Arg Leu Gly Ile Pro Gly Ala Ile Gly Ala
  70                  75                  80                  85

ttt gct ggc gct acc ttc ttg tcc aat att tcc acc gaa gca gca gca   403
Phe Ala Gly Ala Thr Phe Leu Ser Asn Ile Ser Thr Glu Ala Ala Ala
                  90                  95                 100

ccg atc acc tcc ctg att ctt gcc ctg atc ggc atg aac cta gtc tgg   451
Pro Ile Thr Ser Leu Ile Leu Ala Leu Ile Gly Met Asn Leu Val Trp
             105                 110                 115

cga ttc agc aag gga cgc atc cgc cgc gac tat tcc gat cgc ccg cac   499
Arg Phe Ser Lys Gly Arg Ile Arg Arg Asp Tyr Ser Asp Arg Pro His
         120                 125                 130

agc agg gga ttc ctc ggc gga ctc ggt att gtc ggt ggt ttc gtt gac   547
```

```
Ser Arg Gly Phe Leu Gly Gly Leu Gly Ile Val Gly Gly Phe Val Asp
    135                 140                 145

gca tcc ggt ggc ggc gga tgg ggt cca gtg acc acc tct acg ctg ctg   595
Ala Ser Gly Gly Gly Gly Trp Gly Pro Val Thr Thr Ser Thr Leu Leu
150                 155                 160                 165

tct ttg gga cgc acc gaa ccc cgc aaa gta gtc ggc acc gtc aac acc   643
Ser Leu Gly Arg Thr Glu Pro Arg Lys Val Val Gly Thr Val Asn Thr
                170                 175                 180

gca gaa ttc tta gtc tcc cta gcc gca aca ttg ggc ttc gtc gtg gga   691
Ala Glu Phe Leu Val Ser Leu Ala Ala Thr Leu Gly Phe Val Val Gly
            185                 190                 195

ctg tgg gat gac cta gta gct aac ctc tct gca gtt ctc gcg ttg ctc   739
Leu Trp Asp Asp Leu Val Ala Asn Leu Ser Ala Val Leu Ala Leu Leu
        200                 205                 210

atc ggc ggc gca atc gca gca cca atc ggc gcc tgg atg atc tct cgc   787
Ile Gly Gly Ala Ile Ala Ala Pro Ile Gly Ala Trp Met Ile Ser Arg
    215                 220                 225

gtt aat gca acc gtc ctc ggt ggc ttc gtg ggc acc ctg att gtc aca   835
Val Asn Ala Thr Val Leu Gly Gly Phe Val Gly Thr Leu Ile Val Thr
230                 235                 240                 245

ctg aac ctg cca aag gtg ctc aac gtg gtt ggc ctt gat ttc atc ccc   883
Leu Asn Leu Pro Lys Val Leu Asn Val Val Gly Leu Asp Phe Ile Pro
                250                 255                 260

acc ggc ctc atc cag gtc acc gtc ctc ctc atc ggc ctg ccg ctg acg   931
Thr Gly Leu Ile Gln Val Thr Val Leu Leu Ile Gly Leu Pro Leu Thr
            265                 270                 275

tac ctc ggc ttc cgc cgc tac cgc aaa aat ctc ctc aac gag acc atc   979
Tyr Leu Gly Phe Arg Arg Tyr Arg Lys Asn Leu Leu Asn Glu Thr Ile
        280                 285                 290

tcc agc gaa gtt gtc tcc gaa cca aag ggc caa aag att aaa agc act   1027
Ser Ser Glu Val Val Ser Glu Pro Lys Gly Gln Lys Ile Lys Ser Thr
    295                 300                 305

taaaacacgc ttttcgacgc cca                                        1050


<210> 156
<211> 309
<212> PRT
<213> Corynebacterium glutamicum

<400> 156
Met Gln Thr Leu Ile Phe Ile Ala Ile Ala Gly Val Ala Ala Gln Leu
  1               5                  10                  15

Val Asp Gly Gly Leu Gly Met Gly Phe Gly Val Thr Ser Thr Thr Ile
             20                  25                  30

Leu Ile Met Leu Ala Gly Leu Gly Pro Ala Gln Ala Ser Ala Val Val
         35                  40                  45
```

```
His Thr Ala Glu Val Gly Thr Thr Leu Val Ser Gly Leu Ser His Trp
     50                  55                  60

Lys Phe Gly Asn Val Asp Trp Lys Val Val Val Arg Leu Gly Ile Pro
 65                  70                  75                  80

Gly Ala Ile Gly Ala Phe Ala Gly Ala Thr Phe Leu Ser Asn Ile Ser
                 85                  90                  95

Thr Glu Ala Ala Ala Pro Ile Thr Ser Leu Ile Leu Ala Leu Ile Gly
            100                 105                 110

Met Asn Leu Val Trp Arg Phe Ser Lys Gly Arg Ile Arg Arg Asp Tyr
        115                 120                 125

Ser Asp Arg Pro His Ser Arg Gly Phe Leu Gly Gly Leu Gly Ile Val
    130                 135                 140

Gly Gly Phe Val Asp Ala Ser Gly Gly Gly Gly Trp Gly Pro Val Thr
145                 150                 155                 160

Thr Ser Thr Leu Leu Ser Leu Gly Arg Thr Glu Pro Arg Lys Val Val
                165                 170                 175

Gly Thr Val Asn Thr Ala Glu Phe Leu Val Ser Leu Ala Ala Thr Leu
            180                 185                 190

Gly Phe Val Val Gly Leu Trp Asp Asp Leu Val Ala Asn Leu Ser Ala
        195                 200                 205

Val Leu Ala Leu Leu Ile Gly Gly Ala Ile Ala Ala Pro Ile Gly Ala
    210                 215                 220

Trp Met Ile Ser Arg Val Asn Ala Thr Val Leu Gly Gly Phe Val Gly
225                 230                 235                 240

Thr Leu Ile Val Thr Leu Asn Leu Pro Lys Val Leu Asn Val Val Gly
                245                 250                 255

Leu Asp Phe Ile Pro Thr Gly Leu Ile Gln Val Thr Val Leu Leu Ile
            260                 265                 270

Gly Leu Pro Leu Thr Tyr Leu Gly Phe Arg Arg Tyr Arg Lys Asn Leu
        275                 280                 285

Leu Asn Glu Thr Ile Ser Ser Glu Val Val Ser Glu Pro Lys Gly Gln
    290                 295                 300

Lys Ile Lys Ser Thr
305
```

<210> 157
<211> 1050
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1027)
<223> FRXA00247

<400> 157
aacccctaac tactgacctc gcaccacttg ttgcagcccg ttaccacgct gcattgagcg 60

cactgctggc acatatctaa gaccgctaag gaaatcagct atg cag aca tta atc 115
Met Gln Thr Leu Ile
1 5

ttt atc gcc att gca ggc gtc gca gca cag ctt gtt gat ggc ggc ctc 163
Phe Ile Ala Ile Ala Gly Val Ala Ala Gln Leu Val Asp Gly Gly Leu
10 15 20

ggc atg ggg ttc ggc gtc acc tca acc acc atc ctc atc atg ctc gca 211
Gly Met Gly Phe Gly Val Thr Ser Thr Thr Ile Leu Ile Met Leu Ala
25 30 35

ggt tta ggc cct gcg cag gca tcc gcc gtc gtg cac acc gca gag gtt 259
Gly Leu Gly Pro Ala Gln Ala Ser Ala Val Val His Thr Ala Glu Val
40 45 50

gga acc acc tta gtt tct ggt tta agc cac tgg aaa ttt ggc aac gtg 307
Gly Thr Thr Leu Val Ser Gly Leu Ser His Trp Lys Phe Gly Asn Val
55 60 65

gat tgg aaa gta gtt gtc cgg ctc ggt atc ccc ggc gct atc ggc gca 355
Asp Trp Lys Val Val Val Arg Leu Gly Ile Pro Gly Ala Ile Gly Ala
70 75 80 85

ttt gct ggc gct acc ttc ttg tcc aat att tcc acc gaa gca gca gca 403
Phe Ala Gly Ala Thr Phe Leu Ser Asn Ile Ser Thr Glu Ala Ala Ala
90 95 100

ccg atc acc tcc ctg att ctt gcc ctg atc ggc atg aac cta gtc tgg 451
Pro Ile Thr Ser Leu Ile Leu Ala Leu Ile Gly Met Asn Leu Val Trp
105 110 115

cga ttc agc aag gga cgc atc cgc cgc gac tat tcc gat cgc ccg cac 499
Arg Phe Ser Lys Gly Arg Ile Arg Arg Asp Tyr Ser Asp Arg Pro His
120 125 130

agc agg gga ttc ctc ggc gga ctc ggt att gtc ggt ggt ttc gtt gac 547
Ser Arg Gly Phe Leu Gly Gly Leu Gly Ile Val Gly Gly Phe Val Asp
135 140 145

gca tcc ggt ggc ggc gga tgg ggt cca gtg acc acc tct acg ctg ctg 595
Ala Ser Gly Gly Gly Gly Trp Gly Pro Val Thr Thr Ser Thr Leu Leu
150 155 160 165

tct ttg gga cgc acc gaa ccc cgc aaa gta gtc ggc acc gtc aac acc 643
Ser Leu Gly Arg Thr Glu Pro Arg Lys Val Val Gly Thr Val Asn Thr
170 175 180

gca gaa ttc tta gtc tcc cta gcc gca aca ttg ggc ttc gtc gtg gga 691
Ala Glu Phe Leu Val Ser Leu Ala Ala Thr Leu Gly Phe Val Val Gly
185 190 195

ctg tgg gat gac cta gta gct aac ctc tct gca gtt ctc gcg ttg ctc 739
Leu Trp Asp Asp Leu Val Ala Asn Leu Ser Ala Val Leu Ala Leu Leu
200 205 210

atc ggc ggc gca atc gca gca cca atc ggc gcc tgg atg atc tct cgc 787

```
Ile Gly Gly Ala Ile Ala Ala Pro Ile Gly Ala Trp Met Ile Ser Arg
    215                 220                 225

gtt aat gca acc gtc ctc ggt ggc ttc gtg ggc acc ctg att gtc aca   835
Val Asn Ala Thr Val Leu Gly Gly Phe Val Gly Thr Leu Ile Val Thr
230                 235                 240                 245

ctg aac ctg cca aag gtg ctc aac gtg gtt ggc ctt gat ttc atc ccc   883
Leu Asn Leu Pro Lys Val Leu Asn Val Val Gly Leu Asp Phe Ile Pro
                250                 255                 260

acc ggc ctc atc cag gtc acc gtc ctc ctc atc ggc ctg ccg ctg acg   931
Thr Gly Leu Ile Gln Val Thr Val Leu Leu Ile Gly Leu Pro Leu Thr
            265                 270                 275

tac ctc ggc ttc cgc cgc tac cgc aaa aat ctc ctc aac gag acc atc   979
Tyr Leu Gly Phe Arg Arg Tyr Arg Lys Asn Leu Leu Asn Glu Thr Ile
        280                 285                 290

tcc agc gaa gtt gtc tcc gaa cca aag ggc caa aag att aaa agc act   1027
Ser Ser Glu Val Val Ser Glu Pro Lys Gly Gln Lys Ile Lys Ser Thr
    295                 300                 305

taaaacacgc ttttcgacgc cca                                       1050


<210> 158
<211> 309
<212> PRT
<213> Corynebacterium glutamicum

<400> 158
Met Gln Thr Leu Ile Phe Ile Ala Ile Ala Gly Val Ala Ala Gln Leu
  1               5                  10                  15

Val Asp Gly Gly Leu Gly Met Gly Phe Gly Val Thr Ser Thr Thr Ile
             20                  25                  30

Leu Ile Met Leu Ala Gly Leu Gly Pro Ala Gln Ala Ser Ala Val Val
         35                  40                  45

His Thr Ala Glu Val Gly Thr Thr Leu Val Ser Gly Leu Ser His Trp
     50                  55                  60

Lys Phe Gly Asn Val Asp Trp Lys Val Val Val Arg Leu Gly Ile Pro
 65                  70                  75                  80

Gly Ala Ile Gly Ala Phe Ala Gly Ala Thr Phe Leu Ser Asn Ile Ser
                 85                  90                  95

Thr Glu Ala Ala Ala Pro Ile Thr Ser Leu Ile Leu Ala Leu Ile Gly
            100                 105                 110

Met Asn Leu Val Trp Arg Phe Ser Lys Gly Arg Ile Arg Arg Asp Tyr
        115                 120                 125

Ser Asp Arg Pro His Ser Arg Gly Phe Leu Gly Gly Leu Gly Ile Val
    130                 135                 140

Gly Gly Phe Val Asp Ala Ser Gly Gly Gly Gly Trp Gly Pro Val Thr
145                 150                 155                 160
```

```
Thr Ser Thr Leu Leu Ser Leu Gly Arg Thr Glu Pro Arg Lys Val Val
                165                 170                 175

Gly Thr Val Asn Thr Ala Glu Phe Leu Val Ser Leu Ala Ala Thr Leu
            180                 185                 190

Gly Phe Val Val Gly Leu Trp Asp Asp Leu Val Ala Asn Leu Ser Ala
        195                 200                 205

Val Leu Ala Leu Leu Ile Gly Gly Ala Ile Ala Ala Pro Ile Gly Ala
    210                 215                 220

Trp Met Ile Ser Arg Val Asn Ala Thr Val Leu Gly Gly Phe Val Gly
225                 230                 235                 240

Thr Leu Ile Val Thr Leu Asn Leu Pro Lys Val Leu Asn Val Val Gly
                245                 250                 255

Leu Asp Phe Ile Pro Thr Gly Leu Ile Gln Val Thr Val Leu Leu Ile
            260                 265                 270

Gly Leu Pro Leu Thr Tyr Leu Gly Phe Arg Arg Tyr Arg Lys Asn Leu
        275                 280                 285

Leu Asn Glu Thr Ile Ser Ser Glu Val Val Ser Glu Pro Lys Gly Gln
    290                 295                 300

Lys Ile Lys Ser Thr
305
```

<210> 159
<211> 894
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(871)
<223> RXN00256

<400> 159

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aattaatcaa tcagaaaaac atattgaata cttataaatt tctgacatac tcattaatga 60

gatattcgaa gtctttatca aaatgattaa caaaaggagt atg ttt atg tcg cta   115
                                            Met Phe Met Ser Leu
                                              1               5

aaa act cgc cga ata ttc ggc gca ctt gct gtt tcg cta tca atc tct   163
Lys Thr Arg Arg Ile Phe Gly Ala Leu Ala Val Ser Leu Ser Ile Ser
                  10                  15                  20

ttc tca gcc att gct aca cct gca gca tcc gca caa gaa cta gtg gtg   211
Phe Ser Ala Ile Ala Thr Pro Ala Ala Ser Ala Gln Glu Leu Val Val
              25                  30                  35

agc aca tca gca gta aac gaa ttt ggt gta gtt acc agt gac atc acg   259
Ser Thr Ser Ala Val Asn Glu Phe Gly Val Val Thr Ser Asp Ile Thr
          40                  45                  50
```

```
gct gag caa att ctt cag gcg caa gat cta atc gct gag atg aaa cag   307
Ala Glu Gln Ile Leu Gln Ala Gln Asp Leu Ile Ala Glu Met Lys Gln
     55                  60                  65

tca gag gac ata tat gag tat ttc ggt gcc ttg tct gac gtt gaa cag   355
Ser Glu Asp Ile Tyr Glu Tyr Phe Gly Ala Leu Ser Asp Val Glu Gln
 70                  75                  80                  85

aga tcc atc att gca gct gta aag gaa aat cca tat ctc att gag aac   403
Arg Ser Ile Ile Ala Ala Val Lys Glu Asn Pro Tyr Leu Ile Glu Asn
                90                  95                 100

gaa tca ccc cgt atg aga gtc caa agt gaa aca ccc gac gag gaa aca   451
Glu Ser Pro Arg Met Arg Val Gln Ser Glu Thr Pro Asp Glu Glu Thr
            105                 110                 115

cct gat aag aaa aag ccg agc aaa acc tac aag ctc tat atg agc att   499
Pro Asp Lys Lys Lys Pro Ser Lys Thr Tyr Lys Leu Tyr Met Ser Ile
        120                 125                 130

ctc gaa atg atg tca tgt atc aat ctt gtt gat gtt ccg tca tgt gcc   547
Leu Glu Met Met Ser Cys Ile Asn Leu Val Asp Val Pro Ser Cys Ala
    135                 140                 145

caa gcc ctt aaa gcg gca aat ata gct gaa cgc gag gcc aag gcc cgt   595
Gln Ala Leu Lys Ala Ala Asn Ile Ala Glu Arg Glu Ala Lys Ala Arg
150                 155                 160                 165

tac ccc gat tcg gtc act aat ggt aaa ggc gat gcc ctt cgt cat tgt   643
Tyr Pro Asp Ser Val Thr Asn Gly Lys Gly Asp Ala Leu Arg His Cys
                170                 175                 180

gca tgg agc gct ctc atg act att cga atc gga aaa gat gca gcc gaa   691
Ala Trp Ser Ala Leu Met Thr Ile Arg Ile Gly Lys Asp Ala Ala Glu
            185                 190                 195

aga att ggt aac gct cat gaa acc gtt gtg aga ggt gaa ccc gaa gaa   739
Arg Ile Gly Asn Ala His Glu Thr Val Val Arg Gly Glu Pro Glu Glu
        200                 205                 210

aga gaa atg gat ctc atc aat aac gcg ctg ggt aga gac atc ggc gaa   787
Arg Glu Met Asp Leu Ile Asn Asn Ala Leu Gly Arg Asp Ile Gly Glu
    215                 220                 225

aga ttc atc atc aat ggc gat gaa acg ggt gcg ctc agt act tgt gta   835
Arg Phe Ile Ile Asn Gly Asp Glu Thr Gly Ala Leu Ser Thr Cys Val
230                 235                 240                 245

tcc atg gct aat atc ggg cta ctt cat act ctg ttg taaacaaagg        881
Ser Met Ala Asn Ile Gly Leu Leu His Thr Leu Leu
                250                 255

aagtttctat cat                                                   894
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<210> 160
<211> 257
<212> PRT
<213> Corynebacterium glutamicum

<400> 160

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Met Phe Met Ser Leu Lys Thr Arg Arg Ile Phe Gly Ala Leu Ala Val
 1               5                  10                  15

Ser Leu Ser Ile Ser Phe Ser Ala Ile Ala Thr Pro Ala Ala Ser Ala
            20                  25                  30

Gln Glu Leu Val Val Ser Thr Ser Ala Val Asn Glu Phe Gly Val Val
        35                  40                  45

Thr Ser Asp Ile Thr Ala Glu Gln Ile Leu Gln Ala Gln Asp Leu Ile
    50                  55                  60

Ala Glu Met Lys Gln Ser Glu Asp Ile Tyr Glu Tyr Phe Gly Ala Leu
65                  70                  75                  80

Ser Asp Val Glu Gln Arg Ser Ile Ile Ala Ala Val Lys Glu Asn Pro
                85                  90                  95

Tyr Leu Ile Glu Asn Glu Ser Pro Arg Met Arg Val Gln Ser Glu Thr
            100                 105                 110

Pro Asp Glu Glu Thr Pro Asp Lys Lys Lys Pro Ser Lys Thr Tyr Lys
        115                 120                 125

Leu Tyr Met Ser Ile Leu Glu Met Met Ser Cys Ile Asn Leu Val Asp
    130                 135                 140

Val Pro Ser Cys Ala Gln Ala Leu Lys Ala Ala Asn Ile Ala Glu Arg
145                 150                 155                 160

Glu Ala Lys Ala Arg Tyr Pro Asp Ser Val Thr Asn Gly Lys Gly Asp
                165                 170                 175

Ala Leu Arg His Cys Ala Trp Ser Ala Leu Met Thr Ile Arg Ile Gly
            180                 185                 190

Lys Asp Ala Ala Glu Arg Ile Gly Asn Ala His Glu Thr Val Val Arg
        195                 200                 205

Gly Glu Pro Glu Glu Arg Glu Met Asp Leu Ile Asn Asn Ala Leu Gly
    210                 215                 220

Arg Asp Ile Gly Glu Arg Phe Ile Ile Asn Gly Asp Glu Thr Gly Ala
225                 230                 235                 240

Leu Ser Thr Cys Val Ser Met Ala Asn Ile Gly Leu Leu His Thr Leu
                245                 250                 255

Leu
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<210> 161
<211> 894
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(871)
<223> FRXA00256

<400> 161
aattaatcaa tcagaaaaac atattgaata cttataaatt tctgacatac tcattaatga 60

gatattcgaa gtctttatca aaatgattaa caaaaggagt atg ttt atg tcg cta 115
Met Phe Met Ser Leu
1 5

aaa act cgc cga ata ttc ggc gca ctt gct gtt tcg cta tca atc tct 163
Lys Thr Arg Arg Ile Phe Gly Ala Leu Ala Val Ser Leu Ser Ile Ser
10 15 20

ttc tca gcc att gct aca cct gca gca tcc gca caa gaa cta gtg gtg 211
Phe Ser Ala Ile Ala Thr Pro Ala Ala Ser Ala Gln Glu Leu Val Val
25 30 35

agc aca tca gca gta aac gaa ttt ggt gta gtt acc agt gac atc acg 259
Ser Thr Ser Ala Val Asn Glu Phe Gly Val Val Thr Ser Asp Ile Thr
40 45 50

gct gag caa att ctt cag gcg caa gat cta atc gct gag atg aaa cag 307
Ala Glu Gln Ile Leu Gln Ala Gln Asp Leu Ile Ala Glu Met Lys Gln
55 60 65

tca gag gac ata tat gag tat ttc ggt gcc ttg tct gac gtt gaa cag 355
Ser Glu Asp Ile Tyr Glu Tyr Phe Gly Ala Leu Ser Asp Val Glu Gln
70 75 80 85

aga tcc atc att gca gct gta aag gaa aat cca tat ctc att gag aac 403
Arg Ser Ile Ile Ala Ala Val Lys Glu Asn Pro Tyr Leu Ile Glu Asn
90 95 100

gaa tca ccc cgt atg aga gtc caa agt gaa aca ccc gac gag gaa aca 451
Glu Ser Pro Arg Met Arg Val Gln Ser Glu Thr Pro Asp Glu Glu Thr
105 110 115

cct gat aag aaa aag ccg agc aaa acc tac aag ctc tat atg agc att 499
Pro Asp Lys Lys Lys Pro Ser Lys Thr Tyr Lys Leu Tyr Met Ser Ile
120 125 130

ctc gaa atg atg tca tgt atc aat ctt gtt gat gtt ccg tca tgt gcc 547
Leu Glu Met Met Ser Cys Ile Asn Leu Val Asp Val Pro Ser Cys Ala
135 140 145

caa gcc ctt aaa gcg gca aat ata gct gaa cgc gag gcc aag gcc cgt 595
Gln Ala Leu Lys Ala Ala Asn Ile Ala Glu Arg Glu Ala Lys Ala Arg
150 155 160 165

tac ccc gat tcg gtc act aat ggt aaa ggc gat gcc ctt cgt cat tgt 643
Tyr Pro Asp Ser Val Thr Asn Gly Lys Gly Asp Ala Leu Arg His Cys
170 175 180

gca tgg agc gct ctc atg act att cga atc gga aaa gat gca gcc gaa 691
Ala Trp Ser Ala Leu Met Thr Ile Arg Ile Gly Lys Asp Ala Ala Glu
185 190 195

aga att ggt aac gct cat gaa acc gtt gtg aga ggt gaa ccc gaa gaa 739
Arg Ile Gly Asn Ala His Glu Thr Val Val Arg Gly Glu Pro Glu Glu
200 205 210

aga gaa atg gat ctc atc aat aac gcg ctg ggt aga gac atc ggc gaa 787

```
Arg Glu Met Asp Leu Ile Asn Asn Ala Leu Gly Arg Asp Ile Gly Glu
    215                 220                 225

aga ttc atc atc aat ggc gat gaa acg ggt gcg ctc agt act tgt gta   835
Arg Phe Ile Ile Asn Gly Asp Glu Thr Gly Ala Leu Ser Thr Cys Val
230                 235                 240                 245

tcc atg gct aat atc ggg cta ctt cat act ctg ttg taaacaaagg        881
Ser Met Ala Asn Ile Gly Leu Leu His Thr Leu Leu
                250                 255

aagtttctat cat                                                   894


<210> 162
<211> 257
<212> PRT
<213> Corynebacterium glutamicum

<400> 162
Met Phe Met Ser Leu Lys Thr Arg Arg Ile Phe Gly Ala Leu Ala Val
  1               5                  10                  15

Ser Leu Ser Ile Ser Phe Ser Ala Ile Ala Thr Pro Ala Ala Ser Ala
            20                  25                  30

Gln Glu Leu Val Val Ser Thr Ser Ala Val Asn Glu Phe Gly Val Val
        35                  40                  45

Thr Ser Asp Ile Thr Ala Glu Gln Ile Leu Gln Ala Gln Asp Leu Ile
    50                  55                  60

Ala Glu Met Lys Gln Ser Glu Asp Ile Tyr Glu Tyr Phe Gly Ala Leu
65                  70                  75                  80

Ser Asp Val Glu Gln Arg Ser Ile Ile Ala Ala Val Lys Glu Asn Pro
                85                  90                  95

Tyr Leu Ile Glu Asn Glu Ser Pro Arg Met Arg Val Gln Ser Glu Thr
            100                 105                 110

Pro Asp Glu Glu Thr Pro Asp Lys Lys Lys Pro Ser Lys Thr Tyr Lys
        115                 120                 125

Leu Tyr Met Ser Ile Leu Glu Met Met Ser Cys Ile Asn Leu Val Asp
    130                 135                 140

Val Pro Ser Cys Ala Gln Ala Leu Lys Ala Ala Asn Ile Ala Glu Arg
145                 150                 155                 160

Glu Ala Lys Ala Arg Tyr Pro Asp Ser Val Thr Asn Gly Lys Gly Asp
                165                 170                 175

Ala Leu Arg His Cys Ala Trp Ser Ala Leu Met Thr Ile Arg Ile Gly
            180                 185                 190

Lys Asp Ala Ala Glu Arg Ile Gly Asn Ala His Glu Thr Val Val Arg
        195                 200                 205

Gly Glu Pro Glu Glu Arg Glu Met Asp Leu Ile Asn Asn Ala Leu Gly
    210                 215                 220
```

```
Arg Asp Ile Gly Glu Arg Phe Ile Ile Asn Gly Asp Glu Thr Gly Ala
225                 230                 235                 240

Leu Ser Thr Cys Val Ser Met Ala Asn Ile Gly Leu Leu His Thr Leu
                245                 250                 255

Leu
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<210> 163
<211> 501
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(478)
<223> RXN00264

<400> 163

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aaaccggaag ggcccgttta ctcccctact tggcgcagaa atccacatca atccaggtga 60

agcagtcatc tttgatgttg atcccacgtt tgaacacggt ttg ctt gtc gat tcc   115
                                              Leu Leu Val Asp Ser
                                                1               5

ggc gac gtc caa cta gaa ggc gtc acc gtc gag ccc acc cag ctg gcc   163
Gly Asp Val Gln Leu Glu Gly Val Thr Val Glu Pro Thr Gln Leu Ala
                10                  15                  20

tac acc ggc atc aat gaa acc caa ctc cga atc cgt aac atc ggc acc   211
Tyr Thr Gly Ile Asn Glu Thr Gln Leu Arg Ile Arg Asn Ile Gly Thr
            25                  30                  35

aca ccg gcg cgt act gta ctg cta ggt ggc gaa cca ttt acc gaa gac   259
Thr Pro Ala Arg Thr Val Leu Leu Gly Gly Glu Pro Phe Thr Glu Asp
        40                  45                  50

atc gtg atg tgg tgg aac ttc att ggc cgc agc cat gaa gaa att gcc   307
Ile Val Met Trp Trp Asn Phe Ile Gly Arg Ser His Glu Glu Ile Ala
    55                  60                  65

gag tac cgt aaa cag tgg cag gcc gaa gct gat cgt ttt ggt atc acc   355
Glu Tyr Arg Lys Gln Trp Gln Ala Glu Ala Asp Arg Phe Gly Ile Thr
70                  75                  80                  85

cac gga tat atc agc cac cac aaa gat ggg ctc acc agg ctt cca gca   403
His Gly Tyr Ile Ser His His Lys Asp Gly Leu Thr Arg Leu Pro Ala
                90                  95                  100

ccc gag ctt ccc aac gct gct atc aag gca cgt aaa aac cca gca cca   451
Pro Glu Leu Pro Asn Ala Ala Ile Lys Ala Arg Lys Asn Pro Ala Pro
            105                 110                 115

act gca cga cca gaa acg aga att gat taaatgcgct ccgctcacgg         498
Thr Ala Arg Pro Glu Thr Arg Ile Asp
        120                 125

ccc                                                              501
```

<210> 164
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 164
Leu Leu Val Asp Ser Gly Asp Val Gln Leu Glu Gly Val Thr Val Glu
1 5 10 15

Pro Thr Gln Leu Ala Tyr Thr Gly Ile Asn Glu Thr Gln Leu Arg Ile
20 25 30

Arg Asn Ile Gly Thr Thr Pro Ala Arg Thr Val Leu Leu Gly Gly Glu
35 40 45

Pro Phe Thr Glu Asp Ile Val Met Trp Trp Asn Phe Ile Gly Arg Ser
50 55 60

His Glu Glu Ile Ala Glu Tyr Arg Lys Gln Trp Gln Ala Glu Ala Asp
65 70 75 80

Arg Phe Gly Ile Thr His Gly Tyr Ile Ser His His Lys Asp Gly Leu
85 90 95

Thr Arg Leu Pro Ala Pro Glu Leu Pro Asn Ala Ala Ile Lys Ala Arg
100 105 110

Lys Asn Pro Ala Pro Thr Ala Arg Pro Glu Thr Arg Ile Asp
115 120 125

<210> 165
<211> 501
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(478)
<223> FRXA00264

<400> 165
aaaccggaag ggccsgttta ctcccctact tggcgcagaa atccacatca atccaggtga 60

agcagtcatc tttgatgttg atcccacgtt tgaacacggt ttg ctt gtc gat tcc 115
Leu Leu Val Asp Ser
1 5

ggc gac gtc caa cta gaa ggc gtc acc gtc gag ccc acc cag ctg gcc 163
Gly Asp Val Gln Leu Glu Gly Val Thr Val Glu Pro Thr Gln Leu Ala
10 15 20

tac acc ggc atc aat gaa acc caa ctc cga atc cgt aac atc ggc acc 211
Tyr Thr Gly Ile Asn Glu Thr Gln Leu Arg Ile Arg Asn Ile Gly Thr
25 30 35

aca ccg gcg cgt act gta ctg cta ggt ggc gaa cca ttt acc gaa gac 259
Thr Pro Ala Arg Thr Val Leu Leu Gly Gly Glu Pro Phe Thr Glu Asp
40 45 50

```
atc gtg atg tgg tgg aac ttc att ggc cgc agc cat gaa gaa att gcc   307
Ile Val Met Trp Trp Asn Phe Ile Gly Arg Ser His Glu Glu Ile Ala
     55                  60                  65

gag tac cgt aaa cag tgg cag gcc gaa gct gat cgt ttt ggt atc acc   355
Glu Tyr Arg Lys Gln Trp Gln Ala Glu Ala Asp Arg Phe Gly Ile Thr
 70                  75                  80                  85

cac gga tat atc agc cac cac aaa gat ggg ctc acc agg ctt cca gca   403
His Gly Tyr Ile Ser His His Lys Asp Gly Leu Thr Arg Leu Pro Ala
                 90                  95                 100

ccc gag ctt ccc aac gct gct atc aag gca cgt aaa aac cca gca cca   451
Pro Glu Leu Pro Asn Ala Ala Ile Lys Ala Arg Lys Asn Pro Ala Pro
            105                 110                 115

act gca cga cca gaa acg aga att gat taaatgcgct ccgctcacgg         498
Thr Ala Arg Pro Glu Thr Arg Ile Asp
        120                 125

ccc                                                               501
```

<210> 166
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 166

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Leu Leu Val Asp Ser Gly Asp Val Gln Leu Glu Gly Val Thr Val Glu
  1               5                  10                  15

Pro Thr Gln Leu Ala Tyr Thr Gly Ile Asn Glu Thr Gln Leu Arg Ile
            20                  25                  30

Arg Asn Ile Gly Thr Thr Pro Ala Arg Thr Val Leu Leu Gly Gly Glu
        35                  40                  45

Pro Phe Thr Glu Asp Ile Val Met Trp Trp Asn Phe Ile Gly Arg Ser
    50                  55                  60

His Glu Glu Ile Ala Glu Tyr Arg Lys Gln Trp Gln Ala Glu Ala Asp
65                  70                  75                  80

Arg Phe Gly Ile Thr His Gly Tyr Ile Ser His His Lys Asp Gly Leu
                85                  90                  95

Thr Arg Leu Pro Ala Pro Glu Leu Pro Asn Ala Ala Ile Lys Ala Arg
            100                 105                 110

Lys Asn Pro Ala Pro Thr Ala Arg Pro Glu Thr Arg Ile Asp
        115                 120                 125
```

<210> 167
<211> 441
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(418)
<223> RXN00267

<400> 167
gtcgtactta tcttttaaag tcatgcctta aaggatacgg agatcactcc ggcttggctt 60

gggtggcggt gttatcaaag tagtcgtagc gttgagaact atg cga aac tct aag 115
Met Arg Asn Ser Lys
1 5

tct ggc ctg gcc ttt tcc gca gct gca cta ttt tgt gtc gtc gcg gta 163
Ser Gly Leu Ala Phe Ser Ala Ala Ala Leu Phe Cys Val Val Ala Val
10 15 20

atc act cgt att gca agt tcc cca tca ttt atc gct att gtg gcg atc 211
Ile Thr Arg Ile Ala Ser Ser Pro Ser Phe Ile Ala Ile Val Ala Ile
25 30 35

atc gtg gct gcg atc gca ctt ttt gtg ggt ctg aac agt cgt gtg gga 259
Ile Val Ala Ala Ile Ala Leu Phe Val Gly Leu Asn Ser Arg Val Gly
40 45 50

aca aag ctt gtt gat cag cca gtg gtg ttc acc cag gaa caa att gat 307
Thr Lys Leu Val Asp Gln Pro Val Val Phe Thr Gln Glu Gln Ile Asp
55 60 65

caa ttg aaa gag ttg aaa tcc cgc gac cag gag gcg gca gcg atc cgt 355
Gln Leu Lys Glu Leu Lys Ser Arg Asp Gln Glu Ala Ala Ala Ile Arg
70 75 80 85

cag gcg cag ctg tgg agt agg gga tcg tcc agc gaa gcg gtc gca gag 403
Gln Ala Gln Leu Trp Ser Arg Gly Ser Ser Ser Glu Ala Val Ala Glu
90 95 100

gct gtg agg aag ctc taagtcgact taagtgcgcg aag 441
Ala Val Arg Lys Leu
105

<210> 168
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 168
Met Arg Asn Ser Lys Ser Gly Leu Ala Phe Ser Ala Ala Ala Leu Phe
1 5 10 15

Cys Val Val Ala Val Ile Thr Arg Ile Ala Ser Ser Pro Ser Phe Ile
20 25 30

Ala Ile Val Ala Ile Ile Val Ala Ala Ile Ala Leu Phe Val Gly Leu
35 40 45

Asn Ser Arg Val Gly Thr Lys Leu Val Asp Gln Pro Val Val Phe Thr
50 55 60

Gln Glu Gln Ile Asp Gln Leu Lys Glu Leu Lys Ser Arg Asp Gln Glu
65 70 75 80

```
Ala Ala Ala Ile Arg Gln Ala Gln Leu Trp Ser Arg Gly Ser Ser Ser
                 85                  90                  95

Glu Ala Val Ala Glu Ala Val Arg Lys Leu
            100                 105


<210> 169
<211> 358
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (66)..(335)
<223> FRXA00267

<400> 169
cgtagcgttg agaactatgc gaaactctaa gtctggcctg gccttttccg cagctgcact 60

attttgtg tct gtc gcg gta atc act cgt att gca agt tcc cca tca ttt  110
     Val Ser Val Ala Val Ile Thr Arg Ile Ala Ser Ser Pro Ser Phe
       1               5                  10                  15

atc gct att gtg gcg atc atc gtg gct gcg atc gca ctt ttt gtg ggt   158
Ile Ala Ile Val Ala Ile Ile Val Ala Ala Ile Ala Leu Phe Val Gly
                 20                  25                  30

ctg aac agt cgt gtg gga aca aag ctt gtt gat cag cca gtg gtg ttc   206
Leu Asn Ser Arg Val Gly Thr Lys Leu Val Asp Gln Pro Val Val Phe
             35                  40                  45

acc cag gaa caa att gat caa ttg aaa gag ttg aaa tcc cgc gac cag   254
Thr Gln Glu Gln Ile Asp Gln Leu Lys Glu Leu Lys Ser Arg Asp Gln
         50                  55                  60

gag gcg gca gcg atc cgt cag gcg cag ctg tgg agt agg gga tcg tcc   302
Glu Ala Ala Ala Ile Arg Gln Ala Gln Leu Trp Ser Arg Gly Ser Ser
     65                  70                  75

agc gaa gcg gtc gca gag gct gtg agg aag ctc taagtcgact taagtgcgcg 355
Ser Glu Ala Val Ala Glu Ala Val Arg Lys Leu
 80                  85                  90

aag                                                               358


<210> 170
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

<400> 170
Val Ser Val Ala Val Ile Thr Arg Ile Ala Ser Ser Pro Ser Phe Ile
  1               5                  10                  15

Ala Ile Val Ala Ile Ile Val Ala Ala Ile Ala Leu Phe Val Gly Leu
             20                  25                  30

Asn Ser Arg Val Gly Thr Lys Leu Val Asp Gln Pro Val Val Phe Thr
         35                  40                  45
```

```
Gln Glu Gln Ile Asp Gln Leu Lys Glu Leu Lys Ser Arg Asp Gln Glu
     50                  55                  60

Ala Ala Ala Ile Arg Gln Ala Gln Leu Trp Ser Arg Gly Ser Ser Ser
 65                  70                  75                  80

Glu Ala Val Ala Glu Ala Val Arg Lys Leu
                 85                  90


<210> 171
<211> 1113
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1090)
<223> RXN00271

<400> 171
tagtttaaat catgagacat ttcacatatg gttctttatc cgagacatgt gttgacgctg 60

tctgcccctt tttgaaaata acactttaag gagatgtgcc atg ttt tct tcc cgt   115
                                           Met Phe Ser Ser Arg
                                             1               5

tcg aag gta ctc gca agc atc ttt act gtt ggc gcc ttg gcg ttg gct   163
Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly Ala Leu Ala Leu Ala
                 10                  15                  20

tcg tgc tca agc gat tcc agt gac agc tcc acc tcc act gat gct gca   211
Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr Ser Thr Asp Ala Ala
             25                  30                  35

ggt ggc gac tct tac cga gtt ggc atc aac cag ctt gtt cag cac cct   259
Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln Leu Val Gln His Pro
         40                  45                  50

gca ctt gat gca gcg acc act ggt ttc aag gaa gct ttt gaa gag gca   307
Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu Ala Phe Glu Glu Ala
     55                  60                  65

ggc gtt gac gtc acc ttt gat gag caa aac gct aac ggc gag cag ggc   355
Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala Asn Gly Glu Gln Gly
 70                  75                  80                  85

act gca ctg act att tct cag cag ttc gct tct gac aat ttg gat ctc   403
Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser Asp Asn Leu Asp Leu
                 90                  95                 100

gtg ttg gct gtt gca act cca gca gca cag gca act gcg cag aat atc   451
Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala Thr Ala Gln Asn Ile
            105                 110                 115

act gat atc cca gtc ctg ttc acc gca gtt acc gat gca gtg tcg gca   499
Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr Asp Ala Val Ser Ala
        120                 125                 130

gag ctg gtg gat tct aat gaa gca cct ggc gga aac gtc acc ggt act   547
```

```
Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly Asn Val Thr Gly Thr
    135                 140                 145

tct gat atc gca ccg att gag cag cag ttg gag ctt ttg cag cag ctg   595
Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu Leu Leu Gln Gln Leu
150                 155                 160                 165

gtt cct gac gca aag tcc atc ggc atc gtc tac gcg tct ggt gag gtc   643
Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr Ala Ser Gly Glu Val
                170                 175                 180

aac tct cag gtg cag gtc gat gag gtc acc aag gct gct gag cca ctg   691
Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys Ala Ala Glu Pro Leu
            185                 190                 195

ggg ctg tcc gtt aat act cag act gtc act acc gtg aac gag att cag   739
Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr Val Asn Glu Ile Gln
        200                 205                 210

cag gct gtt gaa gct ctc ggc gat gtt gat gtc atc tac gtt cca act   787
Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val Ile Tyr Val Pro Thr
    215                 220                 225

gac aac atg gtt gtt tcc ggt att tct tct ctg gtt cag gtt gct gag   835
Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu Val Gln Val Ala Glu
230                 235                 240                 245

cag aag cag atc cct gtg atc ggc gct gag tcc ggc act gtt gag ggt   883
Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser Gly Thr Val Glu Gly
                250                 255                 260

ggc gca ctg gca acc ctg ggt atc gat tac acc gag ctt ggc cgc cag   931
Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr Glu Leu Gly Arg Gln
            265                 270                 275

act ggt gag atg gct ctg cgt att ctg cag gac ggc gaa gac cca gca   979
Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp Gly Glu Asp Pro Ala
        280                 285                 290

acc atg cct gtg gag act gca act gag ttc acc tac gtg atc aac gaa   1027
Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr Tyr Val Ile Asn Glu
    295                 300                 305

gat gca gca gag cgc cag ggc gtg gag atc cct caa gag att ttg gat   1075
Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro Gln Glu Ile Leu Asp
310                 315                 320                 325

aag gcc gaa cgc gta tgatcggcgc ttttgagttc gga                    1113
Lys Ala Glu Arg Val
                330
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<210> 172
<211> 330
<212> PRT
<213> Corynebacterium glutamicum

<400> 172

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Met Phe Ser Ser Arg Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly
  1               5                  10                  15
```

```
Ala Leu Ala Leu Ala Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr
            20                  25                  30

Ser Thr Asp Ala Ala Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln
        35                  40                  45

Leu Val Gln His Pro Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu
    50                  55                  60

Ala Phe Glu Glu Ala Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala
65                  70                  75                  80

Asn Gly Glu Gln Gly Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser
                85                  90                  95

Asp Asn Leu Asp Leu Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala
            100                 105                 110

Thr Ala Gln Asn Ile Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr
        115                 120                 125

Asp Ala Val Ser Ala Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly
    130                 135                 140

Asn Val Thr Gly Thr Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu
145                 150                 155                 160

Leu Leu Gln Gln Leu Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr
                165                 170                 175

Ala Ser Gly Glu Val Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys
            180                 185                 190

Ala Ala Glu Pro Leu Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr
        195                 200                 205

Val Asn Glu Ile Gln Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val
    210                 215                 220

Ile Tyr Val Pro Thr Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu
225                 230                 235                 240

Val Gln Val Ala Glu Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser
                245                 250                 255

Gly Thr Val Glu Gly Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr
            260                 265                 270

Glu Leu Gly Arg Gln Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp
        275                 280                 285

Gly Glu Asp Pro Ala Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr
    290                 295                 300

Tyr Val Ile Asn Glu Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro
305                 310                 315                 320

Gln Glu Ile Leu Asp Lys Ala Glu Arg Val
                325                 330
```

<210> 173
<211> 1113
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1090)
<223> FRXA00271

<400> 173
tagtttaaat catgagacat ttcacatatg gttctttatc cgagacatgt gttgacgctg 60

tctgcccctt tttgaaaata acactttaag gagatgtgcc atg ttt tct tcc cgt 115
Met Phe Ser Ser Arg
1 5

tcg aag gta ctc gca agc atc ttt act gtt ggc gcc ttg gcg ttg gct 163
Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly Ala Leu Ala Leu Ala
10 15 20

tcg tgc tca agc gat tcc agt gac agc tcc acc tcc act gat gct gca 211
Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr Ser Thr Asp Ala Ala
25 30 35

ggt ggc gac tct tac cga gtt ggc atc aac cag ctt gtt cag cac cct 259
Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln Leu Val Gln His Pro
40 45 50

gca ctt gat gca gcg acc act ggt ttc aag gaa gct ttt gaa gag gca 307
Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu Ala Phe Glu Glu Ala
55 60 65

ggc gtt gac gtc acc ttt gat gag caa aac gct aac ggc gag cag ggc 355
Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala Asn Gly Glu Gln Gly
70 75 80 85

act gca ctg act att tct cag cag ttc gct tct gac aat ttg gat ctc 403
Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser Asp Asn Leu Asp Leu
90 95 100

gtg ttg gct gtt gca act cca gca gca cag gca act gcg cag aat atc 451
Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala Thr Ala Gln Asn Ile
105 110 115

act gat atc cca gtc ctg ttc acc gca gtt acc gat gca gtg tcg gca 499
Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr Asp Ala Val Ser Ala
120 125 130

gag ctg gtg gat tct aat gaa gca cct ggc gga aac gtc acc ggt act 547
Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly Asn Val Thr Gly Thr
135 140 145

tct gat atc gca ccg att gag cag cag ttg gag ctt ttg cag cag ctg 595
Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu Leu Leu Gln Gln Leu
150 155 160 165

gtt cct gac gca aag tcc atc ggc atc gtc tac gcg tct ggt gag gtc 643
Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr Ala Ser Gly Glu Val
170 175 180

```
aac tct cag gtg cag gtc gat gag gtc acc aag gct gct gag cca ctg   691
Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys Ala Ala Glu Pro Leu
            185                 190                 195

ggg ctg tcc gtt aat act cag act gtc act acc gtg aac gag att cag   739
Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr Val Asn Glu Ile Gln
        200                 205                 210

cag gct gtt gaa gct ctc ggc gat gtt gat gtc atc tac gtt cca act   787
Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val Ile Tyr Val Pro Thr
    215                 220                 225

gac aac atg gtt gtt tcc ggt att tct tct ctg gtt cag gtt gct gag   835
Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu Val Gln Val Ala Glu
230                 235                 240                 245

cag aag cag atc cct gtg atc ggc gct gag tcc ggc act gtt gag ggt   883
Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser Gly Thr Val Glu Gly
                250                 255                 260

ggc gca ctg gca acc ctg ggt atc gat tac acc gag ctt ggc cgc cag   931
Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr Glu Leu Gly Arg Gln
            265                 270                 275

act ggt gag atg gct ctg cgt att ctg cag gac ggc gaa gac cca gca   979
Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp Gly Glu Asp Pro Ala
        280                 285                 290

acc atg cct gtg gag act gca act gag ttc acc tac gtg atc aac gaa   1027
Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr Tyr Val Ile Asn Glu
    295                 300                 305

gat gca gca gag cgc cag ggc gtg gag atc cct caa gag att ttg gat   1075
Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro Gln Glu Ile Leu Asp
310                 315                 320                 325

aag gcc gaa cgc gta tgatcggcgc ttttgagttc gga                    1113
Lys Ala Glu Arg Val
                330
```

CONFIDENTIAL

<210> 174
<211> 330
<212> PRT
<213> Corynebacterium glutamicum

<400> 174

```
Met Phe Ser Ser Arg Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly
  1               5                  10                  15

Ala Leu Ala Leu Ala Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr
             20                  25                  30

Ser Thr Asp Ala Ala Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln
         35                  40                  45

Leu Val Gln His Pro Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu
     50                  55                  60

Ala Phe Glu Glu Ala Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala
 65                  70                  75                  80
```

```
Asn Gly Glu Gln Gly Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser
                 85                  90                  95

Asp Asn Leu Asp Leu Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala
            100                 105                 110

Thr Ala Gln Asn Ile Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr
        115                 120                 125

Asp Ala Val Ser Ala Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly
    130                 135                 140

Asn Val Thr Gly Thr Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu
145                 150                 155                 160

Leu Leu Gln Gln Leu Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr
                165                 170                 175

Ala Ser Gly Glu Val Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys
            180                 185                 190

Ala Ala Glu Pro Leu Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr
        195                 200                 205

Val Asn Glu Ile Gln Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val
    210                 215                 220

Ile Tyr Val Pro Thr Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu
225                 230                 235                 240

Val Gln Val Ala Glu Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser
                245                 250                 255

Gly Thr Val Glu Gly Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr
            260                 265                 270

Glu Leu Gly Arg Gln Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp
        275                 280                 285

Gly Glu Asp Pro Ala Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr
    290                 295                 300

Tyr Val Ile Asn Glu Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro
305                 310                 315                 320

Gln Glu Ile Leu Asp Lys Ala Glu Arg Val
                325                 330
```

<210> 175
<211> 495
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(472)
<223> RXN00272

<400> 175

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accgatgcac cagccaccaa cgcgtccaaa tcaatatcag cctggcccac aaggtggaat 60

tccagtgggt ggccatctgc cacaaccagg tgcagggcac atg ccg gaa cca gaa   115
                                            Met Pro Glu Pro Glu
                                              1               5

acc tcc acg atg ggc tcc atc caa aag tcc ggt gaa tgg ctc gtt cct   163
Thr Ser Thr Met Gly Ser Ile Gln Lys Ser Gly Glu Trp Leu Val Pro
                 10                  15                  20

gca tat tcg gca tac aag ctc aac ggt gct gac ctt ttc tta gat atc   211
Ala Tyr Ser Ala Tyr Lys Leu Asn Gly Ala Asp Leu Phe Leu Asp Ile
             25                  30                  35

cgc cat gcc acc gcg gct gct cct gtc att acc ttt gat gtc aac atg   259
Arg His Ala Thr Ala Ala Ala Pro Val Ile Thr Phe Asp Val Asn Met
         40                  45                  50

acc atg ggt tct atg acg ctg att gtt cca ccg ggt gtg tat gtg gaa   307
Thr Met Gly Ser Met Thr Leu Ile Val Pro Pro Gly Val Tyr Val Glu
     55                  60                  65

gtg cag atg gct tcc aag aac tgg tcg gat ttc aag gtt caa aca acc   355
Val Gln Met Ala Ser Lys Asn Trp Ser Asp Phe Lys Val Gln Thr Thr
 70                  75                  80                  85

aat cct ctc ccc ggt gct ccc cga gtg ttc atc act ggt gtt gca cgc   403
Asn Pro Leu Pro Gly Ala Pro Arg Val Phe Ile Thr Gly Val Ala Arg
                 90                  95                 100

gca tca ggg ttg aag gtt ttc acc aag cat cct cat gag cct ttt ggg   451
Ala Ser Gly Leu Lys Val Phe Thr Lys His Pro His Glu Pro Phe Gly
             105                 110                 115

ttc tgg cag aaa atg ttt gag tagcctcggg ccacgcccga acc            495
Phe Trp Gln Lys Met Phe Glu
         120
```

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<210> 176
<211> 124
<212> PRT
<213> Corynebacterium glutamicum

<400> 176

```
Met Pro Glu Pro Glu Thr Ser Thr Met Gly Ser Ile Gln Lys Ser Gly
  1               5                  10                  15

Glu Trp Leu Val Pro Ala Tyr Ser Ala Tyr Lys Leu Asn Gly Ala Asp
             20                  25                  30

Leu Phe Leu Asp Ile Arg His Ala Thr Ala Ala Ala Pro Val Ile Thr
         35                  40                  45

Phe Asp Val Asn Met Thr Met Gly Ser Met Thr Leu Ile Val Pro Pro
     50                  55                  60

Gly Val Tyr Val Glu Val Gln Met Ala Ser Lys Asn Trp Ser Asp Phe
 65                  70                  75                  80

Lys Val Gln Thr Thr Asn Pro Leu Pro Gly Ala Pro Arg Val Phe Ile
```

```
                85                  90                  95

Thr Gly Val Ala Arg Ala Ser Gly Leu Lys Val Phe Thr Lys His Pro
            100                 105                 110

His Glu Pro Phe Gly Phe Trp Gln Lys Met Phe Glu
        115                 120


<210> 177
<211> 495
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(472)
<223> FRXA00272

<400> 177
accgatgcac cagccaccaa cgcgtccaaa tcaatatcag cctggcccac aaggtggaat 60

tccagtgggt ggccatctgc cacaaccagg tgcagggcac atg ccg gaa cca gaa   115
                                              Met Pro Glu Pro Glu
                                                1               5

acc tcc acg atg ggc tcc atc caa aag tcc ggt gaa tgg ctc gtt cct   163
Thr Ser Thr Met Gly Ser Ile Gln Lys Ser Gly Glu Trp Leu Val Pro
                10                  15                  20

gca tat tcg gca tac aag ctc aac ggt gct gac ctt ttc tta gat atc   211
Ala Tyr Ser Ala Tyr Lys Leu Asn Gly Ala Asp Leu Phe Leu Asp Ile
            25                  30                  35

cgc cat gcc acc gcg gct gct cct gtc att acc ttt gat gtc aac atg   259
Arg His Ala Thr Ala Ala Ala Pro Val Ile Thr Phe Asp Val Asn Met
        40                  45                  50

acc atg ggt tct atg acg ctg att gtt cca ccg ggt gtg tat gtg gaa   307
Thr Met Gly Ser Met Thr Leu Ile Val Pro Pro Gly Val Tyr Val Glu
    55                  60                  65

gtg cag atg gct tcc aag aac tgg tcg gat ttc aag gtt caa aca acc   355
Val Gln Met Ala Ser Lys Asn Trp Ser Asp Phe Lys Val Gln Thr Thr
70                  75                  80                  85

aat cct ctc ccc ggt gct ccc cga gtg ttc atc act ggt gtt gca cgc   403
Asn Pro Leu Pro Gly Ala Pro Arg Val Phe Ile Thr Gly Val Ala Arg
                90                  95                 100

gca tca ggg ttg aag gtt ttc acc aag cat cct cat gag cct ttt ggg   451
Ala Ser Gly Leu Lys Val Phe Thr Lys His Pro His Glu Pro Phe Gly
            105                 110                 115

ttc tgg cag aaa atg ttt gag tagcctcggg ccacgcccga acc            495
Phe Trp Gln Lys Met Phe Glu
        120


<210> 178
<211> 124
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<212> PRT
<213> Corynebacterium glutamicum

<400> 178
Met Pro Glu Pro Glu Thr Ser Thr Met Gly Ser Ile Gln Lys Ser Gly
1 5 10 15

Glu Trp Leu Val Pro Ala Tyr Ser Ala Tyr Lys Leu Asn Gly Ala Asp
20 25 30

Leu Phe Leu Asp Ile Arg His Ala Thr Ala Ala Ala Pro Val Ile Thr
35 40 45

Phe Asp Val Asn Met Thr Met Gly Ser Met Thr Leu Ile Val Pro Pro
50 55 60

Gly Val Tyr Val Glu Val Gln Met Ala Ser Lys Asn Trp Ser Asp Phe
65 70 75 80

Lys Val Gln Thr Thr Asn Pro Leu Pro Gly Ala Pro Arg Val Phe Ile
85 90 95

Thr Gly Val Ala Arg Ala Ser Gly Leu Lys Val Phe Thr Lys His Pro
100 105 110

His Glu Pro Phe Gly Phe Trp Gln Lys Met Phe Glu
115 120

<210> 179
<211> 1155
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1132)
<223> RXN00283

<400> 179
gcgttggcat tggcgttttt agcgcgctat gacgccctca tcatggcctt cgtagccatg 60

tggactgtcg gatttatgac atggcgcgca cgataccgcc gtg gct tcc gcg acc 115
Val Ala Ser Ala Thr
1 5

gca tcg gat tcg cac ttg tcg aca tgc tgc tcc tcg tct ggc cga tcg 163
Ala Ser Asp Ser His Leu Ser Thr Cys Cys Ser Ser Ser Gly Arg Ser
10 15 20

gct tcg cct tcg tcg cct gga ctg gcg cca agc tgg ctc act acc ggc 211
Ala Ser Pro Ser Ser Pro Gly Leu Ala Pro Ser Trp Leu Thr Thr Gly
25 30 35

gaa ctc ttt gcc caa ttc acc tcc aca gac ggc aac gct gcg atc atc 259
Glu Leu Phe Ala Gln Phe Thr Ser Thr Asp Gly Asn Ala Ala Ile Ile
40 45 50

gca gca tcc ggc ggc ggc gcc ata ggg ccc caa gcg ctt ttc gac gcc 307
Ala Ala Ser Gly Gly Gly Ala Ile Gly Pro Gln Ala Leu Phe Asp Ala
55 60 65

```
tcc gtc cgc acc ttc ctc atc tcc cca gct ctc cta ctc gtc gca gta   355
Ser Val Arg Thr Phe Leu Ile Ser Pro Ala Leu Leu Leu Val Ala Val
 70                  75                  80                  85

gtt gca gtc ttt ttt gct tat cga cgc cgc gac ccc gaa ccc atc atc   403
Val Ala Val Phe Phe Ala Tyr Arg Arg Arg Asp Pro Glu Pro Ile Ile
                90                  95                 100

ccc tta gct ctc atc ggc tct gtg gtg ttc ttc caa atc att acc tac   451
Pro Leu Ala Leu Ile Gly Ser Val Val Phe Phe Gln Ile Ile Thr Tyr
            105                 110                 115

tca ctt gga tct acc ttc ggc ctg ctg cgc ttt ttc ctc acc gcc ctg   499
Ser Leu Gly Ser Thr Phe Gly Leu Leu Arg Phe Phe Leu Thr Ala Leu
        120                 125                 130

ccg ctc acc att atc ttg ctg ttc caa att atc ccg ccc cgc cac cga   547
Pro Leu Thr Ile Ile Leu Leu Phe Gln Ile Ile Pro Pro Arg His Arg
    135                 140                 145

ttc ccc tca ctg cga cca ggt gcg tgc tac cgc gat cgc gtc acc ggc   595
Phe Pro Ser Leu Arg Pro Gly Ala Cys Tyr Arg Asp Arg Val Thr Gly
150                 155                 160                 165

aag tac gtg ccc aaa aca atc acc ggt gtt tta gtt ctc gcg atc ttc   643
Lys Tyr Val Pro Lys Thr Ile Thr Gly Val Leu Val Leu Ala Ile Phe
                170                 175                 180

ggc ggc acc ggc atc acc ctg tac ggc atg agc agt gct aac tgg gcg   691
Gly Gly Thr Gly Ile Thr Leu Tyr Gly Met Ser Ser Ala Asn Trp Ala
            185                 190                 195

ccc cag gaa tat gcc atc caa gaa cta gtt ttc aac atg gga tcg cca   739
Pro Gln Glu Tyr Ala Ile Gln Glu Leu Val Phe Asn Met Gly Ser Pro
        200                 205                 210

tcg cag gac gcc gtc cac acc ctg aac acc ttc tcc act gaa atg gat   787
Ser Gln Asp Ala Val His Thr Leu Asn Thr Phe Ser Thr Glu Met Asp
    215                 220                 225

gtc gcc gat ttc gtc gac tcc cta aac ctt gga gac ggc gaa gtc ctt   835
Val Ala Asp Phe Val Asp Ser Leu Asn Leu Gly Asp Gly Glu Val Leu
230                 235                 240                 245

ctc tcc acc acc tac ggc ttc gcc gtc ctc acc gca tca aac aac caa   883
Leu Ser Thr Thr Tyr Gly Phe Ala Val Leu Thr Ala Ser Asn Asn Gln
                250                 255                 260

aag caa ttc atc atc ccc tcc gac gaa gac ttc atc acc acc ctc aac   931
Lys Gln Phe Ile Ile Pro Ser Asp Glu Asp Phe Ile Thr Thr Leu Asn
            265                 270                 275

gaa ccc gct gag cac ggc gtt aag tac atc ctc gcc ctc cca cgc gaa   979
Glu Pro Ala Glu His Gly Val Lys Tyr Ile Leu Ala Leu Pro Arg Glu
        280                 285                 290

ggt cgc ggc gcc acc gac ccg atc aac ctg cgc tac cca gac atg tat   1027
Gly Arg Gly Ala Thr Asp Pro Ile Asn Leu Arg Tyr Pro Asp Met Tyr
    295                 300                 305
```

```
gaa acc ggc agc cac atc gcc acg atg gaa atc gaa ttc atc aat caa   1075
Glu Thr Gly Ser His Ile Ala Thr Met Glu Ile Glu Phe Ile Asn Gln
310                 315                 320                 325

ggc caa gga caa cca aat tgg cgc ctc tat cgg gtg ctc acc aca cct   1123
Gly Gln Gly Gln Pro Asn Trp Arg Leu Tyr Arg Val Leu Thr Thr Pro
                330                 335                 340

gaa cag tcg tagactcttt gtaactaccg ttg                             1155
Glu Gln Ser
```

<210> 180
<211> 344
<212> PRT
<213> Corynebacterium glutamicum

<400> 180

```
Val Ala Ser Ala Thr Ala Ser Asp Ser His Leu Ser Thr Cys Cys Ser
  1               5                  10                  15

Ser Ser Gly Arg Ser Ala Ser Pro Ser Ser Pro Gly Leu Ala Pro Ser
             20                  25                  30

Trp Leu Thr Thr Gly Glu Leu Phe Ala Gln Phe Thr Ser Thr Asp Gly
         35                  40                  45

Asn Ala Ala Ile Ile Ala Ala Ser Gly Gly Gly Ala Ile Gly Pro Gln
     50                  55                  60

Ala Leu Phe Asp Ala Ser Val Arg Thr Phe Leu Ile Ser Pro Ala Leu
 65                  70                  75                  80

Leu Leu Val Ala Val Val Ala Val Phe Phe Ala Tyr Arg Arg Arg Asp
                 85                  90                  95

Pro Glu Pro Ile Ile Pro Leu Ala Leu Ile Gly Ser Val Val Phe Phe
            100                 105                 110

Gln Ile Ile Thr Tyr Ser Leu Gly Ser Thr Phe Gly Leu Leu Arg Phe
        115                 120                 125

Phe Leu Thr Ala Leu Pro Leu Thr Ile Ile Leu Leu Phe Gln Ile Ile
    130                 135                 140

Pro Pro Arg His Arg Phe Pro Ser Leu Arg Pro Gly Ala Cys Tyr Arg
145                 150                 155                 160

Asp Arg Val Thr Gly Lys Tyr Val Pro Lys Thr Ile Thr Gly Val Leu
                165                 170                 175

Val Leu Ala Ile Phe Gly Gly Thr Gly Ile Thr Leu Tyr Gly Met Ser
            180                 185                 190

Ser Ala Asn Trp Ala Pro Gln Glu Tyr Ala Ile Gln Glu Leu Val Phe
        195                 200                 205

Asn Met Gly Ser Pro Ser Gln Asp Ala Val His Thr Leu Asn Thr Phe
    210                 215                 220
```

```
Ser Thr Glu Met Asp Val Ala Asp Phe Val Asp Ser Leu Asn Leu Gly
225                 230                 235                 240

Asp Gly Glu Val Leu Leu Ser Thr Thr Tyr Gly Phe Ala Val Leu Thr
                245                 250                 255

Ala Ser Asn Asn Gln Lys Gln Phe Ile Ile Pro Ser Asp Glu Asp Phe
            260                 265                 270

Ile Thr Thr Leu Asn Glu Pro Ala Glu His Gly Val Lys Tyr Ile Leu
        275                 280                 285

Ala Leu Pro Arg Glu Gly Arg Gly Ala Thr Asp Pro Ile Asn Leu Arg
    290                 295                 300

Tyr Pro Asp Met Tyr Glu Thr Gly Ser His Ile Ala Thr Met Glu Ile
305                 310                 315                 320

Glu Phe Ile Asn Gln Gly Gln Gly Gln Pro Asn Trp Arg Leu Tyr Arg
                325                 330                 335

Val Leu Thr Thr Pro Glu Gln Ser
            340
```

CO2007/050030

```
<210> 181
<211> 1251
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1228)
<223> FRXA00283

<400> 181
gaagctccgt tcatttacgc cactctctgg gcggtgcgca ggctgattcg gtggagttct 60

acggaaaacg tccacagacc tcattacctg tggttttgcg ttg gca ttg gcg ttt   115
                                          Leu Ala Leu Ala Phe
                                            1               5

tta gcg cgc tat gac gcc ctc atc atg gcc ttc gta gcc atg tgg act   163
Leu Ala Arg Tyr Asp Ala Leu Ile Met Ala Phe Val Ala Met Trp Thr
                10                  15                  20

gtc gga ttt atg aca tgg cgc gca cga tac cgc cgt ggc ttc cgc gac   211
Val Gly Phe Met Thr Trp Arg Ala Arg Tyr Arg Arg Gly Phe Arg Asp
            25                  30                  35

cgc atc gga ttc gca ctt gtc gac atg ctg ctc ctc gtc tgg ccg atc   259
Arg Ile Gly Phe Ala Leu Val Asp Met Leu Leu Leu Val Trp Pro Ile
        40                  45                  50

ggc ttc gcc ttc gtc gcc tgg act ggc gcc agc tgg ctc act acc ggc   307
Gly Phe Ala Phe Val Ala Trp Thr Gly Ala Ser Trp Leu Thr Thr Gly
    55                  60                  65

gaa ctc ttt gcc caa ttc acc tcc aca gac ggc aac gct gcg atc atc   355
Glu Leu Phe Ala Gln Phe Thr Ser Thr Asp Gly Asn Ala Ala Ile Ile
70                  75                  80                  85
```

```
gca gca tcc ggc ggc ggc gcc ata ggg ccc caa gcg ctt ttc gac gcc   403
Ala Ala Ser Gly Gly Gly Ala Ile Gly Pro Gln Ala Leu Phe Asp Ala
                  90                  95                 100

tcc gtc cgc acc ttc ctc atc tcc cca gct ctc cta ctc gtc gca gta   451
Ser Val Arg Thr Phe Leu Ile Ser Pro Ala Leu Leu Leu Val Ala Val
            105                 110                 115

gtt gca gtc ttt ttt gct tat cga cgc cgc gac ccc gaa ccc atc atc   499
Val Ala Val Phe Phe Ala Tyr Arg Arg Arg Asp Pro Glu Pro Ile Ile
        120                 125                 130

ccc tta gct ctc atc ggc tct gtg gtg ttc ttc caa atc att acc tac   547
Pro Leu Ala Leu Ile Gly Ser Val Val Phe Phe Gln Ile Ile Thr Tyr
    135                 140                 145

tca ctt gga tct acc ttc ggc ctg ctg cgc ttt ttc ctc acc gcc ctg   595
Ser Leu Gly Ser Thr Phe Gly Leu Leu Arg Phe Phe Leu Thr Ala Leu
150                 155                 160                 165

ccg ctc acc att atc ttg ctg ttc caa att atc ccg ccc cgc cac cga   643
Pro Leu Thr Ile Ile Leu Leu Phe Gln Ile Ile Pro Pro Arg His Arg
                170                 175                 180

ttc ccc tca ctg cga cca ggt gcg tgc tac cgc gat cgc gtc acc ggc   691
Phe Pro Ser Leu Arg Pro Gly Ala Cys Tyr Arg Asp Arg Val Thr Gly
            185                 190                 195

aag tac gtg ccc aaa aca atc acc ggt gtt tta gtt ctc gcg atc ttc   739
Lys Tyr Val Pro Lys Thr Ile Thr Gly Val Leu Val Leu Ala Ile Phe
        200                 205                 210

ggc ggc acc ggc atc acc ctg tac ggc atg agc agt gct aac tgg gcg   787
Gly Gly Thr Gly Ile Thr Leu Tyr Gly Met Ser Ser Ala Asn Trp Ala
    215                 220                 225

ccc cag gaa tat gcc atc caa gaa cta gtt ttc aac atg gga tcg cca   835
Pro Gln Glu Tyr Ala Ile Gln Glu Leu Val Phe Asn Met Gly Ser Pro
230                 235                 240                 245

tcg cag gac gcc gtc cac acc ctg aac acc ttc tcc act gaa atg gat   883
Ser Gln Asp Ala Val His Thr Leu Asn Thr Phe Ser Thr Glu Met Asp
                250                 255                 260

gtc gcc gat ttc gtc gac tcc cta aac ctt gga gac ggc gaa gtc ctt   931
Val Ala Asp Phe Val Asp Ser Leu Asn Leu Gly Asp Gly Glu Val Leu
            265                 270                 275

ctc tcc acc acc tac ggc ttc gcc gtc ctc acc gca tca aac aac caa   979
Leu Ser Thr Thr Tyr Gly Phe Ala Val Leu Thr Ala Ser Asn Asn Gln
        280                 285                 290

aag caa ttc atc atc ccc tcc gac gaa gac ttc atc acc acc ctc aac   1027
Lys Gln Phe Ile Ile Pro Ser Asp Glu Asp Phe Ile Thr Thr Leu Asn
    295                 300                 305

gaa ccc gct gag cac ggc gtt aag tac atc ctc gcc ctc cca cgc gaa   1075
Glu Pro Ala Glu His Gly Val Lys Tyr Ile Leu Ala Leu Pro Arg Glu
310                 315                 320                 325
```

```
ggt cgc ggc gcc acc gac ccg atc aac ctg cgc tac cca gac atg tat   1123
Gly Arg Gly Ala Thr Asp Pro Ile Asn Leu Arg Tyr Pro Asp Met Tyr
                330                 335                 340

gaa acc ggc agc cac atc gcc acg atg gaa atc gaa ttc atc aat caa   1171
Glu Thr Gly Ser His Ile Ala Thr Met Glu Ile Glu Phe Ile Asn Gln
            345                 350                 355

ggc caa gga caa cca aat tgg cgc ctc tat cgg gtg ctc acc aca cct   1219
Gly Gln Gly Gln Pro Asn Trp Arg Leu Tyr Arg Val Leu Thr Thr Pro
        360                 365                 370

gaa cag tcg tagactcttt gtaactaccg ttg                            1251
Glu Gln Ser
    375
```

<210> 182
<211> 376
<212> PRT
<213> Corynebacterium glutamicum

<400> 182

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Leu Ala Leu Ala Phe Leu Ala Arg Tyr Asp Ala Leu Ile Met Ala Phe
  1               5                  10                  15

Val Ala Met Trp Thr Val Gly Phe Met Thr Trp Arg Ala Arg Tyr Arg
             20                  25                  30

Arg Gly Phe Arg Asp Arg Ile Gly Phe Ala Leu Val Asp Met Leu Leu
         35                  40                  45

Leu Val Trp Pro Ile Gly Phe Ala Phe Val Ala Trp Thr Gly Ala Ser
     50                  55                  60

Trp Leu Thr Thr Gly Glu Leu Phe Ala Gln Phe Thr Ser Thr Asp Gly
 65                  70                  75                  80

Asn Ala Ala Ile Ile Ala Ala Ser Gly Gly Gly Ala Ile Gly Pro Gln
                 85                  90                  95

Ala Leu Phe Asp Ala Ser Val Arg Thr Phe Leu Ile Ser Pro Ala Leu
            100                 105                 110

Leu Leu Val Ala Val Val Ala Val Phe Phe Ala Tyr Arg Arg Arg Asp
        115                 120                 125

Pro Glu Pro Ile Ile Pro Leu Ala Leu Ile Gly Ser Val Val Phe Phe
    130                 135                 140

Gln Ile Ile Thr Tyr Ser Leu Gly Ser Thr Phe Gly Leu Leu Arg Phe
145                 150                 155                 160

Phe Leu Thr Ala Leu Pro Leu Thr Ile Ile Leu Leu Phe Gln Ile Ile
                165                 170                 175

Pro Pro Arg His Arg Phe Pro Ser Leu Arg Pro Gly Ala Cys Tyr Arg
            180                 185                 190

Asp Arg Val Thr Gly Lys Tyr Val Pro Lys Thr Ile Thr Gly Val Leu
        195                 200                 205
```

```
Val Leu Ala Ile Phe Gly Gly Thr Gly Ile Thr Leu Tyr Gly Met Ser
    210                 215                 220

Ser Ala Asn Trp Ala Pro Gln Glu Tyr Ala Ile Gln Glu Leu Val Phe
225                 230                 235                 240

Asn Met Gly Ser Pro Ser Gln Asp Ala Val His Thr Leu Asn Thr Phe
                245                 250                 255

Ser Thr Glu Met Asp Val Ala Asp Phe Val Asp Ser Leu Asn Leu Gly
            260                 265                 270

Asp Gly Glu Val Leu Leu Ser Thr Thr Tyr Gly Phe Ala Val Leu Thr
        275                 280                 285

Ala Ser Asn Asn Gln Lys Gln Phe Ile Ile Pro Ser Asp Glu Asp Phe
    290                 295                 300

Ile Thr Thr Leu Asn Glu Pro Ala Glu His Gly Val Lys Tyr Ile Leu
305                 310                 315                 320

Ala Leu Pro Arg Glu Gly Arg Gly Ala Thr Asp Pro Ile Asn Leu Arg
                325                 330                 335

Tyr Pro Asp Met Tyr Glu Thr Gly Ser His Ile Ala Thr Met Glu Ile
            340                 345                 350

Glu Phe Ile Asn Gln Gly Gln Gly Gln Pro Asn Trp Arg Leu Tyr Arg
        355                 360                 365

Val Leu Thr Thr Pro Glu Gln Ser
    370                 375


<210> 183
<211> 459
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(436)
<223> RXN00334

<400> 183
ataagccccg catgggatat gagaaaagga atgcacgatg agtattgaat ttccgttagg 60

taatccagcg cctgcacagt ggttttctgg cgaggtccat atg gcc aag ctt gat   115
                                               Met Ala Lys Leu Asp
                                                 1               5

gac aac gtg cag att gag act gtg aac gtg tct ttt gag gca ggc ggt   163
Asp Asn Val Gln Ile Glu Thr Val Asn Val Ser Phe Glu Ala Gly Gly
                10                  15                  20

cgc acc aat tgg cac act cac cca gtc ggt caa aac ata att gtg ctg   211
Arg Thr Asn Trp His Thr His Pro Val Gly Gln Asn Ile Ile Val Leu
            25                  30                  35

tcg ggc ttg ggc att tat gag gcg gag ggg gag cct gct cga ctc ctg   259
```

```
Ser Gly Leu Gly Ile Tyr Glu Ala Glu Gly Glu Pro Ala Arg Leu Leu
         40                  45                  50

gag cct ggc gat gtt gtt ttc gca gcc gcc ggg gtt cgc cac tgg cac   307
Glu Pro Gly Asp Val Val Phe Ala Ala Ala Gly Val Arg His Trp His
     55                  60                  65

ggc gcc gtg tct ggt gca ccg atg ttc cac gtg gtg gtt aac ctc aaa   355
Gly Ala Val Ser Gly Ala Pro Met Phe His Val Val Val Asn Leu Lys
 70                  75                  80                  85

ggc atc gac ggc gag acc gtc gat tgg gag gag ccg gtc gac gag gag   403
Gly Ile Asp Gly Glu Thr Val Asp Trp Glu Glu Pro Val Asp Glu Glu
                 90                  95                 100

cac tac cgc agc gtg agc gcg gag cta caa aga taaaaatgct tttcgacgtc 456
His Tyr Arg Ser Val Ser Ala Glu Leu Gln Arg
            105                 110

cac                                                               459
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<210> 184
<211> 112
<212> PRT
<213> Corynebacterium glutamicum

<400> 184

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Met Ala Lys Leu Asp Asp Asn Val Gln Ile Glu Thr Val Asn Val Ser
  1               5                  10                  15

Phe Glu Ala Gly Gly Arg Thr Asn Trp His Thr His Pro Val Gly Gln
             20                  25                  30

Asn Ile Ile Val Leu Ser Gly Leu Gly Ile Tyr Glu Ala Glu Gly Glu
         35                  40                  45

Pro Ala Arg Leu Leu Glu Pro Gly Asp Val Val Phe Ala Ala Ala Gly
     50                  55                  60

Val Arg His Trp His Gly Ala Val Ser Gly Ala Pro Met Phe His Val
 65                  70                  75                  80

Val Val Asn Leu Lys Gly Ile Asp Gly Glu Thr Val Asp Trp Glu Glu
                 85                  90                  95

Pro Val Asp Glu Glu His Tyr Arg Ser Val Ser Ala Glu Leu Gln Arg
            100                 105                 110
```

<210> 185
<211> 459
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(436)

<223> FRXA00334

<400> 185
ataagccccg catgggatat gagaaaagga atgcacgatg agtattgaat ttccgttagg 60

taatccagcg cctgcacagt ggttttctgg cgaggtccat atg gcc aag ctt gat 115
Met Ala Lys Leu Asp
1 5

gac aac gtg cag att gag act gtg aac gtg tct ttt gag gca ggc ggt 163
Asp Asn Val Gln Ile Glu Thr Val Asn Val Ser Phe Glu Ala Gly Gly
10 15 20

cgc acc aat tgg cac act cac cca gtc ggt caa aac ata att gtg ctg 211
Arg Thr Asn Trp His Thr His Pro Val Gly Gln Asn Ile Ile Val Leu
25 30 35

tcg ggc ttg ggc att tat gag gcg gag ggg gag cct gct cga ctc ctg 259
Ser Gly Leu Gly Ile Tyr Glu Ala Glu Gly Glu Pro Ala Arg Leu Leu
40 45 50

gag cct ggc gat gtt gtt ttc gca gcc gcc ggg gtt cgc cac tgg cac 307
Glu Pro Gly Asp Val Val Phe Ala Ala Ala Gly Val Arg His Trp His
55 60 65

ggc gcc gtg tct ggt gca ccg atg ttc cac gtg gtg gtt aac ctc aaa 355
Gly Ala Val Ser Gly Ala Pro Met Phe His Val Val Val Asn Leu Lys
70 75 80 85

ggc atc gac ggc gag acc gtc gat tgg gag gag ccg gtc gac gag gag 403
Gly Ile Asp Gly Glu Thr Val Asp Trp Glu Glu Pro Val Asp Glu Glu
90 95 100

cac tac cgc agc gtg agc gcg gag cta caa aga taaaaatgct tttcgacgtc 456
His Tyr Arg Ser Val Ser Ala Glu Leu Gln Arg
105 110

cac 459

<210> 186
<211> 112
<212> PRT
<213> Corynebacterium glutamicum

<400> 186
Met Ala Lys Leu Asp Asp Asn Val Gln Ile Glu Thr Val Asn Val Ser
1 5 10 15

Phe Glu Ala Gly Gly Arg Thr Asn Trp His Thr His Pro Val Gly Gln
20 25 30

Asn Ile Ile Val Leu Ser Gly Leu Gly Ile Tyr Glu Ala Glu Gly Glu
35 40 45

Pro Ala Arg Leu Leu Glu Pro Gly Asp Val Val Phe Ala Ala Ala Gly
50 55 60

Val Arg His Trp His Gly Ala Val Ser Gly Ala Pro Met Phe His Val
65 70 75 80

```
Val Val Asn Leu Lys Gly Ile Asp Gly Glu Thr Val Asp Trp Glu Glu
                 85                  90                  95

Pro Val Asp Glu Glu His Tyr Arg Ser Val Ser Ala Glu Leu Gln Arg
            100                 105                 110
```

<210> 187
<211> 1263
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1240)
<223> RXN00338

<400> 187

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tcttagaagg cgtagtcaca ccattaacct tgccagaatt tttcaaggct tggctagact 60

tgggaaacga acatgcggta ccaaccaggg gagttaatgc gtg agt gat gta acc   115
                                              Val Ser Asp Val Thr
                                                1               5

gtt ggc gat att cgc cgc att ttg gat gag gct tat ccg ccg gcg ttg   163
Val Gly Asp Ile Arg Arg Ile Leu Asp Glu Ala Tyr Pro Pro Ala Leu
                10                  15                  20

gcg gaa agc tgg gac aaa gtg ggg ctg atc tgc ggt gat cca aca gag   211
Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys Gly Asp Pro Thr Glu
            25                  30                  35

tcg gtg aag cgt gtc ggt tta gca ctc gat tgc acc cag gca gtg gcc   259
Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys Thr Gln Ala Val Ala
        40                  45                  50

gac aag gct gtg gac atg ggt ttg gac atg ctg atc att cac cac cca   307
Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu Ile Ile His His Pro
    55                  60                  65

ttg ctg ctg cgt ggg gtg acg tct gtt gct gcg gat gag cca aaa ggc   355
Leu Leu Leu Arg Gly Val Thr Ser Val Ala Ala Asp Glu Pro Lys Gly
70                  75                  80                  85

aag gtc att cac acc cta att cgc ggc ggg gtg gca ctg ttt tcc gcg   403
Lys Val Ile His Thr Leu Ile Arg Gly Gly Val Ala Leu Phe Ser Ala
                90                  95                 100

cac act aat gcg gat tcc gcg cgc cca ggt gtc aac gat aaa ctc gcc   451
His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val Asn Asp Lys Leu Ala
            105                 110                 115

gag ctc gtc ggc atc acg gcc ggg cga ccc atc gcg aca cgg ctt tta   499
Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile Ala Thr Arg Leu Leu
        120                 125                 130

ggc ggc atg gac aaa tgg ggc gtg cac gtt ctg ccc aag gat gca gcg   547
Gly Gly Met Asp Lys Trp Gly Val His Val Leu Pro Lys Asp Ala Ala
```

```
    135                 140                 145

tac cta aag aag atg ctt ttc gac gca ggt gcc ggt gcg atc ggc gac   595
Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala Gly Ala Ile Gly Asp
150                 155                 160                 165

tac cga gag tgt gcc ttt gag atc gaa gga acc ggg cag ttt agg ccc   643
Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr Gly Gln Phe Arg Pro
                170                 175                 180

gtg gag ggg gcg aat ccg gca gag ggg gac gtc gat aag ctt ttt aaa   691
Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val Asp Lys Leu Phe Lys
            185                 190                 195

tcc ctt gag ctg cgc atc gag ttt gtt gca ccg cgc aac ctg cgc gcc   739
Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro Arg Asn Leu Arg Ala
        200                 205                 210

cgg ctc acg tcg gtg ctg cgg gag gct cat ccg tat gag gag cct gcc   787
Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro Tyr Glu Glu Pro Ala
    215                 220                 225

ttc gat att gtt gaa atg cac agc gct gag agt tta gaa aat gcg acc   835
Phe Asp Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr
230                 235                 240                 245

gga ttg ggt cgt gtg ggt gaa ttg ccg gag ccg atg cgc ctc gcg gat   883
Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp
                250                 255                 260

ttc gtg caa caa gtg gcc aac aac ctg cct gtc acc gaa tgg ggc gtg   931
Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val
            265                 270                 275

cgc gct acc ggc gat cct gaa caa atg gtg tcc cgt gtg gcg gtt tca   979
Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser
        280                 285                 290

tca ggg tcg ggt gac agt ttc tta aac gat gtg att aag ctc gga gtg   1027
Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val
    295                 300                 305

gac gtt tat gtc act tct gat ctg cgc cac cat cca gtt gat gaa tat   1075
Asp Val Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr
310                 315                 320                 325

ctc cga gaa ggt ggc cct gca gta atc gat act gca cac tgg gcc agc   1123
Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser
                330                 335                 340

gaa ttt cca tgg act tcc caa gcc caa gaa att ttg cag gac aaa gcc   1171
Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala
            345                 350                 355

cca cag gtt gaa gtt gat gtg att tcg atc cgc aca gac ccc tgg acc   1219
Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr
        360                 365                 370

atg tct gcg cga gca gtg aac taaattcttg agaactaaaa aag            1263
Met Ser Ala Arg Ala Val Asn
    375                 380
```

<210> 188
<211> 380
<212> PRT
<213> Corynebacterium glutamicum

<400> 188

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Val Ser Asp Val Thr Val Gly Asp Ile Arg Arg Ile Leu Asp Glu Ala
  1               5                  10                  15

Tyr Pro Pro Ala Leu Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys
             20                  25                  30

Gly Asp Pro Thr Glu Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys
         35                  40                  45

Thr Gln Ala Val Ala Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu
     50                  55                  60

Ile Ile His His Pro Leu Leu Leu Arg Gly Val Thr Ser Val Ala Ala
 65                  70                  75                  80

Asp Glu Pro Lys Gly Lys Val Ile His Thr Leu Ile Arg Gly Gly Val
                 85                  90                  95

Ala Leu Phe Ser Ala His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val
            100                 105                 110

Asn Asp Lys Leu Ala Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile
        115                 120                 125

Ala Thr Arg Leu Leu Gly Gly Met Asp Lys Trp Gly Val His Val Leu
    130                 135                 140

Pro Lys Asp Ala Ala Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala
145                 150                 155                 160

Gly Ala Ile Gly Asp Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr
                165                 170                 175

Gly Gln Phe Arg Pro Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val
            180                 185                 190

Asp Lys Leu Phe Lys Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro
        195                 200                 205

Arg Asn Leu Arg Ala Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro
    210                 215                 220

Tyr Glu Glu Pro Ala Phe Asp Ile Val Glu Met His Ser Ala Glu Ser
225                 230                 235                 240

Leu Glu Asn Ala Thr Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro
                245                 250                 255

Met Arg Leu Ala Asp Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val
            260                 265                 270

Thr Glu Trp Gly Val Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser
        275                 280                 285
```

```
Arg Val Ala Val Ser Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val
    290                 295                 300

Ile Lys Leu Gly Val Asp Val Tyr Val Thr Ser Asp Leu Arg His His
305                 310                 315                 320

Pro Val Asp Glu Tyr Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr
                325                 330                 335

Ala His Trp Ala Ser Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile
            340                 345                 350

Leu Gln Asp Lys Ala Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg
        355                 360                 365

Thr Asp Pro Trp Thr Met Ser Ala Arg Ala Val Asn
    370                 375                 380


<210> 189
<211> 806
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(783)
<223> FRXA00338

<400> 189
gtc ggc atc acg gcc ggg cga ccc atc gcg aca cgg ctt tta ggc ggc   48
Val Gly Ile Thr Ala Gly Arg Pro Ile Ala Thr Arg Leu Leu Gly Gly
  1               5                  10                  15

atg gac aaa tgg ggc gtg cac gtt ctg ccc aag gat gca gcg tac cta   96
Met Asp Lys Trp Gly Val His Val Leu Pro Lys Asp Ala Ala Tyr Leu
             20                  25                  30

aag aag atg ctt ttc gac gca ggt gcc ggt gcg atc ggc gac tac cga  144
Lys Lys Met Leu Phe Asp Ala Gly Ala Gly Ala Ile Gly Asp Tyr Arg
         35                  40                  45

gag tgt gcc ttt gag atc gaa gga acc ggg cag ttt agg ccc gtg gag  192
Glu Cys Ala Phe Glu Ile Glu Gly Thr Gly Gln Phe Arg Pro Val Glu
     50                  55                  60

ggg gcg aat ccg gca gag ggg gac gtc gat aag ctt ttt aaa tcc ctt  240
Gly Ala Asn Pro Ala Glu Gly Asp Val Asp Lys Leu Phe Lys Ser Leu
 65                  70                  75                  80

gag ctg cgc atc gag ttt gtt gca ccg cgc aac ctg cgc gcc cgg ctc  288
Glu Leu Arg Ile Glu Phe Val Ala Pro Arg Asn Leu Arg Ala Arg Leu
                 85                  90                  95

acg tcg gtg ctg cgg gag gct cat ccg tat gag gag cct gcc ttc gat  336
Thr Ser Val Leu Arg Glu Ala His Pro Tyr Glu Glu Pro Ala Phe Asp
            100                 105                 110

att gtt gaa atg cac agc gct gag agt tta gaa aat gcg acc gga ttg  384
Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr Gly Leu
```

```
        115                 120                 125

ggt cgt gtg ggt gaa ttg ccg gag ccg atg cgc ctc gcg gat ttc gtg   432
Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp Phe Val
    130                 135                 140

caa caa gtg gcc aac aac ctg cct gtc acc gaa tgg ggc gtg cgc gct   480
Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val Arg Ala
145                 150                 155                 160

acc ggc gat cct gaa caa atg gtg tcc cgt gtg gcg gtt tca tca ggg   528
Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser Ser Gly
                165                 170                 175

tcg ggt gac agt ttc tta aac gat gtg att aag ctc gga gtg gac gtt   576
Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val Asp Val
            180                 185                 190

tat gtc act tct gat ctg cgc cac cat cca gtt gat gaa tat ctc cga   624
Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr Leu Arg
        195                 200                 205

gaa ggt ggc cct gca gta atc gat act gca cac tgg gcc agc gaa ttt   672
Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser Glu Phe
    210                 215                 220

cca tgg act tcc caa gcc caa gaa att ttg cag gac aaa gcc cca cag   720
Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala Pro Gln
225                 230                 235                 240

gtt gaa gtt gat gtg att tcg atc cgc aca gac ccc tgg acc atg tct   768
Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr Met Ser
                245                 250                 255

gcg cga gca gtg aac taaattcttg agaactaaaa aag                    806
Ala Arg Ala Val Asn
            260
```

<210> 190
<211> 261
<212> PRT
<213> Corynebacterium glutamicum

<400> 190

```
Val Gly Ile Thr Ala Gly Arg Pro Ile Ala Thr Arg Leu Leu Gly Gly
  1               5                  10                  15

Met Asp Lys Trp Gly Val His Val Leu Pro Lys Asp Ala Ala Tyr Leu
             20                  25                  30

Lys Lys Met Leu Phe Asp Ala Gly Ala Gly Ala Ile Gly Asp Tyr Arg
         35                  40                  45

Glu Cys Ala Phe Glu Ile Glu Gly Thr Gly Gln Phe Arg Pro Val Glu
     50                  55                  60

Gly Ala Asn Pro Ala Glu Gly Asp Val Asp Lys Leu Phe Lys Ser Leu
 65                  70                  75                  80

Glu Leu Arg Ile Glu Phe Val Ala Pro Arg Asn Leu Arg Ala Arg Leu
```

```
                 85                  90                  95

Thr Ser Val Leu Arg Glu Ala His Pro Tyr Glu Glu Pro Ala Phe Asp
            100                 105                 110

Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr Gly Leu
        115                 120                 125

Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp Phe Val
    130                 135                 140

Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val Arg Ala
145                 150                 155                 160

Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser Ser Gly
                165                 170                 175

Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val Asp Val
            180                 185                 190

Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr Leu Arg
        195                 200                 205

Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser Glu Phe
    210                 215                 220

Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala Pro Gln
225                 230                 235                 240

Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr Met Ser
                245                 250                 255

Ala Arg Ala Val Asn
            260
```

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<210> 191
<211> 310
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(310)
<223> FRXA00318

<400> 191
tcttagaagg cgtagtcaca ccattaacct tgccagaatt tttcaaggct tggcttgact 60

```
tgggaaacga acatgcggta ccaaccaggg gaggtaatgc gtg agt gat gta acc   115
                                               Val Ser Asp Val Thr
                                                 1               5

gtt ggc gat att ctc cgc att ttg gat gag gct tat ccg ccg gcg ttg   163
Val Gly Asp Ile Leu Arg Ile Leu Asp Glu Ala Tyr Pro Pro Ala Leu
                 10                  15                  20

gcg gaa agc tgg gac aaa gtg gtg ctg atc tgc gtt gat cca aca gag   211
Ala Glu Ser Trp Asp Lys Val Val Leu Ile Cys Val Asp Pro Thr Glu
             25                  30                  35
```

```
tcg gtg aag cgt gtt ggt tta gca ctc gat tgc acc cag gca ctg gcc   259
Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys Thr Gln Ala Leu Ala
         40                  45                  50

gac aag gct gtg gac atg ggt ttg gac atg ctg atc att cac cac cca   307
Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu Ile Ile His His Pro
     55                  60                  65

tta                                                               310
Leu
 70
```

<210> 192
<211> 70
<212> PRT
<213> Corynebacterium glutamicum

<400> 192

```
Val Ser Asp Val Thr Val Gly Asp Ile Leu Arg Ile Leu Asp Glu Ala
  1               5                  10                  15

Tyr Pro Pro Ala Leu Ala Glu Ser Trp Asp Lys Val Val Leu Ile Cys
             20                  25                  30

Val Asp Pro Thr Glu Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys
         35                  40                  45

Thr Gln Ala Leu Ala Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu
     50                  55                  60

Ile Ile His His Pro Leu
 65                  70
```

<210> 193
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> RXN00342

<400> 193

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cggtaatgtg caattcggat atatcaatag ccccgcggtt tcatgttgaa tccatgtaat 60

cgaaaaacac atcggggccc acacgaggag gattattaaa gtg gcc gac gct ccg   115
                                              Val Ala Asp Ala Pro
                                                1               5

ggc gca gtc aag caa ggt gcc cag gat tat gct caa cta ctc ggc att   163
Gly Ala Val Lys Gln Gly Ala Gln Asp Tyr Ala Gln Leu Leu Gly Ile
                10                  15                  20

caa tcg ggt cat atc gtt caa gaa att gga tgg gat gaa gat tcc gac   211
Gln Ser Gly His Ile Val Gln Glu Ile Gly Trp Asp Glu Asp Ser Asp
             25                  30                  35

acg ctg atc agc gag tcc atc gaa gat gca atc ggt gag gaa cta ctc   259
```

```
Thr Leu Ile Ser Glu Ser Ile Glu Asp Ala Ile Gly Glu Glu Leu Leu
         40                  45                  50

gat gaa gaa acc gac gag ctg tgc gat gtc gtg ctg ctc tgg tgg cgc   307
Asp Glu Glu Thr Asp Glu Leu Cys Asp Val Val Leu Leu Trp Trp Arg
     55                  60                  65

gag gat gac ggc gat ctc gtc gac gga ctt gtg gat tcc atc cgc tcc   355
Glu Asp Asp Gly Asp Leu Val Asp Gly Leu Val Asp Ser Ile Arg Ser
 70                  75                  80                  85

ctc gct gag aat ggt cgt atc tgg gtg ttg act cct ggc att ggt aaa   403
Leu Ala Glu Asn Gly Arg Ile Trp Val Leu Thr Pro Gly Ile Gly Lys
                 90                  95                 100

gaa gga gcc ctg gct cct gga gtt atc tct gaa tca gct caa ctg gca   451
Glu Gly Ala Leu Ala Pro Gly Val Ile Ser Glu Ser Ala Gln Leu Ala
            105                 110                 115

ggt ctc gtg cag acc aag gca gaa cgt ctc ggt aat tgg caa ggt tct   499
Gly Leu Val Gln Thr Lys Ala Glu Arg Leu Gly Asn Trp Gln Gly Ser
        120                 125                 130

tgc ctc gtc cag cgt gga aac aag aag cct taacaatcgc taatttccac     549
Cys Leu Val Gln Arg Gly Asn Lys Lys Pro
    135                 140

ggc                                                               552


<210> 194
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 194
Val Ala Asp Ala Pro Gly Ala Val Lys Gln Gly Ala Gln Asp Tyr Ala
  1               5                  10                  15

Gln Leu Leu Gly Ile Gln Ser Gly His Ile Val Gln Glu Ile Gly Trp
            20                  25                  30

Asp Glu Asp Ser Asp Thr Leu Ile Ser Glu Ser Ile Glu Asp Ala Ile
        35                  40                  45

Gly Glu Glu Leu Leu Asp Glu Glu Thr Asp Glu Leu Cys Asp Val Val
    50                  55                  60

Leu Leu Trp Trp Arg Glu Asp Asp Gly Asp Leu Val Asp Gly Leu Val
65                  70                  75                  80

Asp Ser Ile Arg Ser Leu Ala Glu Asn Gly Arg Ile Trp Val Leu Thr
                85                  90                  95

Pro Gly Ile Gly Lys Glu Gly Ala Leu Ala Pro Gly Val Ile Ser Glu
            100                 105                 110

Ser Ala Gln Leu Ala Gly Leu Val Gln Thr Lys Ala Glu Arg Leu Gly
        115                 120                 125

Asn Trp Gln Gly Ser Cys Leu Val Gln Arg Gly Asn Lys Lys Pro
```

130 135 140

<210> 195
<211> 524
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (73)..(501)
<223> FRXA00342

<400> 195
tagccccgcg gtttcatgtt gaatccatgt aatcgaaaac acatcggggc ccacacgagg 60

agaattatta aagtg gcc gac gct ccg ggc gca gtc aag caa ggt gcc cag 111
Val Ala Asp Ala Pro Gly Ala Val Lys Gln Gly Ala Gln
1 5 10

gat tat gct caa cta ctc ggc att caa tcg ggt cat atc gtt caa gaa 159
Asp Tyr Ala Gln Leu Leu Gly Ile Gln Ser Gly His Ile Val Gln Glu
15 20 25

att gga tgg gat gaa gat tcc gac acg ctg atc agc gag tcc atc gaa 207
Ile Gly Trp Asp Glu Asp Ser Asp Thr Leu Ile Ser Glu Ser Ile Glu
30 35 40 45

gat gca atc ggt gag gaa cta ctc gat gaa gaa acc gac gag ctg tgc 255
Asp Ala Ile Gly Glu Glu Leu Leu Asp Glu Glu Thr Asp Glu Leu Cys
50 55 60

gat gtc gtg ctg ctc tgg tgg cgc gag gat gac ggc gat ctc gtc gac 303
Asp Val Val Leu Leu Trp Trp Arg Glu Asp Asp Gly Asp Leu Val Asp
65 70 75

gga ctt gtg gat tcc atc cgc tcc ctc gct gag aat ggt cgt atc tgg 351
Gly Leu Val Asp Ser Ile Arg Ser Leu Ala Glu Asn Gly Arg Ile Trp
80 85 90

gtg ttg act cct ggc att ggt aaa gaa gga gcc ctg gct cct gga gtt 399
Val Leu Thr Pro Gly Ile Gly Lys Glu Gly Ala Leu Ala Pro Gly Val
95 100 105

atc tct gaa tca gct caa ctg gca ggt ctc gtg cag acc aag gca gaa 447
Ile Ser Glu Ser Ala Gln Leu Ala Gly Leu Val Gln Thr Lys Ala Glu
110 115 120 125

cgt ctc ggt aat tgg caa ggt tct tgc ctc gtc cag cgt gga aac aag 495
Arg Leu Gly Asn Trp Gln Gly Ser Cys Leu Val Gln Arg Gly Asn Lys
130 135 140

aag cct taacaatcgc taatttccac ggc 524
Lys Pro

<210> 196
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 196
Val Ala Asp Ala Pro Gly Ala Val Lys Gln Gly Ala Gln Asp Tyr Ala
1 5 10 15

Gln Leu Leu Gly Ile Gln Ser Gly His Ile Val Gln Glu Ile Gly Trp
20 25 30

Asp Glu Asp Ser Asp Thr Leu Ile Ser Glu Ser Ile Glu Asp Ala Ile
35 40 45

Gly Glu Glu Leu Leu Asp Glu Glu Thr Asp Glu Leu Cys Asp Val Val
50 55 60

Leu Leu Trp Trp Arg Glu Asp Asp Gly Asp Leu Val Asp Gly Leu Val
65 70 75 80

Asp Ser Ile Arg Ser Leu Ala Glu Asn Gly Arg Ile Trp Val Leu Thr
85 90 95

Pro Gly Ile Gly Lys Glu Gly Ala Leu Ala Pro Gly Val Ile Ser Glu
100 105 110

Ser Ala Gln Leu Ala Gly Leu Val Gln Thr Lys Ala Glu Arg Leu Gly
115 120 125

Asn Trp Gln Gly Ser Cys Leu Val Gln Arg Gly Asn Lys Lys Pro
130 135 140

<210> 197
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<222> (101)..(979)
<223> RXN00344

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cacggtggct cgcatcaacg acagaatcgt ggtggtttaa gtg gat cta tcc acc 115
Val Asp Leu Ser Thr
1 5

tgg ctt tcc gac acc caa tat ctc atc agc gtc gat ttc gtc cag cac 163
Trp Leu Ser Asp Thr Gln Tyr Leu Ile Ser Val Asp Phe Val Gln His
10 15 20

gca ctc atc gcc tcc gcg ctg ttg ggc ctg ctc tcc ggt gtg atc gcg 211
Ala Leu Ile Ala Ser Ala Leu Leu Gly Leu Leu Ser Gly Val Ile Ala
25 30 35

ccg ctc atc gtg gtg cgc caa cag tcc ttc gca gtc cac ggc acc gcc 259
Pro Leu Ile Val Val Arg Gln Gln Ser Phe Ala Val His Gly Thr Ala
40 45 50

gaa ctc gcc ctc atg gga gcc gcc gcc gcg ctg ctc ttc gga ttg aat 307
Glu Leu Ala Leu Met Gly Ala Ala Ala Ala Leu Leu Phe Gly Leu Asn

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     55                  60                  65

gta ggc ggc ggt gca gtg atc ggt tcc gtg gtc gcc gcg atc cta ctg   355
Val Gly Gly Gly Ala Val Ile Gly Ser Val Val Ala Ala Ile Leu Leu
 70                  75                  80                  85

gca tta ctc ggc atg aaa caa caa gat tcc gcc gtc ggt gcc gtg atg   403
Ala Leu Leu Gly Met Lys Gln Gln Asp Ser Ala Val Gly Ala Val Met
                90                  95                 100

agt ttc gga ctc ggt ctg tcc gtg ctg ttc att cac ctc tac ccc ggc   451
Ser Phe Gly Leu Gly Leu Ser Val Leu Phe Ile His Leu Tyr Pro Gly
            105                 110                 115

cga agc tcc acc gcg ttc tcc ctg ctc aca ggg caa atc gtt ggt gtt   499
Arg Ser Ser Thr Ala Phe Ser Leu Leu Thr Gly Gln Ile Val Gly Val
        120                 125                 130

tcc tca tca tcg ctg tgg atc ctt gtg gca gtc acc gtg atc gtg gtt   547
Ser Ser Ser Ser Leu Trp Ile Leu Val Ala Val Thr Val Ile Val Val
    135                 140                 145

agc gcc gtg gtg att ttc tgg cgc ccg ctg ctt ttc gcc agc gcc gat   595
Ser Ala Val Val Ile Phe Trp Arg Pro Leu Leu Phe Ala Ser Ala Asp
150                 155                 160                 165

ccg atc atg gcg cag gcc tcc gga gta aac gtc cga ttc atc gcc gtt   643
Pro Ile Met Ala Gln Ala Ser Gly Val Asn Val Arg Phe Ile Ala Val
                170                 175                 180

gcc ttc gca gtt ctg gtt ggc ctc acc acg tcc cag tcc gtg cag att   691
Ala Phe Ala Val Leu Val Gly Leu Thr Thr Ser Gln Ser Val Gln Ile
            185                 190                 195

gtc ggt gcg ctg ctg gtc atg gca ttg ctg atc act ccc ggc gcg gcc   739
Val Gly Ala Leu Leu Val Met Ala Leu Leu Ile Thr Pro Gly Ala Ala
        200                 205                 210

gct gtg gcg gtg acc gcc aat cca gtg aaa gcc gtg gtg ctg gca gtc   787
Ala Val Ala Val Thr Ala Asn Pro Val Lys Ala Val Val Leu Ala Val
    215                 220                 225

atc ttc gcg gaa gta tcg gct gtc ggt ggc ctg cta ttg tcg cta gcg   835
Ile Phe Ala Glu Val Ser Ala Val Gly Gly Leu Leu Leu Ser Leu Ala
230                 235                 240                 245

cct ggt ttg ccg gtg agt gtt ttt gtc acc acc atc tct ttt gtg att   883
Pro Gly Leu Pro Val Ser Val Phe Val Thr Thr Ile Ser Phe Val Ile
                250                 255                 260

tac ctg gtc tgc cgc ctg atc ggt tgg ctc cgc ggc cgt gga gct cag   931
Tyr Leu Val Cys Arg Leu Ile Gly Trp Leu Arg Gly Arg Gly Ala Gln
            265                 270                 275

cgt gac gaa gat gct tat cga cgc cgc cag cac gat cac cac cct cac   979
Arg Asp Glu Asp Ala Tyr Arg Arg Arg Gln His Asp His His Pro His
        280                 285                 290

taggcgtttc gaagtcctat ttc                                        1002
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<210> 198
<211> 293
<212> PRT
<213> Corynebacterium glutamicum

<400> 198

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Val Asp Leu Ser Thr Trp Leu Ser Asp Thr Gln Tyr Leu Ile Ser Val
  1               5                  10                  15

Asp Phe Val Gln His Ala Leu Ile Ala Ser Ala Leu Leu Gly Leu Leu
             20                  25                  30

Ser Gly Val Ile Ala Pro Leu Ile Val Val Arg Gln Gln Ser Phe Ala
         35                  40                  45

Val His Gly Thr Ala Glu Leu Ala Leu Met Gly Ala Ala Ala Ala Leu
     50                  55                  60

Leu Phe Gly Leu Asn Val Gly Gly Gly Ala Val Ile Gly Ser Val Val
 65                  70                  75                  80

Ala Ala Ile Leu Leu Ala Leu Leu Gly Met Lys Gln Gln Asp Ser Ala
                 85                  90                  95

Val Gly Ala Val Met Ser Phe Gly Leu Gly Leu Ser Val Leu Phe Ile
            100                 105                 110

His Leu Tyr Pro Gly Arg Ser Ser Thr Ala Phe Ser Leu Leu Thr Gly
        115                 120                 125

Gln Ile Val Gly Val Ser Ser Ser Ser Leu Trp Ile Leu Val Ala Val
    130                 135                 140

Thr Val Ile Val Val Ser Ala Val Val Ile Phe Trp Arg Pro Leu Leu
145                 150                 155                 160

Phe Ala Ser Ala Asp Pro Ile Met Ala Gln Ala Ser Gly Val Asn Val
                165                 170                 175

Arg Phe Ile Ala Val Ala Phe Ala Val Leu Val Gly Leu Thr Thr Ser
            180                 185                 190

Gln Ser Val Gln Ile Val Gly Ala Leu Leu Val Met Ala Leu Leu Ile
        195                 200                 205

Thr Pro Gly Ala Ala Ala Val Ala Val Thr Ala Asn Pro Val Lys Ala
    210                 215                 220

Val Val Leu Ala Val Ile Phe Ala Glu Val Ser Ala Val Gly Gly Leu
225                 230                 235                 240

Leu Leu Ser Leu Ala Pro Gly Leu Pro Val Ser Val Phe Val Thr Thr
                245                 250                 255

Ile Ser Phe Val Ile Tyr Leu Val Cys Arg Leu Ile Gly Trp Leu Arg
            260                 265                 270

Gly Arg Gly Ala Gln Arg Asp Glu Asp Ala Tyr Arg Arg Arg Gln His
        275                 280                 285

Asp His His Pro His
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290

<210> 199
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (1)..(579)
<223> FRXA00344

<400> 199

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Met Ser Phe Gly Leu Gly Leu Ser Val Leu Phe Ile His Leu Tyr Pro
  1               5                  10                  15

ggc cga agc tcc acc gcg ttc tcc ctg ctc aca ggg caa atc gtt ggt   96
Gly Arg Ser Ser Thr Ala Phe Ser Leu Leu Thr Gly Gln Ile Val Gly
             20                  25                  30

gtt tcc tca tca tcg ctg tgg atc ctt gtg gca gtc acc gtg atc gtg   144
Val Ser Ser Ser Ser Leu Trp Ile Leu Val Ala Val Thr Val Ile Val
         35                  40                  45

gtt agc gcc gtg gtg att ttc tgg cgc ccg ctg ctt ttc gcc agc gcc   192
Val Ser Ala Val Val Ile Phe Trp Arg Pro Leu Leu Phe Ala Ser Ala
     50                  55                  60

gat ccg atc atg gcg cag gcc tcc gga gta aac gtc cga ttc atc gcc   240
Asp Pro Ile Met Ala Gln Ala Ser Gly Val Asn Val Arg Phe Ile Ala
 65                  70                  75                  80

gtt gcc ttc gca gtt ctg gtt ggc ctc acc acg tcc cag tcc gtg cag   288
Val Ala Phe Ala Val Leu Val Gly Leu Thr Thr Ser Gln Ser Val Gln
                 85                  90                  95

att gtc ggt gcg ctg ctg gtc atg gca ttg ctg atc act ccc ggc gcg   336
Ile Val Gly Ala Leu Leu Val Met Ala Leu Leu Ile Thr Pro Gly Ala
            100                 105                 110

gcc gct gtg gcg gtg acc gcc aat cca gtg aaa gcc gtg gtg ctg gca   384
Ala Ala Val Ala Val Thr Ala Asn Pro Val Lys Ala Val Val Leu Ala
        115                 120                 125

gtc atc ttc gcg gaa gta tcg gct gtc ggt ggc ctg cta ttg tcg cta   432
Val Ile Phe Ala Glu Val Ser Ala Val Gly Gly Leu Leu Leu Ser Leu
    130                 135                 140

gcg cct ggt ttg ccg gtg agt gtt ttt gtc acc acc atc tct ttt gtg   480
Ala Pro Gly Leu Pro Val Ser Val Phe Val Thr Thr Ile Ser Phe Val
145                 150                 155                 160

att tac ctg gtc tgc cgc ctg atc ggt tgg ctc cgc ggc cgt gga gct   528
Ile Tyr Leu Val Cys Arg Leu Ile Gly Trp Leu Arg Gly Arg Gly Ala
                165                 170                 175

cag cgt gac gaa gat gct tat cga cgc cgc cag cac gat cac cac cct   576
Gln Arg Asp Glu Asp Ala Tyr Arg Arg Arg Gln His Asp His His Pro
            180                 185                 190
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cac taggcgtttc gaagt 594
His

<210> 200
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 200
Met Ser Phe Gly Leu Gly Leu Ser Val Leu Phe Ile His Leu Tyr Pro
1 5 10 15

Gly Arg Ser Ser Thr Ala Phe Ser Leu Leu Thr Gly Gln Ile Val Gly
20 25 30

Val Ser Ser Ser Ser Leu Trp Ile Leu Val Ala Val Thr Val Ile Val
35 40 45

Val Ser Ala Val Val Ile Phe Trp Arg Pro Leu Leu Phe Ala Ser Ala
50 55 60

Asp Pro Ile Met Ala Gln Ala Ser Gly Val Asn Val Arg Phe Ile Ala
65 70 75 80

Val Ala Phe Ala Val Leu Val Gly Leu Thr Thr Ser Gln Ser Val Gln
85 90 95

Ile Val Gly Ala Leu Leu Val Met Ala Leu Leu Ile Thr Pro Gly Ala
100 105 110

Ala Ala Val Ala Val Thr Ala Asn Pro Val Lys Ala Val Val Leu Ala
115 120 125

Val Ile Phe Ala Glu Val Ser Ala Val Gly Gly Leu Leu Leu Ser Leu
130 135 140

Ala Pro Gly Leu Pro Val Ser Val Phe Val Thr Thr Ile Ser Phe Val
145 150 155 160

Ile Tyr Leu Val Cys Arg Leu Ile Gly Trp Leu Arg Gly Arg Gly Ala
165 170 175

Gln Arg Asp Glu Asp Ala Tyr Arg Arg Arg Gln His Asp His His Pro
180 185 190

His

<210> 201
<211> 816
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> RXN00353

<400> 201
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tgcgctgatc tattttcatg gctcccagca gtcaggatct gtg ggg cgc agc ttc 115
Val Gly Arg Ser Phe
1 5

acc aac agg act ttt gat ccg ttg ccg ttc atg gtg gtt tat ccg gat 163
Thr Asn Arg Thr Phe Asp Pro Leu Pro Phe Met Val Val Tyr Pro Asp
10 15 20

ggg gtg gat cag cat tgg aat gat gcg cgg ttg ggt ttg gat gaa aat 211
Gly Val Asp Gln His Trp Asn Asp Ala Arg Leu Gly Leu Asp Glu Asn
25 30 35

acc cgc cat tta ggc att gat gat gtg ggg ttc ttt gta aaa ctc gcc 259
Thr Arg His Leu Gly Ile Asp Asp Val Gly Phe Phe Val Lys Leu Ala
40 45 50

acg cac ttg ggc aac acg tat ggc atc aag agg atc ttt att gtt ggc 307
Thr His Leu Gly Asn Thr Tyr Gly Ile Lys Arg Ile Phe Ile Val Gly
55 60 65

tat tcc aac ggt ggg cag atg gtg ttg cgg ctc atg cat gag gtt ccc 355
Tyr Ser Asn Gly Gly Gln Met Val Leu Arg Leu Met His Glu Val Pro
70 75 80 85

aag atg ctc agt ggc gct gca acc att gca tcc aac atg cca gtt gca 403
Lys Met Leu Ser Gly Ala Ala Thr Ile Ala Ser Asn Met Pro Val Ala
90 95 100

gag aat acg ctg ccg cag gtg aaa acc ttc aag aca cat ccg gtg cct 451
Glu Asn Thr Leu Pro Gln Val Lys Thr Phe Lys Thr His Pro Val Pro
105 110 115

tat ttg gcg atg gct gga act gcc gat act ttt tca ccg tat gag ggt 499
Tyr Leu Ala Met Ala Gly Thr Ala Asp Thr Phe Ser Pro Tyr Glu Gly
120 125 130

ggc gat gcc ggt att ggt cgc gaa cac cgc cgt ggc gtg ggc atg tcc 547
Gly Asp Ala Gly Ile Gly Arg Glu His Arg Arg Gly Val Gly Met Ser
135 140 145

gcc ttt gat tca gct gcc tat att gcc gcc cga aac gga ctg acc gaa 595
Ala Phe Asp Ser Ala Ala Tyr Ile Ala Ala Arg Asn Gly Leu Thr Glu
150 155 160 165

cac cgc cac gac gtg att gat gat gtg gtg tcg atc gat acc tgg gat 643
His Arg His Asp Val Ile Asp Asp Val Val Ser Ile Asp Thr Trp Asp
170 175 180

gga gaa aat ccc gtt gag ttt tgg aca ctc aac ggg atc ggc cac ttg 691
Gly Glu Asn Pro Val Glu Phe Trp Thr Leu Asn Gly Ile Gly His Leu
185 190 195

gta cca agt ggg aaa act tat cca gaa ttt cta ggc ccc tca acc aca 739
Val Pro Ser Gly Lys Thr Tyr Pro Glu Phe Leu Gly Pro Ser Thr Thr
200 205 210

tca gtg ata gcg gct gag gag att ggg aag ttc ttt gat ggg gtc agg 787

Ser Val Ile Ala Ala Glu Glu Ile Gly Lys Phe Phe Asp Gly Val Arg
215 220 225

cgt cga taagctcaag ctttaaaaac gca 816
Arg Arg
230

<210> 202
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 202
Val Gly Arg Ser Phe Thr Asn Arg Thr Phe Asp Pro Leu Pro Phe Met
1 5 10 15

Val Val Tyr Pro Asp Gly Val Asp Gln His Trp Asn Asp Ala Arg Leu
20 25 30

Gly Leu Asp Glu Asn Thr Arg His Leu Gly Ile Asp Asp Val Gly Phe
35 40 45

Phe Val Lys Leu Ala Thr His Leu Gly Asn Thr Tyr Gly Ile Lys Arg
50 55 60

Ile Phe Ile Val Gly Tyr Ser Asn Gly Gly Gln Met Val Leu Arg Leu
65 70 75 80

Met His Glu Val Pro Lys Met Leu Ser Gly Ala Ala Thr Ile Ala Ser
85 90 95

Asn Met Pro Val Ala Glu Asn Thr Leu Pro Gln Val Lys Thr Phe Lys
100 105 110

Thr His Pro Val Pro Tyr Leu Ala Met Ala Gly Thr Ala Asp Thr Phe
115 120 125

Ser Pro Tyr Glu Gly Gly Asp Ala Gly Ile Gly Arg Glu His Arg Arg
130 135 140

Gly Val Gly Met Ser Ala Phe Asp Ser Ala Ala Tyr Ile Ala Ala Arg
145 150 155 160

Asn Gly Leu Thr Glu His Arg His Asp Val Ile Asp Asp Val Val Ser
165 170 175

Ile Asp Thr Trp Asp Gly Glu Asn Pro Val Glu Phe Trp Thr Leu Asn
180 185 190

Gly Ile Gly His Leu Val Pro Ser Gly Lys Thr Tyr Pro Glu Phe Leu
195 200 205

Gly Pro Ser Thr Thr Ser Val Ile Ala Ala Glu Glu Ile Gly Lys Phe
210 215 220

Phe Asp Gly Val Arg Arg Arg
225 230

<210> 203

<211> 816
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<222> (101)..(793)
<223> FRXA00353

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                                              Val Gly Arg Ser Phe
                                                1               5

acc aac agg act ttt gat ccg ttg ccg ttc atg gtg gtt tat ccg gat   163
Thr Asn Arg Thr Phe Asp Pro Leu Pro Phe Met Val Val Tyr Pro Asp
                 10                  15                  20

ggg gtg gat cag cat tgg aat gat gcg cgg ttg ggt ttg gat gaa aat   211
Gly Val Asp Gln His Trp Asn Asp Ala Arg Leu Gly Leu Asp Glu Asn
             25                  30                  35

acc cgc cat tta ggc att gat gat gtg ggg ttc ttt gta aaa ctc gcc   259
Thr Arg His Leu Gly Ile Asp Asp Val Gly Phe Phe Val Lys Leu Ala
         40                  45                  50

acg cac ttg ggc aac acg tat ggc atc aag agg atc ttt att gtt ggc   307
Thr His Leu Gly Asn Thr Tyr Gly Ile Lys Arg Ile Phe Ile Val Gly
     55                  60                  65

tat tcc aac ggt ggg cag atg gtg ttg cgg ctc atg cat gag gtt ccc   355
Tyr Ser Asn Gly Gly Gln Met Val Leu Arg Leu Met His Glu Val Pro
 70                  75                  80                  85

aag atg ctc agt ggc gct gca acc att gca tcc aac atg cca gtt gca   403
Lys Met Leu Ser Gly Ala Ala Thr Ile Ala Ser Asn Met Pro Val Ala
                 90                  95                 100

gag aat acg ctg ccg cag gtg aaa acc ttc aag aca cat ccg gtg cct   451
Glu Asn Thr Leu Pro Gln Val Lys Thr Phe Lys Thr His Pro Val Pro
            105                 110                 115

tat ttg gcg atg gct gga act gcc gat act ttt tca ccg tat gag ggt   499
Tyr Leu Ala Met Ala Gly Thr Ala Asp Thr Phe Ser Pro Tyr Glu Gly
        120                 125                 130

ggc gat gcc ggt att ggt cgc gaa cac cgc cgt ggc gtg ggc atg tcc   547
Gly Asp Ala Gly Ile Gly Arg Glu His Arg Arg Gly Val Gly Met Ser
    135                 140                 145

gcc ttt gat tca gct gcc tat att gcc gcc cga aac gga ctg acc gaa   595
Ala Phe Asp Ser Ala Ala Tyr Ile Ala Ala Arg Asn Gly Leu Thr Glu
150                 155                 160                 165

cac cgc cac gac gtg att gat gat gtg gtg tcg atc gat acc tgg gat   643
His Arg His Asp Val Ile Asp Asp Val Val Ser Ile Asp Thr Trp Asp
                170                 175                 180

gga gaa aat ccc gtt gag ttt tgg aca ctc aac ggg atc ggc cac ttg   691
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Gly Glu Asn Pro Val Glu Phe Trp Thr Leu Asn Gly Ile Gly His Leu
            185                 190                 195

gta cca agt ggg aaa act tat cca gaa ttt cta ggc ccc tca acc aca   739
Val Pro Ser Gly Lys Thr Tyr Pro Glu Phe Leu Gly Pro Ser Thr Thr
        200                 205                 210

tca gtg ata gcg gct gag gag att ggg aag ttc ttt gat ggg gtc agg   787
Ser Val Ile Ala Ala Glu Glu Ile Gly Lys Phe Phe Asp Gly Val Arg
    215                 220                 225

cgt cga taagctcaag ctttaaaaac gca                                 816
Arg Arg
230
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<210> 204
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 204

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Val Gly Arg Ser Phe Thr Asn Arg Thr Phe Asp Pro Leu Pro Phe Met
  1               5                  10                  15

Val Val Tyr Pro Asp Gly Val Asp Gln His Trp Asn Asp Ala Arg Leu
             20                  25                  30

Gly Leu Asp Glu Asn Thr Arg His Leu Gly Ile Asp Asp Val Gly Phe
         35                  40                  45

Phe Val Lys Leu Ala Thr His Leu Gly Asn Thr Tyr Gly Ile Lys Arg
     50                  55                  60

Ile Phe Ile Val Gly Tyr Ser Asn Gly Gly Gln Met Val Leu Arg Leu
 65                  70                  75                  80

Met His Glu Val Pro Lys Met Leu Ser Gly Ala Ala Thr Ile Ala Ser
                 85                  90                  95

Asn Met Pro Val Ala Glu Asn Thr Leu Pro Gln Val Lys Thr Phe Lys
            100                 105                 110

Thr His Pro Val Pro Tyr Leu Ala Met Ala Gly Thr Ala Asp Thr Phe
        115                 120                 125

Ser Pro Tyr Glu Gly Gly Asp Ala Gly Ile Gly Arg Glu His Arg Arg
    130                 135                 140

Gly Val Gly Met Ser Ala Phe Asp Ser Ala Ala Tyr Ile Ala Ala Arg
145                 150                 155                 160

Asn Gly Leu Thr Glu His Arg His Asp Val Ile Asp Asp Val Val Ser
                165                 170                 175

Ile Asp Thr Trp Asp Gly Glu Asn Pro Val Glu Phe Trp Thr Leu Asn
            180                 185                 190

Gly Ile Gly His Leu Val Pro Ser Gly Lys Thr Tyr Pro Glu Phe Leu
        195                 200                 205
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Gly Pro Ser Thr Thr Ser Val Ile Ala Ala Glu Glu Ile Gly Lys Phe
    210                 215                 220

Phe Asp Gly Val Arg Arg Arg
225                 230


<210> 205
<211> 936
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(913)
<223> RXN00354

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ttctcgatta tgtacctcat ttacgcgtaa agtttggggc atg gga aag tta ctt   115
                                             Met Gly Lys Leu Leu
                                               1               5

ttc gta gac atc ggt ggc aca ctg ctg gat tac tca aat gaa gtt ccg   163
Phe Val Asp Ile Gly Gly Thr Leu Leu Asp Tyr Ser Asn Glu Val Pro
                10                  15                  20

cgt tcg gcc gtt gac gcg atc cgt aag gca cgc gcc aaa gga cac cgc   211
Arg Ser Ala Val Asp Ala Ile Arg Lys Ala Arg Ala Lys Gly His Arg
            25                  30                  35

gtg tac ttg agc tct ggt cga agc agc gct gag gtg act tct cag ttg   259
Val Tyr Leu Ser Ser Gly Arg Ser Ser Ala Glu Val Thr Ser Gln Leu
        40                  45                  50

tgg gat atc gga gtg gat ggc ctc att ggc gca aat ggt gga tat gtg   307
Trp Asp Ile Gly Val Asp Gly Leu Ile Gly Ala Asn Gly Gly Tyr Val
    55                  60                  65

gaa agc gca cag gag tct gtg ttc cac cgc cgt ttg tcg ggt gag gag   355
Glu Ser Ala Gln Glu Ser Val Phe His Arg Arg Leu Ser Gly Glu Glu
70                  75                  80                  85

acc cgc cac att gtg gag tgg ctc tac aac cgt ggt ttg gag ttt tat   403
Thr Arg His Ile Val Glu Trp Leu Tyr Asn Arg Gly Leu Glu Phe Tyr
                90                  95                  100

ctc gag tcc aac aac ggt ttg tat gca agc cgt ggt ttc cgt gag gct   451
Leu Glu Ser Asn Asn Gly Leu Tyr Ala Ser Arg Gly Phe Arg Glu Ala
            105                 110                 115

tct aag cca gtg ctg tct cgc ctt tcg gag aag acc gac gtg aca gtc   499
Ser Lys Pro Val Leu Ser Arg Leu Ser Glu Lys Thr Asp Val Thr Val
        120                 125                 130

gat agc atg tac ccg gat atg ttc tgg ggc gcg agc ctt gat cgt gac   547
Asp Ser Met Tyr Pro Asp Met Phe Trp Gly Ala Ser Leu Asp Arg Asp
    135                 140                 145

gat gtg aac aag atc agt tac atc ttc aat tct cag gaa gat ttg gac   595
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Asp Val Asn Lys Ile Ser Tyr Ile Phe Asn Ser Gln Glu Asp Leu Asp
150                 155                 160                 165

gca gcg cgt gag gcg ttc cct aac ctg gag cac acc acg tgg ggt ggt   643
Ala Ala Arg Glu Ala Phe Pro Asn Leu Glu His Thr Thr Trp Gly Gly
                170                 175                 180

cag acg ggt gcg ttg ttc ggc acg atc ggt gtg tct gtc aac aag aag   691
Gln Thr Gly Ala Leu Phe Gly Thr Ile Gly Val Ser Val Asn Lys Lys
            185                 190                 195

atc ggc gtg gat cgc ctg ctg aag tac ctg aac gca gat cgc gca aac   739
Ile Gly Val Asp Arg Leu Leu Lys Tyr Leu Asn Ala Asp Arg Ala Asn
        200                 205                 210

acc att gcg ttc ggc gac agc gat gag gat ctc tcc cta ttt gag gcg   787
Thr Ile Ala Phe Gly Asp Ser Asp Glu Asp Leu Ser Leu Phe Glu Ala
    215                 220                 225

agc gct tac ggc gtc gcg atg ggc gag gcc acc gaa tcg ctc aag gct   835
Ser Ala Tyr Gly Val Ala Met Gly Glu Ala Thr Glu Ser Leu Lys Ala
230                 235                 240                 245

gct gct gac ctg gtc acg gat gct gtt ggg cag gac ggc ttg cgc aat   883
Ala Ala Asp Leu Val Thr Asp Ala Val Gly Gln Asp Gly Leu Arg Asn
                250                 255                 260

gcg ttt tta aag ctt gag ctt atc gac gcc tgaccccatc aaagaacttc     933
Ala Phe Leu Lys Leu Glu Leu Ile Asp Ala
            265                 270

cca                                                              936


<210> 206
<211> 271
<212> PRT
<213> Corynebacterium glutamicum

<400> 206
Met Gly Lys Leu Leu Phe Val Asp Ile Gly Gly Thr Leu Leu Asp Tyr
  1               5                  10                  15

Ser Asn Glu Val Pro Arg Ser Ala Val Asp Ala Ile Arg Lys Ala Arg
             20                  25                  30

Ala Lys Gly His Arg Val Tyr Leu Ser Ser Gly Arg Ser Ser Ala Glu
         35                  40                  45

Val Thr Ser Gln Leu Trp Asp Ile Gly Val Asp Gly Leu Ile Gly Ala
     50                  55                  60

Asn Gly Gly Tyr Val Glu Ser Ala Gln Glu Ser Val Phe His Arg Arg
 65                  70                  75                  80

Leu Ser Gly Glu Glu Thr Arg His Ile Val Glu Trp Leu Tyr Asn Arg
                 85                  90                  95

Gly Leu Glu Phe Tyr Leu Glu Ser Asn Asn Gly Leu Tyr Ala Ser Arg
            100                 105                 110
```

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Gly Phe Arg Glu Ala Ser Lys Pro Val Leu Ser Arg Leu Ser Glu Lys
        115                 120                 125

Thr Asp Val Thr Val Asp Ser Met Tyr Pro Asp Met Phe Trp Gly Ala
    130                 135                 140

Ser Leu Asp Arg Asp Asp Val Asn Lys Ile Ser Tyr Ile Phe Asn Ser
145                 150                 155                 160

Gln Glu Asp Leu Asp Ala Ala Arg Glu Ala Phe Pro Asn Leu Glu His
                165                 170                 175

Thr Thr Trp Gly Gly Gln Thr Gly Ala Leu Phe Gly Thr Ile Gly Val
            180                 185                 190

Ser Val Asn Lys Lys Ile Gly Val Asp Arg Leu Leu Lys Tyr Leu Asn
        195                 200                 205

Ala Asp Arg Ala Asn Thr Ile Ala Phe Gly Asp Ser Asp Glu Asp Leu
    210                 215                 220

Ser Leu Phe Glu Ala Ser Ala Tyr Gly Val Ala Met Gly Glu Ala Thr
225                 230                 235                 240

Glu Ser Leu Lys Ala Ala Ala Asp Leu Val Thr Asp Ala Val Gly Gln
                245                 250                 255

Asp Gly Leu Arg Asn Ala Phe Leu Lys Leu Glu Leu Ile Asp Ala
            260                 265                 270


<210> 207
<211> 1470
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1447)
<223> RXN00362

<400> 207
cacttttttgg gtgaaaattc cacgaagtta atgccgcttt aagtcaattc aatcacatgt 60

aacatgctac ggtttttttcg gtcacttaaa ggaggcgctt atg gga atc att gct   115
                                              Met Gly Ile Ile Ala
                                                1               5

ctg ctc gtt ttt atc gca att gcc gtg ata ttg aat gtg ttt ttg aaa   163
Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu Asn Val Phe Leu Lys
                  10                  15                  20

cga gat att tca gaa gca ttg cta gtt gga tta gta gga act gcg ctt   211
Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu Val Gly Thr Ala Leu
              25                  30                  35

gtc ggc ggt gta aat gca ccg aca tta ctg att gat gct gta gtg gat   259
Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile Asp Ala Val Val Asp
          40                  45                  50

gct gct cag tcg gaa gtt act ttc gca ggt atg gcc ttt gtt ttc atg   307
```

```
Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met Ala Phe Val Phe Met
     55                  60                  65

ggc atc gtt gtg caa tca act gga ttg att gat cga tta atc gca atc   355
Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp Arg Leu Ile Ala Ile
 70                  75                  80                  85

ctt aac tcg att ttt ggt cgg ctt cga ggt ggc gca ggt tat gtt tcc   403
Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly Ala Gly Tyr Val Ser
                 90                  95                 100

act ctt gga tct gcg ctc att gga ctc atc gct gga tca acg gct gga   451
Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala Gly Ser Thr Ala Gly
            105                 110                 115

aac tcc gcg acg gtt ggc tca gtg acg atc cct tgg atg aaa aag acg   499
Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro Trp Met Lys Lys Thr
        120                 125                 130

gga tgg act gct gaa agg tcc gca acg tta gtc gcg ggc aac tct ggc   547
Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala Gly Asn Ser Gly
    135                 140                 145

ctt ggt gtt gcg ttg cct ccc aat tca aca atg ttc atc att ttg gca   595
Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe Ile Ile Leu Ala
150                 155                 160                 165

ttg cca gct gca gca gct tct tcg gcc tct cag gtg tac att gct ttg   643
Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln Val Tyr Ile Ala Leu
                170                 175                 180

gct tgt ggt ggt gcg tat gca gtg ctc tac cgc tta gcg gtc gtc ttt   691
Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu Ala Val Val Phe
            185                 190                 195

tac tgg aca cgt aaa gat aaa att cct gcc acc cct gat gat caa cgg   739
Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro Asp Asp Gln Arg
        200                 205                 210

gtg tca ttc ggt gag gca atg aag act gga tgg cgt tca ccg ttg atc   787
Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg Ser Pro Leu Ile
    215                 220                 225

ttc ctt gga att ttg atc ccc gta atc ctc aca atc ggc cca ttg tct   835
Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile Gly Pro Leu Ser
230                 235                 240                 245

gaa tgg tta aag aca cat gga gtt ggg gag tct ggt gtt aaa tcg atg   883
Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly Val Lys Ser Met
                250                 255                 260

tcg atc atc gtg tgg gtg cca att ctg att acg gca att gct ctg att   931
Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala Ile Ala Leu Ile
            265                 270                 275

gaa ggg cgt aaa cga att gct aac aac atg gca cac ttt agg gtt cag   979
Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His Phe Arg Val Gln
        280                 285                 290

atc tcc aag gac ttg cca caa ttt gcc acc gta gga att tcg ttg ttt   1027
Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly Ile Ser Leu Phe
```

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    295                 300                 305

tct gcg ctt gca gca gcg aac atc atg gaa gaa ctg ggt gtt ggc ccg   1075
Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu Leu Gly Val Gly Pro
310                 315                 320                 325

cag ttg tct aac tgg ctt gat tcc atg gac cta cct aag tct gtc atg   1123
Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro Lys Ser Val Met
                330                 335                 340

gtg atc att gtc tgc atc atg tgc att gtg gtg gca acg cca ctg tcg   1171
Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala Thr Pro Leu Ser
            345                 350                 355

tca aca gca acc gcg gct gcg att ggt gct ccc gct gtc gct gcg ttg   1219
Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala Val Ala Ala Leu
        360                 365                 370

gct gcg gta ggt att gat cca act gtg gcg atc gta gtg atc ttg ctg   1267
Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val Val Ile Leu Leu
    375                 380                 385

tgc act tcc act gaa ggt gca tcc ccg ccg gtg ggc gcg ccg att tac   1315
Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly Ala Pro Ile Tyr
390                 395                 400                 405

ctt tct gct gcg atc gcc gat gca aac cca acg aaa atg ttc gta cca   1363
Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys Met Phe Val Pro
                410                 415                 420

ctg att acg tac ttt gtt gtc ccc atg att ctg ctt gct tgg cta gtt   1411
Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu Ala Trp Leu Val
            425                 430                 435

gga atg gga ttc tta cca gtg att gtt cct acg ggt taaaggggta        1457
Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly
        440                 445

aaaatgaact caa                                                   1470


<210> 208
<211> 449
<212> PRT
<213> Corynebacterium glutamicum

<400> 208
Met Gly Ile Ile Ala Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu
  1               5                  10                  15

Asn Val Phe Leu Lys Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu
             20                  25                  30

Val Gly Thr Ala Leu Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile
         35                  40                  45

Asp Ala Val Val Asp Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met
     50                  55                  60

Ala Phe Val Phe Met Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp
 65                  70                  75                  80
```

```
Arg Leu Ile Ala Ile Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly
                 85                  90                  95

Ala Gly Tyr Val Ser Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala
            100                 105                 110

Gly Ser Thr Ala Gly Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro
        115                 120                 125

Trp Met Lys Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val
    130                 135                 140

Ala Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met
145                 150                 155                 160

Phe Ile Ile Leu Ala Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln
                165                 170                 175

Val Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg
            180                 185                 190

Leu Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr
        195                 200                 205

Pro Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp
    210                 215                 220

Arg Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr
225                 230                 235                 240

Ile Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser
                245                 250                 255

Gly Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr
            260                 265                 270

Ala Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala
        275                 280                 285

His Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val
    290                 295                 300

Gly Ile Ser Leu Phe Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu
305                 310                 315                 320

Leu Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu
                325                 330                 335

Pro Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val
            340                 345                 350

Ala Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro
        355                 360                 365

Ala Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile
    370                 375                 380

Val Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val
385                 390                 395                 400
```

```
Gly Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr
                405                 410                 415

Lys Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu
            420                 425                 430

Leu Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr
        435                 440                 445

Gly
```

<210> 209
<211> 983
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(960)
<223> FRXA00362

<400> 209

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gat gaa aag acg gga tgg act gct gaa agg tcc gca acg tta gtc gcg   48
Asp Glu Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala
  1               5                  10                  15

ggc aac tct ggc ctt ggt gtt gcg ttg cct ccc aat tca aca atg ttc   96
Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe
             20                  25                  30

atc att ttg gca ttg cca gct gca gca gct tct tcg gcc tct cag gtg   144
Ile Ile Leu Ala Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln Val
         35                  40                  45

tac att gct ttg gct tgt ggt ggt gcg tat gca gtg ctc tac cgc tta   192
Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu
     50                  55                  60

gcg gtc gtc ttt tac tgg aca cgt aaa gat aaa att cct gcc acc cct   240
Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro
 65                  70                  75                  80

gat gat caa cgg gtg tca ttc ggt gag gca atg aag act gga tgg cgt   288
Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg
                 85                  90                  95

tca ccg ttg atc ttc ctt gga att ttg atc ccc gta atc ctc aca atc   336
Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile
            100                 105                 110

ggc cca ttg tct gaa tgg tta aag aca cat gga gtt ggg gag tct ggt   384
Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly
        115                 120                 125

gtt aaa tcg atg tcg atc atc gtg tgg gtg cca att ctg att acg gca   432
Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala
    130                 135                 140

att gct ctg att gaa ggg cgt aaa cga att gct aac aac atg gca cac   480
```

```
Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His
145                 150                 155                 160

ttt agg gtt cag atc tcc aag gac ttg cca caa ttt gcc acc gta gga   528
Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly
                165                 170                 175

att tcg ttg ttt tct gcg ctt gca gca gcg aac atc atg gaa gaa ctg   576
Ile Ser Leu Phe Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu Leu
            180                 185                 190

ggt gtt ggc ccg cag ttg tct aac tgg ctt gat tcc atg gac cta cct   624
Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro
        195                 200                 205

aag tct gtc atg gtg atc att gtc tgc atc atg tgc att gtg gtg gca   672
Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala
    210                 215                 220

acg cca ctg tcg tca aca gca acc gcg gct gcg att ggt gct ccc gct   720
Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala
225                 230                 235                 240

gtc gct gcg ttg gct gcg gta ggt att gat cca act gtg gcg atc gta   768
Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val
                245                 250                 255

gtg atc ttg ctg tgc act tcc act gaa ggt gca tcc ccg ccg gtg ggc   816
Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly
            260                 265                 270

gcg ccg att tac ctt tct gct gcg atc gcc gat gca aac cca acg aaa   864
Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys
        275                 280                 285

atg ttc gta cca ctg att acg tac ttt gtt gtc ccc atg att ctg ctt   912
Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu
    290                 295                 300

gct tgg cta gtt gga atg gga ttc tta cca gtg att gtt cct acg ggt   960
Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly
305                 310                 315                 320

taaaggggta aaaatgaact caa                                        983


<210> 210
<211> 320
<212> PRT
<213> Corynebacterium glutamicum

<400> 210
Asp Glu Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala
  1               5                  10                  15

Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe
             20                  25                  30

Ile Ile Leu Ala Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln Val
         35                  40                  45
```

```
Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu
     50                  55                  60

Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro
 65                  70                  75                  80

Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg
                 85                  90                  95

Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile
            100                 105                 110

Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly
        115                 120                 125

Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala
    130                 135                 140

Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His
145                 150                 155                 160

Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly
                165                 170                 175

Ile Ser Leu Phe Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu Leu
            180                 185                 190

Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro
        195                 200                 205

Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala
    210                 215                 220

Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala
225                 230                 235                 240

Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val
                245                 250                 255

Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly
            260                 265                 270

Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys
        275                 280                 285

Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu
    290                 295                 300

Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly
305                 310                 315                 320
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<210> 211
<211> 439
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(439)
<223> RXN00373

<400> 211
cacgtggcgg atctgcgcgc taagggcgag ctgccgccgc cgaggaagaa acgcaggcgt 60

cgaaaagcgt cttaaaaggt ttttcactag ggtgttgtcc atg gac atc cag cag 115
Met Asp Ile Gln Gln
1 5

cta gac gcc gaa aca aca gca tgg aaa gac agc ctc ctg cgc gcc gca 163
Leu Asp Ala Glu Thr Thr Ala Trp Lys Asp Ser Leu Leu Arg Ala Ala
10 15 20

cag gag gct ggt ttt cat ttt gag cca ccg aaa ctc ttc gag gat ttt 211
Gln Glu Ala Gly Phe His Phe Glu Pro Pro Lys Leu Phe Glu Asp Phe
25 30 35

gag acc atg gtg gag cag tac aag cag gca gct gcg agc gac ccg gac 259
Glu Thr Met Val Glu Gln Tyr Lys Gln Ala Ala Ala Ser Asp Pro Asp
40 45 50

att gat gtc act gat att cag caa atg tgg ggc atc gtg gtg ggg gag 307
Ile Asp Val Thr Asp Ile Gln Gln Met Trp Gly Ile Val Val Gly Glu
55 60 65

tac ctg cgc gaa aaa atg ggc atg gaa tgg gtc gtc atc acc gat gac 355
Tyr Leu Arg Glu Lys Met Gly Met Glu Trp Val Val Ile Thr Asp Asp
70 75 80 85

tac ggc act gac ctc gcg att cta gcc acg gca ccc aac ggg gac cac 403
Tyr Gly Thr Asp Leu Ala Ile Leu Ala Thr Ala Pro Asn Gly Asp His
90 95 100

gta tat tcc tgc ccc atc atc gtg gtg ggc aag cgc 439
Val Tyr Ser Cys Pro Ile Ile Val Val Gly Lys Arg
105 110

<210> 212
<211> 113
<212> PRT
<213> Corynebacterium glutamicum

<400> 212
Met Asp Ile Gln Gln Leu Asp Ala Glu Thr Thr Ala Trp Lys Asp Ser
1 5 10 15

Leu Leu Arg Ala Ala Gln Glu Ala Gly Phe His Phe Glu Pro Pro Lys
20 25 30

Leu Phe Glu Asp Phe Glu Thr Met Val Glu Gln Tyr Lys Gln Ala Ala
35 40 45

Ala Ser Asp Pro Asp Ile Asp Val Thr Asp Ile Gln Gln Met Trp Gly
50 55 60

Ile Val Val Gly Glu Tyr Leu Arg Glu Lys Met Gly Met Glu Trp Val
65 70 75 80

```
Val Ile Thr Asp Asp Tyr Gly Thr Asp Leu Ala Ile Leu Ala Thr Ala
                 85                  90                  95

Pro Asn Gly Asp His Val Tyr Ser Cys Pro Ile Ile Val Val Gly Lys
            100                 105                 110

Arg
```

<210> 213
<211> 439
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(439)
<223> FRXA00373

<400> 213

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cacgtggcgg atctgcgcgc taagggcgag ctgccgccgc cgaggaagaa acgcaggcgt 60

cgaaaagcgt cttaaaaggt ttttcactag ggtgttgtcc atg gac atc cag cag   115
                                              Met Asp Ile Gln Gln
                                                1               5

cta gac gcc gaa aca aca gca tgg aaa gac agc ctc ctg cgc gcc gca   163
Leu Asp Ala Glu Thr Thr Ala Trp Lys Asp Ser Leu Leu Arg Ala Ala
                 10                  15                  20

cag gag gct ggt ttt cat ttt gag cca ccg aaa ctc ttc gag gat ttt   211
Gln Glu Ala Gly Phe His Phe Glu Pro Pro Lys Leu Phe Glu Asp Phe
             25                  30                  35

gag acc atg gtg gag cag tac aag cag gca gct gcg agc gac ccg gac   259
Glu Thr Met Val Glu Gln Tyr Lys Gln Ala Ala Ala Ser Asp Pro Asp
         40                  45                  50

att gat gtc act gat att cag caa atg tgg ggc atc gtg gtg ggg gag   307
Ile Asp Val Thr Asp Ile Gln Gln Met Trp Gly Ile Val Val Gly Glu
     55                  60                  65

tac ctg cgc gaa aaa atg ggc atg gaa tgg gtc gtc atc acc gat gac   355
Tyr Leu Arg Glu Lys Met Gly Met Glu Trp Val Val Ile Thr Asp Asp
 70                  75                  80                  85

tac ggc act gac ctc gcg att cta gcc acg gca ccc aac ggg gac cac   403
Tyr Gly Thr Asp Leu Ala Ile Leu Ala Thr Ala Pro Asn Gly Asp His
                 90                  95                 100

gta tat tcc tgc ccc atc atc gtg gtg ggc aag cgc                   439
Val Tyr Ser Cys Pro Ile Ile Val Val Gly Lys Arg
            105                 110
```

<210> 214
<211> 113
<212> PRT
<213> Corynebacterium glutamicum

<400> 214
Met Asp Ile Gln Gln Leu Asp Ala Glu Thr Thr Ala Trp Lys Asp Ser
1 5 10 15

Leu Leu Arg Ala Ala Gln Glu Ala Gly Phe His Phe Glu Pro Pro Lys
20 25 30

Leu Phe Glu Asp Phe Glu Thr Met Val Glu Gln Tyr Lys Gln Ala Ala
35 40 45

Ala Ser Asp Pro Asp Ile Asp Val Thr Asp Ile Gln Gln Met Trp Gly
50 55 60

Ile Val Val Gly Glu Tyr Leu Arg Glu Lys Met Gly Met Glu Trp Val
65 70 75 80

Val Ile Thr Asp Asp Tyr Gly Thr Asp Leu Ala Ile Leu Ala Thr Ala
85 90 95

Pro Asn Gly Asp His Val Tyr Ser Cys Pro Ile Ile Val Val Gly Lys
100 105 110

Arg

<210> 215
<211> 528
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(505)
<223> RXN00390

<400> 215
ggaaatagac cgttaatagc tggtctttac atttgccaga aagctccgac gaaaccccaa 60

tagttgacac ggaaaactaat tcattctagc tttagtgacc atg tca act acc agg 115
Met Ser Thr Thr Arg
1 5

gaa att gca ttc ctc atc gca cgt atc ctc ttg ggc gtc atc ctc atc 163
Glu Ile Ala Phe Leu Ile Ala Arg Ile Leu Leu Gly Val Ile Leu Ile
10 15 20

gcc cac ggc tgg gac aag ttc gcc atc aca gga ctt gaa ggc gtc acc 211
Ala His Gly Trp Asp Lys Phe Ala Ile Thr Gly Leu Glu Gly Val Thr
25 30 35

ggc ttc ttc gat tca ctc ggc atc cca gca gcc ggc atc gcc gca ata 259
Gly Phe Phe Asp Ser Leu Gly Ile Pro Ala Ala Gly Ile Ala Ala Ile
40 45 50

gct gct gca gtc gtc gag ctc cta gga gga atc ctt atc atc cta gga 307
Ala Ala Ala Val Val Glu Leu Leu Gly Gly Ile Leu Ile Ile Leu Gly
55 60 65

gta ttt acc cgc atc gtt gcc gcc ttc gtt gcc ata gac atg ctc ttc 355
Val Phe Thr Arg Ile Val Ala Ala Phe Val Ala Ile Asp Met Leu Phe

```
 70                  75                  80                  85

gca gca ctg ttt gcg cac gtc tcc tcc ggc atc ttt gtc acc aac aat   403
Ala Ala Leu Phe Ala His Val Ser Ser Gly Ile Phe Val Thr Asn Asn
                90                  95                 100

ggt tgg gaa ctc acc ggc gca atc ggc gct ggc gcg ctg ctt ctc atc   451
Gly Trp Glu Leu Thr Gly Ala Ile Gly Ala Gly Ala Leu Leu Leu Ile
            105                 110                 115

gca gtt ggc gca agt gca tgg agc atc gac ggg gtt ctg gca aaa cgc   499
Ala Val Gly Ala Ser Ala Trp Ser Ile Asp Gly Val Leu Ala Lys Arg
        120                 125                 130

aag gcc taaatctagc gccacaactc cga                                 528
Lys Ala
    135


<210> 216
<211> 135
<212> PRT
<213> Corynebacterium glutamicum

<400> 216
Met Ser Thr Thr Arg Glu Ile Ala Phe Leu Ile Ala Arg Ile Leu Leu
  1               5                  10                  15

Gly Val Ile Leu Ile Ala His Gly Trp Asp Lys Phe Ala Ile Thr Gly
             20                  25                  30

Leu Glu Gly Val Thr Gly Phe Phe Asp Ser Leu Gly Ile Pro Ala Ala
         35                  40                  45

Gly Ile Ala Ala Ile Ala Ala Ala Val Val Glu Leu Leu Gly Gly Ile
     50                  55                  60

Leu Ile Ile Leu Gly Val Phe Thr Arg Ile Val Ala Ala Phe Val Ala
 65                  70                  75                  80

Ile Asp Met Leu Phe Ala Ala Leu Phe Ala His Val Ser Ser Gly Ile
                85                  90                  95

Phe Val Thr Asn Asn Gly Trp Glu Leu Thr Gly Ala Ile Gly Ala Gly
            100                 105                 110

Ala Leu Leu Leu Ile Ala Val Gly Ala Ser Ala Trp Ser Ile Asp Gly
        115                 120                 125

Val Leu Ala Lys Arg Lys Ala
    130                 135


<210> 217
<211> 528
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(505)
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<223> FRXA00390

<400> 217
ggaaatagac cgttaatagc tggtctttac atttgccaga aagctccgac gaaaccccaa 60

tagttgacac ggaaactaat tcattctagc tttagtgacc atg tca act acc agg 115
Met Ser Thr Thr Arg
1 5

gaa att gca ttc ctc atc gca cgt atc ctc ttg ggc gtc atc ctc atc 163
Glu Ile Ala Phe Leu Ile Ala Arg Ile Leu Leu Gly Val Ile Leu Ile
10 15 20

gcc cac ggc tgg gac aag ttc gcc atc aca gga ctt gaa ggc gtc acc 211
Ala His Gly Trp Asp Lys Phe Ala Ile Thr Gly Leu Glu Gly Val Thr
25 30 35

ggc ttc ttc gat tca ctc ggc atc cca gca gcc ggc atc gcc gca ata 259
Gly Phe Phe Asp Ser Leu Gly Ile Pro Ala Ala Gly Ile Ala Ala Ile
40 45 50

gct gct gca gtc gtc gag ctc cta gga gga atc ctt atc atc cta gga 307
Ala Ala Ala Val Val Glu Leu Leu Gly Gly Ile Leu Ile Ile Leu Gly
55 60 65

gta ttt acc cgc atc gtt gcc gcc ttc gtt gcc ata gac atg ctc ttc 355
Val Phe Thr Arg Ile Val Ala Ala Phe Val Ala Ile Asp Met Leu Phe
70 75 80 85

gca gca ctg ttt gcg cac gtc tcc tcc ggc atc ttt gtc acc aac aat 403
Ala Ala Leu Phe Ala His Val Ser Ser Gly Ile Phe Val Thr Asn Asn
90 95 100

ggt tgg gaa ctc acc ggc gca atc ggc gct ggc gcg ctg ctt ctc atc 451
Gly Trp Glu Leu Thr Gly Ala Ile Gly Ala Gly Ala Leu Leu Leu Ile
105 110 115

gca gtt ggc gca agt gca tgg agc atc gac ggg gtt ctg gca aaa cgc 499
Ala Val Gly Ala Ser Ala Trp Ser Ile Asp Gly Val Leu Ala Lys Arg
120 125 130

aag gcc taaatctagc gccacaactc cga 528
Lys Ala
135

<210> 218
<211> 135
<212> PRT
<213> Corynebacterium glutamicum

<400> 218
Met Ser Thr Thr Arg Glu Ile Ala Phe Leu Ile Ala Arg Ile Leu Leu
1 5 10 15

Gly Val Ile Leu Ile Ala His Gly Trp Asp Lys Phe Ala Ile Thr Gly
20 25 30

Leu Glu Gly Val Thr Gly Phe Phe Asp Ser Leu Gly Ile Pro Ala Ala
35 40 45

```
Gly Ile Ala Ala Ile Ala Ala Ala Val Val Glu Leu Leu Gly Gly Ile
     50                  55                  60

Leu Ile Ile Leu Gly Val Phe Thr Arg Ile Val Ala Ala Phe Val Ala
 65                  70                  75                  80

Ile Asp Met Leu Phe Ala Ala Leu Phe Ala His Val Ser Ser Gly Ile
                 85                  90                  95

Phe Val Thr Asn Asn Gly Trp Glu Leu Thr Gly Ala Ile Gly Ala Gly
            100                 105                 110

Ala Leu Leu Leu Ile Ala Val Gly Ala Ser Ala Trp Ser Ile Asp Gly
        115                 120                 125

Val Leu Ala Lys Arg Lys Ala
    130                 135


<210> 219
<211> 438
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(415)
<223> RXN00399

<400> 219
ggacattgct atgtcgtgag ttgtagtaac cccaaagccc acggattaat caatagtgaa 60

attcaatgat tttcttttcc cacaggccta aacttaaatc atg agc cac aac gac   115
                                          Met Ser His Asn Asp
                                            1               5

agc cca aac ttt gct cgc cga gcg ctc aat tgg ctc cgc caa ggt tat   163
Ser Pro Asn Phe Ala Arg Arg Ala Leu Asn Trp Leu Arg Gln Gly Tyr
                10                  15                  20

cca acc ggt gtt ccg cgg cac gat act ttc gct ctg ttt tac gtt ttg   211
Pro Thr Gly Val Pro Arg His Asp Thr Phe Ala Leu Phe Tyr Val Leu
            25                  30                  35

gag cgc gaa ctt act gag gaa gat ctc aat gag ctc gca gag ctt ctc   259
Glu Arg Glu Leu Thr Glu Glu Asp Leu Asn Glu Leu Ala Glu Leu Leu
        40                  45                  50

atc gcg gaa ggt gag aac aat ggg ctg cac gat aat ccc att acg cgt   307
Ile Ala Glu Gly Glu Asn Asn Gly Leu His Asp Asn Pro Ile Thr Arg
    55                  60                  65

gaa aaa atc ggc aag ctg atc acg cat gtt cac agt cag cca cct gag   355
Glu Lys Ile Gly Lys Leu Ile Thr His Val His Ser Gln Pro Pro Glu
 70                  75                  80                  85

gat gaa gac atc gat cga att cag aaa aag ctg cag gct gag ggc ttc   403
Asp Glu Asp Ile Asp Arg Ile Gln Lys Lys Leu Gln Ala Glu Gly Phe
                90                  95                  100

ccc acc cgc aat taattaattg gagttttgtt gtt                        438
```

Pro Thr Arg Asn
105

<210> 220
<211> 105
<212> PRT
<213> Corynebacterium glutamicum

<400> 220
Met Ser His Asn Asp Ser Pro Asn Phe Ala Arg Arg Ala Leu Asn Trp
1 5 10 15

Leu Arg Gln Gly Tyr Pro Thr Gly Val Pro Arg His Asp Thr Phe Ala
20 25 30

Leu Phe Tyr Val Leu Glu Arg Glu Leu Thr Glu Glu Asp Leu Asn Glu
35 40 45

Leu Ala Glu Leu Leu Ile Ala Glu Gly Glu Asn Asn Gly Leu His Asp
50 55 60

Asn Pro Ile Thr Arg Glu Lys Ile Gly Lys Leu Ile Thr His Val His
65 70 75 80

Ser Gln Pro Pro Glu Asp Glu Asp Ile Asp Arg Ile Gln Lys Lys Leu
85 90 95

Gln Ala Glu Gly Phe Pro Thr Arg Asn
100 105

<210> 221
<211> 438
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(415)
<223> FRXA00399

<400> 221
ggacattgct atgtcgtgag ttgtagtaac cccaaagccc acggattaat caatagtgaa 60

attcaatgat tttcttttcc cacaggccta aacttaaatc atg agc cac aac gac 115
Met Ser His Asn Asp
1 5

agc cca aac ttt gct cgc cga gcg ctc aat tgg ctc cgc caa ggt tat 163
Ser Pro Asn Phe Ala Arg Arg Ala Leu Asn Trp Leu Arg Gln Gly Tyr
10 15 20

cca acc ggt gtt ccg cgg cac gat act ttc gct ctg ttt tac gtt ttg 211
Pro Thr Gly Val Pro Arg His Asp Thr Phe Ala Leu Phe Tyr Val Leu
25 30 35

gag cgc gaa ctt act gag gaa gat ctc aat gag ctc gca gag ctt ctc 259
Glu Arg Glu Leu Thr Glu Glu Asp Leu Asn Glu Leu Ala Glu Leu Leu
40 45 50

```
atc gcg gaa ggt gag aac aat ggg ctg cac gat aat ccc att acg cgt   307
Ile Ala Glu Gly Glu Asn Asn Gly Leu His Asp Asn Pro Ile Thr Arg
     55                  60                  65

gaa aaa atc ggc aag ctg atc acg cat gtt cac agt cag cca cct gag   355
Glu Lys Ile Gly Lys Leu Ile Thr His Val His Ser Gln Pro Pro Glu
 70                  75                  80                  85

gat gaa gac atc gat cga att cag aaa aag ctg cag gct gag ggc ttc   403
Asp Glu Asp Ile Asp Arg Ile Gln Lys Lys Leu Gln Ala Glu Gly Phe
                 90                  95                 100

ccc acc cgc aat taattaattg gagttttgtt gtt                        438
Pro Thr Arg Asn
            105
```

<210> 222
<211> 105
<212> PRT
<213> Corynebacterium glutamicum

<400> 222

```
Met Ser His Asn Asp Ser Pro Asn Phe Ala Arg Arg Ala Leu Asn Trp
  1               5                  10                  15

Leu Arg Gln Gly Tyr Pro Thr Gly Val Pro Arg His Asp Thr Phe Ala
             20                  25                  30

Leu Phe Tyr Val Leu Glu Arg Glu Leu Thr Glu Glu Asp Leu Asn Glu
         35                  40                  45

Leu Ala Glu Leu Leu Ile Ala Glu Gly Glu Asn Asn Gly Leu His Asp
     50                  55                  60

Asn Pro Ile Thr Arg Glu Lys Ile Gly Lys Leu Ile Thr His Val His
 65                  70                  75                  80

Ser Gln Pro Pro Glu Asp Glu Asp Ile Asp Arg Ile Gln Lys Lys Leu
                 85                  90                  95

Gln Ala Glu Gly Phe Pro Thr Arg Asn
            100                 105
```

<210> 223
<211> 1673
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1650)
<223> RXN00416

<400> 223

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ctg gcg tct tac tta agc cca act gcg ctg gtg gtt gcg gtg ttg gct   48
Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
  1               5                  10                  15

att ccg ctg tct gcg acc cgc ctg tat ttg gac gga atc agc gtt gac   96
```

```
Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
            20                  25                  30

cag ggc ttt aga act cag ttt tta acc cgc atg gct gac gat atc ggc   144
Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
         35                  40                  45

ttg tcg gac atg aac tac atc gat atg cct acc ttc tac cct gct gga   192
Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
     50                  55                  60

tgg ttc tgg ctc ggt ggt cgc ttg gcc aat ctt ttg ggg ctg ccc ggt   240
Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65                  70                  75                  80

tgg gaa gct ttc cag cca tgg gca att gtg tcc atg gca gtt gct gct   288
Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
                85                  90                  95

tct gtg tta gtt cca gtg tgg cag cgc atc acc ggt tcc ctg ccg gtg   336
Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
            100                 105                 110

gca aca ggc att gcg ttg gtg aca acc tgc att atc ttg gcg atg aat   384
Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
        115                 120                 125

tcc gaa gag ccc tac gct gca atc gtt gcg atg ggt att cca gcg atg   432
Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
    130                 135                 140

ctc gtg ctg gct tcc cgc att gcc aag ggc gat aag ttt gcg ctt gcc   480
Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
145                 150                 155                 160

ggc ggc att att tac ttg ggt gtt tcg gct act ttc tat act ttg ttc   528
Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
                165                 170                 175

acc ggt gct atc gcg ctt tct gcg gtc gcg gtg tgc atc gtg gtg gcg   576
Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
            180                 185                 190

gct att gtg cag cgc tcc atc aaa cca ctg ctg tgg ctt gca gtg ctg   624
Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu
        195                 200                 205

ggt ggt gga tcc att gtc att gcg ttg att tct tgg ggt cct tac ctt   672
Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
    210                 215                 220

ctg gcc tcc atc aac gga gcg gag cgc tct ggc gat tcc gca aca cac   720
Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
225                 230                 235                 240

tac ctg cct ctt gaa ggc acc caa ttc ccg gtt cct ttc ttg gca tca   768
Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
                245                 250                 255

agc gtt gtg gga ctg ttg tgt ctt gtt ggc ctg atc tat ttg gtg gtg   816
Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
```

```
                260                 265                 270

cgt ttc cac aac aat gag gtg cgc gcg atg tgg gtc ggc atc gca gtg   864
Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
        275                 280                 285

ttt tat gcc tgg atg ggc atg tcc atg gcg atc acg ctt ttg ggc aac   912
Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn
    290                 295                 300

acg ttg ctt gga ttc cgt ctt gat acg gtg ctg gtg ctt att ttt gcc   960
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala
305                 310                 315                 320

acg gct gga gtg ttg ggc att gca gat ttc cgc ctt gcc agt gtg tat   1008
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr
                325                 330                 335

cag ctc tac ccc acc caa atc aca gag cgc acg gcc acc cat ctg acc   1056
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr
            340                 345                 350

aat cta att gtg gtc ctc gtg ctg ctt ggc ggc ctc tac tac gcg caa   1104
Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln
        355                 360                 365

gat ctg ccg cag aag aac gca cga gct atc gat ctg gcc tat acc gat   1152
Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp
    370                 375                 380

act gat ggc tac ggc gag cgc gcg gat ctg tat ccg gcc gga gct gca   1200
Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala
385                 390                 395                 400

cgt tat tac aag gac atc aac gat cat ctg ctt gat caa gga ttc gag   1248
Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu
                405                 410                 415

cct tcc gaa act gtc gtg ctg aca gac gaa ctc gat ttc atg tcc tac   1296
Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr
            420                 425                 430

tac cct tat cgc gga tac caa gct ttt act tcc cac tac gcc aac ccg   1344
Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro
        435                 440                 445

ctt ggt gag ttc gga aac agg aac gca ttc atc gaa gat ctc gcg atc   1392
Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile
    450                 455                 460

cga agc tgg gat gag ttg gct gat cct caa caa ttc agc gac gcc ttg   1440
Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu
465                 470                 475                 480

aac acc tct cca tgg acg atc cct gag gtg ttc atc ttc cgt ggc tcc   1488
Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser
                485                 490                 495

atc gat gat cct gac gcc ggt tgg aaa tac gac gtg gct gaa gat ctg   1536
Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu
            500                 505                 510
```

```
tac ccg aac aat cca aac gtg cgc ttc cgc ggc gtg tac ttt aac ccg   1584
Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro
        515                 520                 525

gag tca ttt gat cag atg tgg cag acc aag caa gtg gga cct ttc gtg   1632
Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val
    530                 535                 540

gtg gta acg cac aat gag taattcctca ccaaacgacc caa                1673
Val Val Thr His Asn Glu
545                 550
```

<210> 224
<211> 550
<212> PRT
<213> Corynebacterium glutamicum

<400> 224

```
Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
  1               5                  10                  15

Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
             20                  25                  30

Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
         35                  40                  45

Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
     50                  55                  60

Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65                  70                  75                  80

Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
                 85                  90                  95

Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
            100                 105                 110

Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
        115                 120                 125

Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
    130                 135                 140

Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
145                 150                 155                 160

Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
                165                 170                 175

Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
            180                 185                 190

Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu
        195                 200                 205

Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
    210                 215                 220
```

```
Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
225                 230                 235                 240

Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
                245                 250                 255

Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
            260                 265                 270

Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
        275                 280                 285

Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn
    290                 295                 300

Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala
305                 310                 315                 320

Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr
                325                 330                 335

Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr
            340                 345                 350

Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln
        355                 360                 365

Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp
    370                 375                 380

Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala
385                 390                 395                 400

Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu
                405                 410                 415

Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr
            420                 425                 430

Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro
        435                 440                 445

Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile
    450                 455                 460

Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu
465                 470                 475                 480

Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser
                485                 490                 495

Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu
            500                 505                 510

Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro
        515                 520                 525

Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val
    530                 535                 540
```

```
Val Val Thr His Asn Glu
545                 550


<210> 225
<211> 350
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(327)
<223> FRXA00416

<400> 225
act tcc cac tac gcc aac ccg ctt ggt gag ttc gga aac agg aac gca   48
Thr Ser His Tyr Ala Asn Pro Leu Gly Glu Phe Gly Asn Arg Asn Ala
  1               5                  10                  15

ttc atc gaa gat ctc gcg atc cga agc tgg aat gag ttg gct gat cct   96
Phe Ile Glu Asp Leu Ala Ile Arg Ser Trp Asn Glu Leu Ala Asp Pro
             20                  25                  30

caa caa ttc agc gac gcc ttg aac acc tct cca tgg acg atc cct gag   144
Gln Gln Phe Ser Asp Ala Leu Asn Thr Ser Pro Trp Thr Ile Pro Glu
         35                  40                  45

gtg ttc atc ttc cgt ggc tcc atc gat gat cct gac gcc ggt tgg aaa   192
Val Phe Ile Phe Arg Gly Ser Ile Asp Asp Pro Asp Ala Gly Trp Lys
     50                  55                  60

tac gat gtg gct gaa gat ctg tac ccg aac aat cca aac gtg cgc ttc   240
Tyr Asp Val Ala Glu Asp Leu Tyr Pro Asn Asn Pro Asn Val Arg Phe
 65                  70                  75                  80

cgc ggc gtg tac ttt aac ccg gag tca ttt gat cag atg tgg cag acc   288
Arg Gly Val Tyr Phe Asn Pro Glu Ser Phe Asp Gln Met Trp Gln Thr
                 85                  90                  95

aag caa gtg gga cct ttc gtg gtg gta acg cac aat gag taattcctca   337
Lys Gln Val Gly Pro Phe Val Val Val Thr His Asn Glu
            100                 105

ccaaacgacc caa                                                  350


<210> 226
<211> 109
<212> PRT
<213> Corynebacterium glutamicum

<400> 226
Thr Ser His Tyr Ala Asn Pro Leu Gly Glu Phe Gly Asn Arg Asn Ala
  1               5                  10                  15

Phe Ile Glu Asp Leu Ala Ile Arg Ser Trp Asn Glu Leu Ala Asp Pro
             20                  25                  30

Gln Gln Phe Ser Asp Ala Leu Asn Thr Ser Pro Trp Thr Ile Pro Glu
         35                  40                  45
```

```
Val Phe Ile Phe Arg Gly Ser Ile Asp Asp Pro Asp Ala Gly Trp Lys
     50                  55                  60

Tyr Asp Val Ala Glu Asp Leu Tyr Pro Asn Asn Pro Asn Val Arg Phe
 65                  70                  75                  80

Arg Gly Val Tyr Phe Asn Pro Glu Ser Phe Asp Gln Met Trp Gln Thr
                 85                  90                  95

Lys Gln Val Gly Pro Phe Val Val Val Thr His Asn Glu
            100                 105
```

<210> 227
<211> 1065
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1065)
<223> FRXA00418

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<400> 227
ctg gcg tct tac tta agc cca act gcg ctg gtg gtt gcg gtg ttg gct   48
Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
  1               5                  10                  15

att ccg ctg tct gcg acc cgc ctg tat ttg gac gga atc agc gtt gac   96
Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
            20                  25                  30

cag ggc ttt aga act cag ttt tta acc cgc atg gct gac gat atc ggc   144
Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
        35                  40                  45

ttg tcg gac atg aac tac atc gat atg cct acc ttc tac cct gct gga   192
Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
    50                  55                  60

tgg ttc tgg ctc ggt ggt cgc ttg gcc aat ctt ttg ggg ctg ccc ggt   240
Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
65                  70                  75                  80

tgg gaa gct ttc cag cca tgg gca att gtg tcc atg gca gtt gct gct   288
Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
                85                  90                  95

tct gtg tta gtt cca gtg tgg cag cgc atc acc ggt tcc ctg ccg gtg   336
Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
            100                 105                 110

gca aca ggc att gcg ttg gtg aca acc tgc att atc ttg gcg atg aat   384
Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
        115                 120                 125

tcc gaa gag ccc tac gct gca atc gtt gcg atg ggt att cca gcg atg   432
Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
    130                 135                 140

ctc gtg ctg gct tcc cgc att gcc aag ggc gat aag ttt gcg ctt gcc   480
```

```
Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
145                 150                 155                 160

ggc ggc att att tac ttg ggt gtt tcg gct act ttc tat act ttg ttc   528
Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
                165                 170                 175

acc ggt gct atc gcg ctt tct gcg gtc gcg gtg tgc atc gtg gtg gcg   576
Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
            180                 185                 190

gct att gtg cag cgc tcc atc aaa cca ctg ctg tgg ctt gca gtg ctg   624
Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu
        195                 200                 205

ggt ggt gga tcc att gtc att gcg ttg att tct tgg ggt cct tac ctt   672
Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
    210                 215                 220

ctg gcc tcc atc aac gga gcg gag cgc tct ggc gat tcc gca aca cac   720
Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
225                 230                 235                 240

tac ctg cct ctt gaa ggc acc caa ttc ccg gtt cct ttc ttg gca tca   768
Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
                245                 250                 255

agc gtt gtg gga ctg ttg tgt ctt gtt ggc ctg atc tat ttg gtg gtg   816
Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
            260                 265                 270

cgt ttc cac aac aat gag gtg cgc gcg atg tgg gtc ggc atc gca gtg   864
Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
        275                 280                 285

ttt tat gcc tgg atg ggc atg tcc atg gcg atc acg ctt ttg ggc aac   912
Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn
    290                 295                 300

acg ttg ctt gga ttc cgt ctt gat acg gtg ctg gtg ctt att ttt gcc   960
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala
305                 310                 315                 320

acg gct gga gtg ttg ggc att gca gat ttc cgc ctt gcc agt gtg tat   1008
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr
                325                 330                 335

cag ctc tac ccc acc caa atc aca gag cgc acg gcc acc cat ctg acc   1056
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr
            340                 345                 350

aat cta att                                                      1065
Asn Leu Ile
        355
```

<210> 228
<211> 355
<212> PRT
<213> Corynebacterium glutamicum

<400> 228

```
Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
  1               5                  10                  15

Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
             20                  25                  30

Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
         35                  40                  45

Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
     50                  55                  60

Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65                  70                  75                  80

Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
                 85                  90                  95

Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
            100                 105                 110

Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
        115                 120                 125

Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
    130                 135                 140

Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
145                 150                 155                 160

Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
                165                 170                 175

Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
            180                 185                 190

Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu
        195                 200                 205

Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
    210                 215                 220

Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
225                 230                 235                 240

Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
                245                 250                 255

Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
            260                 265                 270

Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
        275                 280                 285

Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn
    290                 295                 300

Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala
305                 310                 315                 320
```

```
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr
                325                 330                 335

Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr
            340                 345                 350

Asn Leu Ile
        355


<210> 229
<211> 1017
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(994)
<223> RXN00422

<400> 229
aagcgccggg cgcggaaggc gctggctgag gccttcggcg cggaggtcca gccactgccg 60

cttgacaccg aataggacaa atgggtctat cctggggcgc atg ccc acg aat tat   115
                                            Met Pro Thr Asn Tyr
                                              1               5

gca cgc gac aac gtc att tcc ttg gcg tct gcc cgc gag cag cgt tcc   163
Ala Arg Asp Asn Val Ile Ser Leu Ala Ser Ala Arg Glu Gln Arg Ser
                10                  15                  20

ggg aaa ccc gag ccc aaa ccc gaa cta aca ctc atc gtc cgc gcc acc   211
Gly Lys Pro Glu Pro Lys Pro Glu Leu Thr Leu Ile Val Arg Ala Thr
            25                  30                  35

aac gtg caa gcg gac ggc gag gtc cac agg caa att ggg ttg aac tcg   259
Asn Val Gln Ala Asp Gly Glu Val His Arg Gln Ile Gly Leu Asn Ser
        40                  45                  50

gcg atg agc ctg gac gag ctg cac aat gta ctc aac atc gtt ttc ggt   307
Ala Met Ser Leu Asp Glu Leu His Asn Val Leu Asn Ile Val Phe Gly
    55                  60                  65

gtt ggc ggc gag cag tca ccc tgg cgt ttc gaa gac caa ttc cac caa   355
Val Gly Gly Glu Gln Ser Pro Trp Arg Phe Glu Asp Gln Phe His Gln
70                  75                  80                  85

ccc agc gcc ccc gac acc aac ctc ggc gaa ctc ctg ccc gaa ccc ggc   403
Pro Ser Ala Pro Asp Thr Asn Leu Gly Glu Leu Leu Pro Glu Pro Gly
                90                  95                  100

gac ttc ctg ttt tac ttc tgg ggc ctg tgg caa ttc aac ctg caa tgc   451
Asp Phe Leu Phe Tyr Phe Trp Gly Leu Trp Gln Phe Asn Leu Gln Cys
            105                 110                 115

gtg gaa atg tac ccg cgc gac aac ggc acc ccg cgc gcg ctg tgc atc   499
Val Glu Met Tyr Pro Arg Asp Asn Gly Thr Pro Arg Ala Leu Cys Ile
        120                 125                 130

ggc ggc tcc ggc ggc ctc ggc gac gac ttc gac caa gcc acc atc aac   547
Gly Gly Ser Gly Gly Leu Gly Asp Asp Phe Asp Gln Ala Thr Ile Asn
```

```
    135                 140                 145

gcc gaa ctc acc ggc acc gac acc atc cgc gac gtc ctc tcc ggc gtg   595
Ala Glu Leu Thr Gly Thr Asp Thr Ile Arg Asp Val Leu Ser Gly Val
150                 155                 160                 165

cgc ccc gaa gtc atc gac ctc gtc gac cgc acc ggc gtc ttc gac ttc   643
Arg Pro Glu Val Ile Asp Leu Val Asp Arg Thr Gly Val Phe Asp Phe
                170                 175                 180

atc cca ctg ctc caa gcg ctc gac ctc aaa aga gaa ccg ctt atc gac   691
Ile Pro Leu Leu Gln Ala Leu Asp Leu Lys Arg Glu Pro Leu Ile Asp
            185                 190                 195

gcc acc cgc tac cac acc tgc cgc acg ctg cca gtg gaa aac agc gcc   739
Ala Thr Arg Tyr His Thr Cys Arg Thr Leu Pro Val Glu Asn Ser Ala
        200                 205                 210

gaa gcc tcc gac gca ttc tgg tcc tgc gta ctc gcc ctg tcc tgc ctc   787
Glu Ala Ser Asp Ala Phe Trp Ser Cys Val Leu Ala Leu Ser Cys Leu
    215                 220                 225

gga aac gac gaa ctt ttc atc gaa gtg atc gaa tcc aca atg agc acc   835
Gly Asn Asp Glu Leu Phe Ile Glu Val Ile Glu Ser Thr Met Ser Thr
230                 235                 240                 245

ctc ggc tgg gtc gcc gac gac ggc tcc cca cta cgt gca cca gag atc   883
Leu Gly Trp Val Ala Asp Asp Gly Ser Pro Leu Arg Ala Pro Glu Ile
                250                 255                 260

acc agc gcc tgc gaa gcc tcc ctg aag ata ctc gcg gaa ctc ggt ggc   931
Thr Ser Ala Cys Glu Ala Ser Leu Lys Ile Leu Ala Glu Leu Gly Gly
            265                 270                 275

tac ggc cca gag cgg ctt gcc ccc gtg gat cgc ctg gac att tat agg   979
Tyr Gly Pro Glu Arg Leu Ala Pro Val Asp Arg Leu Asp Ile Tyr Arg
        280                 285                 290

gag ctg ctg tgt ttc taggtattgt gtaacctcgt gtc                    1017
Glu Leu Leu Cys Phe
    295
```

<210> 230
<211> 298
<212> PRT
<213> Corynebacterium glutamicum

<400> 230

```
Met Pro Thr Asn Tyr Ala Arg Asp Asn Val Ile Ser Leu Ala Ser Ala
  1               5                  10                  15

Arg Glu Gln Arg Ser Gly Lys Pro Glu Pro Lys Pro Glu Leu Thr Leu
             20                  25                  30

Ile Val Arg Ala Thr Asn Val Gln Ala Asp Gly Glu Val His Arg Gln
         35                  40                  45

Ile Gly Leu Asn Ser Ala Met Ser Leu Asp Glu Leu His Asn Val Leu
     50                  55                  60
```

```
Asn Ile Val Phe Gly Val Gly Gly Glu Gln Ser Pro Trp Arg Phe Glu
 65                  70                  75                  80

Asp Gln Phe His Gln Pro Ser Ala Pro Asp Thr Asn Leu Gly Glu Leu
                 85                  90                  95

Leu Pro Glu Pro Gly Asp Phe Leu Phe Tyr Phe Trp Gly Leu Trp Gln
            100                 105                 110

Phe Asn Leu Gln Cys Val Glu Met Tyr Pro Arg Asp Asn Gly Thr Pro
        115                 120                 125

Arg Ala Leu Cys Ile Gly Gly Ser Gly Gly Leu Gly Asp Asp Phe Asp
    130                 135                 140

Gln Ala Thr Ile Asn Ala Glu Leu Thr Gly Thr Asp Thr Ile Arg Asp
145                 150                 155                 160

Val Leu Ser Gly Val Arg Pro Glu Val Ile Asp Leu Val Asp Arg Thr
                165                 170                 175

Gly Val Phe Asp Phe Ile Pro Leu Leu Gln Ala Leu Asp Leu Lys Arg
            180                 185                 190

Glu Pro Leu Ile Asp Ala Thr Arg Tyr His Thr Cys Arg Thr Leu Pro
        195                 200                 205

Val Glu Asn Ser Ala Glu Ala Ser Asp Ala Phe Trp Ser Cys Val Leu
    210                 215                 220

Ala Leu Ser Cys Leu Gly Asn Asp Glu Leu Phe Ile Glu Val Ile Glu
225                 230                 235                 240

Ser Thr Met Ser Thr Leu Gly Trp Val Ala Asp Asp Gly Ser Pro Leu
                245                 250                 255

Arg Ala Pro Glu Ile Thr Ser Ala Cys Glu Ala Ser Leu Lys Ile Leu
            260                 265                 270

Ala Glu Leu Gly Gly Tyr Gly Pro Glu Arg Leu Ala Pro Val Asp Arg
        275                 280                 285

Leu Asp Ile Tyr Arg Glu Leu Leu Cys Phe
    290                 295
```

<210> 231
<211> 523
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(523)
<223> FRXA00422

<400> 231
aagcgccggg cgcggaaggc gctggctgag gccttcggcg cggaggtcca gccactgccg 60

cttgacaccg aataggacaa atgggtctat cctggggcgc atg ccc acg aat tat 115
                                                Met Pro Thr Asn Tyr

```
                                                    1               5

gca cgc gac aac gtc att tcc ttg gcg tct gcc cgc gag cag cgt tcc   163
Ala Arg Asp Asn Val Ile Ser Leu Ala Ser Ala Arg Glu Gln Arg Ser
                10                  15                  20

ggg aaa ccc gag ccc aaa ccc gaa cta aca ctc atc gtc cgc gcc acc   211
Gly Lys Pro Glu Pro Lys Pro Glu Leu Thr Leu Ile Val Arg Ala Thr
            25                  30                  35

aac gtg caa gcg gac ggc gag gtc cac agg caa att ggg ttg aac tcg   259
Asn Val Gln Ala Asp Gly Glu Val His Arg Gln Ile Gly Leu Asn Ser
        40                  45                  50

gcg atg agc ctg gac gag ctg cac aat gta ctc aac atc gtt ttc ggt   307
Ala Met Ser Leu Asp Glu Leu His Asn Val Leu Asn Ile Val Phe Gly
    55                  60                  65

gtt ggc ggc gag cag tca ccc tgg cgt ttc gaa gac caa ttc cac caa   355
Val Gly Gly Glu Gln Ser Pro Trp Arg Phe Glu Asp Gln Phe His Gln
70                  75                  80                  85

ccc agc gcc ccc gac acc aac ctc ggc gaa ctc ctg ccc gaa ccc ggc   403
Pro Ser Ala Pro Asp Thr Asn Leu Gly Glu Leu Leu Pro Glu Pro Gly
                90                  95                  100

gac ttc ctg ttt tac ttc tgg ggc ctg tgg caa ttc aac ctg caa tgc   451
Asp Phe Leu Phe Tyr Phe Trp Gly Leu Trp Gln Phe Asn Leu Gln Cys
            105                 110                 115

gtg gaa atg tac ccg cgc gac aac ggc acc ccg cgc gcg ctg tgc atc   499
Val Glu Met Tyr Pro Arg Asp Asn Gly Thr Pro Arg Ala Leu Cys Ile
        120                 125                 130

ggc ggc tcc ggc ggc ctc ggc gac                                  523
Gly Gly Ser Gly Gly Leu Gly Asp
    135                 140
```

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<210> 232
<211> 141
<212> PRT
<213> Corynebacterium glutamicum

<400> 232

```
Met Pro Thr Asn Tyr Ala Arg Asp Asn Val Ile Ser Leu Ala Ser Ala
  1               5                  10                  15

Arg Glu Gln Arg Ser Gly Lys Pro Glu Pro Lys Pro Glu Leu Thr Leu
            20                  25                  30

Ile Val Arg Ala Thr Asn Val Gln Ala Asp Gly Glu Val His Arg Gln
        35                  40                  45

Ile Gly Leu Asn Ser Ala Met Ser Leu Asp Glu Leu His Asn Val Leu
    50                  55                  60

Asn Ile Val Phe Gly Val Gly Gly Glu Gln Ser Pro Trp Arg Phe Glu
65                  70                  75                  80

Asp Gln Phe His Gln Pro Ser Ala Pro Asp Thr Asn Leu Gly Glu Leu
```

```
                85                  90                  95

Leu Pro Glu Pro Gly Asp Phe Leu Phe Tyr Phe Trp Gly Leu Trp Gln
            100                 105                 110

Phe Asn Leu Gln Cys Val Glu Met Tyr Pro Arg Asp Asn Gly Thr Pro
        115                 120                 125

Arg Ala Leu Cys Ile Gly Gly Ser Gly Gly Leu Gly Asp
    130                 135                 140


<210> 233
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> RXN00447

<400> 233
gagcacggca tcgtgattcg cgcgttcccc gagggtgcgc gcatttcggt gaccaacgcc 60

gaggaaactg acaagctgct gcgcgcgtgg gaggccatca atg ctg ggt agt ctt   115
                                              Met Leu Gly Ser Leu
                                                1               5

tgg cgt ttt gcg gtg cgc acc gca gca ggc gcg gtg gcg ttg tgg gtg   163
Trp Arg Phe Ala Val Arg Thr Ala Ala Gly Ala Val Ala Leu Trp Val
                10                  15                  20

gtt att aag ctt atc gac ggc atc tcc ctg agt ttt ccc acc aca cct   211
Val Ile Lys Leu Ile Asp Gly Ile Ser Leu Ser Phe Pro Thr Thr Pro
            25                  30                  35

ctc tat cag gac ggt cag cac gac aat ctg ctg aca ttc ctg gcg gtg   259
Leu Tyr Gln Asp Gly Gln His Asp Asn Leu Leu Thr Phe Leu Ala Val
        40                  45                  50

gca gca atc att gtc gtg ttg aat gcc acg gtg aaa ccc gtc ttg aag   307
Ala Ala Ile Ile Val Val Leu Asn Ala Thr Val Lys Pro Val Leu Lys
    55                  60                  65

ctg ctt ggt ttg ccg ttg aca atc atc acc ttg ggt ctg ttc tcg ctg   355
Leu Leu Gly Leu Pro Leu Thr Ile Ile Thr Leu Gly Leu Phe Ser Leu
70                  75                  80                  85

gtc atc aac gcg gta atc atg ctg ctg gcg gag tat gtg tca gat ttg   403
Val Ile Asn Ala Val Ile Met Leu Leu Ala Glu Tyr Val Ser Asp Leu
                90                  95                  100

atc ggt ttc ggt cta cgc att gaa acc ttc ggt gcg gcc ttc tgg ggt   451
Ile Gly Phe Gly Leu Arg Ile Glu Thr Phe Gly Ala Ala Phe Trp Gly
            105                 110                 115

gcg att gtg ctg gcg tta gtg aac tgg gtt ctt ggc ccc att acc ggc   499
Ala Ile Val Leu Ala Leu Val Asn Trp Val Leu Gly Pro Ile Thr Gly
        120                 125                 130
```

```
ctc ctc ggt gca aaa aag gac taaccatggc ggatctgagc att                543
Leu Leu Gly Ala Lys Lys Asp
    135                 140


<210> 234
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 234
Met Leu Gly Ser Leu Trp Arg Phe Ala Val Arg Thr Ala Ala Gly Ala
  1               5                  10                  15

Val Ala Leu Trp Val Val Ile Lys Leu Ile Asp Gly Ile Ser Leu Ser
             20                  25                  30

Phe Pro Thr Thr Pro Leu Tyr Gln Asp Gly Gln His Asp Asn Leu Leu
         35                  40                  45

Thr Phe Leu Ala Val Ala Ala Ile Ile Val Val Leu Asn Ala Thr Val
     50                  55                  60

Lys Pro Val Leu Lys Leu Leu Gly Leu Pro Leu Thr Ile Ile Thr Leu
 65                  70                  75                  80

Gly Leu Phe Ser Leu Val Ile Asn Ala Val Ile Met Leu Leu Ala Glu
                 85                  90                  95

Tyr Val Ser Asp Leu Ile Gly Phe Gly Leu Arg Ile Glu Thr Phe Gly
            100                 105                 110

Ala Ala Phe Trp Gly Ala Ile Val Leu Ala Leu Val Asn Trp Val Leu
        115                 120                 125

Gly Pro Ile Thr Gly Leu Leu Gly Ala Lys Lys Asp
    130                 135                 140


<210> 235
<211> 400
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(400)
<223> FRXA00447

<400> 235
gagcacggca tcgtgattcg cgcgttcccc gagggtgcgc gcatttcggt gaccaacgcc 60

gaggaaactg acaagctgct gcgcgcgtgg gaggccatca atg ctg ggt agt ctt   115
                                              Met Leu Gly Ser Leu
                                                1               5

tgg cgt ttt gcg gtg cgc acc gca gca ggc gcg gtg gcg ttg tgg gtg   163
Trp Arg Phe Ala Val Arg Thr Ala Ala Gly Ala Val Ala Leu Trp Val
                 10                  15                  20

gtt att aag ctt atc gac ggc atc tcc ctg agt ttt ccc acc aca cct   211
```

```
Val Ile Lys Leu Ile Asp Gly Ile Ser Leu Ser Phe Pro Thr Thr Pro
            25                  30                  35

ctc tat cag gac ggt cag cac gac aat ctg ctg aca ttc ctg gcg gtg   259
Leu Tyr Gln Asp Gly Gln His Asp Asn Leu Leu Thr Phe Leu Ala Val
        40                  45                  50

gca gca atc att gtc gtg ttg aat gcc acg gtg aaa ccc gtc ttg aag   307
Ala Ala Ile Ile Val Val Leu Asn Ala Thr Val Lys Pro Val Leu Lys
    55                  60                  65

ctg ctt ggt ttg ccg ttg aca atc atc acc ttg ggt ctg ttc tcg ctg   355
Leu Leu Gly Leu Pro Leu Thr Ile Ile Thr Leu Gly Leu Phe Ser Leu
70                  75                  80                  85

gtc atc aac gcg gta atc atg ctg ctg gcg gag tat gtg tca gat       400
Val Ile Asn Ala Val Ile Met Leu Leu Ala Glu Tyr Val Ser Asp
                90                  95                  100


<210> 236
<211> 100
<212> PRT
<213> Corynebacterium glutamicum

<400> 236
Met Leu Gly Ser Leu Trp Arg Phe Ala Val Arg Thr Ala Ala Gly Ala
  1               5                  10                  15

Val Ala Leu Trp Val Val Ile Lys Leu Ile Asp Gly Ile Ser Leu Ser
            20                  25                  30

Phe Pro Thr Thr Pro Leu Tyr Gln Asp Gly Gln His Asp Asn Leu Leu
        35                  40                  45

Thr Phe Leu Ala Val Ala Ala Ile Ile Val Val Leu Asn Ala Thr Val
    50                  55                  60

Lys Pro Val Leu Lys Leu Leu Gly Leu Pro Leu Thr Ile Ile Thr Leu
65                  70                  75                  80

Gly Leu Phe Ser Leu Val Ile Asn Ala Val Ile Met Leu Leu Ala Glu
                85                  90                  95

Tyr Val Ser Asp
            100


<210> 237
<211> 873
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(850)
<223> RXN00455

<400> 237
gaagtgtctg gccgattggc taacaatctc tagttaaatc ccgcctcatg aaaccacgat 60
```

```
gaaaccaaca tgagagtttt ttcatccacg ttttctggct atg gtt gtg gac gtg   115
                                              Met Val Val Asp Val
                                                1               5

caa aat caa tca cac acc cca gaa acc cag cct caa cct ggg cag ggc   163
Gln Asn Gln Ser His Thr Pro Glu Thr Gln Pro Gln Pro Gly Gln Gly
                   10                  15                  20

gca gcc aag aaa acc ccc gtt gcg tcc gga aac tcc acg ttc att cac   211
Ala Ala Lys Lys Thr Pro Val Ala Ser Gly Asn Ser Thr Phe Ile His
               25                  30                  35

att cag cca agc ttg tac ccc att ttg ctg gcg ctg ttt gtt gca gtc   259
Ile Gln Pro Ser Leu Tyr Pro Ile Leu Leu Ala Leu Phe Val Ala Val
           40                  45                  50

ttt cta att tca aat atc acc gca acc aag ggc gta gaa atc ggc ccg   307
Phe Leu Ile Ser Asn Ile Thr Ala Thr Lys Gly Val Glu Ile Gly Pro
       55                  60                  65

ttg gtg aca gac ggt gcg ttc ttc ctc ttc ccc atc tca tat gtg ttg   355
Leu Val Thr Asp Gly Ala Phe Phe Leu Phe Pro Ile Ser Tyr Val Leu
   70                  75                  80                  85

ggc gat gtt cta gcc gaa tgt tac ggc ttc aaa tcc act cgt cgt gcc   403
Gly Asp Val Leu Ala Glu Cys Tyr Gly Phe Lys Ser Thr Arg Arg Ala
                   90                  95                 100

att ctt act ggt ttt ggc atc acg atg ctc gcg gcg ctg tct ttc tac   451
Ile Leu Thr Gly Phe Gly Ile Thr Met Leu Ala Ala Leu Ser Phe Tyr
               105                 110                 115

att tcc atc tgg ctg cct ggc gca agt ttc tgg gaa ggc caa gaa gct   499
Ile Ser Ile Trp Leu Pro Gly Ala Ser Phe Trp Glu Gly Gln Glu Ala
           120                 125                 130

ttc gaa gca acg ctc ggc ctt gtt cca cag atc atc gtg gca tca ctg   547
Phe Glu Ala Thr Leu Gly Leu Val Pro Gln Ile Ile Val Ala Ser Leu
       135                 140                 145

gcg ggc tat att gtg ggt cag ctg ctc aac gcc aaa gtt ctg gtg gct   595
Ala Gly Tyr Ile Val Gly Gln Leu Leu Asn Ala Lys Val Leu Val Ala
   150                 155                 160                 165

atc aaa aag cgc acg ggt gaa aag tcc ctg tgg gcg cgc ctg att ggt   643
Ile Lys Lys Arg Thr Gly Glu Lys Ser Leu Trp Ala Arg Leu Ile Gly
                   170                 175                 180

tcc acc gtt gtc gga gaa ttt gtc gat acc ctg ctg ttt tgc gcc atc   691
Ser Thr Val Val Gly Glu Phe Val Asp Thr Leu Leu Phe Cys Ala Ile
               185                 190                 195

gca gcg cca gtg atc ggt att gcc acc gcc ccg gat ttc atc aac tac   739
Ala Ala Pro Val Ile Gly Ile Ala Thr Ala Pro Asp Phe Ile Asn Tyr
           200                 205                 210

gtt gtg gtg ggc ttc gtg tgg aaa acc ctt cta gag gtc atc ctc atg   787
Val Val Val Gly Phe Val Trp Lys Thr Leu Leu Glu Val Ile Leu Met
       215                 220                 225

ccc atc acc tac gca gtc att agg tgg gtg aaa cgc cgc gaa ggt tat   835
```

```
Pro Ile Thr Tyr Ala Val Ile Arg Trp Val Lys Arg Arg Glu Gly Tyr
230                 235                 240                 245

gaa acc ttc gac gcg tagtaccggc ctaagaattc ttc                    873
Glu Thr Phe Asp Ala
                250
```

<210> 238
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 238

```
Met Val Val Asp Val Gln Asn Gln Ser His Thr Pro Glu Thr Gln Pro
  1               5                  10                  15

Gln Pro Gly Gln Gly Ala Ala Lys Lys Thr Pro Val Ala Ser Gly Asn
            20                  25                  30

Ser Thr Phe Ile His Ile Gln Pro Ser Leu Tyr Pro Ile Leu Leu Ala
        35                  40                  45

Leu Phe Val Ala Val Phe Leu Ile Ser Asn Ile Thr Ala Thr Lys Gly
    50                  55                  60

Val Glu Ile Gly Pro Leu Val Thr Asp Gly Ala Phe Phe Leu Phe Pro
65                  70                  75                  80

Ile Ser Tyr Val Leu Gly Asp Val Leu Ala Glu Cys Tyr Gly Phe Lys
                85                  90                  95

Ser Thr Arg Arg Ala Ile Leu Thr Gly Phe Gly Ile Thr Met Leu Ala
            100                 105                 110

Ala Leu Ser Phe Tyr Ile Ser Ile Trp Leu Pro Gly Ala Ser Phe Trp
        115                 120                 125

Glu Gly Gln Glu Ala Phe Glu Ala Thr Leu Gly Leu Val Pro Gln Ile
    130                 135                 140

Ile Val Ala Ser Leu Ala Gly Tyr Ile Val Gly Gln Leu Leu Asn Ala
145                 150                 155                 160

Lys Val Leu Val Ala Ile Lys Lys Arg Thr Gly Glu Lys Ser Leu Trp
                165                 170                 175

Ala Arg Leu Ile Gly Ser Thr Val Val Gly Glu Phe Val Asp Thr Leu
            180                 185                 190

Leu Phe Cys Ala Ile Ala Ala Pro Val Ile Gly Ile Ala Thr Ala Pro
        195                 200                 205

Asp Phe Ile Asn Tyr Val Val Val Gly Phe Val Trp Lys Thr Leu Leu
    210                 215                 220

Glu Val Ile Leu Met Pro Ile Thr Tyr Ala Val Ile Arg Trp Val Lys
225                 230                 235                 240

Arg Arg Glu Gly Tyr Glu Thr Phe Asp Ala
                245                 250
```

<210> 239
<211> 641
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(618)
<223> FRXA00455

<400> 239

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att ttg ctg gcg ctg ttt gtt gca gtc ttt cta att tca aat atc acc   48
Ile Leu Leu Ala Leu Phe Val Ala Val Phe Leu Ile Ser Asn Ile Thr
  1               5                  10                  15

gca acc aag ggc gta gaa atc ggc ccg ttg gtg aca gac ggt gcg ttc   96
Ala Thr Lys Gly Val Glu Ile Gly Pro Leu Val Thr Asp Gly Ala Phe
             20                  25                  30

ttc ctc ttc ccc atc tca tat gtg ttg ggc gat gtt cta gcc gaa tgt   144
Phe Leu Phe Pro Ile Ser Tyr Val Leu Gly Asp Val Leu Ala Glu Cys
         35                  40                  45

tac ggc ttc aaa tcc act cgt cgt gcc att ctt act ggt ttt ggc atc   192
Tyr Gly Phe Lys Ser Thr Arg Arg Ala Ile Leu Thr Gly Phe Gly Ile
     50                  55                  60

acg atg ctc gcg gcg ctg tct ttc tac att tcc atc tgg ctg cct ggc   240
Thr Met Leu Ala Ala Leu Ser Phe Tyr Ile Ser Ile Trp Leu Pro Gly
 65                  70                  75                  80

gca agt ttc tgg gaa ggc caa gaa gct ttc gaa gca acg ctc ggc ctt   288
Ala Ser Phe Trp Glu Gly Gln Glu Ala Phe Glu Ala Thr Leu Gly Leu
                 85                  90                  95

gtt cca cag atc atc gtg gca tca ctg gcg ggc tat att gtg ggt cag   336
Val Pro Gln Ile Ile Val Ala Ser Leu Ala Gly Tyr Ile Val Gly Gln
            100                 105                 110

ctg ctc aac gcc aaa gtt ctg gtg gct atc aaa aag cgc acg ggt gaa   384
Leu Leu Asn Ala Lys Val Leu Val Ala Ile Lys Lys Arg Thr Gly Glu
        115                 120                 125

aag tcc ctg tgg gcg cgc ctg att ggt tcc acc gtt gtc gga gaa ttt   432
Lys Ser Leu Trp Ala Arg Leu Ile Gly Ser Thr Val Val Gly Glu Phe
    130                 135                 140

gtc gat acc ctg ctg ttt tgc gcc atc gca gcg cca gtg atc ggt att   480
Val Asp Thr Leu Leu Phe Cys Ala Ile Ala Ala Pro Val Ile Gly Ile
145                 150                 155                 160

gcc acc gcc ccg gat ttc atc aac tac gtt gtg gtg ggc ttc gtg tgg   528
Ala Thr Ala Pro Asp Phe Ile Asn Tyr Val Val Val Gly Phe Val Trp
                165                 170                 175

aaa acc ctt cta gag gtc atc ctc atg ccc atc acc tac gca gtc att   576
Lys Thr Leu Leu Glu Val Ile Leu Met Pro Ile Thr Tyr Ala Val Ile
            180                 185                 190
```

```
agg tgg gtg aaa cgc cgc gaa ggt tat gaa acc ttc gac gcg          618
Arg Trp Val Lys Arg Arg Glu Gly Tyr Glu Thr Phe Asp Ala
        195                 200                 205

tagtaccggc ctaagaattc ttc                                       641


<210> 240
<211> 206
<212> PRT
<213> Corynebacterium glutamicum

<400> 240
Ile Leu Leu Ala Leu Phe Val Ala Val Phe Leu Ile Ser Asn Ile Thr
  1               5                  10                  15

Ala Thr Lys Gly Val Glu Ile Gly Pro Leu Val Thr Asp Gly Ala Phe
             20                  25                  30

Phe Leu Phe Pro Ile Ser Tyr Val Leu Gly Asp Val Leu Ala Glu Cys
         35                  40                  45

Tyr Gly Phe Lys Ser Thr Arg Arg Ala Ile Leu Thr Gly Phe Gly Ile
     50                  55                  60

Thr Met Leu Ala Ala Leu Ser Phe Tyr Ile Ser Ile Trp Leu Pro Gly
 65                  70                  75                  80

Ala Ser Phe Trp Glu Gly Gln Glu Ala Phe Glu Ala Thr Leu Gly Leu
                 85                  90                  95

Val Pro Gln Ile Ile Val Ala Ser Leu Ala Gly Tyr Ile Val Gly Gln
            100                 105                 110

Leu Leu Asn Ala Lys Val Leu Val Ala Ile Lys Lys Arg Thr Gly Glu
        115                 120                 125

Lys Ser Leu Trp Ala Arg Leu Ile Gly Ser Thr Val Val Gly Glu Phe
    130                 135                 140

Val Asp Thr Leu Leu Phe Cys Ala Ile Ala Ala Pro Val Ile Gly Ile
145                 150                 155                 160

Ala Thr Ala Pro Asp Phe Ile Asn Tyr Val Val Val Gly Phe Val Trp
                165                 170                 175

Lys Thr Leu Leu Glu Val Ile Leu Met Pro Ile Thr Tyr Ala Val Ile
            180                 185                 190

Arg Trp Val Lys Arg Arg Glu Gly Tyr Glu Thr Phe Asp Ala
        195                 200                 205


<210> 241
<211> 912
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(889)
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<223> RXN00473

<400> 241

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ggggcagctg tggatttttc acaaccaccc cttttctcac accagccccg catgaacagg 60

ctggttgcac accgttgaaa atgagtgttt actggaactc atg agt gga aca ggt   115
                                              Met Ser Gly Thr Gly
                                                1               5

gtt cga aag ttg tgg gga gat ggc act ccg gtg tcg ctc cct gac ctt   163
Val Arg Lys Leu Trp Gly Asp Gly Thr Pro Val Ser Leu Pro Asp Leu
                10                  15                  20

tca gga tta agt aga gcg gag cgc att gat gcg ttg cgt tca cgc atg   211
Ser Gly Leu Ser Arg Ala Glu Arg Ile Asp Ala Leu Arg Ser Arg Met
            25                  30                  35

tcc acc atg ggt gct gcg gtg cca aag ttt gag ccg tcg gtg gaa gaa   259
Ser Thr Met Gly Ala Ala Val Pro Lys Phe Glu Pro Ser Val Glu Glu
        40                  45                  50

agt gct gaa caa aag cag gat tct ctc gcc gaa aaa cag gac ata gtt   307
Ser Ala Glu Gln Lys Gln Asp Ser Leu Ala Glu Lys Gln Asp Ile Val
    55                  60                  65

gca gtt cct tcc gct ttt tct gat ctt ttc cct ggg gat ggt ttg ccg   355
Ala Val Pro Ser Ala Phe Ser Asp Leu Phe Pro Gly Asp Gly Leu Pro
70                  75                  80                  85

cgt cgt gcg gtt act caa ttg gtt gaa cag cca ctt gtg gtg gtg gac   403
Arg Arg Ala Val Thr Gln Leu Val Glu Gln Pro Leu Val Val Val Asp
                90                  95                  100

ttc ctg gct cat att act gcc cag ggt gga cac gct gcg gtg att ggg   451
Phe Leu Ala His Ile Thr Ala Gln Gly Gly His Ala Ala Val Ile Gly
            105                 110                 115

tgg aag gat tta gcc tac gcc ggg gtg att gat tcc gga ggt gtg tgc   499
Trp Lys Asp Leu Ala Tyr Ala Gly Val Ile Asp Ser Gly Gly Val Cys
        120                 125                 130

gag aac atc att gct att cca aat cct ggt acg gag cca ctg aat gtg   547
Glu Asn Ile Ile Ala Ile Pro Asn Pro Gly Thr Glu Pro Leu Asn Val
    135                 140                 145

gca gcg gtg ctg tgt gag ggg ttg gat gtg gtc gtg tac aaa ggc ccg   595
Ala Ala Val Leu Cys Glu Gly Leu Asp Val Val Val Tyr Lys Gly Pro
150                 155                 160                 165

gag att tcc ctg tcg cca acc aga gcg agg ccg ttg ctg gga aag ctg   643
Glu Ile Ser Leu Ser Pro Thr Arg Ala Arg Pro Leu Leu Gly Lys Leu
                170                 175                 180

agg cag ggg act gct gcc ttg gtg atg gtt ggc acg aaa gta agc tca   691
Arg Gln Gly Thr Ala Ala Leu Val Met Val Gly Thr Lys Val Ser Ser
            185                 190                 195

ccg gcg ctg tcg gtg gat gca gag atc act gat tat gtt ggc att ggt   739
Pro Ala Leu Ser Val Asp Ala Glu Ile Thr Asp Tyr Val Gly Ile Gly
        200                 205                 210
```

```
gca ggt agt ggg cgt att cgt ggc gtt gag atg cag gtg cgg gct gtg   787
Ala Gly Ser Gly Arg Ile Arg Gly Val Glu Met Gln Val Arg Ala Val
    215                 220                 225

tcg aaa act cac ggt gtg cgc agc gga aaa gtc ctg atc agt agg cct   835
Ser Lys Thr His Gly Val Arg Ser Gly Lys Val Leu Ile Ser Arg Pro
230                 235                 240                 245

cag gat gca gca ttg ctt gag cct gaa cag cca aca acg ttg cgg gcg   883
Gln Asp Ala Ala Leu Leu Glu Pro Glu Gln Pro Thr Thr Leu Arg Ala
                250                 255                 260

gtc cca tgacgcgggt gatggcattg tgg                                912
Val Pro
```

<210> 242
<211> 263
<212> PRT
<213> Corynebacterium glutamicum

```
<400> 242
Met Ser Gly Thr Gly Val Arg Lys Leu Trp Gly Asp Gly Thr Pro Val
  1               5                  10                  15

Ser Leu Pro Asp Leu Ser Gly Leu Ser Arg Ala Glu Arg Ile Asp Ala
            20                  25                  30

Leu Arg Ser Arg Met Ser Thr Met Gly Ala Ala Val Pro Lys Phe Glu
        35                  40                  45

Pro Ser Val Glu Glu Ser Ala Glu Gln Lys Gln Asp Ser Leu Ala Glu
    50                  55                  60

Lys Gln Asp Ile Val Ala Val Pro Ser Ala Phe Ser Asp Leu Phe Pro
65                  70                  75                  80

Gly Asp Gly Leu Pro Arg Arg Ala Val Thr Gln Leu Val Glu Gln Pro
                85                  90                  95

Leu Val Val Val Asp Phe Leu Ala His Ile Thr Ala Gln Gly Gly His
            100                 105                 110

Ala Ala Val Ile Gly Trp Lys Asp Leu Ala Tyr Ala Gly Val Ile Asp
        115                 120                 125

Ser Gly Gly Val Cys Glu Asn Ile Ile Ala Ile Pro Asn Pro Gly Thr
    130                 135                 140

Glu Pro Leu Asn Val Ala Ala Val Leu Cys Glu Gly Leu Asp Val Val
145                 150                 155                 160

Val Tyr Lys Gly Pro Glu Ile Ser Leu Ser Pro Thr Arg Ala Arg Pro
                165                 170                 175

Leu Leu Gly Lys Leu Arg Gln Gly Thr Ala Ala Leu Val Met Val Gly
            180                 185                 190

Thr Lys Val Ser Ser Pro Ala Leu Ser Val Asp Ala Glu Ile Thr Asp
        195                 200                 205
```

```
Tyr Val Gly Ile Gly Ala Gly Ser Gly Arg Ile Arg Gly Val Glu Met
    210                 215                 220

Gln Val Arg Ala Val Ser Lys Thr His Gly Val Arg Ser Gly Lys Val
225                 230                 235                 240

Leu Ile Ser Arg Pro Gln Asp Ala Ala Leu Leu Glu Pro Glu Gln Pro
                245                 250                 255

Thr Thr Leu Arg Ala Val Pro
            260


<210> 243
<211> 888
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(865)
<223> FRXA00473

<400> 243
ccaccccttt tctcacacca gccccgcatg aacaggctgg ttgcacaccg ttgaaaatga 60

gtgtttactg gaactcatga gtggaacagg tgttcgaaag ttg tgg gga gat ggc   115
                                              Leu Trp Gly Asp Gly
                                                1               5

act ccg gtg tcg ctc cct gac ctt tca gga tta agt aga gcg gag cgc   163
Thr Pro Val Ser Leu Pro Asp Leu Ser Gly Leu Ser Arg Ala Glu Arg
                10                  15                  20

att gat gcg ttg cgt tca cgc atg tcc acc atg ggt gct gcg gtg cca   211
Ile Asp Ala Leu Arg Ser Arg Met Ser Thr Met Gly Ala Ala Val Pro
            25                  30                  35

aag ttt gag ccg tcg gtg gaa gaa agt gct gaa caa aag cag gat tct   259
Lys Phe Glu Pro Ser Val Glu Glu Ser Ala Glu Gln Lys Gln Asp Ser
        40                  45                  50

ctc gcc gaa aaa cag gac ata gtt gca gtt cct tcc gct ttt tct gat   307
Leu Ala Glu Lys Gln Asp Ile Val Ala Val Pro Ser Ala Phe Ser Asp
    55                  60                  65

ctt ttc cct ggg gat ggt ttg ccg cgt cgt gcg gtt act caa ttg gtt   355
Leu Phe Pro Gly Asp Gly Leu Pro Arg Arg Ala Val Thr Gln Leu Val
70                  75                  80                  85

gaa cag cca ctt gtg gtg gtg gac ttc ctg gct cat att act gcc cag   403
Glu Gln Pro Leu Val Val Val Asp Phe Leu Ala His Ile Thr Ala Gln
                90                  95                  100

ggt gga cac gct gcg gtg att ggg tgg aag gat tta gcc tac gcc ggg   451
Gly Gly His Ala Ala Val Ile Gly Trp Lys Asp Leu Ala Tyr Ala Gly
            105                 110                 115

gtg att gat tcc gga ggt gtg tgc gag aac atc att gct att cca aat   499
Val Ile Asp Ser Gly Gly Val Cys Glu Asn Ile Ile Ala Ile Pro Asn
```

```
        120                 125                 130

cct ggt acg gag cca ctg aat gtg gca gcg gtg ctg tgt gag ggg ttg   547
Pro Gly Thr Glu Pro Leu Asn Val Ala Ala Val Leu Cys Glu Gly Leu
    135                 140                 145

gat gtg gtc gtg tac aaa ggc ccg gag att tcc ctg tcg cca acc aga   595
Asp Val Val Val Tyr Lys Gly Pro Glu Ile Ser Leu Ser Pro Thr Arg
150                 155                 160                 165

gcg agg ccg ttg ctg gga aag ctg agg cag ggg act gct gcc ttg gtg   643
Ala Arg Pro Leu Leu Gly Lys Leu Arg Gln Gly Thr Ala Ala Leu Val
                170                 175                 180

atg gtt ggc acg aaa gta agc tca ccg gcg ctg tcg gtg gat gca gag   691
Met Val Gly Thr Lys Val Ser Ser Pro Ala Leu Ser Val Asp Ala Glu
            185                 190                 195

atc act gat tat gtt ggc att ggt gca ggt agt ggg cgt att cgt ggc   739
Ile Thr Asp Tyr Val Gly Ile Gly Ala Gly Ser Gly Arg Ile Arg Gly
        200                 205                 210

gtt gag atg cag gtg cgg gct gtg tcg aaa act cac ggt gtg cgc agc   787
Val Glu Met Gln Val Arg Ala Val Ser Lys Thr His Gly Val Arg Ser
    215                 220                 225

gga aaa gtc ctg atc agt agg cct cag gat gca gca ttg ctt gag cct   835
Gly Lys Val Leu Ile Ser Arg Pro Gln Asp Ala Ala Leu Leu Glu Pro
230                 235                 240                 245

gaa cag cca aca acg ttg cgg gcg gtc cca tgacgcgggt gatggcattg     885
Glu Gln Pro Thr Thr Leu Arg Ala Val Pro
                250                 255

tgg                                                               888
```

<210> 244
<211> 255
<212> PRT
<213> Corynebacterium glutamicum

```
<400> 244
Leu Trp Gly Asp Gly Thr Pro Val Ser Leu Pro Asp Leu Ser Gly Leu
  1               5                  10                  15

Ser Arg Ala Glu Arg Ile Asp Ala Leu Arg Ser Arg Met Ser Thr Met
             20                  25                  30

Gly Ala Ala Val Pro Lys Phe Glu Pro Ser Val Glu Glu Ser Ala Glu
         35                  40                  45

Gln Lys Gln Asp Ser Leu Ala Glu Lys Gln Asp Ile Val Ala Val Pro
     50                  55                  60

Ser Ala Phe Ser Asp Leu Phe Pro Gly Asp Gly Leu Pro Arg Arg Ala
 65                  70                  75                  80

Val Thr Gln Leu Val Glu Gln Pro Leu Val Val Val Asp Phe Leu Ala
                 85                  90                  95
```

```
His Ile Thr Ala Gln Gly Gly His Ala Ala Val Ile Gly Trp Lys Asp
            100                 105                 110

Leu Ala Tyr Ala Gly Val Ile Asp Ser Gly Gly Val Cys Glu Asn Ile
        115                 120                 125

Ile Ala Ile Pro Asn Pro Gly Thr Glu Pro Leu Asn Val Ala Ala Val
    130                 135                 140

Leu Cys Glu Gly Leu Asp Val Val Val Tyr Lys Gly Pro Glu Ile Ser
145                 150                 155                 160

Leu Ser Pro Thr Arg Ala Arg Pro Leu Leu Gly Lys Leu Arg Gln Gly
                165                 170                 175

Thr Ala Ala Leu Val Met Val Gly Thr Lys Val Ser Ser Pro Ala Leu
            180                 185                 190

Ser Val Asp Ala Glu Ile Thr Asp Tyr Val Gly Ile Gly Ala Gly Ser
        195                 200                 205

Gly Arg Ile Arg Gly Val Glu Met Gln Val Arg Ala Val Ser Lys Thr
    210                 215                 220

His Gly Val Arg Ser Gly Lys Val Leu Ile Ser Arg Pro Gln Asp Ala
225                 230                 235                 240

Ala Leu Leu Glu Pro Glu Gln Pro Thr Thr Leu Arg Ala Val Pro
                245                 250                 255
```

<210> 245
<211> 2418
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2395)
<223> RXN00485

<400> 245

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tcaacttcgg cgacgaggtg ggcgctattt ttcattgttt ttcgcgattt tcgcttcggt 60

tgcattgact gttagcgcca ctgcgttgac aaattctttg gtg tcc agt gtt aat   115
                                          Val Ser Ser Val Asn
                                            1               5

gat ctt ttt gcc aag ccg tat gaa aac gct gat ctt gtg gtc acg gtg   163
Asp Leu Phe Ala Lys Pro Tyr Glu Asn Ala Asp Leu Val Val Thr Val
                  10                  15                  20

tct gcg aaa aac gaa gat tcc ttt gca gct ttt gag caa caa tta gct   211
Ser Ala Lys Asn Glu Asp Ser Phe Ala Ala Phe Glu Gln Gln Leu Ala
              25                  30                  35

acg aca cct ggt gtt gaa gct ctg gct ttt gat caa aat ttt gca gcc   259
Thr Thr Pro Gly Val Glu Ala Leu Ala Phe Asp Gln Asn Phe Ala Ala
          40                  45                  50

tct gta aag caa tca gac ggg att tac gcc agt act tca gtc cag tca   307
```

```
Ser Val Lys Gln Ser Asp Gly Ile Tyr Ala Ser Thr Ser Val Gln Ser
     55                  60                  65

att tcg gaa ggc cca ctg cag tgg cgg cca atc cta gaa ggc cga ttg   355
Ile Ser Glu Gly Pro Leu Gln Trp Arg Pro Ile Leu Glu Gly Arg Leu
 70                  75                  80                  85

ccc caa gga cct ggt gag att gca gta aca acg gcc ccg ggt gcg cct   403
Pro Gln Gly Pro Gly Glu Ile Ala Val Thr Thr Ala Pro Gly Ala Pro
                 90                  95                 100

gaa gtt ggt gag cac gta tcc att cgc ctg tcc caa aac act gag gac   451
Glu Val Gly Glu His Val Ser Ile Arg Leu Ser Gln Asn Thr Glu Asp
            105                 110                 115

act gag gtt ctt gtg gtt ggc gtg gtg gag cca gcg gcg cag gaa act   499
Thr Glu Val Leu Val Val Gly Val Val Glu Pro Ala Ala Gln Glu Thr
        120                 125                 130

tta ggt ggc gca ccg ttc gtt gtg gcg tct cct gat gcg ctg atg gag   547
Leu Gly Gly Ala Pro Phe Val Val Ala Ser Pro Asp Ala Leu Met Glu
    135                 140                 145

tgg aat tct tcc ggt gtg cgg ggt gaa ttc cga gtg gca act tcc gat   595
Trp Asn Ser Ser Gly Val Arg Gly Glu Phe Arg Val Ala Thr Ser Asp
150                 155                 160                 165

cct gcc tcg cta gag gct gca agc ttt agc gac gct acg gtg gtg gtt   643
Pro Ala Ser Leu Glu Ala Ala Ser Phe Ser Asp Ala Thr Val Val Val
                170                 175                 180

gct tcg gcg gag ggg cac gtc gat aag ctt gct gat tct tat ttg ggc   691
Ala Ser Ala Glu Gly His Val Asp Lys Leu Ala Asp Ser Tyr Leu Gly
            185                 190                 195

cag cga gat cgc tat ttc ttg ctg ctc gca gcg ttt gtg gca gtg gct   739
Gln Arg Asp Arg Tyr Phe Leu Leu Leu Ala Ala Phe Val Ala Val Ala
        200                 205                 210

gct gcc gtg gcg ttt ttg gtg gtc ttt tct gca tat tcg gtg ctc act   787
Ala Ala Val Ala Phe Leu Val Val Phe Ser Ala Tyr Ser Val Leu Thr
    215                 220                 225

ggt gag cga gtt cgc gag ttc ggg ctg att cgt tca gtg ggc gca tcg   835
Gly Glu Arg Val Arg Glu Phe Gly Leu Ile Arg Ser Val Gly Ala Ser
230                 235                 240                 245

acg ccg cag att ttg ggg tca gtg att ttt gaa gcc ggc atc ctc ggt   883
Thr Pro Gln Ile Leu Gly Ser Val Ile Phe Glu Ala Gly Ile Leu Gly
                250                 255                 260

gtg gtg gct gct ggt ttt ggt gcg ccc gcc gga ttg atg gcg gcg cgt   931
Val Val Ala Ala Gly Phe Gly Ala Pro Ala Gly Leu Met Ala Ala Arg
            265                 270                 275

ttg ttg gcg gat aat gcc gca cgt ttt ggc att cgt gtg ccc att gat   979
Leu Leu Ala Asp Asn Ala Ala Arg Phe Gly Ile Arg Val Pro Ile Asp
        280                 285                 290

gtg att gat ctg cca agt agc acg atg tgg ctc atc gct ggc gtc ggc   1027
Val Ile Asp Leu Pro Ser Ser Thr Met Trp Leu Ile Ala Gly Val Gly
```

```
    295                 300                 305

gtg gtg atg tcc gtg att gcg gca tta ccg gca gtg ttc agt gtg tgc   1075
Val Val Met Ser Val Ile Ala Ala Leu Pro Ala Val Phe Ser Val Cys
310                 315                 320                 325

aga aaa tcc gca gtg gaa tca ctg agt acg cct gct att tcg agg act   1123
Arg Lys Ser Ala Val Glu Ser Leu Ser Thr Pro Ala Ile Ser Arg Thr
                330                 335                 340

tcc ccc tgg ttc ggt gca tta tgg ttg ctg ctc gcg ggc att gtg ggc   1171
Ser Pro Trp Phe Gly Ala Leu Trp Leu Leu Leu Ala Gly Ile Val Gly
            345                 350                 355

gcc ggc gga atg tgg gcg tat gag gca acc tcg gac tac cgc ggc atg   1219
Ala Gly Gly Met Trp Ala Tyr Glu Ala Thr Ser Asp Tyr Arg Gly Met
        360                 365                 370

cgt tca gtg gct tta tcc atc gcc ggt tca ggc gct ttg gtg tgt gcg   1267
Arg Ser Val Ala Leu Ser Ile Ala Gly Ser Gly Ala Leu Val Cys Ala
    375                 380                 385

ttg ttg att gcc acg gcg gtg ctc gtg ccc tgg tta ttg cac gta ttc   1315
Leu Leu Ile Ala Thr Ala Val Leu Val Pro Trp Leu Leu His Val Phe
390                 395                 400                 405

tcc agg att gtg ggc ggc acc gtc cca aca ctt cag ttg gga ttg gcg   1363
Ser Arg Ile Val Gly Gly Thr Val Pro Thr Leu Gln Leu Gly Leu Ala
                410                 415                 420

ttt gca gca aag cag aaa tct cgt tcg gcg gcg ctg atc gct gtg att   1411
Phe Ala Ala Lys Gln Lys Ser Arg Ser Ala Ala Leu Ile Ala Val Ile
            425                 430                 435

ctt gct ggt tct gca tta agc tcc gct gtt ctg cat ggc cag gca cat   1459
Leu Ala Gly Ser Ala Leu Ser Ser Ala Val Leu His Gly Gln Ala His
        440                 445                 450

atc ggc acg cat ttg gtg gcc gtg gct aaa ggc atg ggc ggc aca gac   1507
Ile Gly Thr His Leu Val Ala Val Ala Lys Gly Met Gly Gly Thr Asp
    455                 460                 465

atg atg gtt aca gcg ctt gat ggg gaa atc ccc gcc gga atg ctg gag   1555
Met Met Val Thr Ala Leu Asp Gly Glu Ile Pro Ala Gly Met Leu Glu
470                 475                 480                 485

gaa atc tct agc atc gac ggc gtg aaa act gcc atc gcg cca gcc acc   1603
Glu Ile Ser Ser Ile Asp Gly Val Lys Thr Ala Ile Ala Pro Ala Thr
                490                 495                 500

acc gct gtg gaa ttg gaa gat tcc ggc aat ttc tct gtg ctc atg ctc   1651
Thr Ala Val Glu Leu Glu Asp Ser Gly Asn Phe Ser Val Leu Met Leu
            505                 510                 515

gct gaa gaa gac gga gcc tcc gtg atg cgc gca ggc gat act ggt gca   1699
Ala Glu Glu Asp Gly Ala Ser Val Met Arg Ala Gly Asp Thr Gly Ala
        520                 525                 530

cca gct ggt ggc ctt gtt ttg ggc aga aac tct cct gac cag gat gct   1747
Pro Ala Gly Gly Leu Val Leu Gly Arg Asn Ser Pro Asp Gln Asp Ala
    535                 540                 545
```

```
tac ccg gcc ggc cag gct gca aac atc att gtc gcg gat acc cca acg   1795
Tyr Pro Ala Gly Gln Ala Ala Asn Ile Ile Val Ala Asp Thr Pro Thr
550                 555                 560                 565

cag gcg gaa atc ttc cac agc gac aac tac ttc tcc atg atc gac cca   1843
Gln Ala Glu Ile Phe His Ser Asp Asn Tyr Phe Ser Met Ile Asp Pro
                570                 575                 580

gca ctc gcc acc ggc ccc agc acc aca cgc aac gta ctg atc ctg ctc   1891
Ala Leu Ala Thr Gly Pro Ser Thr Thr Arg Asn Val Leu Ile Leu Leu
            585                 590                 595

gac ggc gac tcc aac cag gcc ccc gac aac gcc acg gcg cag gcg gta   1939
Asp Gly Asp Ser Asn Gln Ala Pro Asp Asn Ala Thr Ala Gln Ala Val
        600                 605                 610

cgc aag acc att tcg ctt ttc gac gga cga tac tcc atc acc gag ggt   1987
Arg Lys Thr Ile Ser Leu Phe Asp Gly Arg Tyr Ser Ile Thr Glu Gly
    615                 620                 625

ttc tcc gcc cgc caa aac act ttt gaa ctg gtt tcc cgc atc acc acc   2035
Phe Ser Ala Arg Gln Asn Thr Phe Glu Leu Val Ser Arg Ile Thr Thr
630                 635                 640                 645

atg tcc aca ctg ctt gcc atc gtg gcc tta gcg atc gct gcc gtt ggc   2083
Met Ser Thr Leu Leu Ala Ile Val Ala Leu Ala Ile Ala Ala Val Gly
                650                 655                 660

ctg atc aac aca gtg gca ctc acc att tct gag cgt gcc cgc gat cgt   2131
Leu Ile Asn Thr Val Ala Leu Thr Ile Ser Glu Arg Ala Arg Asp Arg
            665                 670                 675

tat ttg ctg cgc acc att gga ctg acc tca act ggt cag att ctg gtg   2179
Tyr Leu Leu Arg Thr Ile Gly Leu Thr Ser Thr Gly Gln Ile Leu Val
        680                 685                 690

atg gct att gaa atg atc gcg ctc tca ttg ccg gct gcc att gtt ggt   2227
Met Ala Ile Glu Met Ile Ala Leu Ser Leu Pro Ala Ala Ile Val Gly
    695                 700                 705

gca gtt tcg gga gga ttc tta ggc aga ttc gtt gcc agt tct gcc acc   2275
Ala Val Ser Gly Gly Phe Leu Gly Arg Phe Val Ala Ser Ser Ala Thr
710                 715                 720                 725

aac acc gct gcg acg gca cca ctt caa gta gac att ctc ggc gga acg   2323
Asn Thr Ala Ala Thr Ala Pro Leu Gln Val Asp Ile Leu Gly Gly Thr
                730                 735                 740

gtt ctc gcg atg gtc gca gga tct gta ctg tgc gcg ctc atc gtg ctg   2371
Val Leu Ala Met Val Ala Gly Ser Val Leu Cys Ala Leu Ile Val Leu
            745                 750                 755

gcg aac aaa cga cgt cgg gtg gtt tgattataaa atccaaaaat cga         2418
Ala Asn Lys Arg Arg Arg Val Val
        760                 765
```

<210> 246
<211> 765
<212> PRT

<213> Corynebacterium glutamicum

<400> 246

```
Val Ser Ser Val Asn Asp Leu Phe Ala Lys Pro Tyr Glu Asn Ala Asp
  1               5                  10                  15

Leu Val Val Thr Val Ser Ala Lys Asn Glu Asp Ser Phe Ala Ala Phe
             20                  25                  30

Glu Gln Gln Leu Ala Thr Thr Pro Gly Val Glu Ala Leu Ala Phe Asp
         35                  40                  45

Gln Asn Phe Ala Ala Ser Val Lys Gln Ser Asp Gly Ile Tyr Ala Ser
     50                  55                  60

Thr Ser Val Gln Ser Ile Ser Glu Gly Pro Leu Gln Trp Arg Pro Ile
 65                  70                  75                  80

Leu Glu Gly Arg Leu Pro Gln Gly Pro Gly Glu Ile Ala Val Thr Thr
                 85                  90                  95

Ala Pro Gly Ala Pro Glu Val Gly Glu His Val Ser Ile Arg Leu Ser
            100                 105                 110

Gln Asn Thr Glu Asp Thr Glu Val Leu Val Val Gly Val Val Glu Pro
        115                 120                 125

Ala Ala Gln Glu Thr Leu Gly Gly Ala Pro Phe Val Val Ala Ser Pro
    130                 135                 140

Asp Ala Leu Met Glu Trp Asn Ser Ser Gly Val Arg Gly Glu Phe Arg
145                 150                 155                 160

Val Ala Thr Ser Asp Pro Ala Ser Leu Glu Ala Ala Ser Phe Ser Asp
                165                 170                 175

Ala Thr Val Val Val Ala Ser Ala Glu Gly His Val Asp Lys Leu Ala
            180                 185                 190

Asp Ser Tyr Leu Gly Gln Arg Asp Arg Tyr Phe Leu Leu Leu Ala Ala
        195                 200                 205

Phe Val Ala Val Ala Ala Ala Val Ala Phe Leu Val Val Phe Ser Ala
    210                 215                 220

Tyr Ser Val Leu Thr Gly Glu Arg Val Arg Glu Phe Gly Leu Ile Arg
225                 230                 235                 240

Ser Val Gly Ala Ser Thr Pro Gln Ile Leu Gly Ser Val Ile Phe Glu
                245                 250                 255

Ala Gly Ile Leu Gly Val Val Ala Ala Gly Phe Gly Ala Pro Ala Gly
            260                 265                 270

Leu Met Ala Ala Arg Leu Leu Ala Asp Asn Ala Ala Arg Phe Gly Ile
        275                 280                 285

Arg Val Pro Ile Asp Val Ile Asp Leu Pro Ser Ser Thr Met Trp Leu
    290                 295                 300

Ile Ala Gly Val Gly Val Val Met Ser Val Ile Ala Ala Leu Pro Ala
```

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305                 310                 315                 320

Val Phe Ser Val Cys Arg Lys Ser Ala Val Glu Ser Leu Ser Thr Pro
                325                 330                 335

Ala Ile Ser Arg Thr Ser Pro Trp Phe Gly Ala Leu Trp Leu Leu Leu
            340                 345                 350

Ala Gly Ile Val Gly Ala Gly Gly Met Trp Ala Tyr Glu Ala Thr Ser
        355                 360                 365

Asp Tyr Arg Gly Met Arg Ser Val Ala Leu Ser Ile Ala Gly Ser Gly
    370                 375                 380

Ala Leu Val Cys Ala Leu Leu Ile Ala Thr Ala Val Leu Val Pro Trp
385                 390                 395                 400

Leu Leu His Val Phe Ser Arg Ile Val Gly Gly Thr Val Pro Thr Leu
                405                 410                 415

Gln Leu Gly Leu Ala Phe Ala Ala Lys Gln Lys Ser Arg Ser Ala Ala
            420                 425                 430

Leu Ile Ala Val Ile Leu Ala Gly Ser Ala Leu Ser Ser Ala Val Leu
        435                 440                 445

His Gly Gln Ala His Ile Gly Thr His Leu Val Ala Val Ala Lys Gly
    450                 455                 460

Met Gly Gly Thr Asp Met Met Val Thr Ala Leu Asp Gly Glu Ile Pro
465                 470                 475                 480

Ala Gly Met Leu Glu Glu Ile Ser Ser Ile Asp Gly Val Lys Thr Ala
                485                 490                 495

Ile Ala Pro Ala Thr Thr Ala Val Glu Leu Glu Asp Ser Gly Asn Phe
            500                 505                 510

Ser Val Leu Met Leu Ala Glu Glu Asp Gly Ala Ser Val Met Arg Ala
        515                 520                 525

Gly Asp Thr Gly Ala Pro Ala Gly Gly Leu Val Leu Gly Arg Asn Ser
    530                 535                 540

Pro Asp Gln Asp Ala Tyr Pro Ala Gly Gln Ala Ala Asn Ile Ile Val
545                 550                 555                 560

Ala Asp Thr Pro Thr Gln Ala Glu Ile Phe His Ser Asp Asn Tyr Phe
                565                 570                 575

Ser Met Ile Asp Pro Ala Leu Ala Thr Gly Pro Ser Thr Thr Arg Asn
            580                 585                 590

Val Leu Ile Leu Leu Asp Gly Asp Ser Asn Gln Ala Pro Asp Asn Ala
        595                 600                 605

Thr Ala Gln Ala Val Arg Lys Thr Ile Ser Leu Phe Asp Gly Arg Tyr
    610                 615                 620

Ser Ile Thr Glu Gly Phe Ser Ala Arg Gln Asn Thr Phe Glu Leu Val
625                 630                 635                 640
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```
Ser Arg Ile Thr Thr Met Ser Thr Leu Leu Ala Ile Val Ala Leu Ala
                645                 650                 655

Ile Ala Ala Val Gly Leu Ile Asn Thr Val Ala Leu Thr Ile Ser Glu
            660                 665                 670

Arg Ala Arg Asp Arg Tyr Leu Leu Arg Thr Ile Gly Leu Thr Ser Thr
        675                 680                 685

Gly Gln Ile Leu Val Met Ala Ile Glu Met Ile Ala Leu Ser Leu Pro
    690                 695                 700

Ala Ala Ile Val Gly Ala Val Ser Gly Gly Phe Leu Gly Arg Phe Val
705                 710                 715                 720

Ala Ser Ser Ala Thr Asn Thr Ala Ala Thr Ala Pro Leu Gln Val Asp
                725                 730                 735

Ile Leu Gly Gly Thr Val Leu Ala Met Val Ala Gly Ser Val Leu Cys
            740                 745                 750

Ala Leu Ile Val Leu Ala Asn Lys Arg Arg Arg Val Val
        755                 760                 765
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CONFIDENTIAL

<210> 247
<211> 2166
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2143)
<223> FRXA00485

<400> 247

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tgcagcctct gtaaagcaat cagacgggat ttacgccagt acttcagtcc agtcaatttc 60

ggaaggccca ctgcagtggc ggccaatcct agaaggccga ttg ccc caa gga cct   115
                                              Leu Pro Gln Gly Pro
                                                1               5

ggt gag att gca gta aca acg gcc ccg ggt gcg cct gaa gtt ggt gag   163
Gly Glu Ile Ala Val Thr Thr Ala Pro Gly Ala Pro Glu Val Gly Glu
                10                  15                  20

cac gta tcc att cgc ctg tcc caa aac act gag gac act gag gtt ctt   211
His Val Ser Ile Arg Leu Ser Gln Asn Thr Glu Asp Thr Glu Val Leu
            25                  30                  35

gtg gtt ggc gtg gtg gag cca gcg gcg cag gaa act tta ggt ggc gca   259
Val Val Gly Val Val Glu Pro Ala Ala Gln Glu Thr Leu Gly Gly Ala
        40                  45                  50

ccg ttc gtt gtg gcg tct cct gat gcg ctg atg gag tgg aat tct tcc   307
Pro Phe Val Val Ala Ser Pro Asp Ala Leu Met Glu Trp Asn Ser Ser
    55                  60                  65

ggt gtg cgg ggt gaa ttc cga gtg gca act tcc gat cct gcc tcg cta   355
Gly Val Arg Gly Glu Phe Arg Val Ala Thr Ser Asp Pro Ala Ser Leu
```

```
 70                  75                  80                  85

gag gct gca agc ttt agc gac gct acg gtg gtg gtt gct tcg gcg gag   403
Glu Ala Ala Ser Phe Ser Asp Ala Thr Val Val Val Ala Ser Ala Glu
                 90                  95                 100

ggg cac gtc gat aag ctt gct gat tct tat ttg ggc cag cga gat cgc   451
Gly His Val Asp Lys Leu Ala Asp Ser Tyr Leu Gly Gln Arg Asp Arg
            105                 110                 115

tat ttc ttg ctg ctc gca gcg ttt gtg gca gtg gct gct gcc gtg gcg   499
Tyr Phe Leu Leu Leu Ala Ala Phe Val Ala Val Ala Ala Ala Val Ala
        120                 125                 130

ttt ttg gtg gtc ttt tct gca tat tcg gtg ctc act ggt gag cga gtt   547
Phe Leu Val Val Phe Ser Ala Tyr Ser Val Leu Thr Gly Glu Arg Val
    135                 140                 145

cgc gag ttc ggg ctg att cgt tca gtg ggc gca tcg acg ccg cag att   595
Arg Glu Phe Gly Leu Ile Arg Ser Val Gly Ala Ser Thr Pro Gln Ile
150                 155                 160                 165

ttg ggg tca gtg att ttt gaa gcc ggc atc ctc ggt gtg gtg gct gct   643
Leu Gly Ser Val Ile Phe Glu Ala Gly Ile Leu Gly Val Val Ala Ala
                170                 175                 180

ggt ttt ggt gcg ccc gcc gga ttg atg gcg gcg cgt ttg ttg gcg gat   691
Gly Phe Gly Ala Pro Ala Gly Leu Met Ala Ala Arg Leu Leu Ala Asp
            185                 190                 195

aat gcc gca cgt ttt ggc att cgt gtg ccc att gat gtg att gat ctg   739
Asn Ala Ala Arg Phe Gly Ile Arg Val Pro Ile Asp Val Ile Asp Leu
        200                 205                 210

cca agt agc acg atg tgg ctc atc gct ggc gtc ggc gtg gtg atg tcc   787
Pro Ser Ser Thr Met Trp Leu Ile Ala Gly Val Gly Val Val Met Ser
    215                 220                 225

gtg att gcg gca tta ccg gca gtg ttc agt gtg tgc aga aaa tcc gca   835
Val Ile Ala Ala Leu Pro Ala Val Phe Ser Val Cys Arg Lys Ser Ala
230                 235                 240                 245

gtg gaa tca ctg agt acg cct gct att tcg agg act tcc ccc tgg ttc   883
Val Glu Ser Leu Ser Thr Pro Ala Ile Ser Arg Thr Ser Pro Trp Phe
                250                 255                 260

ggt gca tta tgg ttg ctg ctc gcg ggc att gtg ggc gcc ggc gga atg   931
Gly Ala Leu Trp Leu Leu Leu Ala Gly Ile Val Gly Ala Gly Gly Met
            265                 270                 275

tgg gcg tat gag gca acc tcg gac tac cgc ggc atg cgt tca gtg gct   979
Trp Ala Tyr Glu Ala Thr Ser Asp Tyr Arg Gly Met Arg Ser Val Ala
        280                 285                 290

tta tcc atc gcc ggt tca ggc gct ttg gtg tgt gcg ttg ttg att gcc   1027
Leu Ser Ile Ala Gly Ser Gly Ala Leu Val Cys Ala Leu Leu Ile Ala
    295                 300                 305

acg gcg gtg ctc gtg ccc tgg tta ttg cac gta ttc tcc agg att gtg   1075
Thr Ala Val Leu Val Pro Trp Leu Leu His Val Phe Ser Arg Ile Val
310                 315                 320                 325
```

```
ggc ggc acc gtc cca aca ctt cag ttg gga ttg gcg ttt gca gca aag   1123
Gly Gly Thr Val Pro Thr Leu Gln Leu Gly Leu Ala Phe Ala Ala Lys
                330                 335                 340

cag aaa tct cgt tcg gcg gcg ctg atc gct gtg att ctt gct ggt tct   1171
Gln Lys Ser Arg Ser Ala Ala Leu Ile Ala Val Ile Leu Ala Gly Ser
            345                 350                 355

gca tta agc tcc gct gtt ctg cat ggc cag gca cat atc ggc acg cat   1219
Ala Leu Ser Ser Ala Val Leu His Gly Gln Ala His Ile Gly Thr His
        360                 365                 370

ttg gtg gcc gtg gct aaa ggc atg ggc ggc aca gac atg atg gtt aca   1267
Leu Val Ala Val Ala Lys Gly Met Gly Gly Thr Asp Met Met Val Thr
    375                 380                 385

gcg ctt gat ggg gaa atc ccc gcc gga atg ctg gag gaa atc tct agc   1315
Ala Leu Asp Gly Glu Ile Pro Ala Gly Met Leu Glu Glu Ile Ser Ser
390                 395                 400                 405

atc gac ggc gtg aaa act gcc atc gcg cca gcc acc acc gct gtg gaa   1363
Ile Asp Gly Val Lys Thr Ala Ile Ala Pro Ala Thr Thr Ala Val Glu
                410                 415                 420

ttg gaa gat tcc ggc aat ttc tct gtg ctc atg ctc gct gaa gaa gac   1411
Leu Glu Asp Ser Gly Asn Phe Ser Val Leu Met Leu Ala Glu Glu Asp
            425                 430                 435

gga gcc tcc gtg atg cgc gca ggc gat act ggt gca cca gct ggt ggc   1459
Gly Ala Ser Val Met Arg Ala Gly Asp Thr Gly Ala Pro Ala Gly Gly
        440                 445                 450

ctt gtt ttg ggc aga aac tct cct gac cag gat gct tac ccg gcc ggc   1507
Leu Val Leu Gly Arg Asn Ser Pro Asp Gln Asp Ala Tyr Pro Ala Gly
    455                 460                 465

cag gct gca aac atc att gtc gcg gat acc cca acg cag gcg gaa atc   1555
Gln Ala Ala Asn Ile Ile Val Ala Asp Thr Pro Thr Gln Ala Glu Ile
470                 475                 480                 485

ttc cac agc gac aac tac ttc tcc atg atc gac cca gca ctc gcc acc   1603
Phe His Ser Asp Asn Tyr Phe Ser Met Ile Asp Pro Ala Leu Ala Thr
                490                 495                 500

ggc ccc agc acc aca cgc aac gta ctg atc ctg ctc gac ggc gac tcc   1651
Gly Pro Ser Thr Thr Arg Asn Val Leu Ile Leu Leu Asp Gly Asp Ser
            505                 510                 515

aac cag gcc ccc gac aac gcc acg gcg cag gcg gta cgc aag acc att   1699
Asn Gln Ala Pro Asp Asn Ala Thr Ala Gln Ala Val Arg Lys Thr Ile
        520                 525                 530

tcg ctt ttc gac gga cga tac tcc atc acc gag ggt ttc tcc gcc cgc   1747
Ser Leu Phe Asp Gly Arg Tyr Ser Ile Thr Glu Gly Phe Ser Ala Arg
    535                 540                 545

caa aac act ttt gaa ctg gtt tcc cgc atc acc acc atg tcc aca ctg   1795
Gln Asn Thr Phe Glu Leu Val Ser Arg Ile Thr Thr Met Ser Thr Leu
550                 555                 560                 565
```

```
ctt gcc atc gtg gcc tta gcg atc gct gcc gtt ggc ctg atc aac aca   1843
Leu Ala Ile Val Ala Leu Ala Ile Ala Ala Val Gly Leu Ile Asn Thr
                570                 575                 580

gtg gca ctc acc att tct gag cgt gcc cgc gat cgt tat ttg ctg cgc   1891
Val Ala Leu Thr Ile Ser Glu Arg Ala Arg Asp Arg Tyr Leu Leu Arg
            585                 590                 595

acc att gga ctg acc tca act ggt cag att ctg gtg atg gct att gaa   1939
Thr Ile Gly Leu Thr Ser Thr Gly Gln Ile Leu Val Met Ala Ile Glu
        600                 605                 610

atg atc gcg ctc tca ttg ccg gct gcc att gtt ggt gca gtt tcg gga   1987
Met Ile Ala Leu Ser Leu Pro Ala Ala Ile Val Gly Ala Val Ser Gly
    615                 620                 625

gga ttc tta ggc aga ttc gtt gcc agt tct gcc acc aac acc gct gcg   2035
Gly Phe Leu Gly Arg Phe Val Ala Ser Ser Ala Thr Asn Thr Ala Ala
630                 635                 640                 645

acg gca cca ctt caa gta gac att ctc ggc gga acg gtt ctc gcg atg   2083
Thr Ala Pro Leu Gln Val Asp Ile Leu Gly Gly Thr Val Leu Ala Met
                650                 655                 660

gtc gca gga tct gta ctg tgc gcg ctc atc gtg ctg gcg aac aaa cga   2131
Val Ala Gly Ser Val Leu Cys Ala Leu Ile Val Leu Ala Asn Lys Arg
            665                 670                 675

cgt cgg gtg gtt tgattataaa atccaaaaat cga                        2166
Arg Arg Val Val
        680


<210> 248
<211> 681
<212> PRT
<213> Corynebacterium glutamicum

<400> 248
Leu Pro Gln Gly Pro Gly Glu Ile Ala Val Thr Thr Ala Pro Gly Ala
  1               5                  10                  15

Pro Glu Val Gly Glu His Val Ser Ile Arg Leu Ser Gln Asn Thr Glu
             20                  25                  30

Asp Thr Glu Val Leu Val Val Gly Val Val Glu Pro Ala Ala Gln Glu
         35                  40                  45

Thr Leu Gly Gly Ala Pro Phe Val Val Ala Ser Pro Asp Ala Leu Met
     50                  55                  60

Glu Trp Asn Ser Ser Gly Val Arg Gly Glu Phe Arg Val Ala Thr Ser
 65                  70                  75                  80

Asp Pro Ala Ser Leu Glu Ala Ala Ser Phe Ser Asp Ala Thr Val Val
                 85                  90                  95

Val Ala Ser Ala Glu Gly His Val Asp Lys Leu Ala Asp Ser Tyr Leu
            100                 105                 110

Gly Gln Arg Asp Arg Tyr Phe Leu Leu Leu Ala Ala Phe Val Ala Val
```

```
        115                 120                 125

Ala Ala Ala Val Ala Phe Leu Val Val Phe Ser Ala Tyr Ser Val Leu
    130                 135                 140

Thr Gly Glu Arg Val Arg Glu Phe Gly Leu Ile Arg Ser Val Gly Ala
145                 150                 155                 160

Ser Thr Pro Gln Ile Leu Gly Ser Val Ile Phe Glu Ala Gly Ile Leu
                165                 170                 175

Gly Val Val Ala Ala Gly Phe Gly Ala Pro Ala Gly Leu Met Ala Ala
            180                 185                 190

Arg Leu Leu Ala Asp Asn Ala Ala Arg Phe Gly Ile Arg Val Pro Ile
        195                 200                 205

Asp Val Ile Asp Leu Pro Ser Ser Thr Met Trp Leu Ile Ala Gly Val
    210                 215                 220

Gly Val Val Met Ser Val Ile Ala Ala Leu Pro Ala Val Phe Ser Val
225                 230                 235                 240

Cys Arg Lys Ser Ala Val Glu Ser Leu Ser Thr Pro Ala Ile Ser Arg
                245                 250                 255

Thr Ser Pro Trp Phe Gly Ala Leu Trp Leu Leu Leu Ala Gly Ile Val
            260                 265                 270

Gly Ala Gly Gly Met Trp Ala Tyr Glu Ala Thr Ser Asp Tyr Arg Gly
        275                 280                 285

Met Arg Ser Val Ala Leu Ser Ile Ala Gly Ser Gly Ala Leu Val Cys
    290                 295                 300

Ala Leu Leu Ile Ala Thr Ala Val Leu Val Pro Trp Leu Leu His Val
305                 310                 315                 320

Phe Ser Arg Ile Val Gly Gly Thr Val Pro Thr Leu Gln Leu Gly Leu
                325                 330                 335

Ala Phe Ala Ala Lys Gln Lys Ser Arg Ser Ala Ala Leu Ile Ala Val
            340                 345                 350

Ile Leu Ala Gly Ser Ala Leu Ser Ser Ala Val Leu His Gly Gln Ala
        355                 360                 365

His Ile Gly Thr His Leu Val Ala Val Ala Lys Gly Met Gly Gly Thr
    370                 375                 380

Asp Met Met Val Thr Ala Leu Asp Gly Glu Ile Pro Ala Gly Met Leu
385                 390                 395                 400

Glu Glu Ile Ser Ser Ile Asp Gly Val Lys Thr Ala Ile Ala Pro Ala
                405                 410                 415

Thr Thr Ala Val Glu Leu Glu Asp Ser Gly Asn Phe Ser Val Leu Met
            420                 425                 430

Leu Ala Glu Glu Asp Gly Ala Ser Val Met Arg Ala Gly Asp Thr Gly
        435                 440                 445
```

```
Ala Pro Ala Gly Gly Leu Val Leu Gly Arg Asn Ser Pro Asp Gln Asp
    450                 455                 460

Ala Tyr Pro Ala Gly Gln Ala Ala Asn Ile Ile Val Ala Asp Thr Pro
465                 470                 475                 480

Thr Gln Ala Glu Ile Phe His Ser Asp Asn Tyr Phe Ser Met Ile Asp
                485                 490                 495

Pro Ala Leu Ala Thr Gly Pro Ser Thr Thr Arg Asn Val Leu Ile Leu
            500                 505                 510

Leu Asp Gly Asp Ser Asn Gln Ala Pro Asp Asn Ala Thr Ala Gln Ala
        515                 520                 525

Val Arg Lys Thr Ile Ser Leu Phe Asp Gly Arg Tyr Ser Ile Thr Glu
    530                 535                 540

Gly Phe Ser Ala Arg Gln Asn Thr Phe Glu Leu Val Ser Arg Ile Thr
545                 550                 555                 560

Thr Met Ser Thr Leu Leu Ala Ile Val Ala Leu Ala Ile Ala Ala Val
                565                 570                 575

Gly Leu Ile Asn Thr Val Ala Leu Thr Ile Ser Glu Arg Ala Arg Asp
            580                 585                 590

Arg Tyr Leu Leu Arg Thr Ile Gly Leu Thr Ser Thr Gly Gln Ile Leu
        595                 600                 605

Val Met Ala Ile Glu Met Ile Ala Leu Ser Leu Pro Ala Ala Ile Val
    610                 615                 620

Gly Ala Val Ser Gly Gly Phe Leu Gly Arg Phe Val Ala Ser Ser Ala
625                 630                 635                 640

Thr Asn Thr Ala Ala Thr Ala Pro Leu Gln Val Asp Ile Leu Gly Gly
                645                 650                 655

Thr Val Leu Ala Met Val Ala Gly Ser Val Leu Cys Ala Leu Ile Val
            660                 665                 670

Leu Ala Asn Lys Arg Arg Arg Val Val
        675                 680
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<210> 249
<211> 1149
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1126)
<223> RXN00496

<400> 249
ctgcagagat ggtgggcagc accccaggtg ctgtacgagt tgcccaacac agggcactca 60

cgacacttcg aagcacactt gagcagcagg agaacaagta atg act cga cgt cta 115

```
                                                    Met Thr Arg Arg Leu
                                                      1               5

cat ggt ggt gag cag gat ggc cag gaa cac gtt aaa gga cag cta aag   163
His Gly Gly Glu Gln Asp Gly Gln Glu His Val Lys Gly Gln Leu Lys
                  10                  15                  20

cag ctg ttc gac gac gac gcg ttc ttg act gac ctg tcc cgc ggc gtt   211
Gln Leu Phe Asp Asp Asp Ala Phe Leu Thr Asp Leu Ser Arg Gly Val
              25                  30                  35

gat ccc tca gag ggc gat gac gcc ctc gct ggc ctc ctc ctc gat tta   259
Asp Pro Ser Glu Gly Asp Asp Ala Leu Ala Gly Leu Leu Leu Asp Leu
          40                  45                  50

aca aag gaa gct cag gag ccg ccg gca aca atg ccg gat tgg tct act   307
Thr Lys Glu Ala Gln Glu Pro Pro Ala Thr Met Pro Asp Trp Ser Thr
      55                  60                  65

ttg ctc cct gga att ttg gat cag gat cag gat ttg cca gtg gaa tcc   355
Leu Leu Pro Gly Ile Leu Asp Gln Asp Gln Asp Leu Pro Val Glu Ser
  70                  75                  80                  85

act tcg gac acc acg gtt atg cag gca tca aac cct gca acc caa gaa   403
Thr Ser Asp Thr Thr Val Met Gln Ala Ser Asn Pro Ala Thr Gln Glu
                  90                  95                 100

ttc gca cct gtt tct att tct gat acc ccc aac act gca act aat tca   451
Phe Ala Pro Val Ser Ile Ser Asp Thr Pro Asn Thr Ala Thr Asn Ser
              105                 110                 115

gct gat gca gat gag tcc gca act gtt gtt cca ctt gca gca cgc cgt   499
Ala Asp Ala Asp Glu Ser Ala Thr Val Val Pro Leu Ala Ala Arg Arg
          120                 125                 130

gag aag cgt gcc aag agc gga tca agc ggg gtt cat tca ctg gat gct   547
Glu Lys Arg Ala Lys Ser Gly Ser Ser Gly Val His Ser Leu Asp Ala
      135                 140                 145

tcg gca acc cag cgc aaa tct cac cca ttc ctt agc ggt ttg gtg ggt   595
Ser Ala Thr Gln Arg Lys Ser His Pro Phe Leu Ser Gly Leu Val Gly
150                 155                 160                 165

gct gca gct gca act cta gtc atc gca ggc ggt gga gca gca gtg tac   643
Ala Ala Ala Ala Thr Leu Val Ile Ala Gly Gly Gly Ala Ala Val Tyr
                  170                 175                 180

aac gct gat gaa aac tcc ccg ttg tat ggc atg aat cag cag ctg ttt   691
Asn Ala Asp Glu Asn Ser Pro Leu Tyr Gly Met Asn Gln Gln Leu Phe
              185                 190                 195

ggc aat caa gat tct cca agc gtg gtg gag ctt gcc tcc acg ctg gaa   739
Gly Asn Gln Asp Ser Pro Ser Val Val Glu Leu Ala Ser Thr Leu Glu
          200                 205                 210

gaa gtt gat agt cgt aca gct agt ggc gat gtg gaa ggg gca cgt gct   787
Glu Val Asp Ser Arg Thr Ala Ser Gly Asp Val Glu Gly Ala Arg Ala
      215                 220                 225

cta ctc gag cag gct cga gca atg ctg gat ggc atg gca cct cct cga   835
Leu Leu Glu Gln Ala Arg Ala Met Leu Asp Gly Met Ala Pro Pro Arg
```

```
230                 235                 240                 245

aag gcg ccg tcg gag gca acc cga acg gtt gaa tct gaa cca ggt act   883
Lys Ala Pro Ser Glu Ala Thr Arg Thr Val Glu Ser Glu Pro Gly Thr
                250                 255                 260

cag acg ttg act gca acg gtt act gaa tcc gca agt ccg gaa cca ccg   931
Gln Thr Leu Thr Ala Thr Val Thr Glu Ser Ala Ser Pro Glu Pro Pro
            265                 270                 275

gtc acg gaa act caa act gtt acc tcc acc gag gta cag aca gtg aca   979
Val Thr Glu Thr Gln Thr Val Thr Ser Thr Glu Val Gln Thr Val Thr
        280                 285                 290

acc act gcg gtt gct cca ccg gtc tgg act cct aat cca gag cca aca  1027
Thr Thr Ala Val Ala Pro Pro Val Trp Thr Pro Asn Pro Glu Pro Thr
    295                 300                 305

acc aca gct gcc ccg act tct acg cct tca act ggt ggc ggt gag gga  1075
Thr Thr Ala Ala Pro Thr Ser Thr Pro Ser Thr Gly Gly Gly Glu Gly
310                 315                 320                 325

acc ggc aat gat ggt gac tct gga ctt gtg cca cct cag act cct gga  1123
Thr Gly Asn Asp Gly Asp Ser Gly Leu Val Pro Pro Gln Thr Pro Gly
                330                 335                 340

aac taggtaaaaa tataaaaact gct                                   1149
Asn
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<210> 250
<211> 342
<212> PRT
<213> Corynebacterium glutamicum

<400> 250

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Met Thr Arg Arg Leu His Gly Gly Glu Gln Asp Gly Gln Glu His Val
  1               5                  10                  15

Lys Gly Gln Leu Lys Gln Leu Phe Asp Asp Asp Ala Phe Leu Thr Asp
            20                  25                  30

Leu Ser Arg Gly Val Asp Pro Ser Glu Gly Asp Asp Ala Leu Ala Gly
        35                  40                  45

Leu Leu Leu Asp Leu Thr Lys Glu Ala Gln Glu Pro Pro Ala Thr Met
    50                  55                  60

Pro Asp Trp Ser Thr Leu Leu Pro Gly Ile Leu Asp Gln Asp Gln Asp
65                  70                  75                  80

Leu Pro Val Glu Ser Thr Ser Asp Thr Thr Val Met Gln Ala Ser Asn
                85                  90                  95

Pro Ala Thr Gln Glu Phe Ala Pro Val Ser Ile Ser Asp Thr Pro Asn
            100                 105                 110

Thr Ala Thr Asn Ser Ala Asp Ala Asp Glu Ser Ala Thr Val Val Pro
        115                 120                 125
```

```
Leu Ala Ala Arg Arg Glu Lys Arg Ala Lys Ser Gly Ser Ser Gly Val
    130                 135                 140

His Ser Leu Asp Ala Ser Ala Thr Gln Arg Lys Ser His Pro Phe Leu
145                 150                 155                 160

Ser Gly Leu Val Gly Ala Ala Ala Ala Thr Leu Val Ile Ala Gly Gly
                165                 170                 175

Gly Ala Ala Val Tyr Asn Ala Asp Glu Asn Ser Pro Leu Tyr Gly Met
            180                 185                 190

Asn Gln Gln Leu Phe Gly Asn Gln Asp Ser Pro Ser Val Val Glu Leu
        195                 200                 205

Ala Ser Thr Leu Glu Glu Val Asp Ser Arg Thr Ala Ser Gly Asp Val
    210                 215                 220

Glu Gly Ala Arg Ala Leu Leu Glu Gln Ala Arg Ala Met Leu Asp Gly
225                 230                 235                 240

Met Ala Pro Pro Arg Lys Ala Pro Ser Glu Ala Thr Arg Thr Val Glu
                245                 250                 255

Ser Glu Pro Gly Thr Gln Thr Leu Thr Ala Thr Val Thr Glu Ser Ala
            260                 265                 270

Ser Pro Glu Pro Pro Val Thr Glu Thr Gln Thr Val Thr Ser Thr Glu
        275                 280                 285

Val Gln Thr Val Thr Thr Thr Ala Val Ala Pro Pro Val Trp Thr Pro
    290                 295                 300

Asn Pro Glu Pro Thr Thr Thr Ala Ala Pro Thr Ser Thr Pro Ser Thr
305                 310                 315                 320

Gly Gly Gly Glu Gly Thr Gly Asn Asp Gly Asp Ser Gly Leu Val Pro
                325                 330                 335

Pro Gln Thr Pro Gly Asn
            340
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<210> 251
<211> 502
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(502)
<223> FRXA00496

<400> 251
ctgcagagat ggtgggcagc accccaggtg ctgtacgagt tgcccaacac agggcactca 60

cgacacttcg aagcacactt gagcagcagg agaacaagta atg act cga cgt cta 115
Met Thr Arg Arg Leu
1 5

cat ggt ggt gag cag gat ggc cag gaa cac gtt aaa gga cag cta aag 163

```
His Gly Gly Glu Gln Asp Gly Gln Glu His Val Lys Gly Gln Leu Lys
                10                  15                  20

cag ctg ttc gac gac gac gcg ttc ttg act gac ctg tcc cgc ggc gtt   211
Gln Leu Phe Asp Asp Asp Ala Phe Leu Thr Asp Leu Ser Arg Gly Val
            25                  30                  35

gat ccc tca gag ggc gat gac gcc ctc gct ggc ctc ctc ctc gat tta   259
Asp Pro Ser Glu Gly Asp Asp Ala Leu Ala Gly Leu Leu Leu Asp Leu
        40                  45                  50

aca aag gaa gct cag gag ccg ccg gca aca atg ccg gat tgg tct act   307
Thr Lys Glu Ala Gln Glu Pro Pro Ala Thr Met Pro Asp Trp Ser Thr
    55                  60                  65

ttg ctc cct gga att ttg gat cag gat cag gat ttg cca gtg gaa tcc   355
Leu Leu Pro Gly Ile Leu Asp Gln Asp Gln Asp Leu Pro Val Glu Ser
70                  75                  80                  85

act tcg gac acc acg gtt atg cag gca tca aac cct gca acc caa gaa   403
Thr Ser Asp Thr Thr Val Met Gln Ala Ser Asn Pro Ala Thr Gln Glu
                90                  95                  100

ttc gca cct gtt tct att tct gat acc ccc aac act gca act aat tca   451
Phe Ala Pro Val Ser Ile Ser Asp Thr Pro Asn Thr Ala Thr Asn Ser
            105                 110                 115

gct gat gca gat gag tcc gca act gtt gtt cca ctt gca gca cgc cgt   499
Ala Asp Ala Asp Glu Ser Ala Thr Val Val Pro Leu Ala Ala Arg Arg
        120                 125                 130

gag                                                               502
Glu
```

<210> 252
<211> 134
<212> PRT
<213> Corynebacterium glutamicum

<400> 252

```
Met Thr Arg Arg Leu His Gly Gly Glu Gln Asp Gly Gln Glu His Val
  1               5                  10                  15

Lys Gly Gln Leu Lys Gln Leu Phe Asp Asp Asp Ala Phe Leu Thr Asp
            20                  25                  30

Leu Ser Arg Gly Val Asp Pro Ser Glu Gly Asp Asp Ala Leu Ala Gly
        35                  40                  45

Leu Leu Leu Asp Leu Thr Lys Glu Ala Gln Glu Pro Pro Ala Thr Met
    50                  55                  60

Pro Asp Trp Ser Thr Leu Leu Pro Gly Ile Leu Asp Gln Asp Gln Asp
65                  70                  75                  80

Leu Pro Val Glu Ser Thr Ser Asp Thr Thr Val Met Gln Ala Ser Asn
                85                  90                  95

Pro Ala Thr Gln Glu Phe Ala Pro Val Ser Ile Ser Asp Thr Pro Asn
```

```
            100                 105                 110

Thr Ala Thr Asn Ser Ala Asp Ala Asp Glu Ser Ala Thr Val Val Pro
        115                 120                 125

Leu Ala Ala Arg Arg Glu
    130


<210> 253
<211> 1845
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1822)
<223> RXN00503

<400> 253
aatccacgaa ggtgcccaag aatcaccaat ttcggtcgga actgatcctt ctttgtccgt 60

tgagacccca caggtgtttt aaacatttag tattagttcc atg aaa cca gtc ttc   115
                                            Met Lys Pro Val Phe
                                              1               5

tcc gtt gac caa atc cga cgc gca gaa aac acc ctt ttt gag ctt cag   163
Ser Val Asp Gln Ile Arg Arg Ala Glu Asn Thr Leu Phe Glu Leu Gln
                  10                  15                  20

gca gat ccg gat gag ctg atg atc tcc gcg gca tcg gcg gtg gcc gat   211
Ala Asp Pro Asp Glu Leu Met Ile Ser Ala Ala Ser Ala Val Ala Asp
              25                  30                  35

gtc gcg ttg gca atg gtg gac ggc ccc gct cca gcg gtc tcc agt gag   259
Val Ala Leu Ala Met Val Asp Gly Pro Ala Pro Ala Val Ser Ser Glu
          40                  45                  50

gag tca atc ctg ctg ctg gtc ggc ccc ggt ggc aac ggt ggc gac gcc   307
Glu Ser Ile Leu Leu Leu Val Gly Pro Gly Gly Asn Gly Gly Asp Ala
      55                  60                  65

ttg tat gca ggc gcg ttc ctt gca gaa gaa ggc cac cac gtt gat gct   355
Leu Tyr Ala Gly Ala Phe Leu Ala Glu Glu Gly His His Val Asp Ala
  70                  75                  80                  85

ttg ctg ttg gga aac ggc aaa gtc cat caa tca gca ttg gca tat tat   403
Leu Leu Leu Gly Asn Gly Lys Val His Gln Ser Ala Leu Ala Tyr Tyr
                  90                  95                 100

gag tct ttg ggc ggg cag atc att tcc gat ttt ccc cct cac tac ctc   451
Glu Ser Leu Gly Gly Gln Ile Ile Ser Asp Phe Pro Pro His Tyr Leu
              105                 110                 115

tac cgc ctg gtg att gat ggt ttg ttt ggc atc ggt ggt cgg gga ggg   499
Tyr Arg Leu Val Ile Asp Gly Leu Phe Gly Ile Gly Gly Arg Gly Gly
          120                 125                 130

ctc acc cca gag ctg gcc agt ttg gtg gag tct ttt tcc gct tca ggt   547
Leu Thr Pro Glu Leu Ala Ser Leu Val Glu Ser Phe Ser Ala Ser Gly
      135                 140                 145
```

```
atc ccc att ttg gcg att gat gtg ccg tct ggc gtg cat gcc gat agt   595
Ile Pro Ile Leu Ala Ile Asp Val Pro Ser Gly Val His Ala Asp Ser
150                 155                 160                 165

ggt gaa ctg ccg ccc ggc gtg atg gtg acg gtg gaa gga ttt gat aat   643
Gly Glu Leu Pro Pro Gly Val Met Val Thr Val Glu Gly Phe Asp Asn
                170                 175                 180

gat gca ccg atg gcg cgt cag aaa att ccg gca cac att gac gct gat   691
Asp Ala Pro Met Ala Arg Gln Lys Ile Pro Ala His Ile Asp Ala Asp
            185                 190                 195

gtc acg atc acg ttt ggc ggt ttg aga cgc gcc cac gcg gtc agt cct   739
Val Thr Ile Thr Phe Gly Gly Leu Arg Arg Ala His Ala Val Ser Pro
        200                 205                 210

gcg tgt ggt gaa gtg ctc tgt gct gat atc aac atc gct ggt ggc ggc   787
Ala Cys Gly Glu Val Leu Cys Ala Asp Ile Asn Ile Ala Gly Gly Gly
    215                 220                 225

gga aaa tcg ctg tcc gct gag ttg agt cag gtg cag gca gaa gac gcg   835
Gly Lys Ser Leu Ser Ala Glu Leu Ser Gln Val Gln Ala Glu Asp Ala
230                 235                 240                 245

acc ccg cag atg ttt gcc tcc aag gcg tat caa cgg aaa gat tcg ctt   883
Thr Pro Gln Met Phe Ala Ser Lys Ala Tyr Gln Arg Lys Asp Ser Leu
                250                 255                 260

ttt gag cgc gcg aat ctc aaa gct acg gcg cca cat atc cat agg atc   931
Phe Glu Arg Ala Asn Leu Lys Ala Thr Ala Pro His Ile His Arg Ile
            265                 270                 275

ggc cag cac ttt acc gtg ttg aac atg gag cct ggc ccg gat cat gat   979
Gly Gln His Phe Thr Val Leu Asn Met Glu Pro Gly Pro Asp His Asp
        280                 285                 290

aaa tac agt ggc gga att gtc ggc att gtt gca ggt agt ggc acc tat  1027
Lys Tyr Ser Gly Gly Ile Val Gly Ile Val Ala Gly Ser Gly Thr Tyr
    295                 300                 305

cca ggt gct gct gtg ctg tcg gtg aag gcg gct gtc agg gcc aca agc  1075
Pro Gly Ala Ala Val Leu Ser Val Lys Ala Ala Val Arg Ala Thr Ser
310                 315                 320                 325

gcc atg gtt cga tac gtt ggc cct gcg tta aat ttt gtc atc cag tcg  1123
Ala Met Val Arg Tyr Val Gly Pro Ala Leu Asn Phe Val Ile Gln Ser
                330                 335                 340

ctg ccg gag gtc gtc gca acg caa tca ctt gcc acc gcc ggc cgc gtg  1171
Leu Pro Glu Val Val Ala Thr Gln Ser Leu Ala Thr Ala Gly Arg Val
            345                 350                 355

caa gcg tgg gtg cac ggc ccc gga cgc ggg ctg gag gct gag caa tca  1219
Gln Ala Trp Val His Gly Pro Gly Arg Gly Leu Glu Ala Glu Gln Ser
        360                 365                 370

gcc gag ctt gcg gag ctt ttg agc cgg cct gag cct gtg ctt atc gac  1267
Ala Glu Leu Ala Glu Leu Leu Ser Arg Pro Glu Pro Val Leu Ile Asp
    375                 380                 385
```

```
gcc gac agc ctc tca tta ctc cag ctc tca gcg gag ctt cgg cag gcg   1315
Ala Asp Ser Leu Ser Leu Leu Gln Leu Ser Ala Glu Leu Arg Gln Ala
390                 395                 400                 405

ttg cgc gag cga aaa gca cca acg gtg ctc act ccg cac aag ggc gaa   1363
Leu Arg Glu Arg Lys Ala Pro Thr Val Leu Thr Pro His Lys Gly Glu
                410                 415                 420

ttt gaa cgc atc gca gca gaa tta cgc tct gaa ggc gtc gag att ccc   1411
Phe Glu Arg Ile Ala Ala Glu Leu Arg Ser Glu Gly Val Glu Ile Pro
            425                 430                 435

caa gcg gac aaa gat ccc att ggt gct gcg caa gcg tta gct aaa gaa   1459
Gln Ala Asp Lys Asp Pro Ile Gly Ala Ala Gln Ala Leu Ala Lys Glu
        440                 445                 450

ttt gat tgt tgc gta ctg ctc aag ggg aaa tac acc gtc att gca gct   1507
Phe Asp Cys Cys Val Leu Leu Lys Gly Lys Tyr Thr Val Ile Ala Ala
    455                 460                 465

cac gac ttt gtg cat gcg atc aac gct ggg cat tcc tgg ttg gct aca   1555
His Asp Phe Val His Ala Ile Asn Ala Gly His Ser Trp Leu Ala Thr
470                 475                 480                 485

cct ggc tct ggc gat gtg ttg tca ggt ctt gtc ggt gca cac ttg gct   1603
Pro Gly Ser Gly Asp Val Leu Ser Gly Leu Val Gly Ala His Leu Ala
                490                 495                 500

caa agc tac gca gaa tta aac cgc ttg ccg gag ttt ttc ccc gat gtg   1651
Gln Ser Tyr Ala Glu Leu Asn Arg Leu Pro Glu Phe Phe Pro Asp Val
            505                 510                 515

acc ttg tct gat tcg gcg att tac acc cag att gca cct gct gcg acc   1699
Thr Leu Ser Asp Ser Ala Ile Tyr Thr Gln Ile Ala Pro Ala Ala Thr
        520                 525                 530

atc cac gcg gtt gct gct ggg ttg gcc gca cga acc gaa ttt ggg ttt   1747
Ile His Ala Val Ala Ala Gly Leu Ala Ala Arg Thr Glu Phe Gly Phe
    535                 540                 545

gcg ccg acc tcc gca agt ttg atc gct gat gcc atc cct gca gcg acc   1795
Ala Pro Thr Ser Ala Ser Leu Ile Ala Asp Ala Ile Pro Ala Ala Thr
550                 555                 560                 565

gcc aag gtg gat ttg aag cga att gtc tagctctgca tgaattccgt         1842
Ala Lys Val Asp Leu Lys Arg Ile Val
                570

atg                                                              1845
```

<210> 254
<211> 574
<212> PRT
<213> Corynebacterium glutamicum

<400> 254

```
Met Lys Pro Val Phe Ser Val Asp Gln Ile Arg Arg Ala Glu Asn Thr
  1               5                  10                  15

Leu Phe Glu Leu Gln Ala Asp Pro Asp Glu Leu Met Ile Ser Ala Ala
```

```
         20                  25                  30
Ser Ala Val Ala Asp Val Ala Leu Ala Met Val Asp Gly Pro Ala Pro
        35                  40                  45
Ala Val Ser Ser Glu Glu Ser Ile Leu Leu Leu Val Gly Pro Gly Gly
    50                  55                  60
Asn Gly Gly Asp Ala Leu Tyr Ala Gly Ala Phe Leu Ala Glu Glu Gly
65                  70                  75                  80
His His Val Asp Ala Leu Leu Leu Gly Asn Gly Lys Val His Gln Ser
                85                  90                  95
Ala Leu Ala Tyr Tyr Glu Ser Leu Gly Gly Gln Ile Ile Ser Asp Phe
            100                 105                 110
Pro Pro His Tyr Leu Tyr Arg Leu Val Ile Asp Gly Leu Phe Gly Ile
        115                 120                 125
Gly Gly Arg Gly Gly Leu Thr Pro Glu Leu Ala Ser Leu Val Glu Ser
    130                 135                 140
Phe Ser Ala Ser Gly Ile Pro Ile Leu Ala Ile Asp Val Pro Ser Gly
145                 150                 155                 160
Val His Ala Asp Ser Gly Glu Leu Pro Pro Gly Val Met Val Thr Val
                165                 170                 175
Glu Gly Phe Asp Asn Asp Ala Pro Met Ala Arg Gln Lys Ile Pro Ala
            180                 185                 190
His Ile Asp Ala Asp Val Thr Ile Thr Phe Gly Gly Leu Arg Arg Ala
        195                 200                 205
His Ala Val Ser Pro Ala Cys Gly Glu Val Leu Cys Ala Asp Ile Asn
    210                 215                 220
Ile Ala Gly Gly Gly Gly Lys Ser Leu Ser Ala Glu Leu Ser Gln Val
225                 230                 235                 240
Gln Ala Glu Asp Ala Thr Pro Gln Met Phe Ala Ser Lys Ala Tyr Gln
                245                 250                 255
Arg Lys Asp Ser Leu Phe Glu Arg Ala Asn Leu Lys Ala Thr Ala Pro
            260                 265                 270
His Ile His Arg Ile Gly Gln His Phe Thr Val Leu Asn Met Glu Pro
        275                 280                 285
Gly Pro Asp His Asp Lys Tyr Ser Gly Gly Ile Val Gly Ile Val Ala
    290                 295                 300
Gly Ser Gly Thr Tyr Pro Gly Ala Ala Val Leu Ser Val Lys Ala Ala
305                 310                 315                 320
Val Arg Ala Thr Ser Ala Met Val Arg Tyr Val Gly Pro Ala Leu Asn
                325                 330                 335
Phe Val Ile Gln Ser Leu Pro Glu Val Val Ala Thr Gln Ser Leu Ala
            340                 345                 350
```

```
Thr Ala Gly Arg Val Gln Ala Trp Val His Gly Pro Gly Arg Gly Leu
        355                 360                 365

Glu Ala Glu Gln Ser Ala Glu Leu Ala Glu Leu Leu Ser Arg Pro Glu
    370                 375                 380

Pro Val Leu Ile Asp Ala Asp Ser Leu Ser Leu Leu Gln Leu Ser Ala
385                 390                 395                 400

Glu Leu Arg Gln Ala Leu Arg Glu Arg Lys Ala Pro Thr Val Leu Thr
                405                 410                 415

Pro His Lys Gly Glu Phe Glu Arg Ile Ala Ala Glu Leu Arg Ser Glu
            420                 425                 430

Gly Val Glu Ile Pro Gln Ala Asp Lys Asp Pro Ile Gly Ala Ala Gln
        435                 440                 445

Ala Leu Ala Lys Glu Phe Asp Cys Cys Val Leu Leu Lys Gly Lys Tyr
    450                 455                 460

Thr Val Ile Ala Ala His Asp Phe Val His Ala Ile Asn Ala Gly His
465                 470                 475                 480

Ser Trp Leu Ala Thr Pro Gly Ser Gly Asp Val Leu Ser Gly Leu Val
                485                 490                 495

Gly Ala His Leu Ala Gln Ser Tyr Ala Glu Leu Asn Arg Leu Pro Glu
            500                 505                 510

Phe Phe Pro Asp Val Thr Leu Ser Asp Ser Ala Ile Tyr Thr Gln Ile
        515                 520                 525

Ala Pro Ala Ala Thr Ile His Ala Val Ala Ala Gly Leu Ala Ala Arg
    530                 535                 540

Thr Glu Phe Gly Phe Ala Pro Thr Ser Ala Ser Leu Ile Ala Asp Ala
545                 550                 555                 560

Ile Pro Ala Ala Thr Ala Lys Val Asp Leu Lys Arg Ile Val
                565                 570
```

<210> 255
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> RXN00504

<400> 255
aaggtggatt tgaagcgaat tgtctagctc tgcatgaatt ccgtatgaat tcttttcttt 60

caagtggccg agatgtgaag cgcacggtta attgagaggc atg acc tac gga ttt 115
                                                Met Thr Tyr Gly Phe
                                                  1   5

```
ctt gtc aac aca gat ctc acc cac cgc gcg att gac ttt gat tta gaa   163
Leu Val Asn Thr Asp Leu Thr His Arg Ala Ile Asp Phe Asp Leu Glu
                 10                  15                  20

aac gct gcg aag ttc ctc ggc ggt gcc gat gat ggc cgc gtc gct gtc   211
Asn Ala Ala Lys Phe Leu Gly Gly Ala Asp Asp Gly Arg Val Ala Val
            25                  30                  35

gct ttc caa gag gat ggc acc ttg tac gcc gct ctc tac agc gcc agc   259
Ala Phe Gln Glu Asp Gly Thr Leu Tyr Ala Ala Leu Tyr Ser Ala Ser
        40                  45                  50

gca aaa gat gag ggt gcc gca gca aac cca gta gca tcc ctt ggc cgc   307
Ala Lys Asp Glu Gly Ala Ala Ala Asn Pro Val Ala Ser Leu Gly Arg
    55                  60                  65

aac gcc gct gct acc ggt gat ggc tcc ttc ttc tct gat ccg acc act   355
Asn Ala Ala Ala Thr Gly Asp Gly Ser Phe Phe Ser Asp Pro Thr Thr
70                  75                  80                  85

gca atc tgt ggc cct gtg atc ttc gtg ggg gcc gaa ggc gaa gac atc   403
Ala Ile Cys Gly Pro Val Ile Phe Val Gly Ala Glu Gly Glu Asp Ile
                90                  95                  100

acg ttg gat gaa att gag cga att aag gac ggc att cgc gcc gct cgt   451
Thr Leu Asp Glu Ile Glu Arg Ile Lys Asp Gly Ile Arg Ala Ala Arg
            105                 110                 115

aac tac cgc gat gat tat cca gag gaa ttc aac ctg tgg cgc aac gct   499
Asn Tyr Arg Asp Asp Tyr Pro Glu Glu Phe Asn Leu Trp Arg Asn Ala
        120                 125                 130

gta tat aac ctg cgt acg gct taaagtttgg ctgccatgtg aat             543
Val Tyr Asn Leu Arg Thr Ala
    135                 140
```

<210> 256
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 256

```
Met Thr Tyr Gly Phe Leu Val Asn Thr Asp Leu Thr His Arg Ala Ile
  1               5                  10                  15

Asp Phe Asp Leu Glu Asn Ala Ala Lys Phe Leu Gly Gly Ala Asp Asp
            20                  25                  30

Gly Arg Val Ala Val Ala Phe Gln Glu Asp Gly Thr Leu Tyr Ala Ala
        35                  40                  45

Leu Tyr Ser Ala Ser Ala Lys Asp Glu Gly Ala Ala Ala Asn Pro Val
    50                  55                  60

Ala Ser Leu Gly Arg Asn Ala Ala Ala Thr Gly Asp Gly Ser Phe Phe
65                  70                  75                  80

Ser Asp Pro Thr Thr Ala Ile Cys Gly Pro Val Ile Phe Val Gly Ala
                85                  90                  95
```

```
Glu Gly Glu Asp Ile Thr Leu Asp Glu Ile Glu Arg Ile Lys Asp Gly
            100                 105                 110

Ile Arg Ala Ala Arg Asn Tyr Arg Asp Asp Tyr Pro Glu Glu Phe Asn
        115                 120                 125

Leu Trp Arg Asn Ala Val Tyr Asn Leu Arg Thr Ala
    130                 135                 140


<210> 257
<211> 346
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(346)
<223> FRXA00504

<400> 257
aaggtggatt tgaagcgaat tgtctagctc tgcatgaatt ccgtatgaat tcttttcttt 60

caagtggccg agatgtgaag cgcacggtta attgagaggc atg acc tac gga ttt   115
                                               Met Thr Tyr Gly Phe
                                                 1               5

ctt gtc aac aca gat ctc acc cac cgc gcg att gac ttt gat tta gaa   163
Leu Val Asn Thr Asp Leu Thr His Arg Ala Ile Asp Phe Asp Leu Glu
                10                  15                  20

aac gct gcg aag ttc ctc ggc ggt gcc gat gat ggc cgc gtc gct gtc   211
Asn Ala Ala Lys Phe Leu Gly Gly Ala Asp Asp Gly Arg Val Ala Val
            25                  30                  35

gct ttc caa gag gat ggc acc ttg tac gcc gct ctc tac agc gcc agc   259
Ala Phe Gln Glu Asp Gly Thr Leu Tyr Ala Ala Leu Tyr Ser Ala Ser
        40                  45                  50

gca aaa gat gag ggt gcc gca gca aac cca gta gca tcc ctt ggc cgc   307
Ala Lys Asp Glu Gly Ala Ala Ala Asn Pro Val Ala Ser Leu Gly Arg
    55                  60                  65

aac gcc gct gct acc ggt gat ggc tcc ttc ttc tct gat               346
Asn Ala Ala Ala Thr Gly Asp Gly Ser Phe Phe Ser Asp
70                  75                  80


<210> 258
<211> 82
<212> PRT
<213> Corynebacterium glutamicum

<400> 258
Met Thr Tyr Gly Phe Leu Val Asn Thr Asp Leu Thr His Arg Ala Ile
  1               5                  10                  15

Asp Phe Asp Leu Glu Asn Ala Ala Lys Phe Leu Gly Gly Ala Asp Asp
            20                  25                  30

Gly Arg Val Ala Val Ala Phe Gln Glu Asp Gly Thr Leu Tyr Ala Ala
```

```
         35                  40                  45

Leu Tyr Ser Ala Ser Ala Lys Asp Glu Gly Ala Ala Ala Asn Pro Val
     50                  55                  60

Ala Ser Leu Gly Arg Asn Ala Ala Ala Thr Gly Asp Gly Ser Phe Phe
 65                  70                  75                  80

Ser Asp



<210> 259
<211> 618
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(595)
<223> RXN00505

<400> 259
ttgcggagcg tttagacacc attaactatg aggtagtgtg ccgaccaacc ggccgaactg 60

tccgcgcata tgtttaagtg aatacgttta aggagcagca atg aaa tct gag ttt   115
                                            Met Lys Ser Glu Phe
                                              1               5

ccg gta tcc ggc acg agg cgt ttt gag cat gcc gca gat acc caa aat   163
Pro Val Ser Gly Thr Arg Arg Phe Glu His Ala Ala Asp Thr Gln Asn
                 10                  15                  20

ttt ggg gaa gaa tta ggc agg cat cta gaa gct ggc gat gtg gtg att   211
Phe Gly Glu Glu Leu Gly Arg His Leu Glu Ala Gly Asp Val Val Ile
             25                  30                  35

ttg gac ggc ccg ctg ggt gct gga aaa acc aca ttt act caa ggt atc   259
Leu Asp Gly Pro Leu Gly Ala Gly Lys Thr Thr Phe Thr Gln Gly Ile
         40                  45                  50

gct cgt gga ttg cag gtg aag ggg cgg gtg aca tcg ccg acg ttt gtg   307
Ala Arg Gly Leu Gln Val Lys Gly Arg Val Thr Ser Pro Thr Phe Val
     55                  60                  65

atc gcg agg gaa cac cgc tcg gaa atc ggt ggg cca gat ctg atc cac   355
Ile Ala Arg Glu His Arg Ser Glu Ile Gly Gly Pro Asp Leu Ile His
 70                  75                  80                  85

atg gat gcc tac cga ttg ctg ggc gaa gac agc gag gat gct gat ccg   403
Met Asp Ala Tyr Arg Leu Leu Gly Glu Asp Ser Glu Asp Ala Asp Pro
                 90                  95                 100

atc ggt gcg ctg gac tct ttg gat ttg gat acc gat ttg gac ttg gct   451
Ile Gly Ala Leu Asp Ser Leu Asp Leu Asp Thr Asp Leu Asp Leu Ala
             105                 110                 115

gtg gtt gtt gcg gaa tgg ggc ggt ggc ttg gtg gag cag atc gct gac   499
Val Val Val Ala Glu Trp Gly Gly Gly Leu Val Glu Gln Ile Ala Asp
         120                 125                 130
```

```
tcg tat ctt ttg att acc att gat cga gag acc gct gtg cag gaa gac   547
Ser Tyr Leu Leu Ile Thr Ile Asp Arg Glu Thr Ala Val Gln Glu Asp
    135                 140                 145

ccg gaa tct gag gct cga att ttc cat tgg gaa tgg cgc gaa ggc cgc   595
Pro Glu Ser Glu Ala Arg Ile Phe His Trp Glu Trp Arg Glu Gly Arg
150             155                 160                 165

tgagaaagtt ttccacgcta aaa                                        618
```

<210> 260
<211> 165
<212> PRT
<213> Corynebacterium glutamicum

<400> 260

```
Met Lys Ser Glu Phe Pro Val Ser Gly Thr Arg Arg Phe Glu His Ala
  1               5                  10                  15

Ala Asp Thr Gln Asn Phe Gly Glu Glu Leu Gly Arg His Leu Glu Ala
            20                  25                  30

Gly Asp Val Val Ile Leu Asp Gly Pro Leu Gly Ala Gly Lys Thr Thr
        35                  40                  45

Phe Thr Gln Gly Ile Ala Arg Gly Leu Gln Val Lys Gly Arg Val Thr
    50                  55                  60

Ser Pro Thr Phe Val Ile Ala Arg Glu His Arg Ser Glu Ile Gly Gly
65                  70                  75                  80

Pro Asp Leu Ile His Met Asp Ala Tyr Arg Leu Leu Gly Glu Asp Ser
                85                  90                  95

Glu Asp Ala Asp Pro Ile Gly Ala Leu Asp Ser Leu Asp Leu Asp Thr
            100                 105                 110

Asp Leu Asp Leu Ala Val Val Val Ala Glu Trp Gly Gly Gly Leu Val
        115                 120                 125

Glu Gln Ile Ala Asp Ser Tyr Leu Leu Ile Thr Ile Asp Arg Glu Thr
    130                 135                 140

Ala Val Gln Glu Asp Pro Glu Ser Glu Ala Arg Ile Phe His Trp Glu
145                 150                 155                 160

Trp Arg Glu Gly Arg
                165
```

<210> 261
<211> 275
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(252)
<223> FRXA00505

<400> 261
gat ctg atc cac atg gat gcc tac cga ttg ctg ggc gaa gac agc gag 48
Asp Leu Ile His Met Asp Ala Tyr Arg Leu Leu Gly Glu Asp Ser Glu
1 5 10 15

gat gct gat ccg atc ggt gcg ctg gac tct ttg gat ttg gat acc gat 96
Asp Ala Asp Pro Ile Gly Ala Leu Asp Ser Leu Asp Leu Asp Thr Asp
20 25 30

ttg gac ttg gct gtg gtt gtt gcg gaa tgg ggc ggt ggc ttg gtg gag 144
Leu Asp Leu Ala Val Val Val Ala Glu Trp Gly Gly Gly Leu Val Glu
35 40 45

cag atc gct gac tcg tat ctt ttg att acc att gat cga gag acc gct 192
Gln Ile Ala Asp Ser Tyr Leu Leu Ile Thr Ile Asp Arg Glu Thr Ala
50 55 60

gtg cag gaa gac ccg gaa tct gag gct cga att ttc cat tgg gaa tgg 240
Val Gln Glu Asp Pro Glu Ser Glu Ala Arg Ile Phe His Trp Glu Trp
65 70 75 80

cgc gaa ggc cgc tgagaaagtt ttccacgcta aaa 275
Arg Glu Gly Arg

<210> 262
<211> 84
<212> PRT
<213> Corynebacterium glutamicum

<400> 262
Asp Leu Ile His Met Asp Ala Tyr Arg Leu Leu Gly Glu Asp Ser Glu
1 5 10 15

Asp Ala Asp Pro Ile Gly Ala Leu Asp Ser Leu Asp Leu Asp Thr Asp
20 25 30

Leu Asp Leu Ala Val Val Val Ala Glu Trp Gly Gly Gly Leu Val Glu
35 40 45

Gln Ile Ala Asp Ser Tyr Leu Leu Ile Thr Ile Asp Arg Glu Thr Ala
50 55 60

Val Gln Glu Asp Pro Glu Ser Glu Ala Arg Ile Phe His Trp Glu Trp
65 70 75 80

Arg Glu Gly Arg

<210> 263
<211> 978
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(955)
<223> RXN00507

<400> 263
gttcatgttg aactattgtg ccaccaaccg cggacagaaa tacgattggt gccggggtta 60

gtgccagtat tgccccacgc tttcaactat ccttaaacac gtg gct gag aat ctg 115
Val Ala Glu Asn Leu
1 5

aac aaa cac ctg tcc aaa ctg tcc aag cgc gga ccg cac cgc gtg ctg 163
Asn Lys His Leu Ser Lys Leu Ser Lys Arg Gly Pro His Arg Val Leu
10 15 20

gta ggc gat atg aac tac gcc ggc atc ccg ggc aaa atc tac acc cca 211
Val Gly Asp Met Asn Tyr Ala Gly Ile Pro Gly Lys Ile Tyr Thr Pro
25 30 35

gca gaa ggc gac ggc atc cca ggt gta gct ttc ggc cac gac tgg atg 259
Ala Glu Gly Asp Gly Ile Pro Gly Val Ala Phe Gly His Asp Trp Met
40 45 50

aaa tcc atc aag tac tac cac caa act ttg cga cac ctc gcg tcc tgg 307
Lys Ser Ile Lys Tyr Tyr His Gln Thr Leu Arg His Leu Ala Ser Trp
55 60 65

ggc atc gct gtt gcc gcc cca gac acc gaa aat ggc ttc atg cca gac 355
Gly Ile Ala Val Ala Ala Pro Asp Thr Glu Asn Gly Phe Met Pro Asp
70 75 80 85

cac aaa ggt ttc gcc tct gac ctc gaa tcc tcc att cag att ctc ggc 403
His Lys Gly Phe Ala Ser Asp Leu Glu Ser Ser Ile Gln Ile Leu Gly
90 95 100

ggc gta aaa ctc ggc tcc gga aac gtc acc gtc aac cca gcc tgc ctc 451
Gly Val Lys Leu Gly Ser Gly Asn Val Thr Val Asn Pro Ala Cys Leu
105 110 115

ggt gta gta ggc cac ggc atg ggt gct ggg gct gca gta cta tcc gca 499
Gly Val Val Gly His Gly Met Gly Ala Gly Ala Ala Val Leu Ser Ala
120 125 130

gca aac cgc gac ctc gtg cgc gca gtc gga gca atc tac cca gcg aaa 547
Ala Asn Arg Asp Leu Val Arg Ala Val Gly Ala Ile Tyr Pro Ala Lys
135 140 145

acc tcc ccc tca gca atc gac gcc gcc ttc gct gtc aaa gcc cca ggc 595
Thr Ser Pro Ser Ala Ile Asp Ala Ala Phe Ala Val Lys Ala Pro Gly
150 155 160 165

cta gtc atc gga tcc tcc agc ctc ggc ctc ttt gaa tcc ggc gag cca 643
Leu Val Ile Gly Ser Ser Ser Leu Gly Leu Phe Glu Ser Gly Glu Pro
170 175 180

gca aaa ctc gca gcc aac tgg gcc ggc gat gtc tgc tac cgc gaa tca 691
Ala Lys Leu Ala Ala Asn Trp Ala Gly Asp Val Cys Tyr Arg Glu Ser
185 190 195

gaa aaa ggc aac caa cag ggc ttc tct gaa gac acc atg ttc aaa ctt 739
Glu Lys Gly Asn Gln Gln Gly Phe Ser Glu Asp Thr Met Phe Lys Leu
200 205 210

gtc gca gga atc ggc agc cca caa acc gga gct caa gaa acc gtc cgc 787
Val Ala Gly Ile Gly Ser Pro Gln Thr Gly Ala Gln Glu Thr Val Arg

```
    215                 220                 225

ggc ctc ctc acc gga ttc ctt ctc cac caa ctt gcc gga gaa aag aaa   835
Gly Leu Leu Thr Gly Phe Leu Leu His Gln Leu Ala Gly Glu Lys Lys
230                 235                 240                 245

tac aaa gca ttc tcc gaa cca gac gct gaa gct aag aaa gtt gtc tcc   883
Tyr Lys Ala Phe Ser Glu Pro Asp Ala Glu Ala Lys Lys Val Val Ser
                250                 255                 260

tac ttc ggc cag gag ctg cag gaa cat gcc ttc cct aag gac acg tcc   931
Tyr Phe Gly Gln Glu Leu Gln Glu His Ala Phe Pro Lys Asp Thr Ser
            265                 270                 275

cca ttc gcg ttc ctt aac gag aag tagttcgctt ttcttagtgg gtg         978
Pro Phe Ala Phe Leu Asn Glu Lys
        280                 285


<210> 264
<211> 285
<212> PRT
<213> Corynebacterium glutamicum

<400> 264
Val Ala Glu Asn Leu Asn Lys His Leu Ser Lys Leu Ser Lys Arg Gly
  1               5                  10                  15

Pro His Arg Val Leu Val Gly Asp Met Asn Tyr Ala Gly Ile Pro Gly
             20                  25                  30

Lys Ile Tyr Thr Pro Ala Glu Gly Asp Gly Ile Pro Gly Val Ala Phe
         35                  40                  45

Gly His Asp Trp Met Lys Ser Ile Lys Tyr Tyr His Gln Thr Leu Arg
     50                  55                  60

His Leu Ala Ser Trp Gly Ile Ala Val Ala Ala Pro Asp Thr Glu Asn
 65                  70                  75                  80

Gly Phe Met Pro Asp His Lys Gly Phe Ala Ser Asp Leu Glu Ser Ser
                 85                  90                  95

Ile Gln Ile Leu Gly Gly Val Lys Leu Gly Ser Gly Asn Val Thr Val
            100                 105                 110

Asn Pro Ala Cys Leu Gly Val Val Gly His Gly Met Gly Ala Gly Ala
        115                 120                 125

Ala Val Leu Ser Ala Ala Asn Arg Asp Leu Val Arg Ala Val Gly Ala
    130                 135                 140

Ile Tyr Pro Ala Lys Thr Ser Pro Ser Ala Ile Asp Ala Ala Phe Ala
145                 150                 155                 160

Val Lys Ala Pro Gly Leu Val Ile Gly Ser Ser Ser Leu Gly Leu Phe
                165                 170                 175

Glu Ser Gly Glu Pro Ala Lys Leu Ala Ala Asn Trp Ala Gly Asp Val
            180                 185                 190
```

```
Cys Tyr Arg Glu Ser Glu Lys Gly Asn Gln Gln Gly Phe Ser Glu Asp
        195                 200                 205

Thr Met Phe Lys Leu Val Ala Gly Ile Gly Ser Pro Gln Thr Gly Ala
    210                 215                 220

Gln Glu Thr Val Arg Gly Leu Leu Thr Gly Phe Leu Leu His Gln Leu
225                 230                 235                 240

Ala Gly Glu Lys Lys Tyr Lys Ala Phe Ser Glu Pro Asp Ala Glu Ala
                245                 250                 255

Lys Lys Val Val Ser Tyr Phe Gly Gln Glu Leu Gln Glu His Ala Phe
            260                 265                 270

Pro Lys Asp Thr Ser Pro Phe Ala Phe Leu Asn Glu Lys
        275                 280                 285


<210> 265
<211> 978
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(955)
<223> FRXA00507

<400> 265
gttcatgttg aactattgtg ccaccaaccg cggacagaaa tacgattggt gccggggtta 60

gtgccagtat tgccccacgc tttcaactat ccttaaacac gtg gct gag aat ctg   115
                                              Val Ala Glu Asn Leu
                                                1               5

aac aaa cac ctg tcc aaa ctg tcc aag cgc gga ccg cac cgc gtg ctg   163
Asn Lys His Leu Ser Lys Leu Ser Lys Arg Gly Pro His Arg Val Leu
                  10                  15                  20

gta ggc gat atg aac tac gcc ggc atc ccg ggc aaa atc tac acc cca   211
Val Gly Asp Met Asn Tyr Ala Gly Ile Pro Gly Lys Ile Tyr Thr Pro
              25                  30                  35

gca gaa ggc gac ggc atc cca ggt gta gct ttc ggc cac gac tgg atg   259
Ala Glu Gly Asp Gly Ile Pro Gly Val Ala Phe Gly His Asp Trp Met
          40                  45                  50

aaa tcc atc aag tac tac cac caa act ttg cga cac ctc gcg tcc tgg   307
Lys Ser Ile Lys Tyr Tyr His Gln Thr Leu Arg His Leu Ala Ser Trp
      55                  60                  65

ggc atc gct gtt gcc gcc cca gac acc gaa aat ggc ttc atg cca gac   355
Gly Ile Ala Val Ala Ala Pro Asp Thr Glu Asn Gly Phe Met Pro Asp
  70                  75                  80                  85

cac aaa ggt ttc gcc tct gac ctc gaa tcc tcc att cag att ctc ggc   403
His Lys Gly Phe Ala Ser Asp Leu Glu Ser Ser Ile Gln Ile Leu Gly
                  90                  95                 100

ggc gta aaa ctc ggc tcc gga aac gtc acc gtc aac cca gcc tgc ctc   451
```

```
Gly Val Lys Leu Gly Ser Gly Asn Val Thr Val Asn Pro Ala Cys Leu
            105                 110                 115

ggt gta gta ggc cac ggc atg ggt gct ggg gct gca gta cta tcc gca   499
Gly Val Val Gly His Gly Met Gly Ala Gly Ala Ala Val Leu Ser Ala
        120                 125                 130

gca aac cgc gac ctc gtg cgc gca gtc gga gca atc tac cca gcg aaa   547
Ala Asn Arg Asp Leu Val Arg Ala Val Gly Ala Ile Tyr Pro Ala Lys
    135                 140                 145

acc tcc ccc tca gca atc gac gcc gcc ttc gct gtc aaa gcc cca ggc   595
Thr Ser Pro Ser Ala Ile Asp Ala Ala Phe Ala Val Lys Ala Pro Gly
150                 155                 160                 165

cta gtc atc gga tcc tcc agc ctc ggc ctc ttt gaa tcc ggc gag cca   643
Leu Val Ile Gly Ser Ser Ser Leu Gly Leu Phe Glu Ser Gly Glu Pro
                170                 175                 180

gca aaa ctc gca gcc aac tgg gcc ggc gat gtc tgc tac cgc gaa tca   691
Ala Lys Leu Ala Ala Asn Trp Ala Gly Asp Val Cys Tyr Arg Glu Ser
            185                 190                 195

gaa aaa ggc aac caa cag ggc ttc tct gaa gac acc atg ttc aaa ctt   739
Glu Lys Gly Asn Gln Gln Gly Phe Ser Glu Asp Thr Met Phe Lys Leu
        200                 205                 210

gtc gca gga atc ggc agc cca caa acc gga gct caa gaa acc gtc cgc   787
Val Ala Gly Ile Gly Ser Pro Gln Thr Gly Ala Gln Glu Thr Val Arg
    215                 220                 225

ggc ctc ctc acc gga ttc ctt ctc cac caa ctt gcc gga gaa aag aaa   835
Gly Leu Leu Thr Gly Phe Leu Leu His Gln Leu Ala Gly Glu Lys Lys
230                 235                 240                 245

tac aaa gca ttc tcc gaa cca gac gct gaa gct aag aaa gtt gtc tcc   883
Tyr Lys Ala Phe Ser Glu Pro Asp Ala Glu Ala Lys Lys Val Val Ser
                250                 255                 260

tac ttc ggc cag gag ctg cag gaa cat gcc ttc cct aag gac acg tcc   931
Tyr Phe Gly Gln Glu Leu Gln Glu His Ala Phe Pro Lys Asp Thr Ser
            265                 270                 275

cca ttc gcg ttc ctt aac gag aag tagttcgctt ttcttagtgg gtg         978
Pro Phe Ala Phe Leu Asn Glu Lys
        280                 285
```

<210> 266
<211> 285
<212> PRT
<213> Corynebacterium glutamicum

<400> 266

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Val Ala Glu Asn Leu Asn Lys His Leu Ser Lys Leu Ser Lys Arg Gly
  1               5                  10                  15

Pro His Arg Val Leu Val Gly Asp Met Asn Tyr Ala Gly Ile Pro Gly
             20                  25                  30

Lys Ile Tyr Thr Pro Ala Glu Gly Asp Gly Ile Pro Gly Val Ala Phe
```

```
         35                  40                  45

Gly His Asp Trp Met Lys Ser Ile Lys Tyr Tyr His Gln Thr Leu Arg
     50                  55                  60

His Leu Ala Ser Trp Gly Ile Ala Val Ala Ala Pro Asp Thr Glu Asn
 65                  70                  75                  80

Gly Phe Met Pro Asp His Lys Gly Phe Ala Ser Asp Leu Glu Ser Ser
                 85                  90                  95

Ile Gln Ile Leu Gly Gly Val Lys Leu Gly Ser Gly Asn Val Thr Val
            100                 105                 110

Asn Pro Ala Cys Leu Gly Val Val Gly His Gly Met Gly Ala Gly Ala
        115                 120                 125

Ala Val Leu Ser Ala Ala Asn Arg Asp Leu Val Arg Ala Val Gly Ala
    130                 135                 140

Ile Tyr Pro Ala Lys Thr Ser Pro Ser Ala Ile Asp Ala Ala Phe Ala
145                 150                 155                 160

Val Lys Ala Pro Gly Leu Val Ile Gly Ser Ser Ser Leu Gly Leu Phe
                165                 170                 175

Glu Ser Gly Glu Pro Ala Lys Leu Ala Ala Asn Trp Ala Gly Asp Val
            180                 185                 190

Cys Tyr Arg Glu Ser Glu Lys Gly Asn Gln Gln Gly Phe Ser Glu Asp
        195                 200                 205

Thr Met Phe Lys Leu Val Ala Gly Ile Gly Ser Pro Gln Thr Gly Ala
    210                 215                 220

Gln Glu Thr Val Arg Gly Leu Leu Thr Gly Phe Leu Leu His Gln Leu
225                 230                 235                 240

Ala Gly Glu Lys Lys Tyr Lys Ala Phe Ser Glu Pro Asp Ala Glu Ala
                245                 250                 255

Lys Lys Val Val Ser Tyr Phe Gly Gln Glu Leu Gln Glu His Ala Phe
            260                 265                 270

Pro Lys Asp Thr Ser Pro Phe Ala Phe Leu Asn Glu Lys
        275                 280                 285


<210> 267
<211> 1632
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1609)
<223> RXN00510

<400> 267
acgcttttac ccaaacaacc caagccgccg aggaagaagt taaacgattc gacaataccg 60
```

```
acaaagtttt tggtgccgga tttgatggga ttgatccgaa gtg aat gat cct tta   115
                                            Val Asn Asp Pro Leu
                                              1               5

gcc ggc tac gga gca gtg atc tcc gca cta caa ggc gcc agt ggt ggg   163
Ala Gly Tyr Gly Ala Val Ile Ser Ala Leu Gln Gly Ala Ser Gly Gly
                 10                  15                  20

atg tat cgc gga ccg gcg aaa tcc gaa ggc cag ttg cgc gag atg tac   211
Met Tyr Arg Gly Pro Ala Lys Ser Glu Gly Gln Leu Arg Glu Met Tyr
             25                  30                  35

caa acc atc gaa ggg cta gac acc agc tcg ttg cgc gaa gct gcc gaa   259
Gln Thr Ile Glu Gly Leu Asp Thr Ser Ser Leu Arg Glu Ala Ala Glu
         40                  45                  50

gca gca gtg ggc gga acg aac gaa gcc aga ata caa ggg tgg gtc ggc   307
Ala Ala Val Gly Gly Thr Asn Glu Ala Arg Ile Gln Gly Trp Val Gly
     55                  60                  65

ccg ctc ttg aaa ttc ttc ggg acg gtt ggc ggg gga atg atc gcc acg   355
Pro Leu Leu Lys Phe Phe Gly Thr Val Gly Gly Gly Met Ile Ala Thr
 70                  75                  80                  85

gag ata gct gaa cgg gca gtc gat tgg ttc aaa aac cgt aat gat gtg   403
Glu Ile Ala Glu Arg Ala Val Asp Trp Phe Lys Asn Arg Asn Asp Val
                 90                  95                 100

gaa gaa gtc agc gaa gcc gct gat aaa gcc gcc gat gcg atc gac tcc   451
Glu Glu Val Ser Glu Ala Ala Asp Lys Ala Ala Asp Ala Ile Asp Ser
             105                 110                 115

act gtc aca gag tcc gac cag ggc atg atg cac att atc cag cag ctc   499
Thr Val Thr Glu Ser Asp Gln Gly Met Met His Ile Ile Gln Gln Leu
         120                 125                 130

ttg gac att gtg tct acg ttg acg cag att ctt ggc agc atg gat cgg   547
Leu Asp Ile Val Ser Thr Leu Thr Gln Ile Leu Gly Ser Met Asp Arg
     135                 140                 145

ggg aaa ttt cct caa gaa ttc cgg gac tgt gtc caa act gga gct gat   595
Gly Lys Phe Pro Gln Glu Phe Arg Asp Cys Val Gln Thr Gly Ala Asp
150                 155                 160                 165

ctt att gac cag gca ggg gac atg ctt gaa gga ttg tgc gct gat cga   643
Leu Ile Asp Gln Ala Gly Asp Met Leu Glu Gly Leu Cys Ala Asp Arg
                 170                 175                 180

gat gat gcg att tca cag tgt ttc tcc gcg ttg acc gat cat gga aaa   691
Asp Asp Ala Ile Ser Gln Cys Phe Ser Ala Leu Thr Asp His Gly Lys
             185                 190                 195

caa gtt tgt gaa act gag cca aag ccg ttg tgt agt gca gct tct ggg   739
Gln Val Cys Glu Thr Glu Pro Lys Pro Leu Cys Ser Ala Ala Ser Gly
         200                 205                 210

ggt tca tct ggt gga gcg act tct tcg gct gcg gcc tct tca ggt ggt   787
Gly Ser Ser Gly Gly Ala Thr Ser Ser Ala Ala Ala Ser Ser Gly Gly
     215                 220                 225

tca agc tcg agc act gct agc tct ggg agt tct ggc gga tcg agc agt   835
```

```
Ser Ser Ser Ser Thr Ala Ser Ser Gly Ser Ser Gly Gly Ser Ser Ser
230                 235                 240                 245

gct gcg gat agt tcg acg tcg acc aat gct gaa tcc agt gtt gaa aag   883
Ala Ala Asp Ser Ser Thr Ser Thr Asn Ala Glu Ser Ser Val Glu Lys
                250                 255                 260

gaa aag acc aca cct gct gcc gtt gag aaa cct gac gag aaa cca gtg   931
Glu Lys Thr Thr Pro Ala Ala Val Glu Lys Pro Asp Glu Lys Pro Val
            265                 270                 275

gag aag ccg gtt gaa aag acg cca gaa aag ccg gta gaa aaa cct gtc   979
Glu Lys Pro Val Glu Lys Thr Pro Glu Lys Pro Val Glu Lys Pro Val
        280                 285                 290

gag aag caa gag tgt gaa gaa aag cct gac cct gac ccg gaa aaa tgc   1027
Glu Lys Gln Glu Cys Glu Glu Lys Pro Asp Pro Asp Pro Glu Lys Cys
    295                 300                 305

aaa aca gag ccg gtc gag tgt gag cca aca ccg aaa cct gaa aca gag   1075
Lys Thr Glu Pro Val Glu Cys Glu Pro Thr Pro Lys Pro Glu Thr Glu
310                 315                 320                 325

cct gaa cca aaa ccg aca ccc acg ccc aca ccc gga aca cca aca cca   1123
Pro Glu Pro Lys Pro Thr Pro Thr Pro Thr Pro Gly Thr Pro Thr Pro
                330                 335                 340

ata cct gag cta gag act gag gat tgt gaa cct ggc aag gag acg ggc   1171
Ile Pro Glu Leu Glu Thr Glu Asp Cys Glu Pro Gly Lys Glu Thr Gly
            345                 350                 355

aca gac tca gaa tct gaa tcg gaa gag tgc gcc ccc gag ctc aat gac   1219
Thr Asp Ser Glu Ser Glu Ser Glu Glu Cys Ala Pro Glu Leu Asn Asp
        360                 365                 370

gtt cca gaa gag tcg gat ctg att ggg caa ctc atc aag gga gca atc   1267
Val Pro Glu Glu Ser Asp Leu Ile Gly Gln Leu Ile Lys Gly Ala Ile
    375                 380                 385

ggt att ggg att gtt gtt gta ggc gtt ggg ctg ttg gtg aat ttc ctg   1315
Gly Ile Gly Ile Val Val Val Gly Val Gly Leu Leu Val Asn Phe Leu
390                 395                 400                 405

gag cag tgc gtc cct gtg att gaa gaa gta cct gtg ccg gag ccc gag   1363
Glu Gln Cys Val Pro Val Ile Glu Glu Val Pro Val Pro Glu Pro Glu
                410                 415                 420

cct ata cct gaa ccc gct ccg cag cct gag cca act tca gtg aaa cca   1411
Pro Ile Pro Glu Pro Ala Pro Gln Pro Glu Pro Thr Ser Val Lys Pro
            425                 430                 435

cca gag tct gaa cta gat aag gtg gct gag cct gcg ccg aag cca att   1459
Pro Glu Ser Glu Leu Asp Lys Val Ala Glu Pro Ala Pro Lys Pro Ile
        440                 445                 450

cca caa gct aat tac act gct gct gca gca act aac tat tcc gct ccc   1507
Pro Gln Ala Asn Tyr Thr Ala Ala Ala Ala Thr Asn Tyr Ser Ala Pro
    455                 460                 465

gcg cac gct ccc gtt gtc cca att acg ccg gca gca cct gaa gtt ccg   1555
Ala His Ala Pro Val Val Pro Ile Thr Pro Ala Ala Pro Glu Val Pro
```

```
470                 475                 480                 485

gca gca cca gaa gtg cct gca ccg gcg gtt aat ctt cac aag gcc ggc   1603
Ala Ala Pro Glu Val Pro Ala Pro Ala Val Asn Leu His Lys Ala Gly
                490                 495                 500

ggg tgg tagcggtgga gtatgcggaa ttt                                 1632
Gly Trp
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<210> 268
<211> 503
<212> PRT
<213> Corynebacterium glutamicum

<400> 268

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Val Asn Asp Pro Leu Ala Gly Tyr Gly Ala Val Ile Ser Ala Leu Gln
  1               5                  10                  15

Gly Ala Ser Gly Gly Met Tyr Arg Gly Pro Ala Lys Ser Glu Gly Gln
             20                  25                  30

Leu Arg Glu Met Tyr Gln Thr Ile Glu Gly Leu Asp Thr Ser Ser Leu
         35                  40                  45

Arg Glu Ala Ala Glu Ala Ala Val Gly Gly Thr Asn Glu Ala Arg Ile
     50                  55                  60

Gln Gly Trp Val Gly Pro Leu Leu Lys Phe Phe Gly Thr Val Gly Gly
 65                  70                  75                  80

Gly Met Ile Ala Thr Glu Ile Ala Glu Arg Ala Val Asp Trp Phe Lys
                 85                  90                  95

Asn Arg Asn Asp Val Glu Glu Val Ser Glu Ala Ala Asp Lys Ala Ala
            100                 105                 110

Asp Ala Ile Asp Ser Thr Val Thr Glu Ser Asp Gln Gly Met Met His
        115                 120                 125

Ile Ile Gln Gln Leu Leu Asp Ile Val Ser Thr Leu Thr Gln Ile Leu
    130                 135                 140

Gly Ser Met Asp Arg Gly Lys Phe Pro Gln Glu Phe Arg Asp Cys Val
145                 150                 155                 160

Gln Thr Gly Ala Asp Leu Ile Asp Gln Ala Gly Asp Met Leu Glu Gly
                165                 170                 175

Leu Cys Ala Asp Arg Asp Asp Ala Ile Ser Gln Cys Phe Ser Ala Leu
            180                 185                 190

Thr Asp His Gly Lys Gln Val Cys Glu Thr Glu Pro Lys Pro Leu Cys
        195                 200                 205

Ser Ala Ala Ser Gly Gly Ser Ser Gly Gly Ala Thr Ser Ser Ala Ala
    210                 215                 220

Ala Ser Ser Gly Gly Ser Ser Ser Ser Thr Ala Ser Ser Gly Ser Ser
225                 230                 235                 240
```

```
Gly Gly Ser Ser Ser Ala Ala Asp Ser Ser Thr Ser Thr Asn Ala Glu
                245                 250                 255

Ser Ser Val Glu Lys Glu Lys Thr Thr Pro Ala Ala Val Glu Lys Pro
            260                 265                 270

Asp Glu Lys Pro Val Glu Lys Pro Val Glu Lys Thr Pro Glu Lys Pro
        275                 280                 285

Val Glu Lys Pro Val Glu Lys Gln Glu Cys Glu Glu Lys Pro Asp Pro
    290                 295                 300

Asp Pro Glu Lys Cys Lys Thr Glu Pro Val Glu Cys Glu Pro Thr Pro
305                 310                 315                 320

Lys Pro Glu Thr Glu Pro Glu Pro Lys Pro Thr Pro Thr Pro Thr Pro
                325                 330                 335

Gly Thr Pro Thr Pro Ile Pro Glu Leu Glu Thr Glu Asp Cys Glu Pro
            340                 345                 350

Gly Lys Glu Thr Gly Thr Asp Ser Glu Ser Glu Ser Glu Glu Cys Ala
        355                 360                 365

Pro Glu Leu Asn Asp Val Pro Glu Glu Ser Asp Leu Ile Gly Gln Leu
    370                 375                 380

Ile Lys Gly Ala Ile Gly Ile Gly Ile Val Val Val Gly Val Gly Leu
385                 390                 395                 400

Leu Val Asn Phe Leu Glu Gln Cys Val Pro Val Ile Glu Glu Val Pro
                405                 410                 415

Val Pro Glu Pro Glu Pro Ile Pro Glu Pro Ala Pro Gln Pro Glu Pro
            420                 425                 430

Thr Ser Val Lys Pro Pro Glu Ser Glu Leu Asp Lys Val Ala Glu Pro
        435                 440                 445

Ala Pro Lys Pro Ile Pro Gln Ala Asn Tyr Thr Ala Ala Ala Ala Thr
    450                 455                 460

Asn Tyr Ser Ala Pro Ala His Ala Pro Val Val Pro Ile Thr Pro Ala
465                 470                 475                 480

Ala Pro Glu Val Pro Ala Ala Pro Glu Val Pro Ala Pro Ala Val Asn
                485                 490                 495

Leu His Lys Ala Gly Gly Trp
            500
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<210> 269
<211> 300
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(277)

<223> FRXA00509

<400> 269
cttttctggc gtcttttcaa ccggcttctc cactggtttc tcgtcaggtt tctcaacggc 60

agcaggtgtg gtcttttcct tttcaacact ggattcagca ttg gtc gac gtc gaa 115
Leu Val Asp Val Glu
1 5

cta tcc gca gca ctg ctc gat ccg cca gaa ctc cca gag cta gca gtg 163
Leu Ser Ala Ala Leu Leu Asp Pro Pro Glu Leu Pro Glu Leu Ala Val
10 15 20

ctc gag ctt gaa cca cct gaa gag gcc gca gcc gaa gaa gtc gct cca 211
Leu Glu Leu Glu Pro Pro Glu Glu Ala Ala Ala Glu Glu Val Ala Pro
25 30 35

cca gat gaa ccc cca gaa gct gca cta cac aac ggc ttt ggc tca gtt 259
Pro Asp Glu Pro Pro Glu Ala Ala Leu His Asn Gly Phe Gly Ser Val
40 45 50

tca caa act tgt ttt cca tgatcggtca acgcggagaa aca 300
Ser Gln Thr Cys Phe Pro
55

<210> 270
<211> 59
<212> PRT
<213> Corynebacterium glutamicum

<400> 270
Leu Val Asp Val Glu Leu Ser Ala Ala Leu Leu Asp Pro Pro Glu Leu
1 5 10 15

Pro Glu Leu Ala Val Leu Glu Leu Glu Pro Pro Glu Glu Ala Ala Ala
20 25 30

Glu Glu Val Ala Pro Pro Asp Glu Pro Pro Glu Ala Ala Leu His Asn
35 40 45

Gly Phe Gly Ser Val Ser Gln Thr Cys Phe Pro
50 55

<210> 271
<211> 631
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(631)
<223> FRXA00510

<400> 271
gagcagtgct gcggatagtt cgacgtcgac caatgctgaa tccagtgttg aaaaggaaaa 60

gaccacacct gctgccgttg agaaacctga cgagaaacca gtg gag aag ccg gtt 115
Val Glu Lys Pro Val
1 5

```
gaa aag acg cca gaa aag ccg gta gaa aaa cct gtc gag aag caa gag   163
Glu Lys Thr Pro Glu Lys Pro Val Glu Lys Pro Val Glu Lys Gln Glu
                10                  15                  20

tgt gaa gaa aag cct gac cct gac ccg gaa ana atg caa aan can gag   211
Cys Glu Glu Lys Pro Asp Pro Asp Pro Glu Xaa Met Gln Xaa Xaa Glu
            25                  30                  35

ccg gtc gag tgt gag cca aca ccg aaa cct gaa aca gag cct gaa cca   259
Pro Val Glu Cys Glu Pro Thr Pro Lys Pro Glu Thr Glu Pro Glu Pro
        40                  45                  50

aaa ccn gac acc cac gcc can cna ccc gga aca cca aca cca ata cct   307
Lys Pro Asp Thr His Ala Xaa Xaa Pro Gly Thr Pro Thr Pro Ile Pro
    55                  60                  65

gna gct aga gna ctg agg att gnt gna nac nct gng caa gga gan cgn   355
Xaa Ala Arg Xaa Leu Arg Ile Xaa Xaa Xaa Xaa Xaa Gln Gly Xaa Arg
70                  75                  80                  85

ggc aca gac tca gnn ana tnc tnn nnn nnn gaa tcg gaa gag tgc gcc   403
Gly Thr Asp Ser Xaa Xaa Xaa Xaa Xaa Xaa Glu Ser Glu Glu Cys Ala
                90                  95                  100

ccc gag ctc aat gac gtt cca gaa gag tcg gat ctg att ggg caa ctc   451
Pro Glu Leu Asn Asp Val Pro Glu Glu Ser Asp Leu Ile Gly Gln Leu
            105                 110                 115

atc aag gga gca atc ggt att ggg att gtt gtt gta ggc gtt ggg ctg   499
Ile Lys Gly Ala Ile Gly Ile Gly Ile Val Val Val Gly Val Gly Leu
        120                 125                 130

ttg gtg aat ttc ctg gag cag tgc gtc cct gtg att gaa gaa gta cct   547
Leu Val Asn Phe Leu Glu Gln Cys Val Pro Val Ile Glu Glu Val Pro
    135                 140                 145

gtg ccg gag ccc gag cct ata cct gaa ccc gct ccg cag cct gag cca   595
Val Pro Glu Pro Glu Pro Ile Pro Glu Pro Ala Pro Gln Pro Glu Pro
150                 155                 160                 165

act tca gtg aaa cca cca gag tct gaa cta gat aag                   631
Thr Ser Val Lys Pro Pro Glu Ser Glu Leu Asp Lys
                170                 175
```

<210> 272
<211> 177
<212> PRT
<213> Corynebacterium glutamicum

<400> 272

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Val Glu Lys Pro Val Glu Lys Thr Pro Glu Lys Pro Val Glu Lys Pro
  1               5                  10                  15

Val Glu Lys Gln Glu Cys Glu Glu Lys Pro Asp Pro Asp Pro Glu Xaa
            20                  25                  30

Met Gln Xaa Xaa Glu Pro Val Glu Cys Glu Pro Thr Pro Lys Pro Glu
        35                  40                  45
```

Thr Glu Pro Glu Pro Lys Pro Asp Thr His Ala Xaa Xaa Pro Gly Thr
50 55 60

Pro Thr Pro Ile Pro Xaa Ala Arg Xaa Leu Arg Ile Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Gln Gly Xaa Arg Gly Thr Asp Ser Xaa Xaa Xaa Xaa Xaa Xaa Glu
85 90 95

Ser Glu Glu Cys Ala Pro Glu Leu Asn Asp Val Pro Glu Glu Ser Asp
100 105 110

Leu Ile Gly Gln Leu Ile Lys Gly Ala Ile Gly Ile Gly Ile Val Val
115 120 125

Val Gly Val Gly Leu Leu Val Asn Phe Leu Glu Gln Cys Val Pro Val
130 135 140

Ile Glu Glu Val Pro Val Pro Glu Pro Glu Pro Ile Pro Glu Pro Ala
145 150 155 160

Pro Gln Pro Glu Pro Thr Ser Val Lys Pro Pro Glu Ser Glu Leu Asp
165 170 175

Lys

<210> 273
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> RXN00515

<400> 273
gttgacgcac tgaagaagta aagtctcttc acaaaaagcg ctgtgcttcc tcacatggaa 60

gcacagcgct ttttcatatt tttattgcca taatgggcac atg cgt ttt tct cga 115
Met Arg Phe Ser Arg
1 5

gtt ctt ccc gca ctt ctt atc acc acc gcc gtg agc atc cca aca gca 163
Val Leu Pro Ala Leu Leu Ile Thr Thr Ala Val Ser Ile Pro Thr Ala
10 15 20

tct gct gcc aca ctc acc gcc gac acc gac aag gaa ttg tgc atc gcc 211
Ser Ala Ala Thr Leu Thr Ala Asp Thr Asp Lys Glu Leu Cys Ile Ala
25 30 35

agc aac acc gac gat tcc gcg gtg gtt acc ttc tgg aac tcc att gaa 259
Ser Asn Thr Asp Asp Ser Ala Val Val Thr Phe Trp Asn Ser Ile Glu
40 45 50

gac tcc gtg cgc gaa caa cgc ctc gac gaa cta gac gcc caa gat cca 307
Asp Ser Val Arg Glu Gln Arg Leu Asp Glu Leu Asp Ala Gln Asp Pro
55 60 65

```
gga atc aaa gcg gcg att gaa agc tac atc gcc caa gat gac aac gcc   355
Gly Ile Lys Ala Ala Ile Glu Ser Tyr Ile Ala Gln Asp Asp Asn Ala
 70                  75                  80                  85

cca act gct gct gaa ctg caa gta cgc ctc gat gcc atc gaa tcc ggc   403
Pro Thr Ala Ala Glu Leu Gln Val Arg Leu Asp Ala Ile Glu Ser Gly
                90                  95                 100

gaa ggc cta gcc atg ctc ctc cca gac gat ccc acg ctg gca gac ccc   451
Glu Gly Leu Ala Met Leu Leu Pro Asp Asp Pro Thr Leu Ala Asp Pro
            105                 110                 115

aac gcc gag gaa agt ttc aaa acg gag tac aca tac gac gaa gcc aaa   499
Asn Ala Glu Glu Ser Phe Lys Thr Glu Tyr Thr Tyr Asp Glu Ala Lys
        120                 125                 130

gac atc atc agc gga ttc tcc agc gat cca gcc agc gat gta ctc agc   547
Asp Ile Ile Ser Gly Phe Ser Ser Asp Pro Ala Ser Asp Val Leu Ser
    135                 140                 145

caa ctt caa caa gcc gcc acc acc ggc acc cgc acc gca gaa atc cgc   595
Gln Leu Gln Gln Ala Ala Thr Thr Gly Thr Arg Thr Ala Glu Ile Arg
150                 155                 160                 165

gcc gaa gta ttc gcc gac cgc acc gat gat tac aac gaa tcc caa acc   643
Ala Glu Val Phe Ala Asp Arg Thr Asp Asp Tyr Asn Glu Ser Gln Thr
                170                 175                 180

gct ctt aaa gag gat ttc caa aac tgc atc gat gcc atc gat gac gcc   691
Ala Leu Lys Glu Asp Phe Gln Asn Cys Ile Asp Ala Ile Asp Asp Ala
            185                 190                 195

cgc cca atc cca ctg cag tac atc ctg att gga ggc gcc atc gct ttg   739
Arg Pro Ile Pro Leu Gln Tyr Ile Leu Ile Gly Gly Ala Ile Ala Leu
        200                 205                 210

gcg gtc atc gtc ctc ggg atc agg gcg tgg act aac tca agg aag cag   787
Ala Val Ile Val Leu Gly Ile Arg Ala Trp Thr Asn Ser Arg Lys Gln
    215                 220                 225

tcc aag cac agc cag taatacgcca agcaaaaaat tgc                    825
Ser Lys His Ser Gln
230
```

<210> 274
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 274

```
Met Arg Phe Ser Arg Val Leu Pro Ala Leu Leu Ile Thr Thr Ala Val
  1               5                  10                  15

Ser Ile Pro Thr Ala Ser Ala Ala Thr Leu Thr Ala Asp Thr Asp Lys
             20                  25                  30

Glu Leu Cys Ile Ala Ser Asn Thr Asp Asp Ser Ala Val Val Thr Phe
         35                  40                  45

Trp Asn Ser Ile Glu Asp Ser Val Arg Glu Gln Arg Leu Asp Glu Leu
```

```
     50                  55                  60

Asp Ala Gln Asp Pro Gly Ile Lys Ala Ala Ile Glu Ser Tyr Ile Ala
 65                  70                  75                  80

Gln Asp Asp Asn Ala Pro Thr Ala Ala Glu Leu Gln Val Arg Leu Asp
                 85                  90                  95

Ala Ile Glu Ser Gly Glu Gly Leu Ala Met Leu Leu Pro Asp Asp Pro
            100                 105                 110

Thr Leu Ala Asp Pro Asn Ala Glu Glu Ser Phe Lys Thr Glu Tyr Thr
        115                 120                 125

Tyr Asp Glu Ala Lys Asp Ile Ile Ser Gly Phe Ser Ser Asp Pro Ala
    130                 135                 140

Ser Asp Val Leu Ser Gln Leu Gln Gln Ala Ala Thr Thr Gly Thr Arg
145                 150                 155                 160

Thr Ala Glu Ile Arg Ala Glu Val Phe Ala Asp Arg Thr Asp Asp Tyr
                165                 170                 175

Asn Glu Ser Gln Thr Ala Leu Lys Glu Asp Phe Gln Asn Cys Ile Asp
            180                 185                 190

Ala Ile Asp Asp Ala Arg Pro Ile Pro Leu Gln Tyr Ile Leu Ile Gly
        195                 200                 205

Gly Ala Ile Ala Leu Ala Val Ile Val Leu Gly Ile Arg Ala Trp Thr
    210                 215                 220

Asn Ser Arg Lys Gln Ser Lys His Ser Gln
225                 230


<210> 275
<211> 503
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(480)
<223> FRXA00515

<400> 275
att gaa agc tac atc gcc caa gat gac aac gcc cca act gct gct gaa   48
Ile Glu Ser Tyr Ile Ala Gln Asp Asp Asn Ala Pro Thr Ala Ala Glu
  1               5                  10                  15

ctg caa gta cgc ctc gat gcc atc gaa tcc ggc gaa ggc cta gcc atg   96
Leu Gln Val Arg Leu Asp Ala Ile Glu Ser Gly Glu Gly Leu Ala Met
             20                  25                  30

ctc ctc cca gac gat ccc acg ctg gca gac ccc aac gcc gag gaa agt   144
Leu Leu Pro Asp Asp Pro Thr Leu Ala Asp Pro Asn Ala Glu Glu Ser
         35                  40                  45

ttc aaa acg gag tac aca tac gac gaa gcc aaa gac atc atc agc gga   192
Phe Lys Thr Glu Tyr Thr Tyr Asp Glu Ala Lys Asp Ile Ile Ser Gly
```

```
     50                  55                  60

ttc tcc agc gat cca gcc agc gat gta ctc agc caa ctt caa caa gcc   240
Phe Ser Ser Asp Pro Ala Ser Asp Val Leu Ser Gln Leu Gln Gln Ala
 65                  70                  75                  80

gcc acc acc ggc acc cgc acc gca gaa atc cgc gcc gaa gta ttc gcc   288
Ala Thr Thr Gly Thr Arg Thr Ala Glu Ile Arg Ala Glu Val Phe Ala
                85                  90                  95

gac cgc acc gat gat tac aac gaa tcc caa acc gct ctt aaa gag gat   336
Asp Arg Thr Asp Asp Tyr Asn Glu Ser Gln Thr Ala Leu Lys Glu Asp
            100                 105                 110

ttc caa aac tgc atc gat gcc atc gat gac gcc cgc cca atc cca ctg   384
Phe Gln Asn Cys Ile Asp Ala Ile Asp Asp Ala Arg Pro Ile Pro Leu
        115                 120                 125

cag tac atc ctg att gga ggc gcc atc gct ttg gcg gtc atc gtc ctc   432
Gln Tyr Ile Leu Ile Gly Gly Ala Ile Ala Leu Ala Val Ile Val Leu
    130                 135                 140

ggg atc agg gcg tgg act aac tca agg aag cag tcc aag cac agc cag   480
Gly Ile Arg Ala Trp Thr Asn Ser Arg Lys Gln Ser Lys His Ser Gln
145                 150                 155                 160

taatacgcca agcaaaaaat tgc                                        503


<210> 276
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 276
Ile Glu Ser Tyr Ile Ala Gln Asp Asp Asn Ala Pro Thr Ala Ala Glu
  1               5                  10                  15

Leu Gln Val Arg Leu Asp Ala Ile Glu Ser Gly Glu Gly Leu Ala Met
             20                  25                  30

Leu Leu Pro Asp Asp Pro Thr Leu Ala Asp Pro Asn Ala Glu Glu Ser
         35                  40                  45

Phe Lys Thr Glu Tyr Thr Tyr Asp Glu Ala Lys Asp Ile Ile Ser Gly
     50                  55                  60

Phe Ser Ser Asp Pro Ala Ser Asp Val Leu Ser Gln Leu Gln Gln Ala
 65                  70                  75                  80

Ala Thr Thr Gly Thr Arg Thr Ala Glu Ile Arg Ala Glu Val Phe Ala
                85                  90                  95

Asp Arg Thr Asp Asp Tyr Asn Glu Ser Gln Thr Ala Leu Lys Glu Asp
            100                 105                 110

Phe Gln Asn Cys Ile Asp Ala Ile Asp Asp Ala Arg Pro Ile Pro Leu
        115                 120                 125

Gln Tyr Ile Leu Ile Gly Gly Ala Ile Ala Leu Ala Val Ile Val Leu
    130                 135                 140
```

```
Gly Ile Arg Ala Trp Thr Asn Ser Arg Lys Gln Ser Lys His Ser Gln
145                 150                 155                 160
```

<210> 277
<211> 298
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(298)
<223> FRXA00520

<400> 277
gttgacgcac tgaagaagta aagtctcttc acaaaaagcg ctgtgcttcc tcacatggaa 60

```
gcacagcgct ttttcatatt tttattgcca taatgggcac atg cgt ttt tct cga   115
                                            Met Arg Phe Ser Arg
                                              1               5

gtt ctt ccc gca ctt ctt atc acc acc gcc gtg agc atc cca aca gca   163
Val Leu Pro Ala Leu Leu Ile Thr Thr Ala Val Ser Ile Pro Thr Ala
                 10                  15                  20

tct gct gcc aca ctc acc ggc gac acc gac aag gaa ttg tgc atc gcc   211
Ser Ala Ala Thr Leu Thr Gly Asp Thr Asp Lys Glu Leu Cys Ile Ala
             25                  30                  35

agc aac acc gac gat tcc gcg gtg gtt acc ttc tgg aac tcc att gaa   259
Ser Asn Thr Asp Asp Ser Ala Val Val Thr Phe Trp Asn Ser Ile Glu
         40                  45                  50

gac tcc gtg cgc gaa caa cgc ctc gac gaa cta gac gcc               298
Asp Ser Val Arg Glu Gln Arg Leu Asp Glu Leu Asp Ala
     55                  60                  65
```

<210> 278
<211> 66
<212> PRT
<213> Corynebacterium glutamicum

<400> 278

```
Met Arg Phe Ser Arg Val Leu Pro Ala Leu Leu Ile Thr Thr Ala Val
  1               5                  10                  15

Ser Ile Pro Thr Ala Ser Ala Ala Thr Leu Thr Gly Asp Thr Asp Lys
             20                  25                  30

Glu Leu Cys Ile Ala Ser Asn Thr Asp Asp Ser Ala Val Val Thr Phe
         35                  40                  45

Trp Asn Ser Ile Glu Asp Ser Val Arg Glu Gln Arg Leu Asp Glu Leu
     50                  55                  60

Asp Ala
```

65

<210> 279
<211> 1887
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1864)
<223> RXN00527

<400> 279
ttccttggcc ccgaagaaat taatcattgt ggccgtggtc ctgattttga tcattgcggc 60

tgcctcgttt tattttctgc gttcatcatc gaatgaccag gtg att gcc act tct 115
Val Ile Ala Thr Ser
1 5

gat gtt cgg gag att tcc tcc gag gga atc gtg gcg cgt gtg tct gtc 163
Asp Val Arg Glu Ile Ser Ser Glu Gly Ile Val Ala Arg Val Ser Val
10 15 20

aac gga aat att gaa gct gcg cga acc acc acc att tac acc agt ctg 211
Asn Gly Asn Ile Glu Ala Ala Arg Thr Thr Thr Ile Tyr Thr Ser Leu
25 30 35

act gtg ccg gtc gcg aac ttg ccg gtt gcg gtt ggt gac cgt gtg gca 259
Thr Val Pro Val Ala Asn Leu Pro Val Ala Val Gly Asp Arg Val Ala
40 45 50

gct gat cag gtg ttg gct gag ttg gat gcc tct gcc ctg caa cga cag 307
Ala Asp Gln Val Leu Ala Glu Leu Asp Ala Ser Ala Leu Gln Arg Gln
55 60 65

ttg gat gaa act gat gcc aac aat gcg cgt gca gcc atg gcg aac cgc 355
Leu Asp Glu Thr Asp Ala Asn Asn Ala Arg Ala Ala Met Ala Asn Arg
70 75 80 85

aat tcc atc gcg cag tcg cag caa gca tat gag cag tcc agg gaa ctt 403
Asn Ser Ile Ala Gln Ser Gln Gln Ala Tyr Glu Gln Ser Arg Glu Leu
90 95 100

ctt gat agt ggt ttg agc ccg gag atc aac tcg gcg cgg tcc tcg ttg 451
Leu Asp Ser Gly Leu Ser Pro Glu Ile Asn Ser Ala Arg Ser Ser Leu
105 110 115

cgg gcg tcc tca cag gca tat cag gat gcg atc cgc agt ttt gaa gcg 499
Arg Ala Ser Ser Gln Ala Tyr Gln Asp Ala Ile Arg Ser Phe Glu Ala
120 125 130

aag cag cga gat gtg gat ggc gga ttg gat tcc acc atg gtc gct caa 547
Lys Gln Arg Asp Val Asp Gly Gly Leu Asp Ser Thr Met Val Ala Gln
135 140 145

tcg gat gct ctc aag gca gct cgt gag caa gca gat gct gct gaa att 595
Ser Asp Ala Leu Lys Ala Ala Arg Glu Gln Ala Asp Ala Ala Glu Ile
150 155 160 165

gaa cga ctg cgc gcg gac ttc gga ctg ctc aac aac gat cgc agc aac 643

```
Glu Arg Leu Arg Ala Asp Phe Gly Leu Leu Asn Asn Asp Arg Ser Asn
                170                 175                 180

ctc aac gat gtc att ggt ctg ctc gat gag aga gaa tct ttg gct tct   691
Leu Asn Asp Val Ile Gly Leu Leu Asp Glu Arg Glu Ser Leu Ala Ser
            185                 190                 195

gcg gaa tcc gaa cta gct caa gcc cgc gct gca ggt gac cta gag gca   739
Ala Glu Ser Glu Leu Ala Gln Ala Arg Ala Ala Gly Asp Leu Glu Ala
        200                 205                 210

gtc gct gca gct gaa gca aag gtt gca ggc ctg gaa caa tca att gct   787
Val Ala Ala Ala Glu Ala Lys Val Ala Gly Leu Glu Gln Ser Ile Ala
    215                 220                 225

tcc aaa acc tcc acg tgg cct agc caa gat cag act tac ttg cag tcc   835
Ser Lys Thr Ser Thr Trp Pro Ser Gln Asp Gln Thr Tyr Leu Gln Ser
230                 235                 240                 245

tac acc gct ttg gag gaa gct gag cga cgc gtc gca tcc acc act gaa   883
Tyr Thr Ala Leu Glu Glu Ala Glu Arg Arg Val Ala Ser Thr Thr Glu
                250                 255                 260

gct cta gaa ata gcc gag cgg atc tac att gat tca ctc gga aaa gtt   931
Ala Leu Glu Ile Ala Glu Arg Ile Tyr Ile Asp Ser Leu Gly Lys Val
            265                 270                 275

gac tca gaa cta gcc gcc gca cag cgc gcc gtt gcc gaa gcc cac tca   979
Asp Ser Glu Leu Ala Ala Ala Gln Arg Ala Val Ala Glu Ala His Ser
        280                 285                 290

gca caa caa gac gca gca ctt ggc ctc gag acc gcg cag ctt tcc acc  1027
Ala Gln Gln Asp Ala Ala Leu Gly Leu Glu Thr Ala Gln Leu Ser Thr
    295                 300                 305

caa cac caa ttg gaa gcc caa tca agc gcc atc gat gca gct tta ggt  1075
Gln His Gln Leu Glu Ala Gln Ser Ser Ala Ile Asp Ala Ala Leu Gly
310                 315                 320                 325

ttg gca tca gta gat aat gaa gcc gcc acc aga tcc acg tcc cag ctg  1123
Leu Ala Ser Val Asp Asn Glu Ala Ala Thr Arg Ser Thr Ser Gln Leu
                330                 335                 340

cgg atg gat atc aac aac acc acc gtt cgc tcc cca tac tca ggc att  1171
Arg Met Asp Ile Asn Asn Thr Thr Val Arg Ser Pro Tyr Ser Gly Ile
            345                 350                 355

gtt tca tcc gtg cag gca gcc caa ggt caa cca gca gcc ggc gca ctg  1219
Val Ser Ser Val Gln Ala Ala Gln Gly Gln Pro Ala Ala Gly Ala Leu
        360                 365                 370

ttg agt gtt gct gat gat tcc gaa ctg aag atc acc gcg aat gta aaa  1267
Leu Ser Val Ala Asp Asp Ser Glu Leu Lys Ile Thr Ala Asn Val Lys
    375                 380                 385

gaa gcg gag atc agc aac gtc acc atc gga tcc cgc gtc acc ttc act  1315
Glu Ala Glu Ile Ser Asn Val Thr Ile Gly Ser Arg Val Thr Phe Thr
390                 395                 400                 405

acc cca tcg acc gga acc aaa gaa ttc gcc ggc cga gta tcc aaa gtc  1363
Thr Pro Ser Thr Gly Thr Lys Glu Phe Ala Gly Arg Val Ser Lys Val
```

```
                410                 415                 420

tcc ccc att gca gct gcc gcc agt gcc cca gct aca ggt gaa gga gct   1411
Ser Pro Ile Ala Ala Ala Ala Ser Ala Pro Ala Thr Gly Glu Gly Ala
            425                 430                 435

gcc gca ggc gcc aca acc acc aac act gac gtc acc ttc ccc atc gaa   1459
Ala Ala Gly Ala Thr Thr Thr Asn Thr Asp Val Thr Phe Pro Ile Glu
        440                 445                 450

att tcc gtc acc ggc gac cgc gaa ggc ctc aac ctc ggc gga tcc gct   1507
Ile Ser Val Thr Gly Asp Arg Glu Gly Leu Asn Leu Gly Gly Ser Ala
    455                 460                 465

cga gta cgc atc gtc cat gaa atc gca cca cac gta ctg acc gtt cct   1555
Arg Val Arg Ile Val His Glu Ile Ala Pro His Val Leu Thr Val Pro
470                 475                 480                 485

ttg gaa gct gtg tac aaa aat gat gac ggc aaa gac gct gtt ttg atc   1603
Leu Glu Ala Val Tyr Lys Asn Asp Asp Gly Lys Asp Ala Val Leu Ile
                490                 495                 500

atc agc gac gac aac aaa gta gaa gaa gta gaa gta aaa aca gct gaa   1651
Ile Ser Asp Asp Asn Lys Val Glu Glu Val Glu Val Lys Thr Ala Glu
            505                 510                 515

tcc gat gac ttt gat atc gca gtc agc ggt gct gga att tca gaa gac   1699
Ser Asp Asp Phe Asp Ile Ala Val Ser Gly Ala Gly Ile Ser Glu Asp
        520                 525                 530

gct cga gtg ctc acc cag cct gga aac tac cgg ggc ctc atc gga gaa   1747
Ala Arg Val Leu Thr Gln Pro Gly Asn Tyr Arg Gly Leu Ile Gly Glu
    535                 540                 545

act gtg aaa ctt cac gca gat acg gtg gag cag gcg gcg gct cct ttt   1795
Thr Val Lys Leu His Ala Asp Thr Val Glu Gln Ala Ala Ala Pro Phe
550                 555                 560                 565

agt cct gcg gcc cct ttt gac cct gca gcc cct gcc gtt tct gcc aag   1843
Ser Pro Ala Ala Pro Phe Asp Pro Ala Ala Pro Ala Val Ser Ala Lys
                570                 575                 580

caa acc gtg ggc cag gtg att tagcctatga gcctcatcga aat             1887
Gln Thr Val Gly Gln Val Ile
            585
```

CCA GTC GAC TCT AGA GGA TCC CCG GGT ACC GAG CTC GAA TTC

<210> 280
<211> 588
<212> PRT
<213> Corynebacterium glutamicum

<400> 280

```
Val Ile Ala Thr Ser Asp Val Arg Glu Ile Ser Ser Glu Gly Ile Val
  1               5                  10                  15

Ala Arg Val Ser Val Asn Gly Asn Ile Glu Ala Ala Arg Thr Thr Thr
             20                  25                  30

Ile Tyr Thr Ser Leu Thr Val Pro Val Ala Asn Leu Pro Val Ala Val
         35                  40                  45
```

```
Gly Asp Arg Val Ala Ala Asp Gln Val Leu Ala Glu Leu Asp Ala Ser
     50                  55                  60

Ala Leu Gln Arg Gln Leu Asp Glu Thr Asp Ala Asn Asn Ala Arg Ala
 65                  70                  75                  80

Ala Met Ala Asn Arg Asn Ser Ile Ala Gln Ser Gln Gln Ala Tyr Glu
                 85                  90                  95

Gln Ser Arg Glu Leu Leu Asp Ser Gly Leu Ser Pro Glu Ile Asn Ser
            100                 105                 110

Ala Arg Ser Ser Leu Arg Ala Ser Ser Gln Ala Tyr Gln Asp Ala Ile
        115                 120                 125

Arg Ser Phe Glu Ala Lys Gln Arg Asp Val Asp Gly Gly Leu Asp Ser
    130                 135                 140

Thr Met Val Ala Gln Ser Asp Ala Leu Lys Ala Ala Arg Glu Gln Ala
145                 150                 155                 160

Asp Ala Ala Glu Ile Glu Arg Leu Arg Ala Asp Phe Gly Leu Leu Asn
                165                 170                 175

Asn Asp Arg Ser Asn Leu Asn Asp Val Ile Gly Leu Leu Asp Glu Arg
            180                 185                 190

Glu Ser Leu Ala Ser Ala Glu Ser Glu Leu Ala Gln Ala Arg Ala Ala
        195                 200                 205

Gly Asp Leu Glu Ala Val Ala Ala Ala Glu Ala Lys Val Ala Gly Leu
    210                 215                 220

Glu Gln Ser Ile Ala Ser Lys Thr Ser Thr Trp Pro Ser Gln Asp Gln
225                 230                 235                 240

Thr Tyr Leu Gln Ser Tyr Thr Ala Leu Glu Glu Ala Glu Arg Arg Val
                245                 250                 255

Ala Ser Thr Thr Glu Ala Leu Glu Ile Ala Glu Arg Ile Tyr Ile Asp
            260                 265                 270

Ser Leu Gly Lys Val Asp Ser Glu Leu Ala Ala Ala Gln Arg Ala Val
        275                 280                 285

Ala Glu Ala His Ser Ala Gln Gln Asp Ala Ala Leu Gly Leu Glu Thr
    290                 295                 300

Ala Gln Leu Ser Thr Gln His Gln Leu Glu Ala Gln Ser Ser Ala Ile
305                 310                 315                 320

Asp Ala Ala Leu Gly Leu Ala Ser Val Asp Asn Glu Ala Ala Thr Arg
                325                 330                 335

Ser Thr Ser Gln Leu Arg Met Asp Ile Asn Asn Thr Thr Val Arg Ser
            340                 345                 350

Pro Tyr Ser Gly Ile Val Ser Ser Val Gln Ala Ala Gln Gly Gln Pro
        355                 360                 365
```

```
Ala Ala Gly Ala Leu Leu Ser Val Ala Asp Asp Ser Glu Leu Lys Ile
    370                 375                 380

Thr Ala Asn Val Lys Glu Ala Glu Ile Ser Asn Val Thr Ile Gly Ser
385                 390                 395                 400

Arg Val Thr Phe Thr Thr Pro Ser Thr Gly Thr Lys Glu Phe Ala Gly
                405                 410                 415

Arg Val Ser Lys Val Ser Pro Ile Ala Ala Ala Ala Ser Ala Pro Ala
            420                 425                 430

Thr Gly Glu Gly Ala Ala Ala Gly Ala Thr Thr Thr Asn Thr Asp Val
        435                 440                 445

Thr Phe Pro Ile Glu Ile Ser Val Thr Gly Asp Arg Glu Gly Leu Asn
    450                 455                 460

Leu Gly Gly Ser Ala Arg Val Arg Ile Val His Glu Ile Ala Pro His
465                 470                 475                 480

Val Leu Thr Val Pro Leu Glu Ala Val Tyr Lys Asn Asp Asp Gly Lys
                485                 490                 495

Asp Ala Val Leu Ile Ile Ser Asp Asp Asn Lys Val Glu Glu Val Glu
            500                 505                 510

Val Lys Thr Ala Glu Ser Asp Asp Phe Asp Ile Ala Val Ser Gly Ala
        515                 520                 525

Gly Ile Ser Glu Asp Ala Arg Val Leu Thr Gln Pro Gly Asn Tyr Arg
    530                 535                 540

Gly Leu Ile Gly Glu Thr Val Lys Leu His Ala Asp Thr Val Glu Gln
545                 550                 555                 560

Ala Ala Ala Pro Phe Ser Pro Ala Ala Pro Phe Asp Pro Ala Ala Pro
                565                 570                 575

Ala Val Ser Ala Lys Gln Thr Val Gly Gln Val Ile
            580                 585
```

<210> 281
<211> 1887
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1864)
<223> FRXA00527

<400> 281
ttccttggcc ccgaagaaat taatcattgt ggccgtggtc ctgattttga tcattgcggc 60

tgcctcgttt tattttctgc gttcatcatc gaatgaccag gtg att gcc act tct 115
                                                Val Ile Ala Thr Ser
                                                  1   5

gat gtt cgg gag att tcc tcc gag gga atc gtg gcg cgt gtg tct gtc 163

```
Asp Val Arg Glu Ile Ser Ser Glu Gly Ile Val Ala Arg Val Ser Val
                 10                  15                  20

aac gga aat att gaa gct gcg cga acc acc acc att tac acc agt ctg   211
Asn Gly Asn Ile Glu Ala Ala Arg Thr Thr Thr Ile Tyr Thr Ser Leu
            25                  30                  35

act gtg ccg gtc gcg aac ttg ccg gtt gcg gtt ggt gac cgt gtg gca   259
Thr Val Pro Val Ala Asn Leu Pro Val Ala Val Gly Asp Arg Val Ala
        40                  45                  50

gct gat cag gtg ttg gct gag ttg gat gcc tct gcc ctg caa cga cag   307
Ala Asp Gln Val Leu Ala Glu Leu Asp Ala Ser Ala Leu Gln Arg Gln
    55                  60                  65

ttg gat gaa act gat gcc aac aat gcg cgt gca gcc atg gcg aac cgc   355
Leu Asp Glu Thr Asp Ala Asn Asn Ala Arg Ala Ala Met Ala Asn Arg
70                  75                  80                  85

aat tcc atc gcg cag tcg cag caa gca tat gag cag tcc agg gaa ctt   403
Asn Ser Ile Ala Gln Ser Gln Gln Ala Tyr Glu Gln Ser Arg Glu Leu
                90                  95                 100

ctt gat agt ggt ttg agc ccg gag atc aac tcg gcg cgg tcc tcg ttg   451
Leu Asp Ser Gly Leu Ser Pro Glu Ile Asn Ser Ala Arg Ser Ser Leu
            105                 110                 115

cgg gcg tcc tca cag gca tat cag gat gcg atc cgc agt ttt gaa gcg   499
Arg Ala Ser Ser Gln Ala Tyr Gln Asp Ala Ile Arg Ser Phe Glu Ala
        120                 125                 130

aag cag cga gat gtg gat ggc gga ttg gat tcc acc atg gtc gct caa   547
Lys Gln Arg Asp Val Asp Gly Gly Leu Asp Ser Thr Met Val Ala Gln
    135                 140                 145

tcg gat gct ctc aag gca gct cgt gag caa gca gat gct gct gaa att   595
Ser Asp Ala Leu Lys Ala Ala Arg Glu Gln Ala Asp Ala Ala Glu Ile
150                 155                 160                 165

gaa cga ctg cgc gcg gac ttc gga ctg ctc aac aac gat cgc agc aac   643
Glu Arg Leu Arg Ala Asp Phe Gly Leu Leu Asn Asn Asp Arg Ser Asn
                170                 175                 180

ctc aac gat gtc att ggt ctg ctc gat gag aga gaa tct ttg gct tct   691
Leu Asn Asp Val Ile Gly Leu Leu Asp Glu Arg Glu Ser Leu Ala Ser
            185                 190                 195

gcg gaa tcc gaa cta gct caa gcc cgc gct gca ggt gac cta gag gca   739
Ala Glu Ser Glu Leu Ala Gln Ala Arg Ala Ala Gly Asp Leu Glu Ala
        200                 205                 210

gtc gct gca gct gaa gca aag gtt gca ggc ctg gaa caa tca att gct   787
Val Ala Ala Ala Glu Ala Lys Val Ala Gly Leu Glu Gln Ser Ile Ala
    215                 220                 225

tcc aaa acc tcc acg tgg cct agc caa gat cag act tac ttg cag tcc   835
Ser Lys Thr Ser Thr Trp Pro Ser Gln Asp Gln Thr Tyr Leu Gln Ser
230                 235                 240                 245

tac acc gct ttg gag gaa gct gag cga cgc gtc gca tcc acc act gaa   883
Tyr Thr Ala Leu Glu Glu Ala Glu Arg Arg Val Ala Ser Thr Thr Glu
```

```
                    250                 255                 260

gct cta gaa ata gcc gag cgg atc tac att gat tca ctc gga aaa gtt   931
Ala Leu Glu Ile Ala Glu Arg Ile Tyr Ile Asp Ser Leu Gly Lys Val
            265                 270                 275

gac tca gaa cta gcc gcc gca cag cgc gcc gtt gcc gaa gcc cac tca   979
Asp Ser Glu Leu Ala Ala Ala Gln Arg Ala Val Ala Glu Ala His Ser
        280                 285                 290

gca caa caa gac gca gca ctt ggc ctc gag acc gcg cag ctt tcc acc  1027
Ala Gln Gln Asp Ala Ala Leu Gly Leu Glu Thr Ala Gln Leu Ser Thr
    295                 300                 305

caa cac caa ttg gaa gcc caa tca agc gcc atc gat gca gct tta ggt  1075
Gln His Gln Leu Glu Ala Gln Ser Ser Ala Ile Asp Ala Ala Leu Gly
310                 315                 320                 325

ttg gca tca gta gat aat gaa gcc gcc acc aga tcc acg tcc cag ctg  1123
Leu Ala Ser Val Asp Asn Glu Ala Ala Thr Arg Ser Thr Ser Gln Leu
                330                 335                 340

cgg atg gat atc aac aac acc acc gtt cgc tcc cca tac tca ggc att  1171
Arg Met Asp Ile Asn Asn Thr Thr Val Arg Ser Pro Tyr Ser Gly Ile
            345                 350                 355

gtt tca tcc gtg cag gca gcc caa ggt caa cca gca gcc ggc gca ctg  1219
Val Ser Ser Val Gln Ala Ala Gln Gly Gln Pro Ala Ala Gly Ala Leu
        360                 365                 370

ttg agt gtt gct gat gat tcc gaa ctg aag atc acc gcg aat gta aaa  1267
Leu Ser Val Ala Asp Asp Ser Glu Leu Lys Ile Thr Ala Asn Val Lys
    375                 380                 385

gaa gcg gag atc agc aac gtc acc atc gga tcc cgc gtc acc ttc act  1315
Glu Ala Glu Ile Ser Asn Val Thr Ile Gly Ser Arg Val Thr Phe Thr
390                 395                 400                 405

acc cca tcg acc gga acc aaa gaa ttc gcc ggc cga gta tcc aaa gtc  1363
Thr Pro Ser Thr Gly Thr Lys Glu Phe Ala Gly Arg Val Ser Lys Val
                410                 415                 420

tcc ccc att gca gct gcc gcc agt gcc cca gct aca ggt gaa gga gct  1411
Ser Pro Ile Ala Ala Ala Ala Ser Ala Pro Ala Thr Gly Glu Gly Ala
            425                 430                 435

gcc gca ggc gcc aca acc acc aac act gac gtc acc ttc ccc atc gaa  1459
Ala Ala Gly Ala Thr Thr Thr Asn Thr Asp Val Thr Phe Pro Ile Glu
        440                 445                 450

att tcc gtc acc ggc gac cgc gaa ggc ctc aac ctc ggc gga tcc gct  1507
Ile Ser Val Thr Gly Asp Arg Glu Gly Leu Asn Leu Gly Gly Ser Ala
    455                 460                 465

cga gta cgc atc gtc cat gaa atc gca cca cac gta ctg acc gtt cct  1555
Arg Val Arg Ile Val His Glu Ile Ala Pro His Val Leu Thr Val Pro
470                 475                 480                 485

ttg gaa gct gtg tac aaa aat gat gac ggc aaa gac gct gtt ttg atc  1603
Leu Glu Ala Val Tyr Lys Asn Asp Asp Gly Lys Asp Ala Val Leu Ile
                490                 495                 500
```

```
atc agc gac gac aac aaa gta gaa gaa gta gaa gta aaa aca gct gaa   1651
Ile Ser Asp Asp Asn Lys Val Glu Glu Val Glu Val Lys Thr Ala Glu
            505                 510                 515

tcc gat gac ttt gat atc gca gtc agc ggt gct gga att tca gaa gac   1699
Ser Asp Asp Phe Asp Ile Ala Val Ser Gly Ala Gly Ile Ser Glu Asp
        520                 525                 530

gct cga gtg ctc acc cag cct gga aac tac cgg ggc ctc atc gga gaa   1747
Ala Arg Val Leu Thr Gln Pro Gly Asn Tyr Arg Gly Leu Ile Gly Glu
    535                 540                 545

act gtg aaa ctt cac gca gat acg gtg gag cag gcg gcg gct cct ttt   1795
Thr Val Lys Leu His Ala Asp Thr Val Glu Gln Ala Ala Ala Pro Phe
550                 555                 560                 565

agt cct gcg gcc cct ttt gac cct gca gcc cct gcc gtt tct gcc aag   1843
Ser Pro Ala Ala Pro Phe Asp Pro Ala Ala Pro Ala Val Ser Ala Lys
                570                 575                 580

caa acc gtg ggc cag gtg att tagcctatga gcctcatcga aat             1887
Gln Thr Val Gly Gln Val Ile
            585
```

<210> 282
<211> 588
<212> PRT
<213> Corynebacterium glutamicum

<400> 282

```
Val Ile Ala Thr Ser Asp Val Arg Glu Ile Ser Ser Glu Gly Ile Val
  1               5                  10                  15

Ala Arg Val Ser Val Asn Gly Asn Ile Glu Ala Ala Arg Thr Thr Thr
             20                  25                  30

Ile Tyr Thr Ser Leu Thr Val Pro Val Ala Asn Leu Pro Val Ala Val
         35                  40                  45

Gly Asp Arg Val Ala Ala Asp Gln Val Leu Ala Glu Leu Asp Ala Ser
     50                  55                  60

Ala Leu Gln Arg Gln Leu Asp Glu Thr Asp Ala Asn Asn Ala Arg Ala
 65                  70                  75                  80

Ala Met Ala Asn Arg Asn Ser Ile Ala Gln Ser Gln Gln Ala Tyr Glu
                 85                  90                  95

Gln Ser Arg Glu Leu Leu Asp Ser Gly Leu Ser Pro Glu Ile Asn Ser
            100                 105                 110

Ala Arg Ser Ser Leu Arg Ala Ser Ser Gln Ala Tyr Gln Asp Ala Ile
        115                 120                 125

Arg Ser Phe Glu Ala Lys Gln Arg Asp Val Asp Gly Gly Leu Asp Ser
    130                 135                 140

Thr Met Val Ala Gln Ser Asp Ala Leu Lys Ala Ala Arg Glu Gln Ala
145                 150                 155                 160
```

```
Asp Ala Ala Glu Ile Glu Arg Leu Arg Ala Asp Phe Gly Leu Leu Asn
                  165                 170                 175

Asn Asp Arg Ser Asn Leu Asn Asp Val Ile Gly Leu Leu Asp Glu Arg
             180                 185                 190

Glu Ser Leu Ala Ser Ala Glu Ser Glu Leu Ala Gln Ala Arg Ala Ala
         195                 200                 205

Gly Asp Leu Glu Ala Val Ala Ala Ala Glu Ala Lys Val Ala Gly Leu
     210                 215                 220

Glu Gln Ser Ile Ala Ser Lys Thr Ser Thr Trp Pro Ser Gln Asp Gln
225                 230                 235                 240

Thr Tyr Leu Gln Ser Tyr Thr Ala Leu Glu Glu Ala Glu Arg Arg Val
                  245                 250                 255

Ala Ser Thr Thr Glu Ala Leu Glu Ile Ala Glu Arg Ile Tyr Ile Asp
             260                 265                 270

Ser Leu Gly Lys Val Asp Ser Glu Leu Ala Ala Ala Gln Arg Ala Val
         275                 280                 285

Ala Glu Ala His Ser Ala Gln Gln Asp Ala Ala Leu Gly Leu Glu Thr
     290                 295                 300

Ala Gln Leu Ser Thr Gln His Gln Leu Glu Ala Gln Ser Ser Ala Ile
305                 310                 315                 320

Asp Ala Ala Leu Gly Leu Ala Ser Val Asp Asn Glu Ala Ala Thr Arg
                  325                 330                 335

Ser Thr Ser Gln Leu Arg Met Asp Ile Asn Asn Thr Thr Val Arg Ser
             340                 345                 350

Pro Tyr Ser Gly Ile Val Ser Ser Val Gln Ala Ala Gln Gly Gln Pro
         355                 360                 365

Ala Ala Gly Ala Leu Leu Ser Val Ala Asp Asp Ser Glu Leu Lys Ile
     370                 375                 380

Thr Ala Asn Val Lys Glu Ala Glu Ile Ser Asn Val Thr Ile Gly Ser
385                 390                 395                 400

Arg Val Thr Phe Thr Thr Pro Ser Thr Gly Thr Lys Glu Phe Ala Gly
                  405                 410                 415

Arg Val Ser Lys Val Ser Pro Ile Ala Ala Ala Ala Ser Ala Pro Ala
             420                 425                 430

Thr Gly Glu Gly Ala Ala Ala Gly Ala Thr Thr Thr Asn Thr Asp Val
         435                 440                 445

Thr Phe Pro Ile Glu Ile Ser Val Thr Gly Asp Arg Glu Gly Leu Asn
     450                 455                 460

Leu Gly Gly Ser Ala Arg Val Arg Ile Val His Glu Ile Ala Pro His
465                 470                 475                 480
```

```
Val Leu Thr Val Pro Leu Glu Ala Val Tyr Lys Asn Asp Asp Gly Lys
                485                 490                 495

Asp Ala Val Leu Ile Ile Ser Asp Asp Asn Lys Val Glu Glu Val Glu
            500                 505                 510

Val Lys Thr Ala Glu Ser Asp Asp Phe Asp Ile Ala Val Ser Gly Ala
        515                 520                 525

Gly Ile Ser Glu Asp Ala Arg Val Leu Thr Gln Pro Gly Asn Tyr Arg
    530                 535                 540

Gly Leu Ile Gly Glu Thr Val Lys Leu His Ala Asp Thr Val Glu Gln
545                 550                 555                 560

Ala Ala Ala Pro Phe Ser Pro Ala Ala Pro Phe Asp Pro Ala Ala Pro
                565                 570                 575

Ala Val Ser Ala Lys Gln Thr Val Gly Gln Val Ile
            580                 585
```

<210> 283
<211> 1521
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1498)
<223> RXN00547

<400> 283

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ggtcgtagcc taaacgacct taaaaaggag ccgaccgccg atggaccaga aattggacca 60

gcagaaggta gaccgcgtat cgcccggtga tagtgaaccg gtg gca cgg gat ttt   115
                                            Val Ala Arg Asp Phe
                                              1               5

atc aat gca atc ggc ggt cgg ttt ggt cgt ttt gcg cag gtg ggc act   163
Ile Asn Ala Ile Gly Gly Arg Phe Gly Arg Phe Ala Gln Val Gly Thr
                 10                  15                  20

cag cgg ttc tgg act ccc ctg cgt gtt ttg atc acc act tcc ctg gtg   211
Gln Arg Phe Trp Thr Pro Leu Arg Val Leu Ile Thr Thr Ser Leu Val
             25                  30                  35

ttt ttg gcc atg ggg ttt tta aca aaa gcc aat tgc atc cag ggt tct   259
Phe Leu Ala Met Gly Phe Leu Thr Lys Ala Asn Cys Ile Gln Gly Ser
         40                  45                  50

aga ggt act gat ggt gtg gtt tct ttg aac tgg tcg gga agt cgc cag   307
Arg Gly Thr Asp Gly Val Val Ser Leu Asn Trp Ser Gly Ser Arg Gln
     55                  60                  65

tac acc tca gcc tgt tac aac gac atc gtt ccg ctc tat ggg ggg cgc   355
Tyr Thr Ser Ala Cys Tyr Asn Asp Ile Val Pro Leu Tyr Gly Gly Arg
 70                  75                  80                  85

gga att gat gcg cca ggt ttc cct tat gcc ttt tcg tgg cag gaa ggt   403
Gly Ile Asp Ala Pro Gly Phe Pro Tyr Ala Phe Ser Trp Gln Glu Gly
```

```
                    90                  95                 100

gat ctc acc agg tac atg gag tac ccg gtg ttg ggc gga att ttc cag   451
Asp Leu Thr Arg Tyr Met Glu Tyr Pro Val Leu Gly Gly Ile Phe Gln
            105                 110                 115

tgg att tgt ggc att atc acg cgg ttt ttg tac ccg gtt gtt gat gtc   499
Trp Ile Cys Gly Ile Ile Thr Arg Phe Leu Tyr Pro Val Val Asp Val
        120                 125                 130

att ccg ttt cat acg ctg cct gaa tct ggt ctt tat ttc atc gtc acc   547
Ile Pro Phe His Thr Leu Pro Glu Ser Gly Leu Tyr Phe Ile Val Thr
    135                 140                 145

gcg ctt gcg ttg gcg ttc ttt tgg gtg ttg gtc atc cgc atg atg gtg   595
Ala Leu Ala Leu Ala Phe Phe Trp Val Leu Val Ile Arg Met Met Val
150                 155                 160                 165

gag ctc act ggc aat cga gtg tgg gat acc gtc ctt gtt gcg gcg tct   643
Glu Leu Thr Gly Asn Arg Val Trp Asp Thr Val Leu Val Ala Ala Ser
                170                 175                 180

ccc ctg gtt gct gtg cat gcg ttt acc aac tgg gat act cca gcc att   691
Pro Leu Val Ala Val His Ala Phe Thr Asn Trp Asp Thr Pro Ala Ile
            185                 190                 195

gcg gcg gtg att ggt gcg atg ctt gcg gtg aaa cgc gga aac ccc ttg   739
Ala Ala Val Ile Gly Ala Met Leu Ala Val Lys Arg Gly Asn Pro Leu
        200                 205                 210

gtt gcg ggt gtg ctg atc ggc gcg ggt acg gcg ttc aaa ttg tgg ccg   787
Val Ala Gly Val Leu Ile Gly Ala Gly Thr Ala Phe Lys Leu Trp Pro
    215                 220                 225

ctt tat ctt ctt ggt gcg tat ttg gtg ctg gcg gtc aag aat aag aat   835
Leu Tyr Leu Leu Gly Ala Tyr Leu Val Leu Ala Val Lys Asn Lys Asn
230                 235                 240                 245

ctc aag ccg ttt atc acc atg gct gca gcg gct gcg gtg aca tgg ctc   883
Leu Lys Pro Phe Ile Thr Met Ala Ala Ala Ala Ala Val Thr Trp Leu
                250                 255                 260

gtg gtg aat gtg cca gtg atg atc gcg tac ccc aag gcg tgg aat gaa   931
Val Val Asn Val Pro Val Met Ile Ala Tyr Pro Lys Ala Trp Asn Glu
            265                 270                 275

ttc ttg cgc ctg aac cgg gag cgt ggt gcg gag tgg acc acg att tac   979
Phe Leu Arg Leu Asn Arg Glu Arg Gly Ala Glu Trp Thr Thr Ile Tyr
        280                 285                 290

cag gtc atc gac cgt aat ttg ccg atc aat ttg aat gat cca gtg ctg   1027
Gln Val Ile Asp Arg Asn Leu Pro Ile Asn Leu Asn Asp Pro Val Leu
    295                 300                 305

ctt aat gtg ctg agc ttc ggc ttg ttt ggt gca tcg tgt gtg gcc att   1075
Leu Asn Val Leu Ser Phe Gly Leu Phe Gly Ala Ser Cys Val Ala Ile
310                 315                 320                 325

ttg atc ctt ggg ctc aag gtg cag cgc act ccc cga gtc gct gag ctg   1123
Leu Ile Leu Gly Leu Lys Val Gln Arg Thr Pro Arg Val Ala Glu Leu
                330                 335                 340
```

```
gcc ttt ttg att gtc gcg gcg ttt ttg ctg ttt aac aag gtg tgg agt   1171
Ala Phe Leu Ile Val Ala Ala Phe Leu Leu Phe Asn Lys Val Trp Ser
            345                 350                 355

cct cag tat tca ctg tgg ctg gtc ccg ttg gct gtt ctg gca ttt cct   1219
Pro Gln Tyr Ser Leu Trp Leu Val Pro Leu Ala Val Leu Ala Phe Pro
        360                 365                 370

cag tgg aaa gtg ctg ttc ccg tgg atg gtt aca gac gcc atg gtg tgg   1267
Gln Trp Lys Val Leu Phe Pro Trp Met Val Thr Asp Ala Met Val Trp
    375                 380                 385

cca att ttg atg tgg cac atg ctc ggc acg gac aac aag gga ctc ccc   1315
Pro Ile Leu Met Trp His Met Leu Gly Thr Asp Asn Lys Gly Leu Pro
390                 395                 400                 405

cat gaa atg ttg gat ctc atc gtg att tcc cga gat gcc ttc att gtg   1363
His Glu Met Leu Asp Leu Ile Val Ile Ser Arg Asp Ala Phe Ile Val
                410                 415                 420

gtc atg ata gta ggt gta atc cgg cag atg ctc gga cga cgt gca gat   1411
Val Met Ile Val Gly Val Ile Arg Gln Met Leu Gly Arg Arg Ala Asp
            425                 430                 435

ccg gtg atg gat gcg cac gcc ggg cgc gat ttg ttg gcc ggg ccc ttc   1459
Pro Val Met Asp Ala His Ala Gly Arg Asp Leu Leu Ala Gly Pro Phe
        440                 445                 450

ggc gca ggc gag cgt cga aaa gca ttg aag gaa gta agt tgagcacaac    1508
Gly Ala Gly Glu Arg Arg Lys Ala Leu Lys Glu Val Ser
    455                 460                 465

agttttgctg gtc                                                   1521
```

<210> 284
<211> 466
<212> PRT
<213> Corynebacterium glutamicum

<400> 284

```
Val Ala Arg Asp Phe Ile Asn Ala Ile Gly Gly Arg Phe Gly Arg Phe
  1               5                  10                  15

Ala Gln Val Gly Thr Gln Arg Phe Trp Thr Pro Leu Arg Val Leu Ile
             20                  25                  30

Thr Thr Ser Leu Val Phe Leu Ala Met Gly Phe Leu Thr Lys Ala Asn
         35                  40                  45

Cys Ile Gln Gly Ser Arg Gly Thr Asp Gly Val Val Ser Leu Asn Trp
     50                  55                  60

Ser Gly Ser Arg Gln Tyr Thr Ser Ala Cys Tyr Asn Asp Ile Val Pro
 65                  70                  75                  80

Leu Tyr Gly Gly Arg Gly Ile Asp Ala Pro Gly Phe Pro Tyr Ala Phe
                 85                  90                  95

Ser Trp Gln Glu Gly Asp Leu Thr Arg Tyr Met Glu Tyr Pro Val Leu
```

```
            100                 105                 110

Gly Gly Ile Phe Gln Trp Ile Cys Gly Ile Ile Thr Arg Phe Leu Tyr
        115                 120                 125

Pro Val Val Asp Val Ile Pro Phe His Thr Leu Pro Glu Ser Gly Leu
    130                 135                 140

Tyr Phe Ile Val Thr Ala Leu Ala Leu Ala Phe Phe Trp Val Leu Val
145                 150                 155                 160

Ile Arg Met Met Val Glu Leu Thr Gly Asn Arg Val Trp Asp Thr Val
                165                 170                 175

Leu Val Ala Ala Ser Pro Leu Val Ala Val His Ala Phe Thr Asn Trp
            180                 185                 190

Asp Thr Pro Ala Ile Ala Ala Val Ile Gly Ala Met Leu Ala Val Lys
        195                 200                 205

Arg Gly Asn Pro Leu Val Ala Gly Val Leu Ile Gly Ala Gly Thr Ala
    210                 215                 220

Phe Lys Leu Trp Pro Leu Tyr Leu Leu Gly Ala Tyr Leu Val Leu Ala
225                 230                 235                 240

Val Lys Asn Lys Asn Leu Lys Pro Phe Ile Thr Met Ala Ala Ala Ala
                245                 250                 255

Ala Val Thr Trp Leu Val Val Asn Val Pro Val Met Ile Ala Tyr Pro
            260                 265                 270

Lys Ala Trp Asn Glu Phe Leu Arg Leu Asn Arg Glu Arg Gly Ala Glu
        275                 280                 285

Trp Thr Thr Ile Tyr Gln Val Ile Asp Arg Asn Leu Pro Ile Asn Leu
    290                 295                 300

Asn Asp Pro Val Leu Leu Asn Val Leu Ser Phe Gly Leu Phe Gly Ala
305                 310                 315                 320

Ser Cys Val Ala Ile Leu Ile Leu Gly Leu Lys Val Gln Arg Thr Pro
                325                 330                 335

Arg Val Ala Glu Leu Ala Phe Leu Ile Val Ala Ala Phe Leu Leu Phe
            340                 345                 350

Asn Lys Val Trp Ser Pro Gln Tyr Ser Leu Trp Leu Val Pro Leu Ala
        355                 360                 365

Val Leu Ala Phe Pro Gln Trp Lys Val Leu Phe Pro Trp Met Val Thr
    370                 375                 380

Asp Ala Met Val Trp Pro Ile Leu Met Trp His Met Leu Gly Thr Asp
385                 390                 395                 400

Asn Lys Gly Leu Pro His Glu Met Leu Asp Leu Ile Val Ile Ser Arg
                405                 410                 415

Asp Ala Phe Ile Val Val Met Ile Val Gly Val Ile Arg Gln Met Leu
            420                 425                 430
```

```
Gly Arg Arg Ala Asp Pro Val Met Asp Ala His Ala Gly Arg Asp Leu
        435                 440                 445

Leu Ala Gly Pro Phe Gly Ala Gly Glu Arg Arg Lys Ala Leu Lys Glu
    450                 455                 460

Val Ser
465
```

<210> 285
<211> 514
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(514)
<223> FRXA00547

<400> 285

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accacgattt accaggtcat cgaccgtaat ttgccgatca atttgaatga tccagtgctg 60

cttaatgtgc tgagcttcgg cttgtttggt gcatcagtgt gtg gcc att ttg atc   115
                                          Val Ala Ile Leu Ile
                                            1               5

ctt ggg ctc aag gtg cag cgc act ccc cga gtc gct gag ctg gcc ttt   163
Leu Gly Leu Lys Val Gln Arg Thr Pro Arg Val Ala Glu Leu Ala Phe
                  10                  15                  20

ttg att gtc gcg gcg ttt ttg ctg ttt aac aag gtg tgg agt cct cag   211
Leu Ile Val Ala Ala Phe Leu Leu Phe Asn Lys Val Trp Ser Pro Gln
             25                  30                  35

tat tca ctg tgg ctg gtc ccg ttg gct gtt ctg gca ttt cct cag tgg   259
Tyr Ser Leu Trp Leu Val Pro Leu Ala Val Leu Ala Phe Pro Gln Trp
         40                  45                  50

aaa gtg ctg ttc ccg tgg atg gtt aca gac gcc atg gtg tgg cca att   307
Lys Val Leu Phe Pro Trp Met Val Thr Asp Ala Met Val Trp Pro Ile
     55                  60                  65

ttg atg tgg cac atg ctc ggc acg gac aac aag gga ctc ccc cat gaa   355
Leu Met Trp His Met Leu Gly Thr Asp Asn Lys Gly Leu Pro His Glu
 70                  75                  80                  85

atg ttg gat ctc atc gtg att tcc cga gat gcc ttc att gtg gtc atg   403
Met Leu Asp Leu Ile Val Ile Ser Arg Asp Ala Phe Ile Val Val Met
                 90                  95                 100

ata agt agg tgt aat ccg gca gat gct cgg acg acg tgc aaa tcc ggt   451
Ile Ser Arg Cys Asn Pro Ala Asp Ala Arg Thr Thr Cys Lys Ser Gly
            105                 110                 115

gat gga tgc gca cgc cgg gcg cga att gtt ggc cgg gcc ctt cgg cgc   499
Asp Gly Cys Ala Arg Arg Ala Arg Ile Val Gly Arg Ala Leu Arg Arg
        120                 125                 130

aag cga agc gtc gaa                                              514
```

```
Lys Arg Ser Val Glu
    135


<210> 286
<211> 138
<212> PRT
<213> Corynebacterium glutamicum

<400> 286
Val Ala Ile Leu Ile Leu Gly Leu Lys Val Gln Arg Thr Pro Arg Val
  1               5                  10                  15

Ala Glu Leu Ala Phe Leu Ile Val Ala Ala Phe Leu Leu Phe Asn Lys
            20                  25                  30

Val Trp Ser Pro Gln Tyr Ser Leu Trp Leu Val Pro Leu Ala Val Leu
        35                  40                  45

Ala Phe Pro Gln Trp Lys Val Leu Phe Pro Trp Met Val Thr Asp Ala
    50                  55                  60

Met Val Trp Pro Ile Leu Met Trp His Met Leu Gly Thr Asp Asn Lys
65                  70                  75                  80

Gly Leu Pro His Glu Met Leu Asp Leu Ile Val Ile Ser Arg Asp Ala
                85                  90                  95

Phe Ile Val Val Met Ile Ser Arg Cys Asn Pro Ala Asp Ala Arg Thr
            100                 105                 110

Thr Cys Lys Ser Gly Asp Gly Cys Ala Arg Arg Ala Arg Ile Val Gly
        115                 120                 125

Arg Ala Leu Arg Arg Lys Arg Ser Val Glu
    130                 135


<210> 287
<211> 713
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(690)
<223> FRXA00546

<400> 287
ccg gtg ttg ggc gga att ttc cag tgg att tgt ggc att atc acg cgg   48
Pro Val Leu Gly Gly Ile Phe Gln Trp Ile Cys Gly Ile Ile Thr Arg
  1               5                  10                  15

ttt ttg tac ccg gtt gtt gat gtc att ccg ttt cat acg ctg cct gaa   96
Phe Leu Tyr Pro Val Val Asp Val Ile Pro Phe His Thr Leu Pro Glu
            20                  25                  30

tct ggt ctt tat ttc atc gtc acc gcg ctt gcg ttg gcg ttc ttt tgg  144
Ser Gly Leu Tyr Phe Ile Val Thr Ala Leu Ala Leu Ala Phe Phe Trp
        35                  40                  45
```

```
gtg ttg gtc atc cgc atg atg gtg gag ctc act ggc aat cga gtg tgg   192
Val Leu Val Ile Arg Met Met Val Glu Leu Thr Gly Asn Arg Val Trp
     50                  55                  60

gat acc gtc ctt gtt gcg gcg tct ccc ctg gtt gct gtg cat gcg ttt   240
Asp Thr Val Leu Val Ala Ala Ser Pro Leu Val Ala Val His Ala Phe
 65                  70                  75                  80

acc aac tgg gat act cca gcc att gcg gcg gtg att ggt gcg atg ctt   288
Thr Asn Trp Asp Thr Pro Ala Ile Ala Ala Val Ile Gly Ala Met Leu
                85                  90                  95

gcg gtg aaa cgc gga aac ccc ttg gtt gcg ggt gtg ctg atc ggc gcg   336
Ala Val Lys Arg Gly Asn Pro Leu Val Ala Gly Val Leu Ile Gly Ala
            100                 105                 110

ggt acg gcg ttc aaa ttg tgg ccg ctt tat ctt ctt ggt gcg tat ttg   384
Gly Thr Ala Phe Lys Leu Trp Pro Leu Tyr Leu Leu Gly Ala Tyr Leu
        115                 120                 125

gtg ctg gcg gtc aag aat aag aat ctc aag ccg ttt atc acc atg gct   432
Val Leu Ala Val Lys Asn Lys Asn Leu Lys Pro Phe Ile Thr Met Ala
    130                 135                 140

gca gcg gct gcg gtg aca tgg ctc gtg gtg aat gtg cca gtg atg atc   480
Ala Ala Ala Ala Val Thr Trp Leu Val Val Asn Val Pro Val Met Ile
145                 150                 155                 160

gcg tac ccc aag gcg tgg aat gaa ttc ttg cgc ctg aac cgg gag cgt   528
Ala Tyr Pro Lys Ala Trp Asn Glu Phe Leu Arg Leu Asn Arg Glu Arg
                165                 170                 175

ggt gcg gag tgg acc acg att tac cag gtc atc gac cgt aat ttg ccg   576
Gly Ala Glu Trp Thr Thr Ile Tyr Gln Val Ile Asp Arg Asn Leu Pro
            180                 185                 190

atc aat ttg aat gat cca gtg ctg ctt aat gtg ctg agc ttc ggc ttg   624
Ile Asn Leu Asn Asp Pro Val Leu Leu Asn Val Leu Ser Phe Gly Leu
        195                 200                 205

ttt ggt gca tca gtg tgt ggc cat ttt gat cct tgg gct caa ggt gca   672
Phe Gly Ala Ser Val Cys Gly His Phe Asp Pro Trp Ala Gln Gly Ala
    210                 215                 220

gcg cac tcc ccg agt cgc tgagctggcc tttttgattg tcg                713
Ala His Ser Pro Ser Arg
225                 230
```

<210> 288
<211> 230
<212> PRT
<213> Corynebacterium glutamicum

<400> 288

```
Pro Val Leu Gly Gly Ile Phe Gln Trp Ile Cys Gly Ile Ile Thr Arg
  1               5                  10                  15

Phe Leu Tyr Pro Val Val Asp Val Ile Pro Phe His Thr Leu Pro Glu
             20                  25                  30
```

```
Ser Gly Leu Tyr Phe Ile Val Thr Ala Leu Ala Leu Ala Phe Phe Trp
         35                  40                  45

Val Leu Val Ile Arg Met Met Val Glu Leu Thr Gly Asn Arg Val Trp
     50                  55                  60

Asp Thr Val Leu Val Ala Ala Ser Pro Leu Val Ala Val His Ala Phe
 65                  70                  75                  80

Thr Asn Trp Asp Thr Pro Ala Ile Ala Ala Val Ile Gly Ala Met Leu
                 85                  90                  95

Ala Val Lys Arg Gly Asn Pro Leu Val Ala Gly Val Leu Ile Gly Ala
            100                 105                 110

Gly Thr Ala Phe Lys Leu Trp Pro Leu Tyr Leu Leu Gly Ala Tyr Leu
        115                 120                 125

Val Leu Ala Val Lys Asn Lys Asn Leu Lys Pro Phe Ile Thr Met Ala
    130                 135                 140

Ala Ala Ala Ala Val Thr Trp Leu Val Val Asn Val Pro Val Met Ile
145                 150                 155                 160

Ala Tyr Pro Lys Ala Trp Asn Glu Phe Leu Arg Leu Asn Arg Glu Arg
                165                 170                 175

Gly Ala Glu Trp Thr Thr Ile Tyr Gln Val Ile Asp Arg Asn Leu Pro
            180                 185                 190

Ile Asn Leu Asn Asp Pro Val Leu Leu Asn Val Leu Ser Phe Gly Leu
        195                 200                 205

Phe Gly Ala Ser Val Cys Gly His Phe Asp Pro Trp Ala Gln Gly Ala
    210                 215                 220

Ala His Ser Pro Ser Arg
225                 230
```

<210> 289
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1036)
<223> RXN00552

<400> 289
ccgccaacaa ggcagcaaag ctcgatccaa ttgacgcctt gcgttatgag taaaagcctc 60

gtttttaagg tagccacaca tcgcactaga ctgaagaact gtg gct acc tca aaa 115
                                                Val Ala Thr Ser Lys
                                                  1   5

att ctt ctt tat tac gca ttc acc ccg ctc tct gac cct aaa gcg gtt 163
Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser Asp Pro Lys Ala Val
                10   15   20

```
cag ctg tgg cag cgt gag ctc tgc gag tca ctg aat ctt cgt ggc cgc   211
Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu Asn Leu Arg Gly Arg
            25                  30                  35

atc ctg atc tcc act cac ggc atc aat gga acc gtg ggc gga gat att   259
Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr Val Gly Gly Asp Ile
        40                  45                  50

gat gat tgc aag gcg tac att aaa aag acc cgc gag tac cca ggt ttc   307
Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg Glu Tyr Pro Gly Phe
    55                  60                  65

aac cgc atg cag ttt aag tgg tcc gag ggt ggc gct gag gat ttc cca   355
Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro
70                  75                  80                  85

aag ctc agt gtc aaa gtc cgc gat gag atc gtt gcc ttc ggc gct cca   403
Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro
                90                  95                  100

gat gag ctc aaa gtg gat gaa aac ggc gtc gtc ggt ggc ggc gtt cac   451
Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His
            105                 110                 115

ctg aaa cca cag cag gtc aat gag ctt gtg gaa gcc cgt ggc gat gaa   499
Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu
        120                 125                 130

gtt gtg ttc ttt gac ggc cgc aac gca atg gaa gcc cag atc ggc aag   547
Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys
    135                 140                 145

ttc aag gac gct gtt gtc cct gac gta gaa acc act cat gat ttc atc   595
Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile
150                 155                 160                 165

gca gaa att gag tct gga aaa tac gac gat ctc aaa gac aag cct gtg   643
Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val
                170                 175                 180

gtc acc tac tgc acc ggc gga att cgt tgt gag atc ctg agt tca ctc   691
Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu
            185                 190                 195

atg atc aac cgt ggt ttc aaa gag gtc tac caa atc gat ggc ggc atc   739
Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile
        200                 205                 210

gtt cgc tac ggc gag cag ttt ggc aac aag ggc ctg tgg gaa ggc tcc   787
Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser
    215                 220                 225

ctc tac gtt ttc gat aag cgc atg cat atg gaa ttc ggc gag gat tac   835
Leu Tyr Val Phe Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr
230                 235                 240                 245

aaa gag gtc gga cac tgc atc cat tgc gat act ccc acc aac aaa ttt   883
Lys Glu Val Gly His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe
                250                 255                 260

gag cac tgc ctc aac gaa gat gat tgc cgc gag ctc gtg ttg atg tgc   931
```

```
Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys
            265                 270                 275

cct gat tgc ttc gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc   979
Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg
        280                 285                 290

tgt gca gca att gct gcg gat ttc gct gag caa gga att gat ccg ctc   1027
Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu
    295                 300                 305

gtt act tct taaaaagggt atggtggctg ggt                            1059
Val Thr Ser
310
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<210> 290
<211> 312
<212> PRT
<213> Corynebacterium glutamicum

<400> 290

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Val Ala Thr Ser Lys Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser
  1               5                  10                  15

Asp Pro Lys Ala Val Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu
             20                  25                  30

Asn Leu Arg Gly Arg Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr
         35                  40                  45

Val Gly Gly Asp Ile Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg
     50                  55                  60

Glu Tyr Pro Gly Phe Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly
 65                  70                  75                  80

Ala Glu Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val
                 85                  90                  95

Ala Phe Gly Ala Pro Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val
            100                 105                 110

Gly Gly Gly Val His Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu
        115                 120                 125

Ala Arg Gly Asp Glu Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu
    130                 135                 140

Ala Gln Ile Gly Lys Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr
145                 150                 155                 160

Thr His Asp Phe Ile Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu
                165                 170                 175

Lys Asp Lys Pro Val Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu
            180                 185                 190

Ile Leu Ser Ser Leu Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln
        195                 200                 205
```

```
Ile Asp Gly Gly Ile Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly
    210                 215                 220

Leu Trp Glu Gly Ser Leu Tyr Val Phe Asp Lys Arg Met His Met Glu
225                 230                 235                 240

Phe Gly Glu Asp Tyr Lys Glu Val Gly His Cys Ile His Cys Asp Thr
                245                 250                 255

Pro Thr Asn Lys Phe Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu
            260                 265                 270

Leu Val Leu Met Cys Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His
        275                 280                 285

Cys Lys Arg Glu Arg Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln
    290                 295                 300

Gly Ile Asp Pro Leu Val Thr Ser
305                 310
```

09/10/2003 09:50:50 AM

<210> 291
<211> 740
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(717)
<223> FRXA00552

<400> 291

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ttt aag tgg tcc gag ggt ggc gct gag gat ttc cca aag ctc agt gtc   48
Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro Lys Leu Ser Val
  1               5                  10                  15

aaa gtc cgc gat gag atc gtt gcc ttc ggc gct cca gat gag ctc aaa   96
Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro Asp Glu Leu Lys
             20                  25                  30

gtg gat gaa aac ggc gtc gtc ggt ggc ggc gtt cac ctg aaa cca cag   144
Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His Leu Lys Pro Gln
         35                  40                  45

cag gtc aat gag ctt gtg gaa gcc cgt ggc gat gaa gtt gtg ttc ttt   192
Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu Val Val Phe Phe
     50                  55                  60

gac ggc cgc aac gca atg gaa gcc cag atc ggc aag ttc aag gac gct   240
Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys Phe Lys Asp Ala
 65                  70                  75                  80

gtt gtc cct gac gta gaa acc act cat gat ttc atc gca gaa att gag   288
Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile Ala Glu Ile Glu
                 85                  90                  95

tct gga aaa tac gac gat ctc aaa gac aag cct gtg gtc acc tac tgc   336
Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val Val Thr Tyr Cys
            100                 105                 110
```

```
acc ggc gga att cgt tgt gag atc ctg agt tca ctc atg atc aac cgt   384
Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu Met Ile Asn Arg
        115                 120                 125

ggt ttc aaa gag gtc tac caa atc gat ggc ggc atc gtt cgc tac ggc   432
Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile Val Arg Tyr Gly
    130                 135                 140

gag cag ttt ggc aac aag ggc ctg tgg gaa ggc tcc ctc tac gtt ttc   480
Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser Leu Tyr Val Phe
145                 150                 155                 160

gat aag cgc atg cat atg gaa ttc ggc gag gat tac aaa gag gtc gga   528
Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr Lys Glu Val Gly
                165                 170                 175

cac tgc atc cat tgc gat act ccc acc aac aaa ttt gag cac tgc ctc   576
His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe Glu His Cys Leu
            180                 185                 190

aac gaa gat gat tgc cgc gag ctc gtg ttg atg tgc cct gat tgc ttc   624
Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys Pro Asp Cys Phe
        195                 200                 205

gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc tgt gca gca att   672
Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg Cys Ala Ala Ile
    210                 215                 220

gct gcg gat ttc gct gag caa gga att gat ccg ctc gtt act tct       717
Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu Val Thr Ser
225                 230                 235

taaaaagggt atggtggctg ggt                                        740
```

20050208a.ST25

<210> 292
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 292

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Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro Lys Leu Ser Val
  1               5                  10                  15

Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro Asp Glu Leu Lys
             20                  25                  30

Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His Leu Lys Pro Gln
         35                  40                  45

Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu Val Val Phe Phe
     50                  55                  60

Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys Phe Lys Asp Ala
 65                  70                  75                  80

Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile Ala Glu Ile Glu
                 85                  90                  95

Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val Val Thr Tyr Cys
            100                 105                 110
```

```
Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu Met Ile Asn Arg
        115                 120                 125

Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile Val Arg Tyr Gly
    130                 135                 140

Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser Leu Tyr Val Phe
145                 150                 155                 160

Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr Lys Glu Val Gly
                165                 170                 175

His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe Glu His Cys Leu
            180                 185                 190

Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys Pro Asp Cys Phe
        195                 200                 205

Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg Cys Ala Ala Ile
    210                 215                 220

Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu Val Thr Ser
225                 230                 235


<210> 293
<211> 1062
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1039)
<223> RXN00555

<400> 293
cctggtggat atcattactg agcttgcaga ggtgtacggt agctggaaag agaccgacag 60

cggttcttaa cagttttctc catctcaact ccggaatttg atg aaa caa ccc ctt   115
                                              Met Lys Gln Pro Leu
                                                1               5

cgc gta ctt att tct tgt cga ccc gaa gaa aat tcg ggt ggc aaa cgt   163
Arg Val Leu Ile Ser Cys Arg Pro Glu Glu Asn Ser Gly Gly Lys Arg
                10                  15                  20

agt gaa caa aat gat gct gtt ttt gag ttc gcc gca tgg cta gct cgt   211
Ser Glu Gln Asn Asp Ala Val Phe Glu Phe Ala Ala Trp Leu Ala Arg
            25                  30                  35

act tca gac atc aat gtt cgt gga atc aca act ttc ata cgc cct tgg   259
Thr Ser Asp Ile Asn Val Arg Gly Ile Thr Thr Phe Ile Arg Pro Trp
        40                  45                  50

ccg tct tcc tcc atc agt aag ctc gga gga aaa tat cat aag tgg tat   307
Pro Ser Ser Ser Ile Ser Lys Leu Gly Gly Lys Tyr His Lys Trp Tyr
    55                  60                  65

aag aat tta gat tct tac tac cgc agt cgc acg atc aag gga ctc aaa   355
Lys Asn Leu Asp Ser Tyr Tyr Arg Ser Arg Thr Ile Lys Gly Leu Lys
```

```
 70                  75                  80                  85

gag gcc gga gtt gag aag tcc caa tgg gac gat gat gtt tca gtt ttt   403
Glu Ala Gly Val Glu Lys Ser Gln Trp Asp Asp Asp Val Ser Val Phe
                90                  95                 100

gta gat ggt cct tct gaa tcc acg ctg ctc acc cat gct gct gaa gaa   451
Val Asp Gly Pro Ser Glu Ser Thr Leu Leu Thr His Ala Ala Glu Glu
            105                 110                 115

ttc gaa gcg gac ctc att ctg ctt ggc tct gat gcg acc gca cca aaa   499
Phe Glu Ala Asp Leu Ile Leu Leu Gly Ser Asp Ala Thr Ala Pro Lys
        120                 125                 130

ggc cgc ttt ctg gcc agc tcc acc gca gat gcc ctc ctt cac tcc tcg   547
Gly Arg Phe Leu Ala Ser Ser Thr Ala Asp Ala Leu Leu His Ser Ser
    135                 140                 145

ccc gtc cca cta gga ctt gtg ccg cga ggg gtg aag ctt tcc aaa aag   595
Pro Val Pro Leu Gly Leu Val Pro Arg Gly Val Lys Leu Ser Lys Lys
150                 155                 160                 165

ggt gtc acc cgc gtc aac tac gct ttc acc aat gaa agc gat gac ttt   643
Gly Val Thr Arg Val Asn Tyr Ala Phe Thr Asn Glu Ser Asp Asp Phe
                170                 175                 180

gag caa ggt tta cgc tct tcc gcg gag ctc gcc acc aat tgg aac gtt   691
Glu Gln Gly Leu Arg Ser Ser Ala Glu Leu Ala Thr Asn Trp Asn Val
            185                 190                 195

cct ctt cgg atc ctt gct ttt tca ccc aca ggc att act tcc gca cca   739
Pro Leu Arg Ile Leu Ala Phe Ser Pro Thr Gly Ile Thr Ser Ala Pro
        200                 205                 210

acg tcg cgg agc ttg gat att tcc act gag ctt tcc tcc gag tgg cgt   787
Thr Ser Arg Ser Leu Asp Ile Ser Thr Glu Leu Ser Ser Glu Trp Arg
    215                 220                 225

gaa cta acg ctc gcc atg ctt gat cga gcc cgt gat ggc gtc ctc aca   835
Glu Leu Thr Leu Ala Met Leu Asp Arg Ala Arg Asp Gly Val Leu Thr
230                 235                 240                 245

gac cac cca aac ttg agc gtg agc agt gaa acc ggt tct ggc tgg ggt   883
Asp His Pro Asn Leu Ser Val Ser Ser Glu Thr Gly Ser Gly Trp Gly
                250                 255                 260

tgg agc ggt gca att gat gct ttg cga tgg aag aaa ggt gac ctg ctg   931
Trp Ser Gly Ala Ile Asp Ala Leu Arg Trp Lys Lys Gly Asp Leu Leu
            265                 270                 275

tgc atg gga agc cat cgc aca gac acc ctt tca cgt gtc ttt gtc ggt   979
Cys Met Gly Ser His Arg Thr Asp Thr Leu Ser Arg Val Phe Val Gly
        280                 285                 290

tcg gaa aca atg gaa att atc cga aac tct cct gta ccg acc atc att   1027
Ser Glu Thr Met Glu Ile Ile Arg Asn Ser Pro Val Pro Thr Ile Ile
    295                 300                 305

tat ccc ggt ctt taggctctcc aacagcagag gac                        1062
Tyr Pro Gly Leu
310
```

<210> 294
<211> 313
<212> PRT
<213> Corynebacterium glutamicum

<400> 294
Met Lys Gln Pro Leu Arg Val Leu Ile Ser Cys Arg Pro Glu Glu Asn
1 5 10 15

Ser Gly Gly Lys Arg Ser Glu Gln Asn Asp Ala Val Phe Glu Phe Ala
20 25 30

Ala Trp Leu Ala Arg Thr Ser Asp Ile Asn Val Arg Gly Ile Thr Thr
35 40 45

Phe Ile Arg Pro Trp Pro Ser Ser Ser Ile Ser Lys Leu Gly Gly Lys
50 55 60

Tyr His Lys Trp Tyr Lys Asn Leu Asp Ser Tyr Tyr Arg Ser Arg Thr
65 70 75 80

Ile Lys Gly Leu Lys Glu Ala Gly Val Glu Lys Ser Gln Trp Asp Asp
85 90 95

Asp Val Ser Val Phe Val Asp Gly Pro Ser Glu Ser Thr Leu Leu Thr
100 105 110

His Ala Ala Glu Glu Phe Glu Ala Asp Leu Ile Leu Leu Gly Ser Asp
115 120 125

Ala Thr Ala Pro Lys Gly Arg Phe Leu Ala Ser Ser Thr Ala Asp Ala
130 135 140

Leu Leu His Ser Ser Pro Val Pro Leu Gly Leu Val Pro Arg Gly Val
145 150 155 160

Lys Leu Ser Lys Lys Gly Val Thr Arg Val Asn Tyr Ala Phe Thr Asn
165 170 175

Glu Ser Asp Asp Phe Glu Gln Gly Leu Arg Ser Ser Ala Glu Leu Ala
180 185 190

Thr Asn Trp Asn Val Pro Leu Arg Ile Leu Ala Phe Ser Pro Thr Gly
195 200 205

Ile Thr Ser Ala Pro Thr Ser Arg Ser Leu Asp Ile Ser Thr Glu Leu
210 215 220

Ser Ser Glu Trp Arg Glu Leu Thr Leu Ala Met Leu Asp Arg Ala Arg
225 230 235 240

Asp Gly Val Leu Thr Asp His Pro Asn Leu Ser Val Ser Ser Glu Thr
245 250 255

Gly Ser Gly Trp Gly Trp Ser Gly Ala Ile Asp Ala Leu Arg Trp Lys
260 265 270

Lys Gly Asp Leu Leu Cys Met Gly Ser His Arg Thr Asp Thr Leu Ser
275 280 285

```
Arg Val Phe Val Gly Ser Glu Thr Met Glu Ile Ile Arg Asn Ser Pro
    290                 295                 300

Val Pro Thr Ile Ile Tyr Pro Gly Leu
305                 310


<210> 295
<211> 914
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(891)
<223> FRXA00555

<400> 295
tcg ggt ggc aaa cgt agt gaa caa aat gat gct gtt ttt gag ttc gcc   48
Ser Gly Gly Lys Arg Ser Glu Gln Asn Asp Ala Val Phe Glu Phe Ala
  1               5                  10                  15

gca tgg cta gct cgt act tca gac atc aat gtt cgt gga atc aca act   96
Ala Trp Leu Ala Arg Thr Ser Asp Ile Asn Val Arg Gly Ile Thr Thr
             20                  25                  30

ttc ata cgc cct tgg ccg tct tcc tcc atc agt aag ctc gga gga aaa   144
Phe Ile Arg Pro Trp Pro Ser Ser Ser Ile Ser Lys Leu Gly Gly Lys
         35                  40                  45

tat cat aag tgg tat aag aat tta gat tct tac tac cgc agt cgc acg   192
Tyr His Lys Trp Tyr Lys Asn Leu Asp Ser Tyr Tyr Arg Ser Arg Thr
     50                  55                  60

atc aag gga ctc aaa gag gcc gga gtt gag aag tcc caa tgg gac gat   240
Ile Lys Gly Leu Lys Glu Ala Gly Val Glu Lys Ser Gln Trp Asp Asp
 65                  70                  75                  80

gat gtt tca gtt ttt gta gat ggt cct tct gaa tcc acg ctg ctc acc   288
Asp Val Ser Val Phe Val Asp Gly Pro Ser Glu Ser Thr Leu Leu Thr
                 85                  90                  95

cat gct gct gaa gaa ttc gaa gcg gac ctc att ctg ctt ggc tct gat   336
His Ala Ala Glu Glu Phe Glu Ala Asp Leu Ile Leu Leu Gly Ser Asp
            100                 105                 110

gcg acc gca cca aaa ggc cgc ttt ctg gcc agc tcc acc gca gat gcc   384
Ala Thr Ala Pro Lys Gly Arg Phe Leu Ala Ser Ser Thr Ala Asp Ala
        115                 120                 125

ctc ctt cac tcc tcg ccc gtc cca cta gga ctt gtg ccg cga ggg gtg   432
Leu Leu His Ser Ser Pro Val Pro Leu Gly Leu Val Pro Arg Gly Val
    130                 135                 140

aag ctt tcc aaa aag ggt gtc acc cgc gtc aac tac gct ttc acc aat   480
Lys Leu Ser Lys Lys Gly Val Thr Arg Val Asn Tyr Ala Phe Thr Asn
145                 150                 155                 160

gaa agc gat gac ttt gag caa ggt tta cgc tct tcc gcg gag ctc gcc   528
Glu Ser Asp Asp Phe Glu Gln Gly Leu Arg Ser Ser Ala Glu Leu Ala
```

```
                165                 170                 175

acc aat tgg aac gtt cct ctt cgg atc ctt gct ttt tca ccc aca ggc   576
Thr Asn Trp Asn Val Pro Leu Arg Ile Leu Ala Phe Ser Pro Thr Gly
            180                 185                 190

att act tcc gca cca acg tcg cgg agc ttg gat att tcc act gag ctt   624
Ile Thr Ser Ala Pro Thr Ser Arg Ser Leu Asp Ile Ser Thr Glu Leu
        195                 200                 205

tcc tcc gag tgg cgt gaa cta acg ctc gcc atg ctt gat cga gcc cgt   672
Ser Ser Glu Trp Arg Glu Leu Thr Leu Ala Met Leu Asp Arg Ala Arg
    210                 215                 220

gat ggc gtc ctc aca gac cac cca aac ttg agc gtg agc agt gaa acc   720
Asp Gly Val Leu Thr Asp His Pro Asn Leu Ser Val Ser Ser Glu Thr
225                 230                 235                 240

ggt tct ggc tgg ggt tgg agc ggt gca att gat gct ttg cga tgg aag   768
Gly Ser Gly Trp Gly Trp Ser Gly Ala Ile Asp Ala Leu Arg Trp Lys
                245                 250                 255

aaa ggt gac ctg ctg tgc atg gga agc cat cgc aca gac acc ctt tca   816
Lys Gly Asp Leu Leu Cys Met Gly Ser His Arg Thr Asp Thr Leu Ser
            260                 265                 270

cgt gtc ttt gtc ggt tcg gaa aca atg gaa att atc cga aac tct cct   864
Arg Val Phe Val Gly Ser Glu Thr Met Glu Ile Ile Arg Asn Ser Pro
        275                 280                 285

gta ccg acc atc att tat ccc ggt ctt taggctctcc aacagcagag         911
Val Pro Thr Ile Ile Tyr Pro Gly Leu
    290                 295

gac                                                               914
```

09 08 07 06 05 04 03 02 01 00 99 98 97 96 95 94 93 92 91 90 89 88 87 86 85 84 83 82 81 80 79 78 77 76 75 74 73 72 71 70 69 68 67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44 43 42 41 40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 09 08 07 06 05 04 03 02 01

<210> 296
<211> 297
<212> PRT
<213> Corynebacterium glutamicum

<400> 296

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Ser Gly Gly Lys Arg Ser Glu Gln Asn Asp Ala Val Phe Glu Phe Ala
  1               5                  10                  15

Ala Trp Leu Ala Arg Thr Ser Asp Ile Asn Val Arg Gly Ile Thr Thr
             20                  25                  30

Phe Ile Arg Pro Trp Pro Ser Ser Ser Ile Ser Lys Leu Gly Gly Lys
         35                  40                  45

Tyr His Lys Trp Tyr Lys Asn Leu Asp Ser Tyr Tyr Arg Ser Arg Thr
     50                  55                  60

Ile Lys Gly Leu Lys Glu Ala Gly Val Glu Lys Ser Gln Trp Asp Asp
 65                  70                  75                  80

Asp Val Ser Val Phe Val Asp Gly Pro Ser Glu Ser Thr Leu Leu Thr
                 85                  90                  95
```

```
His Ala Ala Glu Glu Phe Glu Ala Asp Leu Ile Leu Leu Gly Ser Asp
            100                 105                 110

Ala Thr Ala Pro Lys Gly Arg Phe Leu Ala Ser Ser Thr Ala Asp Ala
        115                 120                 125

Leu Leu His Ser Ser Pro Val Pro Leu Gly Leu Val Pro Arg Gly Val
    130                 135                 140

Lys Leu Ser Lys Lys Gly Val Thr Arg Val Asn Tyr Ala Phe Thr Asn
145                 150                 155                 160

Glu Ser Asp Asp Phe Glu Gln Gly Leu Arg Ser Ser Ala Glu Leu Ala
                165                 170                 175

Thr Asn Trp Asn Val Pro Leu Arg Ile Leu Ala Phe Ser Pro Thr Gly
            180                 185                 190

Ile Thr Ser Ala Pro Thr Ser Arg Ser Leu Asp Ile Ser Thr Glu Leu
        195                 200                 205

Ser Ser Glu Trp Arg Glu Leu Thr Leu Ala Met Leu Asp Arg Ala Arg
    210                 215                 220

Asp Gly Val Leu Thr Asp His Pro Asn Leu Ser Val Ser Ser Glu Thr
225                 230                 235                 240

Gly Ser Gly Trp Gly Trp Ser Gly Ala Ile Asp Ala Leu Arg Trp Lys
                245                 250                 255

Lys Gly Asp Leu Leu Cys Met Gly Ser His Arg Thr Asp Thr Leu Ser
            260                 265                 270

Arg Val Phe Val Gly Ser Glu Thr Met Glu Ile Ile Arg Asn Ser Pro
        275                 280                 285

Val Pro Thr Ile Ile Tyr Pro Gly Leu
    290                 295
```

<210> 297
<211> 498
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(475)
<223> RXN00560

<400> 297
aaggacgact tctggggagc ggtgtggatt ctcacgggga ttctcatgcg gattatcaga 60

catatggaca ctttaacggt tcgtactagg ctgatgcttc atg agg att gat ccg 115
Met Arg Ile Asp Pro
1 5

ctg gaa acc cgg caa gcc gta ttg gcc gtc aaa gac tgg att gaa ggg 163
Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys Asp Trp Ile Glu Gly
10 15 20

```
gag gga gac gtc aaa aag cct ggt cgt gcg gca ctt gcc gcc gca act   211
Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala Leu Ala Ala Ala Thr
            25                  30                  35

cgc ctg agc gtc cga ctg ctc gcg caa cac gcg ccg gga aac agc gtg   259
Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala Pro Gly Asn Ser Val
        40                  45                  50

gag gtg cgg gta ccc cca ttt gtt gcg gtg caa tgc ata gag ggg cca   307
Glu Val Arg Val Pro Pro Phe Val Ala Val Gln Cys Ile Glu Gly Pro
    55                  60                  65

aaa cat aca cgc ggc aca cca ccc aac gtg gtg gag acc gac gcc aag   355
Lys His Thr Arg Gly Thr Pro Pro Asn Val Val Glu Thr Asp Ala Lys
70                  75                  80                  85

acc tgg tta cgc tta gca cct ggg caa acc aca ttt gat gca gaa ttt   403
Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr Phe Asp Ala Glu Phe
                90                  95                  100

gaa agc gga aaa att agc gca tca ggt acc cga gcc aaa gag att gcg   451
Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg Ala Lys Glu Ile Ala
            105                 110                 115

gac tgg tta cca gtg gtc aaa ctt tagatttcct aatgctcatt agt         498
Asp Trp Leu Pro Val Val Lys Leu
        120                 125
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<210> 298
<211> 125
<212> PRT
<213> Corynebacterium glutamicum

<400> 298

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Met Arg Ile Asp Pro Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys
  1               5                  10                  15

Asp Trp Ile Glu Gly Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala
            20                  25                  30

Leu Ala Ala Ala Thr Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala
        35                  40                  45

Pro Gly Asn Ser Val Glu Val Arg Val Pro Pro Phe Val Ala Val Gln
    50                  55                  60

Cys Ile Glu Gly Pro Lys His Thr Arg Gly Thr Pro Pro Asn Val Val
65                  70                  75                  80

Glu Thr Asp Ala Lys Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr
                85                  90                  95

Phe Asp Ala Glu Phe Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg
            100                 105                 110

Ala Lys Glu Ile Ala Asp Trp Leu Pro Val Val Lys Leu
        115                 120                 125
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<210> 299

<211> 337
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(337)
<223> FRXA00560

<400> 299
aaggacgact tctggggagc ggtgtggatt ctcacgggga ttctcatgcg gattatcaga 60

catatggaca ctttaacggt tcgtactagg ctgatgcttc atg agg att gat ccg 115
Met Arg Ile Asp Pro
1 5

ctg gaa acc cgg caa gcc gta ttg gcc gtc aaa gac tgg att gaa ggg 163
Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys Asp Trp Ile Glu Gly
10 15 20

gag gga gac gtc aaa aag cct ggt cgt gcg gca ctt gcc gcc gca act 211
Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala Leu Ala Ala Ala Thr
25 30 35

cgc ctg agc gtc cga ctg ctc gcg caa cac gcg ccg gga aac agc gtg 259
Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala Pro Gly Asn Ser Val
40 45 50

gag gtg cgg gta ccc cca ttt gtt gcg gtg caa tgc ata gag ggg cca 307
Glu Val Arg Val Pro Pro Phe Val Ala Val Gln Cys Ile Glu Gly Pro
55 60 65

aaa cat aca cgc ggc aca cca ccc aac gtg 337
Lys His Thr Arg Gly Thr Pro Pro Asn Val
70 75

<210> 300
<211> 79
<212> PRT
<213> Corynebacterium glutamicum

<400> 300
Met Arg Ile Asp Pro Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys
1 5 10 15

Asp Trp Ile Glu Gly Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala
20 25 30

Leu Ala Ala Ala Thr Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala
35 40 45

Pro Gly Asn Ser Val Glu Val Arg Val Pro Pro Phe Val Ala Val Gln
50 55 60

Cys Ile Glu Gly Pro Lys His Thr Arg Gly Thr Pro Pro Asn Val
65 70 75

<210> 301
<211> 1002

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(979)
<223> RXN00574

<400> 301
aactgctggg cactactgag attcccatgt gggatgtgga ccggtggcaa ccatcgcttc 60

tcaagcccgg tgattcagtt cgatttgtgc aggtgaagaa atg agc ttc aaa gta 115
Met Ser Phe Lys Val
1 5

att tcc act ggc ccc caa gcc atc ttc caa gac cga ggt cgc ttc ggt 163
Ile Ser Thr Gly Pro Gln Ala Ile Phe Gln Asp Arg Gly Arg Phe Gly
10 15 20

ttt gcc agc gct ggt gtt gga acc tca gga tcc ttt gat cgt tta tcc 211
Phe Ala Ser Ala Gly Val Gly Thr Ser Gly Ser Phe Asp Arg Leu Ser
25 30 35

gct gct cgc gcg aat cac gct tta ggt aat gat ccc aat gca acc gtg 259
Ala Ala Arg Ala Asn His Ala Leu Gly Asn Asp Pro Asn Ala Thr Val
40 45 50

gta gag att ctg ctc ggt ggc ttt gag gtg gag gcg ttg cac acc acc 307
Val Glu Ile Leu Leu Gly Gly Phe Glu Val Glu Ala Leu His Thr Thr
55 60 65

tcg atc gtg ttc acg gga act gaa gct gaa gtg atg gtt cga acg gct 355
Ser Ile Val Phe Thr Gly Thr Glu Ala Glu Val Met Val Arg Thr Ala
70 75 80 85

ggt gga caa tcc aaa aat gcc acc acc aac acc atc atc gat gtt gca 403
Gly Gly Gln Ser Lys Asn Ala Thr Thr Asn Thr Ile Ile Asp Val Ala
90 95 100

gct ggt gaa cgt atc cgc gtc gag ccc gca acc tat ggc atg cgt gcc 451
Ala Gly Glu Arg Ile Arg Val Glu Pro Ala Thr Tyr Gly Met Arg Ala
105 110 115

tac ttt gct gct cgc ggt gga ttt gca gta aaa aaa act ttg gga tct 499
Tyr Phe Ala Ala Arg Gly Gly Phe Ala Val Lys Lys Thr Leu Gly Ser
120 125 130

gct tca acc gat ctg atc tcc cac atg ggc cct tgc ccg atc gag ccc 547
Ala Ser Thr Asp Leu Ile Ser His Met Gly Pro Cys Pro Ile Glu Pro
135 140 145

ggg gat gtc att gac gta gca aca gac att gca gat tct cag tgg tgg 595
Gly Asp Val Ile Asp Val Ala Thr Asp Ile Ala Asp Ser Gln Trp Trp
150 155 160 165

cca aaa ctt cgg caa ctg ccc acc tta tgg aaa cgc atg cca aca gaa 643
Pro Lys Leu Arg Gln Leu Pro Thr Leu Trp Lys Arg Met Pro Thr Glu
170 175 180

acg ctt acc gtc atc cga ggt cca cgt gac aaa tgg ttc acg caa gaa 691
Thr Leu Thr Val Ile Arg Gly Pro Arg Asp Lys Trp Phe Thr Gln Glu

```
            185                 190                 195

tcc ctc aac aac ttt ttt act cag gtg ttt acg gtg agc aat gac tcc   739
Ser Leu Asn Asn Phe Phe Thr Gln Val Phe Thr Val Ser Asn Asp Ser
        200                 205                 210

aac cgg att ggt ttg cgc atg cac tca agc gag ccg atc caa cat cgt   787
Asn Arg Ile Gly Leu Arg Met His Ser Ser Glu Pro Ile Gln His Arg
    215                 220                 225

gtg gaa ggc gag ctg aaa agt gaa gga atg gtc cgg ggg tcc atc cag   835
Val Glu Gly Glu Leu Lys Ser Glu Gly Met Val Arg Gly Ser Ile Gln
230                 235                 240                 245

att ccg cct ggt gga aac ccc gtg gtg ttt ggt ccc gat cat cct gtg   883
Ile Pro Pro Gly Gly Asn Pro Val Val Phe Gly Pro Asp His Pro Val
                250                 255                 260

acc ggt ggc tat cca gta ata gca gta ctt aca tca agg tcg tgt gat   931
Thr Gly Gly Tyr Pro Val Ile Ala Val Leu Thr Ser Arg Ser Cys Asp
            265                 270                 275

cgt tcg gcc cag ctg ttg ccg ggc gat aaa gtc aga ttt aaa ttg ctt   979
Arg Ser Ala Gln Leu Leu Pro Gly Asp Lys Val Arg Phe Lys Leu Leu
        280                 285                 290

taggaacttt gagcttgctc tgg                                        1002


<210> 302
<211> 293
<212> PRT
<213> Corynebacterium glutamicum

<400> 302
Met Ser Phe Lys Val Ile Ser Thr Gly Pro Gln Ala Ile Phe Gln Asp
  1               5                  10                  15

Arg Gly Arg Phe Gly Phe Ala Ser Ala Gly Val Gly Thr Ser Gly Ser
             20                  25                  30

Phe Asp Arg Leu Ser Ala Ala Arg Ala Asn His Ala Leu Gly Asn Asp
         35                  40                  45

Pro Asn Ala Thr Val Val Glu Ile Leu Leu Gly Gly Phe Glu Val Glu
 *   50                  55                  60

Ala Leu His Thr Thr Ser Ile Val Phe Thr Gly Thr Glu Ala Glu Val
 65                  70                  75                  80

Met Val Arg Thr Ala Gly Gly Gln Ser Lys Asn Ala Thr Thr Asn Thr
                 85                  90                  95

Ile Ile Asp Val Ala Ala Gly Glu Arg Ile Arg Val Glu Pro Ala Thr
            100                 105                 110

Tyr Gly Met Arg Ala Tyr Phe Ala Ala Arg Gly Gly Phe Ala Val Lys
        115                 120                 125

Lys Thr Leu Gly Ser Ala Ser Thr Asp Leu Ile Ser His Met Gly Pro
    130                 135                 140
```

```
Cys Pro Ile Glu Pro Gly Asp Val Ile Asp Val Ala Thr Asp Ile Ala
145                 150                 155                 160

Asp Ser Gln Trp Trp Pro Lys Leu Arg Gln Leu Pro Thr Leu Trp Lys
                165                 170                 175

Arg Met Pro Thr Glu Thr Leu Thr Val Ile Arg Gly Pro Arg Asp Lys
            180                 185                 190

Trp Phe Thr Gln Glu Ser Leu Asn Asn Phe Phe Thr Gln Val Phe Thr
        195                 200                 205

Val Ser Asn Asp Ser Asn Arg Ile Gly Leu Arg Met His Ser Ser Glu
    210                 215                 220

Pro Ile Gln His Arg Val Glu Gly Glu Leu Lys Ser Glu Gly Met Val
225                 230                 235                 240

Arg Gly Ser Ile Gln Ile Pro Pro Gly Gly Asn Pro Val Val Phe Gly
                245                 250                 255

Pro Asp His Pro Val Thr Gly Gly Tyr Pro Val Ile Ala Val Leu Thr
            260                 265                 270

Ser Arg Ser Cys Asp Arg Ser Ala Gln Leu Leu Pro Gly Asp Lys Val
        275                 280                 285

Arg Phe Lys Leu Leu
    290


<210> 303
<211> 1002
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(979)
<223> FRXA00574

<400> 303
aactgctggg cactactgag attcccatgt gggatgtgga ccggtggcaa ccatcgcttc 60

tcaagcccgg tgattcagtt cgatttgtgc aggtgaagaa atg agc ttc aaa gta   115
                                            Met Ser Phe Lys Val
                                              1               5

att tcc act ggc ccc caa gcc atc ttc caa gac cga ggt cgc ttc ggt   163
Ile Ser Thr Gly Pro Gln Ala Ile Phe Gln Asp Arg Gly Arg Phe Gly
                  10                  15                  20

ttt gcc agc gct ggt gtt gga acc tca gga tcc ttt gat cgt tta tcc   211
Phe Ala Ser Ala Gly Val Gly Thr Ser Gly Ser Phe Asp Arg Leu Ser
              25                  30                  35

gct gct cgc gcg aat cac gct tta ggt aat gat ccc aat gca acc gtg   259
Ala Ala Arg Ala Asn His Ala Leu Gly Asn Asp Pro Asn Ala Thr Val
          40                  45                  50
```

```
gta gag att ctg ctc ggt ggc ttt gag gtg gag gcg ttg cac acc acc   307
Val Glu Ile Leu Leu Gly Gly Phe Glu Val Glu Ala Leu His Thr Thr
     55                  60                  65

tcg atc gtg ttc acg gga act gaa gct gaa gtg atg gtt cga acg gct   355
Ser Ile Val Phe Thr Gly Thr Glu Ala Glu Val Met Val Arg Thr Ala
 70                  75                  80                  85

ggt gga caa tcc aaa aat gcc acc acc aac acc atc atc gat gtt gca   403
Gly Gly Gln Ser Lys Asn Ala Thr Thr Asn Thr Ile Ile Asp Val Ala
                 90                  95                 100

gct ggt gaa cgt atc cgc gtc gag ccc gca acc tat ggc atg cgt gcc   451
Ala Gly Glu Arg Ile Arg Val Glu Pro Ala Thr Tyr Gly Met Arg Ala
            105                 110                 115

tac ttt gct gct cgc ggt gga ttt gca gta aaa aaa act ttg gga tct   499
Tyr Phe Ala Ala Arg Gly Gly Phe Ala Val Lys Lys Thr Leu Gly Ser
        120                 125                 130

gct tca acc gat ctg atc tcc cac atg ggc cct tgc ccg atc gag ccc   547
Ala Ser Thr Asp Leu Ile Ser His Met Gly Pro Cys Pro Ile Glu Pro
    135                 140                 145

ggg gat gtc att gac gta gca aca gac att gca gat tct cag tgg tgg   595
Gly Asp Val Ile Asp Val Ala Thr Asp Ile Ala Asp Ser Gln Trp Trp
150                 155                 160                 165

cca aaa ctt cgg caa ctg ccc acc tta tgg aaa cgc atg cca aca gaa   643
Pro Lys Leu Arg Gln Leu Pro Thr Leu Trp Lys Arg Met Pro Thr Glu
                170                 175                 180

acg ctt acc gtc atc cga ggt cca cgt gac aaa tgg ttc acg caa gaa   691
Thr Leu Thr Val Ile Arg Gly Pro Arg Asp Lys Trp Phe Thr Gln Glu
            185                 190                 195

tcc ctc aac aac ttt ttt act cag gtg ttt acg gtg agc aat gac tcc   739
Ser Leu Asn Asn Phe Phe Thr Gln Val Phe Thr Val Ser Asn Asp Ser
        200                 205                 210

aac cgg att ggt ttg cgc atg cac tca agc gag ccg atc caa cat cgt   787
Asn Arg Ile Gly Leu Arg Met His Ser Ser Glu Pro Ile Gln His Arg
    215                 220                 225

gtg gaa ggc gag ctg aaa agt gaa gga atg gtc cgg ggg tcc atc cag   835
Val Glu Gly Glu Leu Lys Ser Glu Gly Met Val Arg Gly Ser Ile Gln
230                 235                 240                 245

att ccg cct ggt gga aac ccc gtg gtg ttt ggt ccc gat cat cct gtg   883
Ile Pro Pro Gly Gly Asn Pro Val Val Phe Gly Pro Asp His Pro Val
                250                 255                 260

acc ggt ggc tat cca gta ata gca gta ctt aca tca agg tcg tgt gat   931
Thr Gly Gly Tyr Pro Val Ile Ala Val Leu Thr Ser Arg Ser Cys Asp
            265                 270                 275

cgt tcg gcc cag ctg ttg ccg ggc gat aaa gtc aga ttt aaa ttg ctt   979
Arg Ser Ala Gln Leu Leu Pro Gly Asp Lys Val Arg Phe Lys Leu Leu
        280                 285                 290

taggaacttt gagcttgctc tgg                                        1002
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<210> 304
<211> 293
<212> PRT
<213> Corynebacterium glutamicum

<400> 304
Met Ser Phe Lys Val Ile Ser Thr Gly Pro Gln Ala Ile Phe Gln Asp
1 5 10 15

Arg Gly Arg Phe Gly Phe Ala Ser Ala Gly Val Gly Thr Ser Gly Ser
20 25 30

Phe Asp Arg Leu Ser Ala Ala Arg Ala Asn His Ala Leu Gly Asn Asp
35 40 45

Pro Asn Ala Thr Val Val Glu Ile Leu Leu Gly Gly Phe Glu Val Glu
50 55 60

Ala Leu His Thr Thr Ser Ile Val Phe Thr Gly Thr Glu Ala Glu Val
65 70 75 80

Met Val Arg Thr Ala Gly Gly Gln Ser Lys Asn Ala Thr Thr Asn Thr
85 90 95

Ile Ile Asp Val Ala Ala Gly Glu Arg Ile Arg Val Glu Pro Ala Thr
100 105 110

Tyr Gly Met Arg Ala Tyr Phe Ala Ala Arg Gly Gly Phe Ala Val Lys
115 120 125

Lys Thr Leu Gly Ser Ala Ser Thr Asp Leu Ile Ser His Met Gly Pro
130 135 140

Cys Pro Ile Glu Pro Gly Asp Val Ile Asp Val Ala Thr Asp Ile Ala
145 150 155 160

Asp Ser Gln Trp Trp Pro Lys Leu Arg Gln Leu Pro Thr Leu Trp Lys
165 170 175

Arg Met Pro Thr Glu Thr Leu Thr Val Ile Arg Gly Pro Arg Asp Lys
180 185 190

Trp Phe Thr Gln Glu Ser Leu Asn Asn Phe Phe Thr Gln Val Phe Thr
195 200 205

Val Ser Asn Asp Ser Asn Arg Ile Gly Leu Arg Met His Ser Ser Glu
210 215 220

Pro Ile Gln His Arg Val Glu Gly Glu Leu Lys Ser Glu Gly Met Val
225 230 235 240

Arg Gly Ser Ile Gln Ile Pro Pro Gly Gly Asn Pro Val Val Phe Gly
245 250 255

Pro Asp His Pro Val Thr Gly Gly Tyr Pro Val Ile Ala Val Leu Thr
260 265 270

Ser Arg Ser Cys Asp Arg Ser Ala Gln Leu Leu Pro Gly Asp Lys Val
275 280 285

Arg Phe Lys Leu Leu
290

<210> 305
<211> 573
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(550)
<223> RXN00589

<400> 305
ccgttatctc cgtaactgtt gtttctgcag aaccatacaa ctcagcaaaa gccgcgacac 60

tccgcggcaa aaactaacca aggatttaaa agtcttcaaa atg aca act ctt tca 115
Met Thr Thr Leu Ser
1 5

cgt aag ttc ttc gtt tct gct acc aca gcc ctg gcg gca gtc gca ctg 163
Arg Lys Phe Phe Val Ser Ala Thr Thr Ala Leu Ala Ala Val Ala Leu
10 15 20

gtt gcg tgt tcc cct aat gag att gat tct gaa ctg aag gtg cca acg 211
Val Ala Cys Ser Pro Asn Glu Ile Asp Ser Glu Leu Lys Val Pro Thr
25 30 35

gca act ggc gtt tct tta cct tcg aag aac gtt tcc gcg acc tca act 259
Ala Thr Gly Val Ser Leu Pro Ser Lys Asn Val Ser Ala Thr Ser Thr
40 45 50

gct act aca gat gag gat gcg cct ggc tac att gat tgc gta gcc gca 307
Ala Thr Thr Asp Glu Asp Ala Pro Gly Tyr Ile Asp Cys Val Ala Ala
55 60 65

cca act cag caa cct gct gaa atc tca cta aac tgt gca atg gat att 355
Pro Thr Gln Gln Pro Ala Glu Ile Ser Leu Asn Cys Ala Met Asp Ile
70 75 80 85

gat cgg ctc acg gat att tct tgg agc gaa tgg gat act gat tcc gca 403
Asp Arg Leu Thr Asp Ile Ser Trp Ser Glu Trp Asp Thr Asp Ser Ala
90 95 100

act gga acc ggt acc cgc atc gta acc gct gca aat ggt caa gag acc 451
Thr Gly Thr Gly Thr Arg Ile Val Thr Ala Ala Asn Gly Gln Glu Thr
105 110 115

gaa acc gaa gat att gag gtg aag ctt tcc ttc ccc acc gag tct tcc 499
Glu Thr Glu Asp Ile Glu Val Lys Leu Ser Phe Pro Thr Glu Ser Ser
120 125 130

caa ggc cta gtg ttc act cag gtc acc gtc gat gga cag gtt ctc ttc 547
Gln Gly Leu Val Phe Thr Gln Val Thr Val Asp Gly Gln Val Leu Phe
135 140 145

ctc taatcctcca taattagaga gcg 573
Leu
150

<210> 306
<211> 150
<212> PRT
<213> Corynebacterium glutamicum

<400> 306
Met Thr Thr Leu Ser Arg Lys Phe Phe Val Ser Ala Thr Thr Ala Leu
1 5 10 15

Ala Ala Val Ala Leu Val Ala Cys Ser Pro Asn Glu Ile Asp Ser Glu
20 25 30

Leu Lys Val Pro Thr Ala Thr Gly Val Ser Leu Pro Ser Lys Asn Val
35 40 45

Ser Ala Thr Ser Thr Ala Thr Thr Asp Glu Asp Ala Pro Gly Tyr Ile
50 55 60

Asp Cys Val Ala Ala Pro Thr Gln Gln Pro Ala Glu Ile Ser Leu Asn
65 70 75 80

Cys Ala Met Asp Ile Asp Arg Leu Thr Asp Ile Ser Trp Ser Glu Trp
85 90 95

Asp Thr Asp Ser Ala Thr Gly Thr Gly Thr Arg Ile Val Thr Ala Ala
100 105 110

Asn Gly Gln Glu Thr Glu Thr Glu Asp Ile Glu Val Lys Leu Ser Phe
115 120 125

Pro Thr Glu Ser Ser Gln Gly Leu Val Phe Thr Gln Val Thr Val Asp
130 135 140

Gly Gln Val Leu Phe Leu
145 150

<210> 307
<211> 463
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(463)
<223> FRXA00589

<400> 307
ccgttatctc cgtaactgtt gtttctgcag aaccatacaa ctcagcaaaa gccgcgacac 60

tccgcggcaa aaactaacca aggatttaaa agtcttcaaa atg aca act ctt tca 115
Met Thr Thr Leu Ser
1 5

cgt aag ttc ttc gtt tct gct acc aca gcc ctg gcg gca gtc gca ctg 163
Arg Lys Phe Phe Val Ser Ala Thr Thr Ala Leu Ala Ala Val Ala Leu
10 15 20

gtt gcg tgt tcc cct aat gag att gat tct gaa ctg aag gtg cca acg 211

```
Val Ala Cys Ser Pro Asn Glu Ile Asp Ser Glu Leu Lys Val Pro Thr
            25                  30                  35

gca act ggc gtt tct tta cct tcg aag aac gtt tcc gcg acc tca act   259
Ala Thr Gly Val Ser Leu Pro Ser Lys Asn Val Ser Ala Thr Ser Thr
        40                  45                  50

gct act aca gat gag gat gcg cct ggc tac att gat tgc gta gcc gca   307
Ala Thr Thr Asp Glu Asp Ala Pro Gly Tyr Ile Asp Cys Val Ala Ala
    55                  60                  65

cca act cag caa cct gct gaa atc tca cta aac tgt gca atg gat att   355
Pro Thr Gln Gln Pro Ala Glu Ile Ser Leu Asn Cys Ala Met Asp Ile
70                  75                  80                  85

gat cgg ctc acg gat att tct tgg agc gaa tgg gat act gat tcc gca   403
Asp Arg Leu Thr Asp Ile Ser Trp Ser Glu Trp Asp Thr Asp Ser Ala
                90                  95                  100

act gga acc ggt acc cgc atc gta acc gct gca aat ggt caa gag acc   451
Thr Gly Thr Gly Thr Arg Ile Val Thr Ala Ala Asn Gly Gln Glu Thr
            105                 110                 115

gaa acc gaa gat                                                  463
Glu Thr Glu Asp
        120
```

<210> 308
<211> 121
<212> PRT
<213> Corynebacterium glutamicum

<400> 308

```
Met Thr Thr Leu Ser Arg Lys Phe Phe Val Ser Ala Thr Thr Ala Leu
  1               5                  10                  15

Ala Ala Val Ala Leu Val Ala Cys Ser Pro Asn Glu Ile Asp Ser Glu
            20                  25                  30

Leu Lys Val Pro Thr Ala Thr Gly Val Ser Leu Pro Ser Lys Asn Val
        35                  40                  45

Ser Ala Thr Ser Thr Ala Thr Thr Asp Glu Asp Ala Pro Gly Tyr Ile
    50                  55                  60

Asp Cys Val Ala Ala Pro Thr Gln Gln Pro Ala Glu Ile Ser Leu Asn
65                  70                  75                  80

Cys Ala Met Asp Ile Asp Arg Leu Thr Asp Ile Ser Trp Ser Glu Trp
                85                  90                  95

Asp Thr Asp Ser Ala Thr Gly Thr Gly Thr Arg Ile Val Thr Ala Ala
            100                 105                 110

Asn Gly Gln Glu Thr Glu Thr Glu Asp
        115                 120
```

<210> 309
<211> 468

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(445)
<223> RXN00616

<400> 309
aaccgcaacc tcgcgcactt ggagtgaaaa ttctcatctt catttcatct tggtgcctaa 60

caatggaata cagattgagt tgatcaaagg agaaccccca atg aaa tca ctc ccc 115
Met Lys Ser Leu Pro
1 5

cgt ttc gcc cca ctg att acg att ctg gct ctg ctc gta ctc gtt gcc 163
Arg Phe Ala Pro Leu Ile Thr Ile Leu Ala Leu Leu Val Leu Val Ala
10 15 20

atc gga gga tct gca ctg gca aat aat cgt gct acc cct aat gtg gaa 211
Ile Gly Gly Ser Ala Leu Ala Asn Asn Arg Ala Thr Pro Asn Val Glu
25 30 35

agt gaa ccc gcc acg gtc aac cag cgt tcc act ccc aca act tcc gcg 259
Ser Glu Pro Ala Thr Val Asn Gln Arg Ser Thr Pro Thr Thr Ser Ala
40 45 50

tat gag ccc cct gct aca gaa tct ccg gaa gaa cca acc aca caa att 307
Tyr Glu Pro Pro Ala Thr Glu Ser Pro Glu Glu Pro Thr Thr Gln Ile
55 60 65

caa gaa tcc cca gta caa ccc cca gtt cct gcc ccc gct caa att cct 355
Gln Glu Ser Pro Val Gln Pro Pro Val Pro Ala Pro Ala Gln Ile Pro
70 75 80 85

caa gcc cca caa gtt cca ctc aat tat cag tac tat gac gat gac tgg 403
Gln Ala Pro Gln Val Pro Leu Asn Tyr Gln Tyr Tyr Asp Asp Asp Trp
90 95 100

gac gac gac gat gat gac ttc gac gac gac tgg gac gac gac 445
Asp Asp Asp Asp Asp Asp Phe Asp Asp Asp Trp Asp Asp Asp
105 110 115

taactaaccc ctgaggcact ttc 468

<210> 310
<211> 115
<212> PRT
<213> Corynebacterium glutamicum

<400> 310
Met Lys Ser Leu Pro Arg Phe Ala Pro Leu Ile Thr Ile Leu Ala Leu
1 5 10 15

Leu Val Leu Val Ala Ile Gly Gly Ser Ala Leu Ala Asn Asn Arg Ala
20 25 30

Thr Pro Asn Val Glu Ser Glu Pro Ala Thr Val Asn Gln Arg Ser Thr
35 40 45

```
Pro Thr Thr Ser Ala Tyr Glu Pro Pro Ala Thr Glu Ser Pro Glu Glu
     50                  55                  60

Pro Thr Thr Gln Ile Gln Glu Ser Pro Val Gln Pro Pro Val Pro Ala
 65                  70                  75                  80

Pro Ala Gln Ile Pro Gln Ala Pro Gln Val Pro Leu Asn Tyr Gln Tyr
                 85                  90                  95

Tyr Asp Asp Asp Trp Asp Asp Asp Asp Asp Asp Phe Asp Asp Asp Trp
            100                 105                 110

Asp Asp Asp
        115
```

<210> 311
<211> 468
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(445)
<223> FRXA00616

<400> 311

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aaccgcaacc tcgcgcactt ggagtgaaaa ttctcatctt catttcatct tggtgcctaa 60

caatggaata cagattgagt tgatcaaagg agaaccccca atg aaa tca ctc ccc   115
                                               Met Lys Ser Leu Pro
                                                 1               5

cgt ttc gcc cca ctg att acg att ctg gct ctg ctc gta ctc gtt gcc   163
Arg Phe Ala Pro Leu Ile Thr Ile Leu Ala Leu Leu Val Leu Val Ala
                10                  15                  20

atc gga gga tct gca ctg gca aat aat cgt gct acc cct aat gtg gaa   211
Ile Gly Gly Ser Ala Leu Ala Asn Asn Arg Ala Thr Pro Asn Val Glu
            25                  30                  35

agt gaa ccc gcc acg gtc aac cag cgt tcc act ccc aca act tcc gcg   259
Ser Glu Pro Ala Thr Val Asn Gln Arg Ser Thr Pro Thr Thr Ser Ala
        40                  45                  50

tat gag ccc cct gct aca gaa tct ccg gaa gaa cca acc aca caa att   307
Tyr Glu Pro Pro Ala Thr Glu Ser Pro Glu Glu Pro Thr Thr Gln Ile
    55                  60                  65

caa gaa tcc cca gta caa ccc cca gtt cct gcc ccc gct caa att cct   355
Gln Glu Ser Pro Val Gln Pro Pro Val Pro Ala Pro Ala Gln Ile Pro
70                  75                  80                  85

caa gcc cca caa gtt cca ctc aat tat cag tac tat gac gat gac tgg   403
Gln Ala Pro Gln Val Pro Leu Asn Tyr Gln Tyr Tyr Asp Asp Asp Trp
                90                  95                 100

gac gac gac gat gat gac ttc gac gac gac tgg gac gac gac           445
Asp Asp Asp Asp Asp Asp Phe Asp Asp Asp Trp Asp Asp Asp
            105                 110                 115
```

taactaaccc ctgaggcact ttc 468

<210> 312
<211> 115
<212> PRT
<213> Corynebacterium glutamicum

<400> 312
Met Lys Ser Leu Pro Arg Phe Ala Pro Leu Ile Thr Ile Leu Ala Leu
1 5 10 15

Leu Val Leu Val Ala Ile Gly Gly Ser Ala Leu Ala Asn Asn Arg Ala
20 25 30

Thr Pro Asn Val Glu Ser Glu Pro Ala Thr Val Asn Gln Arg Ser Thr
35 40 45

Pro Thr Thr Ser Ala Tyr Glu Pro Pro Ala Thr Glu Ser Pro Glu Glu
50 55 60

Pro Thr Thr Gln Ile Gln Glu Ser Pro Val Gln Pro Pro Val Pro Ala
65 70 75 80

Pro Ala Gln Ile Pro Gln Ala Pro Gln Val Pro Leu Asn Tyr Gln Tyr
85 90 95

Tyr Asp Asp Asp Trp Asp Asp Asp Asp Asp Asp Phe Asp Asp Asp Trp
100 105 110

Asp Asp Asp
115

<210> 313
<211> 756
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)
<223> RXN00647

<400> 313
tgcattcttc ccacaatgac atgagcttat tgcaacatcg tgggtaaagt tgaatcgaga 60

agtcgagaaa taaccgaccg atgaaagagt tgagacgata atg ggc atc ttc gaa 115
Met Gly Ile Phe Glu
1 5

gcc atc cga gcc gca cgc gcg aag acc aaa gct gag atc aaa gca gcc 163
Ala Ile Arg Ala Ala Arg Ala Lys Thr Lys Ala Glu Ile Lys Ala Ala
10 15 20

gag gca aaa gta aaa act gag gcg aaa aac aaa gca aag cta gat ctc 211
Glu Ala Lys Val Lys Thr Glu Ala Lys Asn Lys Ala Lys Leu Asp Leu
25 30 35

aag cgc gag aag ctt ctt gtc cag cag gaa aag aat ctg ctc aag gtt 259
Lys Arg Glu Lys Leu Leu Val Gln Gln Glu Lys Asn Leu Leu Lys Val

```
         40                  45                  50

gaa gaa aag ggc ctg aag aag cgc aac aag cat gag ctg aag atg gcc   307
Glu Glu Lys Gly Leu Lys Lys Arg Asn Lys His Glu Leu Lys Met Ala
     55                  60                  65

aaa aat atc ctt gag caa aag cgc caa gga cgc cta aac aaa gac aag   355
Lys Asn Ile Leu Glu Gln Lys Arg Gln Gly Arg Leu Asn Lys Asp Lys
 70                  75                  80                  85

gtg aag cgc tgg gct ggc acc gca cgt gtg ctc act cca cta ctg ctg   403
Val Lys Arg Trp Ala Gly Thr Ala Arg Val Leu Thr Pro Leu Leu Leu
                 90                  95                 100

cct att att tat cga ctc tcc acc gaa gca cgc gat cag gtt gtt aag   451
Pro Ile Ile Tyr Arg Leu Ser Thr Glu Ala Arg Asp Gln Val Val Lys
            105                 110                 115

gga cgt gcc cgt cgt gca ggt gtc acc gcg gag cag ctt agc caa ttc   499
Gly Arg Ala Arg Arg Ala Gly Val Thr Ala Glu Gln Leu Ser Gln Phe
        120                 125                 130

gca ggt cac gca gca gcg ctg aag gct cgt att caa ggt gtt cgc gaa   547
Ala Gly His Ala Ala Ala Leu Lys Ala Arg Ile Gln Gly Val Arg Glu
    135                 140                 145

acc gca aag aac tcc agc ctc cct gct ggc ttt gta cgc gat gtt gaa   595
Thr Ala Lys Asn Ser Ser Leu Pro Ala Gly Phe Val Arg Asp Val Glu
150                 155                 160                 165

gag cgt ctc aat gag ctc gag gct gct gcg aat aac tct gag ttc atg   643
Glu Arg Leu Asn Glu Leu Glu Ala Ala Ala Asn Asn Ser Glu Phe Met
                170                 175                 180

tct cca cag cag agg aac cgt gcg cac cag tcg atc agt cgt gat ctg   691
Ser Pro Gln Gln Arg Asn Arg Ala His Gln Ser Ile Ser Arg Asp Leu
            185                 190                 195

aac cag gtg tca gat cag att cag gat cga cta ctg gac aag           733
Asn Gln Val Ser Asp Gln Ile Gln Asp Arg Leu Leu Asp Lys
        200                 205                 210

tagctgctgg tcgagtcgct gcc                                        756


<210> 314
<211> 211
<212> PRT
<213> Corynebacterium glutamicum

<400> 314
Met Gly Ile Phe Glu Ala Ile Arg Ala Ala Arg Ala Lys Thr Lys Ala
  1               5                  10                  15

Glu Ile Lys Ala Ala Glu Ala Lys Val Lys Thr Glu Ala Lys Asn Lys
             20                  25                  30

Ala Lys Leu Asp Leu Lys Arg Glu Lys Leu Leu Val Gln Gln Glu Lys
         35                  40                  45

Asn Leu Leu Lys Val Glu Glu Lys Gly Leu Lys Lys Arg Asn Lys His
```

```
     50                  55                  60

Glu Leu Lys Met Ala Lys Asn Ile Leu Glu Gln Lys Arg Gln Gly Arg
 65                  70                  75                  80

Leu Asn Lys Asp Lys Val Lys Arg Trp Ala Gly Thr Ala Arg Val Leu
                 85                  90                  95

Thr Pro Leu Leu Leu Pro Ile Ile Tyr Arg Leu Ser Thr Glu Ala Arg
            100                 105                 110

Asp Gln Val Val Lys Gly Arg Ala Arg Arg Ala Gly Val Thr Ala Glu
        115                 120                 125

Gln Leu Ser Gln Phe Ala Gly His Ala Ala Ala Leu Lys Ala Arg Ile
    130                 135                 140

Gln Gly Val Arg Glu Thr Ala Lys Asn Ser Ser Leu Pro Ala Gly Phe
145                 150                 155                 160

Val Arg Asp Val Glu Glu Arg Leu Asn Glu Leu Glu Ala Ala Ala Asn
                165                 170                 175

Asn Ser Glu Phe Met Ser Pro Gln Gln Arg Asn Arg Ala His Gln Ser
            180                 185                 190

Ile Ser Arg Asp Leu Asn Gln Val Ser Asp Gln Ile Gln Asp Arg Leu
        195                 200                 205

Leu Asp Lys
    210


<210> 315
<211> 756
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)
<223> FRXA00647

<400> 315
tgcattcttc ccacaatgac atgagcttat tgcaacatcg tgggtaaagt tgaatcgaga 60

agtcgagaaa taaccgaccg atgaaagagt tgagacgata atg ggc atc ttc gaa   115
                                          Met Gly Ile Phe Glu
                                            1               5

gcc atc cga gcc gca cgc gcg aag acc aaa gct gag atc aaa gca gcc   163
Ala Ile Arg Ala Ala Arg Ala Lys Thr Lys Ala Glu Ile Lys Ala Ala
                10                  15                  20

gag gca aaa gta aaa act gag gcg aaa aac aaa gca aag cta gat ctc   211
Glu Ala Lys Val Lys Thr Glu Ala Lys Asn Lys Ala Lys Leu Asp Leu
            25                  30                  35

aag cgc gag aag ctt ctt gtc cag cag gaa aag aat ctg ctc aag gtt   259
Lys Arg Glu Lys Leu Leu Val Gln Gln Glu Lys Asn Leu Leu Lys Val
        40                  45                  50
```

```
gaa gaa aag ggc ctg aag aag cgc aac aag cat gag ctg aag atg gcc   307
Glu Glu Lys Gly Leu Lys Lys Arg Asn Lys His Glu Leu Lys Met Ala
     55                  60                  65

aaa aat atc ctt gag caa aag cgc caa gga cgc cta aac aaa gac aag   355
Lys Asn Ile Leu Glu Gln Lys Arg Gln Gly Arg Leu Asn Lys Asp Lys
 70                  75                  80                  85

gtg aag cgc tgg gct ggc acc gca cgt gtg ctc act cca cta ctg ctg   403
Val Lys Arg Trp Ala Gly Thr Ala Arg Val Leu Thr Pro Leu Leu Leu
                 90                  95                 100

cct att att tat cga ctc tcc acc gaa gca cgc gat cag gtt gtt aag   451
Pro Ile Ile Tyr Arg Leu Ser Thr Glu Ala Arg Asp Gln Val Val Lys
            105                 110                 115

gga cgt gcc cgt cgt gca ggt gtc acc gcg gag cag ctt agc caa ttc   499
Gly Arg Ala Arg Arg Ala Gly Val Thr Ala Glu Gln Leu Ser Gln Phe
        120                 125                 130

gca ggt cac gca gca gcg ctg aag gct cgt att caa ggt gtt cgc gaa   547
Ala Gly His Ala Ala Ala Leu Lys Ala Arg Ile Gln Gly Val Arg Glu
    135                 140                 145

acc gca aag aac tcc agc ctc cct gct ggc ttt gta cgc gat gtt gaa   595
Thr Ala Lys Asn Ser Ser Leu Pro Ala Gly Phe Val Arg Asp Val Glu
150                 155                 160                 165

gag cgt ctc aat gag ctc gag gct gct gcg aat aac tct gag ttc atg   643
Glu Arg Leu Asn Glu Leu Glu Ala Ala Ala Asn Asn Ser Glu Phe Met
                170                 175                 180

tct cca cag cag agg aac cgt gcg cac cag tcg atc agt cgt gat ctg   691
Ser Pro Gln Gln Arg Asn Arg Ala His Gln Ser Ile Ser Arg Asp Leu
            185                 190                 195

aac cag gtg tca gat cag att cag gat cga cta ctg gac aag           733
Asn Gln Val Ser Asp Gln Ile Gln Asp Arg Leu Leu Asp Lys
        200                 205                 210

tagctgctgg tcgagtcgct gcc                                        756
```

<210> 316
<211> 211
<212> PRT
<213> Corynebacterium glutamicum

<400> 316

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Met Gly Ile Phe Glu Ala Ile Arg Ala Ala Arg Ala Lys Thr Lys Ala
  1               5                  10                  15

Glu Ile Lys Ala Ala Glu Ala Lys Val Lys Thr Glu Ala Lys Asn Lys
             20                  25                  30

Ala Lys Leu Asp Leu Lys Arg Glu Lys Leu Leu Val Gln Gln Glu Lys
         35                  40                  45

Asn Leu Leu Lys Val Glu Glu Lys Gly Leu Lys Lys Arg Asn Lys His
     50                  55                  60
```

```
Glu Leu Lys Met Ala Lys Asn Ile Leu Glu Gln Lys Arg Gln Gly Arg
 65                  70                  75                  80

Leu Asn Lys Asp Lys Val Lys Arg Trp Ala Gly Thr Ala Arg Val Leu
                85                  90                  95

Thr Pro Leu Leu Leu Pro Ile Ile Tyr Arg Leu Ser Thr Glu Ala Arg
            100                 105                 110

Asp Gln Val Val Lys Gly Arg Ala Arg Arg Ala Gly Val Thr Ala Glu
        115                 120                 125

Gln Leu Ser Gln Phe Ala Gly His Ala Ala Ala Leu Lys Ala Arg Ile
    130                 135                 140

Gln Gly Val Arg Glu Thr Ala Lys Asn Ser Ser Leu Pro Ala Gly Phe
145                 150                 155                 160

Val Arg Asp Val Glu Glu Arg Leu Asn Glu Leu Glu Ala Ala Ala Asn
                165                 170                 175

Asn Ser Glu Phe Met Ser Pro Gln Gln Arg Asn Arg Ala His Gln Ser
            180                 185                 190

Ile Ser Arg Asp Leu Asn Gln Val Ser Asp Gln Ile Gln Asp Arg Leu
        195                 200                 205

Leu Asp Lys
    210
```

09350350

<210> 317
<211> 888
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(865)
<223> RXN00653

<400> 317
gttgagattc gcctaacaaa gattttggac gaaaacagta acgatgacag ccacgttaag 60

```
cgcggaatct tctcgcaatg gtaaaaagcc gcggcctcga gtg agt gtt tcc cag   115
                                            Val Ser Val Ser Gln
                                              1               5

gtt gtt ggt gaa atc ttg ctc acc gta ggc att ttg gcc ttg tta ttc   163
Val Val Gly Glu Ile Leu Leu Thr Val Gly Ile Leu Ala Leu Leu Phe
                10                  15                  20

gca tac tat gag gcc tat tgg acc aac gtg gaa tct ggg aaa tta caa   211
Ala Tyr Tyr Glu Ala Tyr Trp Thr Asn Val Glu Ser Gly Lys Leu Gln
            25                  30                  35

gaa tcg gct ggt caa aag ctt gat gaa gac tgg aat gaa gct cgg gtg   259
Glu Ser Ala Gly Gln Lys Leu Asp Glu Asp Trp Asn Glu Ala Arg Val
        40                  45                  50
```

```
aat cct cga caa aag ctc acc ccg gaa ctt ggt gag gca ttt gcc cgg   307
Asn Pro Arg Gln Lys Leu Thr Pro Glu Leu Gly Glu Ala Phe Ala Arg
     55                  60                  65

atg tat gtt cca gct ttc ggc tct gac ttc aac ttc gca gtg att gaa   355
Met Tyr Val Pro Ala Phe Gly Ser Asp Phe Asn Phe Ala Val Ile Glu
 70                  75                  80                  85

gga acc gat gag gaa gac ctt ctt gcc ggt cct ggc cgt tat gtg gat   403
Gly Thr Asp Glu Glu Asp Leu Leu Ala Gly Pro Gly Arg Tyr Val Asp
                 90                  95                 100

tcc caa atg cct ggt gaa gcc gga aac ttt gca gtg gca ggc cac cga   451
Ser Gln Met Pro Gly Glu Ala Gly Asn Phe Ala Val Ala Gly His Arg
            105                 110                 115

gtg ggc aag ggt gcg cca ttc aat gat cta gga aac ctg gaa gtc tgc   499
Val Gly Lys Gly Ala Pro Phe Asn Asp Leu Gly Asn Leu Glu Val Cys
        120                 125                 130

gat gcg atc gtg gtg gag act tac aat tcc tgg gat gtg tac cgc gtg   547
Asp Ala Ile Val Val Glu Thr Tyr Asn Ser Trp Asp Val Tyr Arg Val
    135                 140                 145

atg ccg atg tcc acc aac ggt gca gat cgt gca gca gaa gct gcg gat   595
Met Pro Met Ser Thr Asn Gly Ala Asp Arg Ala Ala Glu Ala Ala Asp
150                 155                 160                 165

tgc ttc aac gaa aac cag gtc agc cgc atg gct gaa ggt gac tat gtg   643
Cys Phe Asn Glu Asn Gln Val Ser Arg Met Ala Glu Gly Asp Tyr Val
                170                 175                 180

aat gtg tcc gga cga agc atc acc act ccg gat cgc atc gat gcc acc   691
Asn Val Ser Gly Arg Ser Ile Thr Thr Pro Asp Arg Ile Asp Ala Thr
            185                 190                 195

tac ccc aca ccg ggc gtc ttc gac act gca gtg cgt gaa gga tca gaa   739
Tyr Pro Thr Pro Gly Val Phe Asp Thr Ala Val Arg Glu Gly Ser Glu
        200                 205                 210

gct ctg ctt acc ttg acc acg tgt cac ccg cag ttc tcc aac gct gag   787
Ala Leu Leu Thr Leu Thr Thr Cys His Pro Gln Phe Ser Asn Ala Glu
    215                 220                 225

cgc atg att gtg cac gca atg ttg gtg gaa gaa atc gat aaa tca agt   835
Arg Met Ile Val His Ala Met Leu Val Glu Glu Ile Asp Lys Ser Ser
230                 235                 240                 245

ggc gaa cgc cct gca gct ttg gag gaa aac taaatgtatt cacttctgtg     885
Gly Glu Arg Pro Ala Ala Leu Glu Glu Asn
                250                 255

gca                                                               888
```

<210> 318
<211> 255
<212> PRT
<213> Corynebacterium glutamicum

<400> 318

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Val Ser Val Ser Gln Val Val Gly Glu Ile Leu Leu Thr Val Gly Ile
  1               5                  10                  15

Leu Ala Leu Leu Phe Ala Tyr Tyr Glu Ala Tyr Trp Thr Asn Val Glu
            20                  25                  30

Ser Gly Lys Leu Gln Glu Ser Ala Gly Gln Lys Leu Asp Glu Asp Trp
        35                  40                  45

Asn Glu Ala Arg Val Asn Pro Arg Gln Lys Leu Thr Pro Glu Leu Gly
    50                  55                  60

Glu Ala Phe Ala Arg Met Tyr Val Pro Ala Phe Gly Ser Asp Phe Asn
65                  70                  75                  80

Phe Ala Val Ile Glu Gly Thr Asp Glu Glu Asp Leu Leu Ala Gly Pro
                85                  90                  95

Gly Arg Tyr Val Asp Ser Gln Met Pro Gly Glu Ala Gly Asn Phe Ala
            100                 105                 110

Val Ala Gly His Arg Val Gly Lys Gly Ala Pro Phe Asn Asp Leu Gly
        115                 120                 125

Asn Leu Glu Val Cys Asp Ala Ile Val Val Glu Thr Tyr Asn Ser Trp
    130                 135                 140

Asp Val Tyr Arg Val Met Pro Met Ser Thr Asn Gly Ala Asp Arg Ala
145                 150                 155                 160

Ala Glu Ala Ala Asp Cys Phe Asn Glu Asn Gln Val Ser Arg Met Ala
                165                 170                 175

Glu Gly Asp Tyr Val Asn Val Ser Gly Arg Ser Ile Thr Thr Pro Asp
            180                 185                 190

Arg Ile Asp Ala Thr Tyr Pro Thr Pro Gly Val Phe Asp Thr Ala Val
        195                 200                 205

Arg Glu Gly Ser Glu Ala Leu Leu Thr Leu Thr Thr Cys His Pro Gln
    210                 215                 220

Phe Ser Asn Ala Glu Arg Met Ile Val His Ala Met Leu Val Glu Glu
225                 230                 235                 240

Ile Asp Lys Ser Ser Gly Glu Arg Pro Ala Ala Leu Glu Glu Asn
                245                 250                 255
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<210> 319
<211> 888
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(865)
<223> FRXA00653

<400> 319
gttgagattc gcctaacaaa gattttggac gaaaacagta acgatgacag ccacgttaag 60

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cgcggaatct tctcgcaatg gtaaaaagcc gcggcctcga gtg agt gtt tcc cag   115
                                              Val Ser Val Ser Gln
                                                1               5

gtt gtt ggt gaa atc ttg ctc acc gta ggc att ttg gcc ttg tta ttc   163
Val Val Gly Glu Ile Leu Leu Thr Val Gly Ile Leu Ala Leu Leu Phe
                10                  15                  20

gca tac tat gag gcc tat tgg acc aac gtg gaa tct ggg aaa tta caa   211
Ala Tyr Tyr Glu Ala Tyr Trp Thr Asn Val Glu Ser Gly Lys Leu Gln
            25                  30                  35

gaa tcg gct ggt caa aag ctt gat gaa gac tgg aat gaa gct cgg gtg   259
Glu Ser Ala Gly Gln Lys Leu Asp Glu Asp Trp Asn Glu Ala Arg Val
        40                  45                  50

aat cct cga caa aag ctc acc ccg gaa ctt ggt gag gca ttt gcc cgg   307
Asn Pro Arg Gln Lys Leu Thr Pro Glu Leu Gly Glu Ala Phe Ala Arg
    55                  60                  65

atg tat gtt cca gct ttc ggc tct gac ttc aac ttc gca gtg att gaa   355
Met Tyr Val Pro Ala Phe Gly Ser Asp Phe Asn Phe Ala Val Ile Glu
70                  75                  80                  85

gga acc gat gag gaa gac ctt ctt gcc ggt cct ggc cgt tat gtg gat   403
Gly Thr Asp Glu Glu Asp Leu Leu Ala Gly Pro Gly Arg Tyr Val Asp
                90                  95                  100

tcc caa atg cct ggt gaa gcc gga aac ttt gca gtg gca ggc cac cga   451
Ser Gln Met Pro Gly Glu Ala Gly Asn Phe Ala Val Ala Gly His Arg
            105                 110                 115

gtg ggc aag ggt gcg cca ttc aat gat cta gga aac ctg gaa gtc tgc   499
Val Gly Lys Gly Ala Pro Phe Asn Asp Leu Gly Asn Leu Glu Val Cys
        120                 125                 130

gat gcg atc gtg gtg gag act tac aat tcc tgg gat gtg tac cgc gtg   547
Asp Ala Ile Val Val Glu Thr Tyr Asn Ser Trp Asp Val Tyr Arg Val
    135                 140                 145

atg ccg atg tcc acc aac ggt gca gat cgt gca gca gaa gct gcg gat   595
Met Pro Met Ser Thr Asn Gly Ala Asp Arg Ala Ala Glu Ala Ala Asp
150                 155                 160                 165

tgc ttc aac gaa aac cag gtc agc cgc atg gct gaa ggt gac tat gtg   643
Cys Phe Asn Glu Asn Gln Val Ser Arg Met Ala Glu Gly Asp Tyr Val
                170                 175                 180

aat gtg tcc gga cga agc atc acc act ccg gat cgc atc gat gcc acc   691
Asn Val Ser Gly Arg Ser Ile Thr Thr Pro Asp Arg Ile Asp Ala Thr
            185                 190                 195

tac ccc aca ccg ggc gtc ttc gac act gca gtg cgt gaa gga tca gaa   739
Tyr Pro Thr Pro Gly Val Phe Asp Thr Ala Val Arg Glu Gly Ser Glu
        200                 205                 210

gct ctg ctt acc ttg acc acg tgt cac ccg cag ttc tcc aac gct gag   787
Ala Leu Leu Thr Leu Thr Thr Cys His Pro Gln Phe Ser Asn Ala Glu
    215                 220                 225
```

```
cgc atg att gtg cac gca atg ttg gtg gaa gaa atc gat aaa tca agt   835
Arg Met Ile Val His Ala Met Leu Val Glu Glu Ile Asp Lys Ser Ser
230                 235                 240                 245

ggc gaa cgc cct gca gct ttg gag gaa aac taaatgtatt cacttctgtg     885
Gly Glu Arg Pro Ala Ala Leu Glu Glu Asn
                250                 255

gca                                                               888
```

<210> 320
<211> 255
<212> PRT
<213> Corynebacterium glutamicum

<400> 320

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Val Ser Val Ser Gln Val Val Gly Glu Ile Leu Leu Thr Val Gly Ile
  1               5                  10                  15

Leu Ala Leu Leu Phe Ala Tyr Tyr Glu Ala Tyr Trp Thr Asn Val Glu
             20                  25                  30

Ser Gly Lys Leu Gln Glu Ser Ala Gly Gln Lys Leu Asp Glu Asp Trp
         35                  40                  45

Asn Glu Ala Arg Val Asn Pro Arg Gln Lys Leu Thr Pro Glu Leu Gly
     50                  55                  60

Glu Ala Phe Ala Arg Met Tyr Val Pro Ala Phe Gly Ser Asp Phe Asn
 65                  70                  75                  80

Phe Ala Val Ile Glu Gly Thr Asp Glu Glu Asp Leu Leu Ala Gly Pro
                 85                  90                  95

Gly Arg Tyr Val Asp Ser Gln Met Pro Gly Glu Ala Gly Asn Phe Ala
            100                 105                 110

Val Ala Gly His Arg Val Gly Lys Gly Ala Pro Phe Asn Asp Leu Gly
        115                 120                 125

Asn Leu Glu Val Cys Asp Ala Ile Val Val Glu Thr Tyr Asn Ser Trp
    130                 135                 140

Asp Val Tyr Arg Val Met Pro Met Ser Thr Asn Gly Ala Asp Arg Ala
145                 150                 155                 160

Ala Glu Ala Ala Asp Cys Phe Asn Glu Asn Gln Val Ser Arg Met Ala
                165                 170                 175

Glu Gly Asp Tyr Val Asn Val Ser Gly Arg Ser Ile Thr Thr Pro Asp
            180                 185                 190

Arg Ile Asp Ala Thr Tyr Pro Thr Pro Gly Val Phe Asp Thr Ala Val
        195                 200                 205

Arg Glu Gly Ser Glu Ala Leu Leu Thr Leu Thr Thr Cys His Pro Gln
    210                 215                 220

Phe Ser Asn Ala Glu Arg Met Ile Val His Ala Met Leu Val Glu Glu
225                 230                 235                 240
```

```
Ile Asp Lys Ser Ser Gly Glu Arg Pro Ala Ala Leu Glu Glu Asn
                245                 250                 255


<210> 321
<211> 1392
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1369)
<223> RXN00662

<400> 321
ccctcatcat agttttaaat ctggggcaga ggcgggaatt taaacacctc tgatacagcg 60

tttactggct atagtgttgc gcgtgccaaa tcgagttcct gtg tca acc att ccg   115
                                        Val Ser Thr Ile Pro
                                          1               5

ctg aat cgt cta gcc gtt atc gct gcc atc att ggt gtc ggt acc ggg   163
Leu Asn Arg Leu Ala Val Ile Ala Ala Ile Ile Gly Val Gly Thr Gly
                 10                  15                  20

ctg ttt gtt gct gca ctg aac tgg tct gcc att ggc gtg gag cgt tta   211
Leu Phe Val Ala Ala Leu Asn Trp Ser Ala Ile Gly Val Glu Arg Leu
             25                  30                  35

gtt tat ggc gct gac cat ttg cat aat tac aat ccg gtg gcc aat gtg   259
Val Tyr Gly Ala Asp His Leu His Asn Tyr Asn Pro Val Ala Asn Val
         40                  45                  50

tcg cca ctt cgc ctg tcc atc acg gtg att gtg ctt agc gtg gtg gcc   307
Ser Pro Leu Arg Leu Ser Ile Thr Val Ile Val Leu Ser Val Val Ala
     55                  60                  65

tcc tgg gcg tgg ttt ttt gtg cac cgc acg ggg ccg aaa gag gtt tcg   355
Ser Trp Ala Trp Phe Phe Val His Arg Thr Gly Pro Lys Glu Val Ser
 70                  75                  80                  85

att gtg ggt gcg atc cgg ggc gag aag atg ccg att ttg gag acc ata   403
Ile Val Gly Ala Ile Arg Gly Glu Lys Met Pro Ile Leu Glu Thr Ile
                 90                  95                 100

gcg tcc gca ttt ttg cag gtc acc acg gtt gct gcg ggt gcg ccg gtg   451
Ala Ser Ala Phe Leu Gln Val Thr Thr Val Ala Ala Gly Ala Pro Val
            105                 110                 115

ggt gca gag aac gct cca cgt att gct gga gcc ttg gtg gga gag cgg   499
Gly Ala Glu Asn Ala Pro Arg Ile Ala Gly Ala Leu Val Gly Glu Arg
        120                 125                 130

ttt agt cgg tgg ttg cag ctc gat att gat gca aag cgc atc ttg gtg   547
Phe Ser Arg Trp Leu Gln Leu Asp Ile Asp Ala Lys Arg Ile Leu Val
    135                 140                 145

gcc tct gcc gcg gga gct ggt ttg gga gca agc ttc cac ctt ccc cta   595
Ala Ser Ala Ala Gly Ala Gly Leu Gly Ala Ser Phe His Leu Pro Leu
150                 155                 160                 165
```

```
gca ggc gtg ctg ttt gcc ctt gag gtc cta ctg gtt gag gcc tcc act   643
Ala Gly Val Leu Phe Ala Leu Glu Val Leu Leu Val Glu Ala Ser Thr
                170                 175                 180

cgg acc gtg gtt atc gca att atc acc acg acc gcc gcc gtt gcc acc   691
Arg Thr Val Val Ile Ala Ile Ile Thr Thr Thr Ala Ala Val Ala Thr
            185                 190                 195

act gga ttt ttc gtg caa acc cca gat gtg ttc agc act gtc ccg ctg   739
Thr Gly Phe Phe Val Gln Thr Pro Asp Val Phe Ser Thr Val Pro Leu
        200                 205                 210

acg gaa agc cca tgg atg ctg ctt gcc gcg atg gtc acc gga gta gtc   787
Thr Glu Ser Pro Trp Met Leu Leu Ala Ala Met Val Thr Gly Val Val
    215                 220                 225

gcc ggc atg tgc ggg cac tgg ttt tca gcg gcg gcg cac aaa atg gcg   835
Ala Gly Met Cys Gly His Trp Phe Ser Ala Ala Ala His Lys Met Ala
230                 235                 240                 245

cag gcc tcg ccc aag ggt gtg aag att ttg tgg cag atg ccg ttg ggt   883
Gln Ala Ser Pro Lys Gly Val Lys Ile Leu Trp Gln Met Pro Leu Gly
                250                 255                 260

ttc gtg gtg atc gct gcg gtg att tat ttc ttc ccc gaa acc ctg gcg   931
Phe Val Val Ile Ala Ala Val Ile Tyr Phe Phe Pro Glu Thr Leu Ala
            265                 270                 275

aat ccc cgt tgg ctt gcc gat tcc atg ctc ggc gat ggc ctg atc ctc   979
Asn Pro Arg Trp Leu Ala Asp Ser Met Leu Gly Asp Gly Leu Ile Leu
        280                 285                 290

agc acc att tta ttg gta ctt gtt ctg cgc acc gcc atg ttt ttg ctc   1027
Ser Thr Ile Leu Leu Val Leu Val Leu Arg Thr Ala Met Phe Leu Leu
    295                 300                 305

gcc ttc cgc gtg ggc atg gtc ggc ggt aac ctg atc ccc gca ttc gca   1075
Ala Phe Arg Val Gly Met Val Gly Gly Asn Leu Ile Pro Ala Phe Ala
310                 315                 320                 325

ctc gga tcc atg gtc ggt ggg gta gtg ggt gct gta ttg gaa ccc atc   1123
Leu Gly Ser Met Val Gly Gly Val Val Gly Ala Val Leu Glu Pro Ile
                330                 335                 340

act aac gtc ccg atc gcc gct ttt gcg ctg ctt ggc gcc gcc gca ttt   1171
Thr Asn Val Pro Ile Ala Ala Phe Ala Leu Leu Gly Ala Ala Ala Phe
            345                 350                 355

ttg tcc acc acc atg gca gcg cca ctg ttc ggg ctc atc gcc gca gtg   1219
Leu Ser Thr Thr Met Ala Ala Pro Leu Phe Gly Leu Ile Ala Ala Val
        360                 365                 370

gaa ttc acc gac atg gaa gcc caa ggc tac ctt ccg att ttc ctc gca   1267
Glu Phe Thr Asp Met Glu Ala Gln Gly Tyr Leu Pro Ile Phe Leu Ala
    375                 380                 385

gta gcc tcc gcg gtc ctc gcc gtg cgc gtg tgg tct gtc atc gcc aag   1315
Val Ala Ser Ala Val Leu Ala Val Arg Val Trp Ser Val Ile Ala Lys
390                 395                 400                 405
```

```
cac gag ctc cgc gcc atc ccg atc acg tac gcg agc tgg acg ggc gag   1363
His Glu Leu Arg Ala Ile Pro Ile Thr Tyr Ala Ser Trp Thr Gly Glu
                410                 415                 420

ctt aaa taagcttgtc gacgcctccc tcc                                1392
Leu Lys
```

<210> 322
<211> 423
<212> PRT
<213> Corynebacterium glutamicum

<400> 322

```
Val Ser Thr Ile Pro Leu Asn Arg Leu Ala Val Ile Ala Ala Ile Ile
  1               5                  10                  15

Gly Val Gly Thr Gly Leu Phe Val Ala Ala Leu Asn Trp Ser Ala Ile
             20                  25                  30

Gly Val Glu Arg Leu Val Tyr Gly Ala Asp His Leu His Asn Tyr Asn
         35                  40                  45

Pro Val Ala Asn Val Ser Pro Leu Arg Leu Ser Ile Thr Val Ile Val
     50                  55                  60

Leu Ser Val Val Ala Ser Trp Ala Trp Phe Phe Val His Arg Thr Gly
 65                  70                  75                  80

Pro Lys Glu Val Ser Ile Val Gly Ala Ile Arg Gly Glu Lys Met Pro
                 85                  90                  95

Ile Leu Glu Thr Ile Ala Ser Ala Phe Leu Gln Val Thr Thr Val Ala
            100                 105                 110

Ala Gly Ala Pro Val Gly Ala Glu Asn Ala Pro Arg Ile Ala Gly Ala
        115                 120                 125

Leu Val Gly Glu Arg Phe Ser Arg Trp Leu Gln Leu Asp Ile Asp Ala
    130                 135                 140

Lys Arg Ile Leu Val Ala Ser Ala Ala Gly Ala Gly Leu Gly Ala Ser
145                 150                 155                 160

Phe His Leu Pro Leu Ala Gly Val Leu Phe Ala Leu Glu Val Leu Leu
                165                 170                 175

Val Glu Ala Ser Thr Arg Thr Val Val Ile Ala Ile Ile Thr Thr Thr
            180                 185                 190

Ala Ala Val Ala Thr Thr Gly Phe Phe Val Gln Thr Pro Asp Val Phe
        195                 200                 205

Ser Thr Val Pro Leu Thr Glu Ser Pro Trp Met Leu Leu Ala Ala Met
    210                 215                 220

Val Thr Gly Val Val Ala Gly Met Cys Gly His Trp Phe Ser Ala Ala
225                 230                 235                 240

Ala His Lys Met Ala Gln Ala Ser Pro Lys Gly Val Lys Ile Leu Trp
```

```
                245                 250                 255

Gln Met Pro Leu Gly Phe Val Val Ile Ala Ala Val Ile Tyr Phe Phe
            260                 265                 270

Pro Glu Thr Leu Ala Asn Pro Arg Trp Leu Ala Asp Ser Met Leu Gly
        275                 280                 285

Asp Gly Leu Ile Leu Ser Thr Ile Leu Leu Val Leu Val Leu Arg Thr
    290                 295                 300

Ala Met Phe Leu Leu Ala Phe Arg Val Gly Met Val Gly Gly Asn Leu
305                 310                 315                 320

Ile Pro Ala Phe Ala Leu Gly Ser Met Val Gly Gly Val Val Gly Ala
                325                 330                 335

Val Leu Glu Pro Ile Thr Asn Val Pro Ile Ala Ala Phe Ala Leu Leu
            340                 345                 350

Gly Ala Ala Ala Phe Leu Ser Thr Thr Met Ala Ala Pro Leu Phe Gly
        355                 360                 365

Leu Ile Ala Ala Val Glu Phe Thr Asp Met Glu Ala Gln Gly Tyr Leu
    370                 375                 380

Pro Ile Phe Leu Ala Val Ala Ser Ala Val Leu Ala Val Arg Val Trp
385                 390                 395                 400

Ser Val Ile Ala Lys His Glu Leu Arg Ala Ile Pro Ile Thr Tyr Ala
                405                 410                 415

Ser Trp Thr Gly Glu Leu Lys
            420


<210> 323
<211> 1392
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1369)
<223> FRXA00662

<400> 323
ccctcatcat agttttaaat ctggggcaga ggcgggaatt taaacacctc tgatacagcg 60

tttactggct atagtgttgc gcgtgccaaa tcgagttcct gtg tca acc att ccg   115
                                        Val Ser Thr Ile Pro
                                          1               5

ctg aat cgt cta gcc gtt atc gct gcc atc att ggt gtc ggt acc ggg   163
Leu Asn Arg Leu Ala Val Ile Ala Ala Ile Ile Gly Val Gly Thr Gly
                  10                  15                  20

ctg ttt gtt gct gca ctg aac tgg tct gcc att ggc gtg gag cgt tta   211
Leu Phe Val Ala Ala Leu Asn Trp Ser Ala Ile Gly Val Glu Arg Leu
          25                  30                  35
```

```
gtt tat ggc gct gac cat ttg cat aat tac aat ccg gtg gcc aat gtg   259
Val Tyr Gly Ala Asp His Leu His Asn Tyr Asn Pro Val Ala Asn Val
         40                  45                  50

tcg cca ctt cgc ctg tcc atc acg gtg att gtg ctt agc gtg gtg gcc   307
Ser Pro Leu Arg Leu Ser Ile Thr Val Ile Val Leu Ser Val Val Ala
     55                  60                  65

tcc tgg gcg tgg ttt ttt gtg cac cgc acg ggg ccg aaa gag gtt tcg   355
Ser Trp Ala Trp Phe Phe Val His Arg Thr Gly Pro Lys Glu Val Ser
 70                  75                  80                  85

att gtg ggt gcg atc cgg ggc gag aag atg ccg att ttg gag acc ata   403
Ile Val Gly Ala Ile Arg Gly Glu Lys Met Pro Ile Leu Glu Thr Ile
                 90                  95                 100

gcg tcc gca ttt ttg cag gtc acc acg gtt gct gcg ggt gcg ccg gtg   451
Ala Ser Ala Phe Leu Gln Val Thr Thr Val Ala Ala Gly Ala Pro Val
            105                 110                 115

ggt gca gag aac gct cca cgt att gct gga gcc ttg gtg gga gag cgg   499
Gly Ala Glu Asn Ala Pro Arg Ile Ala Gly Ala Leu Val Gly Glu Arg
        120                 125                 130

ttt agt cgg tgg ttg cag ctc gat att gat gca aag cgc atc ttg gtg   547
Phe Ser Arg Trp Leu Gln Leu Asp Ile Asp Ala Lys Arg Ile Leu Val
    135                 140                 145

gcc tct gcc gcg gga gct ggt ttg gga gca agc ttc cac ctt ccc cta   595
Ala Ser Ala Ala Gly Ala Gly Leu Gly Ala Ser Phe His Leu Pro Leu
150                 155                 160                 165

gca ggc gtg ctg ttt gcc ctt gag gtc cta ctg gtt gag gcc tcc act   643
Ala Gly Val Leu Phe Ala Leu Glu Val Leu Leu Val Glu Ala Ser Thr
                170                 175                 180

cgg acc gtg gtt atc gca att atc acc acg acc gcc gcc gtt gcc acc   691
Arg Thr Val Val Ile Ala Ile Ile Thr Thr Thr Ala Ala Val Ala Thr
            185                 190                 195

act gga ttt ttc gtg caa acc cca gat gtg ttc agc act gtc ccg ctg   739
Thr Gly Phe Phe Val Gln Thr Pro Asp Val Phe Ser Thr Val Pro Leu
        200                 205                 210

acg gaa agc cca tgg atg ctg ctt gcc gcg atg gtc acc gga gta gtc   787
Thr Glu Ser Pro Trp Met Leu Leu Ala Ala Met Val Thr Gly Val Val
    215                 220                 225

gcc ggc atg tgc ggg cac tgg ttt tca gcg gcg gcg cac aaa atg gcg   835
Ala Gly Met Cys Gly His Trp Phe Ser Ala Ala Ala His Lys Met Ala
230                 235                 240                 245

cag gcc tcg ccc aag ggt gtg aag att ttg tgg cag atg ccg ttg ggt   883
Gln Ala Ser Pro Lys Gly Val Lys Ile Leu Trp Gln Met Pro Leu Gly
                250                 255                 260

ttc gtg gtg atc gct gcg gtg att tat ttc ttc ccc gaa acc ctg gcg   931
Phe Val Val Ile Ala Ala Val Ile Tyr Phe Phe Pro Glu Thr Leu Ala
            265                 270                 275

aat ccc cgt tgg ctt gcc gat tcc atg ctc ggc gat ggc ctg atc ctc   979
```

```
Asn Pro Arg Trp Leu Ala Asp Ser Met Leu Gly Asp Gly Leu Ile Leu
        280                 285                 290

agc acc att tta ttg gta ctt gtt ctg cgc acc gcc atg ttt ttg ctc   1027
Ser Thr Ile Leu Leu Val Leu Val Leu Arg Thr Ala Met Phe Leu Leu
    295                 300                 305

gcc ttc cgc gtg ggc atg gtc ggc ggt aac ctg atc ccc gca ttc gca   1075
Ala Phe Arg Val Gly Met Val Gly Gly Asn Leu Ile Pro Ala Phe Ala
310                 315                 320                 325

ctc gga tcc atg gtc ggt ggg gta gtg ggt gct gta ttg gaa ccc atc   1123
Leu Gly Ser Met Val Gly Gly Val Val Gly Ala Val Leu Glu Pro Ile
                330                 335                 340

act aac gtc ccg atc gcc gct ttt gcg ctg ctt ggc gcc gcc gca ttt   1171
Thr Asn Val Pro Ile Ala Ala Phe Ala Leu Leu Gly Ala Ala Ala Phe
            345                 350                 355

ttg tcc acc acc atg gca gcg cca ctg ttc ggg ctc atc gcc gca gtg   1219
Leu Ser Thr Thr Met Ala Ala Pro Leu Phe Gly Leu Ile Ala Ala Val
        360                 365                 370

gaa ttc acc gac atg gaa gcc caa ggc tac ctt ccg att ttc ctc gca   1267
Glu Phe Thr Asp Met Glu Ala Gln Gly Tyr Leu Pro Ile Phe Leu Ala
    375                 380                 385

gta gcc tcc gcg gtc ctc gcc gtg cgc gtg tgg tct gtc atc gcc aag   1315
Val Ala Ser Ala Val Leu Ala Val Arg Val Trp Ser Val Ile Ala Lys
390                 395                 400                 405

cac gag ctc cgc gcc atc ccg atc acg tac gcg agc tgg acg ggc gag   1363
His Glu Leu Arg Ala Ile Pro Ile Thr Tyr Ala Ser Trp Thr Gly Glu
                410                 415                 420

ctt aaa taagcttgtc gacgcctccc tcc                                 1392
Leu Lys
```

09360705.030705

<210> 324
<211> 423
<212> PRT
<213> Corynebacterium glutamicum

<400> 324

```
Val Ser Thr Ile Pro Leu Asn Arg Leu Ala Val Ile Ala Ala Ile Ile
  1               5                  10                  15

Gly Val Gly Thr Gly Leu Phe Val Ala Ala Leu Asn Trp Ser Ala Ile
             20                  25                  30

Gly Val Glu Arg Leu Val Tyr Gly Ala Asp His Leu His Asn Tyr Asn
         35                  40                  45

Pro Val Ala Asn Val Ser Pro Leu Arg Leu Ser Ile Thr Val Ile Val
     50                  55                  60

Leu Ser Val Val Ala Ser Trp Ala Trp Phe Phe Val His Arg Thr Gly
 65                  70                  75                  80
```

```
Pro Lys Glu Val Ser Ile Val Gly Ala Ile Arg Gly Glu Lys Met Pro
                 85                  90                  95

Ile Leu Glu Thr Ile Ala Ser Ala Phe Leu Gln Val Thr Thr Val Ala
            100                 105                 110

Ala Gly Ala Pro Val Gly Ala Glu Asn Ala Pro Arg Ile Ala Gly Ala
        115                 120                 125

Leu Val Gly Glu Arg Phe Ser Arg Trp Leu Gln Leu Asp Ile Asp Ala
    130                 135                 140

Lys Arg Ile Leu Val Ala Ser Ala Ala Gly Ala Gly Leu Gly Ala Ser
145                 150                 155                 160

Phe His Leu Pro Leu Ala Gly Val Leu Phe Ala Leu Glu Val Leu Leu
                165                 170                 175

Val Glu Ala Ser Thr Arg Thr Val Val Ile Ala Ile Ile Thr Thr Thr
            180                 185                 190

Ala Ala Val Ala Thr Thr Gly Phe Phe Val Gln Thr Pro Asp Val Phe
        195                 200                 205

Ser Thr Val Pro Leu Thr Glu Ser Pro Trp Met Leu Leu Ala Ala Met
    210                 215                 220

Val Thr Gly Val Val Ala Gly Met Cys Gly His Trp Phe Ser Ala Ala
225                 230                 235                 240

Ala His Lys Met Ala Gln Ala Ser Pro Lys Gly Val Lys Ile Leu Trp
                245                 250                 255

Gln Met Pro Leu Gly Phe Val Val Ile Ala Ala Val Ile Tyr Phe Phe
            260                 265                 270

Pro Glu Thr Leu Ala Asn Pro Arg Trp Leu Ala Asp Ser Met Leu Gly
        275                 280                 285

Asp Gly Leu Ile Leu Ser Thr Ile Leu Leu Val Leu Val Leu Arg Thr
    290                 295                 300

Ala Met Phe Leu Leu Ala Phe Arg Val Gly Met Val Gly Gly Asn Leu
305                 310                 315                 320

Ile Pro Ala Phe Ala Leu Gly Ser Met Val Gly Gly Val Val Gly Ala
                325                 330                 335

Val Leu Glu Pro Ile Thr Asn Val Pro Ile Ala Ala Phe Ala Leu Leu
            340                 345                 350

Gly Ala Ala Ala Phe Leu Ser Thr Thr Met Ala Ala Pro Leu Phe Gly
        355                 360                 365

Leu Ile Ala Ala Val Glu Phe Thr Asp Met Glu Ala Gln Gly Tyr Leu
    370                 375                 380

Pro Ile Phe Leu Ala Val Ala Ser Ala Val Leu Ala Val Arg Val Trp
385                 390                 395                 400

Ser Val Ile Ala Lys His Glu Leu Arg Ala Ile Pro Ile Thr Tyr Ala
```

```
                405                 410                 415

Ser Trp Thr Gly Glu Leu Lys
            420


<210> 325
<211> 1038
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1015)
<223> RXN00666

<400> 325
agtggtgaat gctggataag tttttaacat gtctagtgta gtcggggaag gcccaaaacc 60

acgattgagc gtgcttgatc tcgtcgcgct gagtgaaggg atg acg gcc ggc gag   115
                                              Met Thr Ala Gly Glu
                                                1               5

gcc att gca cac agt gtt cgc gct gcg cag atc gcc gaa gag cac aat   163
Ala Ile Ala His Ser Val Arg Ala Ala Gln Ile Ala Glu Glu His Asn
                  10                  15                  20

tat gcg cgt ttc tgg gtg gcg gag cac cac aac tcg gaa ggc ttg gca   211
Tyr Ala Arg Phe Trp Val Ala Glu His His Asn Ser Glu Gly Leu Ala
            25                  30                  35

tct tcc gcg acg acg ctg ctc atg ggt cat att gca ggc cac act tca   259
Ser Ser Ala Thr Thr Leu Leu Met Gly His Ile Ala Gly His Thr Ser
        40                  45                  50

cgc att cgc gtt ggc tcc ggt ggc atc atg atg ccc aac cac tcc gcg   307
Arg Ile Arg Val Gly Ser Gly Gly Ile Met Met Pro Asn His Ser Ala
    55                  60                  65

ctg cac gtc gcc gaa gaa ctc ggc acc ctt gag gcc att tac ccc ggc   355
Leu His Val Ala Glu Glu Leu Gly Thr Leu Glu Ala Ile Tyr Pro Gly
70                  75                  80                  85

cgc atc gag gcc ggc cta ggg cgc gca cca gga acc gac ccc atg acg   403
Arg Ile Glu Ala Gly Leu Gly Arg Ala Pro Gly Thr Asp Pro Met Thr
                90                  95                 100

gcg cgg gaa ttg ggt cgg gca agt tcg ctt gtc gac gac gtc ctc tcc   451
Ala Arg Glu Leu Gly Arg Ala Ser Ser Leu Val Asp Asp Val Leu Ser
            105                 110                 115

aca atc gtc tcc ctc cag aat tat ttg gac acc ccc gaa gaa cgc ccg   499
Thr Ile Val Ser Leu Gln Asn Tyr Leu Asp Thr Pro Glu Glu Arg Pro
        120                 125                 130

aac atc atc gcg cat cca gga ata aat tcc cgt gtg ccg cta ttc atg   547
Asn Ile Ile Ala His Pro Gly Ile Asn Ser Arg Val Pro Leu Phe Met
    135                 140                 145

ctg gga tct tcc ctc aac ggc gct gcg atg gcc gct aaa tta gac ctt   595
Leu Gly Ser Ser Leu Asn Gly Ala Ala Met Ala Ala Lys Leu Asp Leu
```

```
150                 155                 160                 165

cca ttc gcc ttc gcc agc cac ttc gca ccc ttc caa atg ggg ccc gcc   643
Pro Phe Ala Phe Ala Ser His Phe Ala Pro Phe Gln Met Gly Pro Ala
                170                 175                 180

atc gcc tcc tat cgc gaa cta gca gcc aat cct tat gtc atg gcc gca   691
Ile Ala Ser Tyr Arg Glu Leu Ala Ala Asn Pro Tyr Val Met Ala Ala
            185                 190                 195

gcg aat gtc ctg gtg tgc gac acc gag gaa gaa gcc gaa ttc cag atc   739
Ala Asn Val Leu Val Cys Asp Thr Glu Glu Glu Ala Glu Phe Gln Ile
        200                 205                 210

tcc aca ctg cac caa atg ttc gcc gga atc gtg acg aac tcc cgc ggc   787
Ser Thr Leu His Gln Met Phe Ala Gly Ile Val Thr Asn Ser Arg Gly
    215                 220                 225

aaa ctt gcc cca cca gtg cgg aat ctg aaa gac aaa ctc gac ccg atg   835
Lys Leu Ala Pro Pro Val Arg Asn Leu Lys Asp Lys Leu Asp Pro Met
230                 235                 240                 245

atc tgg aaa cac atc gaa gat tca ttg gaa atg act ttc atc gga aca   883
Ile Trp Lys His Ile Glu Asp Ser Leu Glu Met Thr Phe Ile Gly Thr
                250                 255                 260

gcc gaa tca gtg gta tta caa ctg cag gaa ttc gct gat cgc tac aag   931
Ala Glu Ser Val Val Leu Gln Leu Gln Glu Phe Ala Asp Arg Tyr Lys
            265                 270                 275

tta gat gag atc att aca gtc acc tac tcc tac gac ccc gaa gtc agg   979
Leu Asp Glu Ile Ile Thr Val Thr Tyr Ser Tyr Asp Pro Glu Val Arg
        280                 285                 290

ttc cgc tcc ata gct gca ctt ggc acg gca tgg aat tagtgtcaaa        1025
Phe Arg Ser Ile Ala Ala Leu Gly Thr Ala Trp Asn
    295                 300                 305

agcctcaaaa ata                                                   1038
```

<210> 326
<211> 305
<212> PRT
<213> Corynebacterium glutamicum

<400> 326

```
Met Thr Ala Gly Glu Ala Ile Ala His Ser Val Arg Ala Ala Gln Ile
  1               5                  10                  15

Ala Glu Glu His Asn Tyr Ala Arg Phe Trp Val Ala Glu His His Asn
             20                  25                  30

Ser Glu Gly Leu Ala Ser Ser Ala Thr Thr Leu Leu Met Gly His Ile
         35                  40                  45

Ala Gly His Thr Ser Arg Ile Arg Val Gly Ser Gly Gly Ile Met Met
     50                  55                  60

Pro Asn His Ser Ala Leu His Val Ala Glu Glu Leu Gly Thr Leu Glu
 65                  70                  75                  80
```

```
Ala Ile Tyr Pro Gly Arg Ile Glu Ala Gly Leu Gly Arg Ala Pro Gly
                 85                  90                  95

Thr Asp Pro Met Thr Ala Arg Glu Leu Gly Arg Ala Ser Ser Leu Val
            100                 105                 110

Asp Asp Val Leu Ser Thr Ile Val Ser Leu Gln Asn Tyr Leu Asp Thr
        115                 120                 125

Pro Glu Glu Arg Pro Asn Ile Ile Ala His Pro Gly Ile Asn Ser Arg
    130                 135                 140

Val Pro Leu Phe Met Leu Gly Ser Ser Leu Asn Gly Ala Ala Met Ala
145                 150                 155                 160

Ala Lys Leu Asp Leu Pro Phe Ala Phe Ala Ser His Phe Ala Pro Phe
                165                 170                 175

Gln Met Gly Pro Ala Ile Ala Ser Tyr Arg Glu Leu Ala Ala Asn Pro
            180                 185                 190

Tyr Val Met Ala Ala Ala Asn Val Leu Val Cys Asp Thr Glu Glu Glu
        195                 200                 205

Ala Glu Phe Gln Ile Ser Thr Leu His Gln Met Phe Ala Gly Ile Val
    210                 215                 220

Thr Asn Ser Arg Gly Lys Leu Ala Pro Pro Val Arg Asn Leu Lys Asp
225                 230                 235                 240

Lys Leu Asp Pro Met Ile Trp Lys His Ile Glu Asp Ser Leu Glu Met
                245                 250                 255

Thr Phe Ile Gly Thr Ala Glu Ser Val Val Leu Gln Leu Gln Glu Phe
            260                 265                 270

Ala Asp Arg Tyr Lys Leu Asp Glu Ile Ile Thr Val Thr Tyr Ser Tyr
        275                 280                 285

Asp Pro Glu Val Arg Phe Arg Ser Ile Ala Ala Leu Gly Thr Ala Trp
    290                 295                 300

Asn
305
```

<210> 327
<211> 487
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(487)
<223> FRXA00666

<400> 327
agtggtgaat gctggataag tttttaacat gtctagtgta gtcggggaag gcccaaaacc 60

acgattgagc gtgcttgatc tcgtcgcgct gagtgaaggg atg acg gcc ggc gag 115

```
                                                    Met Thr Ala Gly Glu
                                                      1               5

gcc att gca cac agt gtt cgc gct gcg cag atc gcc gaa gag cac aat   163
Ala Ile Ala His Ser Val Arg Ala Ala Gln Ile Ala Glu Glu His Asn
                 10                  15                  20

tat gcg cgt ttc tgg gtg gcg gag cac cac aac tcg gaa ggc ttg gca   211
Tyr Ala Arg Phe Trp Val Ala Glu His His Asn Ser Glu Gly Leu Ala
             25                  30                  35

tct tcc gcg acg acg ctg ctc atg ggt cat att gca ggc cac act tca   259
Ser Ser Ala Thr Thr Leu Leu Met Gly His Ile Ala Gly His Thr Ser
         40                  45                  50

cgc att cgc gtt ggc tcc ggt ggc atc atg atg ccc aac cac tcc gcg   307
Arg Ile Arg Val Gly Ser Gly Gly Ile Met Met Pro Asn His Ser Ala
     55                  60                  65

ctg cac gtc gcc gaa gaa ctc ggc acc ctt gag gcc att tac ccc ggc   355
Leu His Val Ala Glu Glu Leu Gly Thr Leu Glu Ala Ile Tyr Pro Gly
 70                  75                  80                  85

cgc atc gag gcc ggc cta ggg cgc gca cca gga acc gac ccc atg acg   403
Arg Ile Glu Ala Gly Leu Gly Arg Ala Pro Gly Thr Asp Pro Met Thr
                 90                  95                 100

gcg cgg gaa ttg ggt cgg gca agt tcg ctt gtc gac gac gtc ctc tcc   451
Ala Arg Glu Leu Gly Arg Ala Ser Ser Leu Val Asp Asp Val Leu Ser
             105                 110                 115

aca atc gtc tcc ctc cag aat tat ttg gac acc ccc                   487
Thr Ile Val Ser Leu Gln Asn Tyr Leu Asp Thr Pro
         120                 125


<210> 328
<211> 129
<212> PRT
<213> Corynebacterium glutamicum

<400> 328
Met Thr Ala Gly Glu Ala Ile Ala His Ser Val Arg Ala Ala Gln Ile
 1               5                  10                  15

Ala Glu Glu His Asn Tyr Ala Arg Phe Trp Val Ala Glu His His Asn
             20                  25                  30

Ser Glu Gly Leu Ala Ser Ser Ala Thr Thr Leu Leu Met Gly His Ile
         35                  40                  45

Ala Gly His Thr Ser Arg Ile Arg Val Gly Ser Gly Gly Ile Met Met
     50                  55                  60

Pro Asn His Ser Ala Leu His Val Ala Glu Glu Leu Gly Thr Leu Glu
 65                  70                  75                  80

Ala Ile Tyr Pro Gly Arg Ile Glu Ala Gly Leu Gly Arg Ala Pro Gly
                 85                  90                  95

Thr Asp Pro Met Thr Ala Arg Glu Leu Gly Arg Ala Ser Ser Leu Val
```

```
            100                 105                 110

Asp Asp Val Leu Ser Thr Ile Val Ser Leu Gln Asn Tyr Leu Asp Thr
        115                 120                 125

Pro
```

<210> 329
<211> 750
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(727)
<223> RXN00704

<400> 329

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tcaaattctg cgcacaaagt gttctaagac gacgtctgcc catcggcgct ctaatgcaca 60

ttacagcgtt tacagaattg aaaatgaaag gttcaaagcc ttg acc att act ttt   115
                                          Leu Thr Ile Thr Phe
                                            1               5

agc cgc gtt gct ctg acc acc ctg gca gtc acc gca acc act ttg tcc   163
Ser Arg Val Ala Leu Thr Thr Leu Ala Val Thr Ala Thr Thr Leu Ser
                  10                  15                  20

ctg agc act gct gcg aat gca cag tct tcc ttg ttg gat aag act ctt   211
Leu Ser Thr Ala Ala Asn Ala Gln Ser Ser Leu Leu Asp Lys Thr Leu
              25                  30                  35

gat gcc cgt cag tgc atc gat gca gac aac gtc tgg gtc tca gtt gac   259
Asp Ala Arg Gln Cys Ile Asp Ala Asp Asn Val Trp Val Ser Val Asp
          40                  45                  50

tat ggt gca gat tcc gaa aaa gaa cca gag ggc gca tgt gcc acc gag   307
Tyr Gly Ala Asp Ser Glu Lys Glu Pro Glu Gly Ala Cys Ala Thr Glu
      55                  60                  65

ttc act gat ggt gtt gta gct ctt gaa tct gct ggg ttc aaa ctg acc   355
Phe Thr Asp Gly Val Val Ala Leu Glu Ser Ala Gly Phe Lys Leu Thr
  70                  75                  80                  85

ttt gac gaa tct gaa atg ggc aaa tac atg acc ggt atc aac gga gtt   403
Phe Asp Glu Ser Glu Met Gly Lys Tyr Met Thr Gly Ile Asn Gly Val
                  90                  95                 100

gtt cct gat tgg gtt gaa act gga act tac tgg agt tac tac tct ggt   451
Val Pro Asp Trp Val Glu Thr Gly Thr Tyr Trp Ser Tyr Tyr Ser Gly
              105                 110                 115

gaa gtc gca gat gat tac agc gtg gac tac acc tac tac gag gtt ggt   499
Glu Val Ala Asp Asp Tyr Ser Val Asp Tyr Thr Tyr Tyr Glu Val Gly
          120                 125                 130

gca tct aat tct gaa cct gaa ggt gga act gtt gag gct tgg gtt gtt   547
Ala Ser Asn Ser Glu Pro Glu Gly Gly Thr Val Glu Ala Trp Val Val
      135                 140                 145
```

```
ggc acc ggc gag gaa aca cca gca ctc gag act ctt cct gaa act cca   595
Gly Thr Gly Glu Glu Thr Pro Ala Leu Glu Thr Leu Pro Glu Thr Pro
150                 155                 160                 165

gca gca acc gga tct tct gaa gac ggc ggc tgg att gca gtc atc gca   643
Ala Ala Thr Gly Ser Ser Glu Asp Gly Gly Trp Ile Ala Val Ile Ala
                170                 175                 180

ggt ctt ctc gca ctg atc ggt ggt gga gtt gca gct ttg tac cag ggc   691
Gly Leu Leu Ala Leu Ile Gly Gly Gly Val Ala Ala Leu Tyr Gln Gly
            185                 190                 195

ttg atc act atc cca ggt ctg gtt ctg cct aag ttt taagcaacct       737
Leu Ile Thr Ile Pro Gly Leu Val Leu Pro Lys Phe
        200                 205

aacctaaagc ttc                                                   750


<210> 330
<211> 209
<212> PRT
<213> Corynebacterium glutamicum

<400> 330
Leu Thr Ile Thr Phe Ser Arg Val Ala Leu Thr Thr Leu Ala Val Thr
  1               5                  10                  15

Ala Thr Thr Leu Ser Leu Ser Thr Ala Ala Asn Ala Gln Ser Ser Leu
             20                  25                  30

Leu Asp Lys Thr Leu Asp Ala Arg Gln Cys Ile Asp Ala Asp Asn Val
         35                  40                  45

Trp Val Ser Val Asp Tyr Gly Ala Asp Ser Glu Lys Glu Pro Glu Gly
     50                  55                  60

Ala Cys Ala Thr Glu Phe Thr Asp Gly Val Val Ala Leu Glu Ser Ala
 65                  70                  75                  80

Gly Phe Lys Leu Thr Phe Asp Glu Ser Glu Met Gly Lys Tyr Met Thr
                 85                  90                  95

Gly Ile Asn Gly Val Val Pro Asp Trp Val Glu Thr Gly Thr Tyr Trp
            100                 105                 110

Ser Tyr Tyr Ser Gly Glu Val Ala Asp Asp Tyr Ser Val Asp Tyr Thr
        115                 120                 125

Tyr Tyr Glu Val Gly Ala Ser Asn Ser Glu Pro Glu Gly Gly Thr Val
    130                 135                 140

Glu Ala Trp Val Val Gly Thr Gly Glu Glu Thr Pro Ala Leu Glu Thr
145                 150                 155                 160

Leu Pro Glu Thr Pro Ala Ala Thr Gly Ser Ser Glu Asp Gly Gly Trp
                165                 170                 175

Ile Ala Val Ile Ala Gly Leu Leu Ala Leu Ile Gly Gly Gly Val Ala
            180                 185                 190
```

```
Ala Leu Tyr Gln Gly Leu Ile Thr Ile Pro Gly Leu Val Leu Pro Lys
        195                 200                 205

Phe



<210> 331
<211> 636
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(613)
<223> FRXA00704

<400> 331
tcaaattctg cgcacaaagt gttctaagac gacgtctgcc catcggcgct ctaatgcaca 60

ttacagcgtt tacagaattg aaaatgaaag gttcaaagcc ttg acc att act ttt   115
                                          Leu Thr Ile Thr Phe
                                            1               5

agc cgc gtt gct ctg acc acc ctg gca gtc acc gca acc act ttg tcc   163
Ser Arg Val Ala Leu Thr Thr Leu Ala Val Thr Ala Thr Thr Leu Ser
                  10                  15                  20

ctg agc act gct gcg aat gca cag tct tcc ttg ttg gat aag act ctt   211
Leu Ser Thr Ala Ala Asn Ala Gln Ser Ser Leu Leu Asp Lys Thr Leu
            25                  30                  35

gat gcc cgt cag tgc atc gat gca gac aac gtc tgg gtc tca gtt gac   259
Asp Ala Arg Gln Cys Ile Asp Ala Asp Asn Val Trp Val Ser Val Asp
         40                  45                  50

tat ggt gca gat tcc gaa aaa gaa cca gag ggc gca tgt gcc acc gag   307
Tyr Gly Ala Asp Ser Glu Lys Glu Pro Glu Gly Ala Cys Ala Thr Glu
     55                  60                  65

ttc act gat ggt gtt gta gct ctt gaa tct gct ggg ttc aaa ctg acc   355
Phe Thr Asp Gly Val Val Ala Leu Glu Ser Ala Gly Phe Lys Leu Thr
 70                  75                  80                  85

ttt gac gaa tct gaa atg ggc aaa tac atg acc ggt atc aac gga gtt   403
Phe Asp Glu Ser Glu Met Gly Lys Tyr Met Thr Gly Ile Asn Gly Val
                 90                  95                 100

gtt cct gat tgg gtt gaa act gga act tac tgg agt tac tac tct ggt   451
Val Pro Asp Trp Val Glu Thr Gly Thr Tyr Trp Ser Tyr Tyr Ser Gly
            105                 110                 115

gaa gtc gca gat gat tac agc gtg gac tac acc tac tac gag gtt ggt   499
Glu Val Ala Asp Asp Tyr Ser Val Asp Tyr Thr Tyr Tyr Glu Val Gly
        120                 125                 130

gca tct aat tct gaa cct gaa ggt gga act gtt gag gct tgg gtt gtt   547
Ala Ser Asn Ser Glu Pro Glu Gly Gly Thr Val Glu Ala Trp Val Val
    135                 140                 145
```

```
ggc acc ggc gag gaa aca cca gca ctc gag act ctt tct gaa act tca   595
Gly Thr Gly Glu Glu Thr Pro Ala Leu Glu Thr Leu Ser Glu Thr Ser
150                 155                 160                 165

gca gca acc gga tct tct taagacggcg gctggattgc agt                636
Ala Ala Thr Gly Ser Ser
               170
```

<210> 332
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 332

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Leu Thr Ile Thr Phe Ser Arg Val Ala Leu Thr Thr Leu Ala Val Thr
  1               5                  10                  15

Ala Thr Thr Leu Ser Leu Ser Thr Ala Ala Asn Ala Gln Ser Ser Leu
             20                  25                  30

Leu Asp Lys Thr Leu Asp Ala Arg Gln Cys Ile Asp Ala Asp Asn Val
         35                  40                  45

Trp Val Ser Val Asp Tyr Gly Ala Asp Ser Glu Lys Glu Pro Glu Gly
     50                  55                  60

Ala Cys Ala Thr Glu Phe Thr Asp Gly Val Val Ala Leu Glu Ser Ala
 65                  70                  75                  80

Gly Phe Lys Leu Thr Phe Asp Glu Ser Glu Met Gly Lys Tyr Met Thr
                 85                  90                  95

Gly Ile Asn Gly Val Val Pro Asp Trp Val Glu Thr Gly Thr Tyr Trp
            100                 105                 110

Ser Tyr Tyr Ser Gly Glu Val Ala Asp Asp Tyr Ser Val Asp Tyr Thr
        115                 120                 125

Tyr Tyr Glu Val Gly Ala Ser Asn Ser Glu Pro Glu Gly Gly Thr Val
    130                 135                 140

Glu Ala Trp Val Val Gly Thr Gly Glu Glu Thr Pro Ala Leu Glu Thr
145                 150                 155                 160

Leu Ser Glu Thr Ser Ala Ala Thr Gly Ser Ser
                165                 170
```

<210> 333
<211> 819
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(796)
<223> RXN00712

<400> 333

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tgttgcgcgt taataaggaa caatatcggt gtgattcgcg atatattaat cagcttgttt 60
```

```
tcccagcata agtagtcgcc tagtttagga ggtacatggc atg tcc cta cgc aag   115
                                            Met Ser Leu Arg Lys
                                              1               5

aat ctc gcc ctc gga agc agc aca gta cta ctc aca gcc gtg cta agc   163
Asn Leu Ala Leu Gly Ser Ser Thr Val Leu Leu Thr Ala Val Leu Ser
                  10                  15                  20

ggg tgt gtt tcc ctt gat gag cgc tcc act gat aca tcc acg gag aat   211
Gly Cys Val Ser Leu Asp Glu Arg Ser Thr Asp Thr Ser Thr Glu Asn
             25                  30                  35

gtc acc acg gta act gcc aca ctc act tcc acc gcc gca gca gaa ccc   259
Val Thr Thr Val Thr Ala Thr Leu Thr Ser Thr Ala Ala Ala Glu Pro
         40                  45                  50

acc act aga acg act gtg caa agt gct aca gaa gcc tcc act act gca   307
Thr Thr Arg Thr Thr Val Gln Ser Ala Thr Glu Ala Ser Thr Thr Ala
     55                  60                  65

cca gtg caa tgc aat ttg gat ccc cgt acc tcg gat ttt ggg cca tat   355
Pro Val Gln Cys Asn Leu Asp Pro Arg Thr Ser Asp Phe Gly Pro Tyr
 70                  75                  80                  85

ctt gca caa tct cgc acc ccg gtt ggt gag cta gct gga tct gca gat   403
Leu Ala Gln Ser Arg Thr Pro Val Gly Glu Leu Ala Gly Ser Ala Asp
                 90                  95                 100

tcc gtc gtg cag gtt cct gac tgg ttc tat cac ttc caa atg ggc gac   451
Ser Val Val Gln Val Pro Asp Trp Phe Tyr His Phe Gln Met Gly Asp
            105                 110                 115

aac ggc tac gat tcc tgt tcc aag ctc agc tat gtg gtt ctc aac ggt   499
Asn Gly Tyr Asp Ser Cys Ser Lys Leu Ser Tyr Val Val Leu Asn Gly
        120                 125                 130

tcc aat gga gac gcc gaa cgt tct act gga acg ggt gct gcg atc gcc   547
Ser Asn Gly Asp Ala Glu Arg Ser Thr Gly Thr Gly Ala Ala Ile Ala
    135                 140                 145

gac gtg gtg gtg ctg ttt atc gac ggc cat atg gtt gct cgt cct gct   595
Asp Val Val Val Leu Phe Ile Asp Gly His Met Val Ala Arg Pro Ala
150                 155                 160                 165

cct ttt gaa atg aag acc gtg gaa tcc gtc acc aga gtg tca gat tca   643
Pro Phe Glu Met Lys Thr Val Glu Ser Val Thr Arg Val Ser Asp Ser
                170                 175                 180

gaa atc caa gtt gtt tac gga cat gcc ggc cga tct act gcc gaa ggt   691
Glu Ile Gln Val Val Tyr Gly His Ala Gly Arg Ser Thr Ala Glu Gly
            185                 190                 195

gtt acg gac tat ttc acc ttt aac ttc ttc gtt gac aac ggc gtt ctt   739
Val Thr Asp Tyr Phe Thr Phe Asn Phe Phe Val Asp Asn Gly Val Leu
        200                 205                 210

tca gga cgc ggc gat ctc cca gaa cac atc gat act cac atg cgt cta   787
Ser Gly Arg Gly Asp Leu Pro Glu His Ile Asp Thr His Met Arg Leu
    215                 220                 225
```

```
tat ctg ctg tagccccatc taaaaactct tga                                  819
Tyr Leu Leu
230


<210> 334
<211> 232
<212> PRT
<213> Corynebacterium glutamicum

<400> 334
Met Ser Leu Arg Lys Asn Leu Ala Leu Gly Ser Ser Thr Val Leu Leu
 1               5                  10                  15

Thr Ala Val Leu Ser Gly Cys Val Ser Leu Asp Glu Arg Ser Thr Asp
            20                  25                  30

Thr Ser Thr Glu Asn Val Thr Thr Val Thr Ala Thr Leu Thr Ser Thr
        35                  40                  45

Ala Ala Ala Glu Pro Thr Thr Arg Thr Thr Val Gln Ser Ala Thr Glu
    50                  55                  60

Ala Ser Thr Thr Ala Pro Val Gln Cys Asn Leu Asp Pro Arg Thr Ser
65                  70                  75                  80

Asp Phe Gly Pro Tyr Leu Ala Gln Ser Arg Thr Pro Val Gly Glu Leu
                85                  90                  95

Ala Gly Ser Ala Asp Ser Val Val Gln Val Pro Asp Trp Phe Tyr His
            100                 105                 110

Phe Gln Met Gly Asp Asn Gly Tyr Asp Ser Cys Ser Lys Leu Ser Tyr
        115                 120                 125

Val Val Leu Asn Gly Ser Asn Gly Asp Ala Glu Arg Ser Thr Gly Thr
    130                 135                 140

Gly Ala Ala Ile Ala Asp Val Val Val Leu Phe Ile Asp Gly His Met
145                 150                 155                 160

Val Ala Arg Pro Ala Pro Phe Glu Met Lys Thr Val Glu Ser Val Thr
                165                 170                 175

Arg Val Ser Asp Ser Glu Ile Gln Val Val Tyr Gly His Ala Gly Arg
            180                 185                 190

Ser Thr Ala Glu Gly Val Thr Asp Tyr Phe Thr Phe Asn Phe Phe Val
        195                 200                 205

Asp Asn Gly Val Leu Ser Gly Arg Gly Asp Leu Pro Glu His Ile Asp
    210                 215                 220

Thr His Met Arg Leu Tyr Leu Leu
225                 230


<210> 335
<211> 572
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (1)..(549)
<223> FRXA00712

<400> 335

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gca gca gaa ccc acc act aga acg act gtg caa agt gct aca gaa gcc   48
Ala Ala Glu Pro Thr Thr Arg Thr Thr Val Gln Ser Ala Thr Glu Ala
  1               5                  10                  15

tcc act act gca cca gtg caa tgc aat ttg gat ccc cgt acc tcg gat   96
Ser Thr Thr Ala Pro Val Gln Cys Asn Leu Asp Pro Arg Thr Ser Asp
             20                  25                  30

ttt ggg cca tat ctt gca caa tct cgc acc ccg gtt ggt gag cta gct   144
Phe Gly Pro Tyr Leu Ala Gln Ser Arg Thr Pro Val Gly Glu Leu Ala
         35                  40                  45

gga tct gca gat tcc gtc gtg cag gtt cct gac tgg ttc tat cac ttc   192
Gly Ser Ala Asp Ser Val Val Gln Val Pro Asp Trp Phe Tyr His Phe
     50                  55                  60

caa atg ggc gac aac ggc tac gat tcc tgt tcc aag ctc agc tat gtg   240
Gln Met Gly Asp Asn Gly Tyr Asp Ser Cys Ser Lys Leu Ser Tyr Val
 65                  70                  75                  80

gtt ctc aac ggt tcc aat gga gac gcc gaa cgt tct act gga acg ggt   288
Val Leu Asn Gly Ser Asn Gly Asp Ala Glu Arg Ser Thr Gly Thr Gly
                 85                  90                  95

gct gcg atc gcc gac gtg gtg gtg ctg ttt atc gac ggc cat atg gtt   336
Ala Ala Ile Ala Asp Val Val Val Leu Phe Ile Asp Gly His Met Val
            100                 105                 110

gct cgt cct gct cct ttt gaa atg aag acc gtg gaa tcc gtc acc aga   384
Ala Arg Pro Ala Pro Phe Glu Met Lys Thr Val Glu Ser Val Thr Arg
        115                 120                 125

gtg tca gat tca gaa atc caa gtt gtt tac gga cat gcc ggc cga tct   432
Val Ser Asp Ser Glu Ile Gln Val Val Tyr Gly His Ala Gly Arg Ser
    130                 135                 140

act gcc gaa ggt gtt acg gac tat ttc acc ttt aac ttc ttc gtt gac   480
Thr Ala Glu Gly Val Thr Asp Tyr Phe Thr Phe Asn Phe Phe Val Asp
145                 150                 155                 160

aac ggc gtt ctt tca gga cgc ggc gat ctc cca gaa cac atc gat act   528
Asn Gly Val Leu Ser Gly Arg Gly Asp Leu Pro Glu His Ile Asp Thr
                165                 170                 175

cac atg cgt cta tat ctg ctg tagccccatc taaaaactct tga             572
His Met Arg Leu Tyr Leu Leu
            180
```

<210> 336
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 336
Ala Ala Glu Pro Thr Thr Arg Thr Thr Val Gln Ser Ala Thr Glu Ala
1 5 10 15

Ser Thr Thr Ala Pro Val Gln Cys Asn Leu Asp Pro Arg Thr Ser Asp
20 25 30

Phe Gly Pro Tyr Leu Ala Gln Ser Arg Thr Pro Val Gly Glu Leu Ala
35 40 45

Gly Ser Ala Asp Ser Val Val Gln Val Pro Asp Trp Phe Tyr His Phe
50 55 60

Gln Met Gly Asp Asn Gly Tyr Asp Ser Cys Ser Lys Leu Ser Tyr Val
65 70 75 80

Val Leu Asn Gly Ser Asn Gly Asp Ala Glu Arg Ser Thr Gly Thr Gly
85 90 95

Ala Ala Ile Ala Asp Val Val Val Leu Phe Ile Asp Gly His Met Val
100 105 110

Ala Arg Pro Ala Pro Phe Glu Met Lys Thr Val Glu Ser Val Thr Arg
115 120 125

Val Ser Asp Ser Glu Ile Gln Val Val Tyr Gly His Ala Gly Arg Ser
130 135 140

Thr Ala Glu Gly Val Thr Asp Tyr Phe Thr Phe Asn Phe Phe Val Asp
145 150 155 160

Asn Gly Val Leu Ser Gly Arg Gly Asp Leu Pro Glu His Ile Asp Thr
165 170 175

His Met Arg Leu Tyr Leu Leu
180

<210> 337
<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(766)
<223> RXN00720

<400> 337
ctgatctata cgtcctgttg aagtagagaa gctttctggt caagttcctt gagtatggtg 60

gtcgaagacc agcactccag attcaaggaa cttataaaac atg gca tca ccg cgc 115
Met Ala Ser Pro Arg
1 5

cgc cca cag gtt gca gca cca cgc atc aaa gaa ctt cgc cta aca ggc 163
Arg Pro Gln Val Ala Ala Pro Arg Ile Lys Glu Leu Arg Leu Thr Gly
10 15 20

ctt gac aac gct gac cct caa gac atc gaa tcg aat gag cag ata gag 211
Leu Asp Asn Ala Asp Pro Gln Asp Ile Glu Ser Asn Glu Gln Ile Glu

```
          25                  30                  35

tca tgc cgt ttt aac gag gcc gag ctt tcc gaa cgc gat ctt tct ggt   259
Ser Cys Arg Phe Asn Glu Ala Glu Leu Ser Glu Arg Asp Leu Ser Gly
         40                  45                  50

gct ggt ttc att gaa tgt gaa ttc ctt ggg ctg gaa gca cac gaa acc   307
Ala Gly Phe Ile Glu Cys Glu Phe Leu Gly Leu Glu Ala His Glu Thr
     55                  60                  65

gag cta cgc cgg gct caa ttc gtg gaa aca cgc atc gaa aga gcc aat   355
Glu Leu Arg Arg Ala Gln Phe Val Glu Thr Arg Ile Glu Arg Ala Asn
 70                  75                  80                  85

gct cca tct ttt aag gca gcc cgc tcc atc tgg cgc aac gca acg att   403
Ala Pro Ser Phe Lys Ala Ala Arg Ser Ile Trp Arg Asn Ala Thr Ile
                 90                  95                 100

tcc gac tcc cgc ttt ggt gcc gtc gaa atg tat gaa gca acc gtc caa   451
Ser Asp Ser Arg Phe Gly Ala Val Glu Met Tyr Glu Ala Thr Val Gln
            105                 110                 115

gct ttg aaa atc tct gat tct aag ctg tcg ttt gtc aat ctg cgg ggt   499
Ala Leu Lys Ile Ser Asp Ser Lys Leu Ser Phe Val Asn Leu Arg Gly
        120                 125                 130

gca tcg tta cgg gat gtg ctc ttt gag aac tgt gtc atc gac gag ctt   547
Ala Ser Leu Arg Asp Val Leu Phe Glu Asn Cys Val Ile Asp Glu Leu
    135                 140                 145

gat ctt ggc caa gcc aga gca gaa cgc atc gct ttt aaa gac tgc acg   595
Asp Leu Gly Gln Ala Arg Ala Glu Arg Ile Ala Phe Lys Asp Cys Thr
150                 155                 160                 165

gtg cat tcg ctc acc ttt gat cat gcc gtg ctc agc aat gtg gat ctt   643
Val His Ser Leu Thr Phe Asp His Ala Val Leu Ser Asn Val Asp Leu
                170                 175                 180

cgc ggt tta gat atc gag cgc atc agt ggc gtg gag tcc atg tcc gga   691
Arg Gly Leu Asp Ile Glu Arg Ile Ser Gly Val Glu Ser Met Ser Gly
            185                 190                 195

acc gtg atc tca tcc ctg cag gct gct gac ctg tcg gga gca ttt gca   739
Thr Val Ile Ser Ser Leu Gln Ala Ala Asp Leu Ser Gly Ala Phe Ala
        200                 205                 210

cgg cat tta gga att act gta aac gat tagaaatccg ctcttttgaa         786
Arg His Leu Gly Ile Thr Val Asn Asp
    215                 220

caa                                                               789


<210> 338
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 338
Met Ala Ser Pro Arg Arg Pro Gln Val Ala Ala Pro Arg Ile Lys Glu
  1               5                  10                  15
```

```
Leu Arg Leu Thr Gly Leu Asp Asn Ala Asp Pro Gln Asp Ile Glu Ser
            20                  25                  30

Asn Glu Gln Ile Glu Ser Cys Arg Phe Asn Glu Ala Glu Leu Ser Glu
        35                  40                  45

Arg Asp Leu Ser Gly Ala Gly Phe Ile Glu Cys Glu Phe Leu Gly Leu
    50                  55                  60

Glu Ala His Glu Thr Glu Leu Arg Arg Ala Gln Phe Val Glu Thr Arg
65                  70                  75                  80

Ile Glu Arg Ala Asn Ala Pro Ser Phe Lys Ala Ala Arg Ser Ile Trp
                85                  90                  95

Arg Asn Ala Thr Ile Ser Asp Ser Arg Phe Gly Ala Val Glu Met Tyr
            100                 105                 110

Glu Ala Thr Val Gln Ala Leu Lys Ile Ser Asp Ser Lys Leu Ser Phe
        115                 120                 125

Val Asn Leu Arg Gly Ala Ser Leu Arg Asp Val Leu Phe Glu Asn Cys
    130                 135                 140

Val Ile Asp Glu Leu Asp Leu Gly Gln Ala Arg Ala Glu Arg Ile Ala
145                 150                 155                 160

Phe Lys Asp Cys Thr Val His Ser Leu Thr Phe Asp His Ala Val Leu
                165                 170                 175

Ser Asn Val Asp Leu Arg Gly Leu Asp Ile Glu Arg Ile Ser Gly Val
            180                 185                 190

Glu Ser Met Ser Gly Thr Val Ile Ser Ser Leu Gln Ala Ala Asp Leu
        195                 200                 205

Ser Gly Ala Phe Ala Arg His Leu Gly Ile Thr Val Asn Asp
    210                 215                 220
```

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<210> 339
<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(766)
<223> FRXA00720

<400> 339
ctgatctata cgtcctgttg aagtagagaa gctttctggt caagttcctt gagtatggtg 60

gtcgaagacc agcactccag attcaaggaa cttataaaac atg gca tca ccg cgc 115
                                                Met Ala Ser Pro Arg
                                                  1   5

cgc cca cag gtt gca gca cca cgc atc aaa gaa ctt cgc cta aca ggc 163
Arg Pro Gln Val Ala Ala Pro Arg Ile Lys Glu Leu Arg Leu Thr Gly
                10   15   20

```
ctt gac aac gct gac cct caa gac atc gaa tcg aat gag cag ata gag   211
Leu Asp Asn Ala Asp Pro Gln Asp Ile Glu Ser Asn Glu Gln Ile Glu
            25                  30                  35

tca tgc cgt ttt aac gag gcc gag ctt tcc gaa cgc gat ctt tct ggt   259
Ser Cys Arg Phe Asn Glu Ala Glu Leu Ser Glu Arg Asp Leu Ser Gly
        40                  45                  50

gct ggt ttc att gaa tgt gaa ttc ctt ggg ctg gaa gca cac gaa acc   307
Ala Gly Phe Ile Glu Cys Glu Phe Leu Gly Leu Glu Ala His Glu Thr
    55                  60                  65

gag cta cgc cgg gct caa ttc gtg gaa aca cgc atc gaa aga gcc aat   355
Glu Leu Arg Arg Ala Gln Phe Val Glu Thr Arg Ile Glu Arg Ala Asn
70                  75                  80                  85

gct cca tct ttt aag gca gcc cgc tcc atc tgg cgc aac gca acg att   403
Ala Pro Ser Phe Lys Ala Ala Arg Ser Ile Trp Arg Asn Ala Thr Ile
                90                  95                  100

tcc gac tcc cgc ttt ggt gcc gtc gaa atg tat gaa gca acc gtc caa   451
Ser Asp Ser Arg Phe Gly Ala Val Glu Met Tyr Glu Ala Thr Val Gln
            105                 110                 115

gct ttg aaa atc tct gat tct aag ctg tcg ttt gtc aat ctg cgg ggt   499
Ala Leu Lys Ile Ser Asp Ser Lys Leu Ser Phe Val Asn Leu Arg Gly
        120                 125                 130

gca tcg tta cgg gat gtg ctc ttt gag aac tgt gtc atc gac gag ctt   547
Ala Ser Leu Arg Asp Val Leu Phe Glu Asn Cys Val Ile Asp Glu Leu
    135                 140                 145

gat ctt ggc caa gcc aga gca gaa cgc atc gct ttt aaa gac tgc acg   595
Asp Leu Gly Gln Ala Arg Ala Glu Arg Ile Ala Phe Lys Asp Cys Thr
150                 155                 160                 165

gtg cat tcg ctc acc ttt gat cat gcc gtg ctc agc aat gtg gat ctt   643
Val His Ser Leu Thr Phe Asp His Ala Val Leu Ser Asn Val Asp Leu
                170                 175                 180

cgc ggt tta gat atc gag cgc atc agt ggc gtg gag tcc atg tcc gga   691
Arg Gly Leu Asp Ile Glu Arg Ile Ser Gly Val Glu Ser Met Ser Gly
            185                 190                 195

acc gtg atc tca tcc ctg cag gct gct gac ctg tcg gga gca ttt gca   739
Thr Val Ile Ser Ser Leu Gln Ala Ala Asp Leu Ser Gly Ala Phe Ala
        200                 205                 210

cgg cat tta gga att act gta aac gat tagaaatccg ctcttttgaa         786
Arg His Leu Gly Ile Thr Val Asn Asp
    215                 220

caa                                                               789
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<210> 340
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 340
Met Ala Ser Pro Arg Arg Pro Gln Val Ala Ala Pro Arg Ile Lys Glu
1 5 10 15

Leu Arg Leu Thr Gly Leu Asp Asn Ala Asp Pro Gln Asp Ile Glu Ser
20 25 30

Asn Glu Gln Ile Glu Ser Cys Arg Phe Asn Glu Ala Glu Leu Ser Glu
35 40 45

Arg Asp Leu Ser Gly Ala Gly Phe Ile Glu Cys Glu Phe Leu Gly Leu
50 55 60

Glu Ala His Glu Thr Glu Leu Arg Arg Ala Gln Phe Val Glu Thr Arg
65 70 75 80

Ile Glu Arg Ala Asn Ala Pro Ser Phe Lys Ala Ala Arg Ser Ile Trp
85 90 95

Arg Asn Ala Thr Ile Ser Asp Ser Arg Phe Gly Ala Val Glu Met Tyr
100 105 110

Glu Ala Thr Val Gln Ala Leu Lys Ile Ser Asp Ser Lys Leu Ser Phe
115 120 125

Val Asn Leu Arg Gly Ala Ser Leu Arg Asp Val Leu Phe Glu Asn Cys
130 135 140

Val Ile Asp Glu Leu Asp Leu Gly Gln Ala Arg Ala Glu Arg Ile Ala
145 150 155 160

Phe Lys Asp Cys Thr Val His Ser Leu Thr Phe Asp His Ala Val Leu
165 170 175

Ser Asn Val Asp Leu Arg Gly Leu Asp Ile Glu Arg Ile Ser Gly Val
180 185 190

Glu Ser Met Ser Gly Thr Val Ile Ser Ser Leu Gln Ala Ala Asp Leu
195 200 205

Ser Gly Ala Phe Ala Arg His Leu Gly Ile Thr Val Asn Asp
210 215 220

<210> 341
<211> 1088
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1065)
<223> RXN00722

<400> 341
gct gtt ctc cga gaa gcc gga gtt gtt gat gcc ggg gga cag ggc cta 48
Ala Val Leu Arg Glu Ala Gly Val Val Asp Ala Gly Gly Gln Gly Leu
1 5 10 15

gtt att ctc ctg gag tcc ctg gcc gaa caa atc aac gga aac cca cct 96
Val Ile Leu Leu Glu Ser Leu Ala Glu Gln Ile Asn Gly Asn Pro Pro

```
                20                  25                  30

cac cat cca tcg cac cac agt gaa cca gcc gaa gaa ccc tcc ttc cac   144
His His Pro Ser His His Ser Glu Pro Ala Glu Glu Pro Ser Phe His
         35                  40                  45

ggc aaa acc ggc gac cta gaa gtg atg ttt tac att gca tgc gac tcc   192
Gly Lys Thr Gly Asp Leu Glu Val Met Phe Tyr Ile Ala Cys Asp Ser
     50                  55                  60

gcg caa aca ctc gat gct ctc cac aac gaa ctt gaa aca cta ggc gac   240
Ala Gln Thr Leu Asp Ala Leu His Asn Glu Leu Glu Thr Leu Gly Asp
 65                  70                  75                  80

agc ctg ctc atc gcc cga gaa acc aat acc cgc ggc acc gtt cac atc   288
Ser Leu Leu Ile Ala Arg Glu Thr Asn Thr Arg Gly Thr Val His Ile
                 85                  90                  95

cat tcg cgc cgg gca ggc gag gtc atc caa aaa gca ttt gcc gca gga   336
His Ser Arg Arg Ala Gly Glu Val Ile Gln Lys Ala Phe Ala Ala Gly
            100                 105                 110

gac gtc agc gaa ctc cgc ctt gaa atc ctc ccc gat act tcc ggc agc   384
Asp Val Ser Glu Leu Arg Leu Glu Ile Leu Pro Asp Thr Ser Gly Ser
        115                 120                 125

ttc acg gaa gaa cca cgc cgg gtc ctc atg gct gtc gca cct gac ggc   432
Phe Thr Glu Glu Pro Arg Arg Val Leu Met Ala Val Ala Pro Asp Gly
    130                 135                 140

ctg gtg gcg gag ctg tac cgc agc gct gga gtg aag gtg gtg gcc cgc   480
Leu Val Ala Glu Leu Tyr Arg Ser Ala Gly Val Lys Val Val Ala Arg
145                 150                 155                 160

aac atc gcg caa tcc aag tct gat gat gtg gtg gca aag atc gtt tcc   528
Asn Ile Ala Gln Ser Lys Ser Asp Asp Val Val Ala Lys Ile Val Ser
                165                 170                 175

atc gcg cgc aag tct ggt gcc gat gag gtg atc ttg ctg ccc aac ggt   576
Ile Ala Arg Lys Ser Gly Ala Asp Glu Val Ile Leu Leu Pro Asn Gly
            180                 185                 190

ctt ttg acc aag cgt gag ctg gtt tcc att gag cgt tcc agc cat gct   624
Leu Leu Thr Lys Arg Glu Leu Val Ser Ile Glu Arg Ser Ser His Ala
        195                 200                 205

ttt gag caa agt gtg gtt att ttg cct act gcc acg ttg gtt gca ggt   672
Phe Glu Gln Ser Val Val Ile Leu Pro Thr Ala Thr Leu Val Ala Gly
    210                 215                 220

ctt gca gcg gtg tcc gtt cat gag cca gcg caa ccc ctg gcg gtg gat   720
Leu Ala Ala Val Ser Val His Glu Pro Ala Gln Pro Leu Ala Val Asp
225                 230                 235                 240

tcc tat gcc atg gca gag gcc gcc ggt tcc atg cgc acg gcc acg atc   768
Ser Tyr Ala Met Ala Glu Ala Ala Gly Ser Met Arg Thr Ala Thr Ile
                245                 250                 255

cgc gcc gcc acc agc gcc gcg ctc acc cag gcc ggc gca tgc tcc aag   816
Arg Ala Ala Thr Ser Ala Ala Leu Thr Gln Ala Gly Ala Cys Ser Lys
            260                 265                 270
```

```
ggt gat cta tta agc ttc atc ggc ccg gag ata gct ctg gtc tcc gag   864
Gly Asp Leu Leu Ser Phe Ile Gly Pro Glu Ile Ala Leu Val Ser Glu
        275                 280                 285

gag ctc aac gac gcg cta tcg cgc acc gct tta agg ctt ctc gac ggc   912
Glu Leu Asn Asp Ala Leu Ser Arg Thr Ala Leu Arg Leu Leu Asp Gly
    290                 295                 300

tcc agc gag caa att acc ctt ctc ata gcg caa gac cgt cag tcc gcc   960
Ser Ser Glu Gln Ile Thr Leu Leu Ile Ala Gln Asp Arg Gln Ser Ala
305                 310                 315                 320

ttc gac gaa gat gtt ttc cgc cgt ggc ctg gga act cac acg gat gtg   1008
Phe Asp Glu Asp Val Phe Arg Arg Gly Leu Gly Thr His Thr Asp Val
                325                 330                 335

gag atc acg gtc tat cct gct act gga atg gag aat ctg gta gag atc   1056
Glu Ile Thr Val Tyr Pro Ala Thr Gly Met Glu Asn Leu Val Glu Ile
            340                 345                 350

gga gtg gag tagccacatg ttgggttggc atg                           1088
Gly Val Glu
        355


<210> 342
<211> 355
<212> PRT
<213> Corynebacterium glutamicum

<400> 342
Ala Val Leu Arg Glu Ala Gly Val Val Asp Ala Gly Gly Gln Gly Leu
  1               5                  10                  15

Val Ile Leu Leu Glu Ser Leu Ala Glu Gln Ile Asn Gly Asn Pro Pro
             20                  25                  30

His His Pro Ser His His Ser Glu Pro Ala Glu Glu Pro Ser Phe His
         35                  40                  45

Gly Lys Thr Gly Asp Leu Glu Val Met Phe Tyr Ile Ala Cys Asp Ser
     50                  55                  60

Ala Gln Thr Leu Asp Ala Leu His Asn Glu Leu Glu Thr Leu Gly Asp
 65                  70                  75                  80

Ser Leu Leu Ile Ala Arg Glu Thr Asn Thr Arg Gly Thr Val His Ile
                85                  90                  95

His Ser Arg Arg Ala Gly Glu Val Ile Gln Lys Ala Phe Ala Ala Gly
            100                 105                 110

Asp Val Ser Glu Leu Arg Leu Glu Ile Leu Pro Asp Thr Ser Gly Ser
        115                 120                 125

Phe Thr Glu Glu Pro Arg Arg Val Leu Met Ala Val Ala Pro Asp Gly
    130                 135                 140

Leu Val Ala Glu Leu Tyr Arg Ser Ala Gly Val Lys Val Val Ala Arg
145                 150                 155                 160
```

```
Asn Ile Ala Gln Ser Lys Ser Asp Asp Val Val Ala Lys Ile Val Ser
                165                 170                 175

Ile Ala Arg Lys Ser Gly Ala Asp Glu Val Ile Leu Leu Pro Asn Gly
            180                 185                 190

Leu Leu Thr Lys Arg Glu Leu Val Ser Ile Glu Arg Ser Ser His Ala
        195                 200                 205

Phe Glu Gln Ser Val Val Ile Leu Pro Thr Ala Thr Leu Val Ala Gly
    210                 215                 220

Leu Ala Ala Val Ser Val His Glu Pro Ala Gln Pro Leu Ala Val Asp
225                 230                 235                 240

Ser Tyr Ala Met Ala Glu Ala Ala Gly Ser Met Arg Thr Ala Thr Ile
                245                 250                 255

Arg Ala Ala Thr Ser Ala Ala Leu Thr Gln Ala Gly Ala Cys Ser Lys
            260                 265                 270

Gly Asp Leu Leu Ser Phe Ile Gly Pro Glu Ile Ala Leu Val Ser Glu
        275                 280                 285

Glu Leu Asn Asp Ala Leu Ser Arg Thr Ala Leu Arg Leu Leu Asp Gly
    290                 295                 300

Ser Ser Glu Gln Ile Thr Leu Leu Ile Ala Gln Asp Arg Gln Ser Ala
305                 310                 315                 320

Phe Asp Glu Asp Val Phe Arg Arg Gly Leu Gly Thr His Thr Asp Val
                325                 330                 335

Glu Ile Thr Val Tyr Pro Ala Thr Gly Met Glu Asn Leu Val Glu Ile
            340                 345                 350

Gly Val Glu
        355
```

<210> 343
<211> 542
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (16)..(519)
<223> FRXA00722

<400> 343

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ccccccccgg tgatcttg ctg ccc aac ggt ctt ttg acc aag cgt gag ctg   51
               Leu Leu Pro Asn Gly Leu Leu Thr Lys Arg Glu Leu
                 1               5                  10

gtt tcc att gag cgt tcc agc cat gct ttt gag caa agt gtg gtt att   99
Val Ser Ile Glu Arg Ser Ser His Ala Phe Glu Gln Ser Val Val Ile
         15                  20                  25

ttg cct act gcc acg ttg gtt gca ggt ctt gca gcg gtg tcc gtt cat   147
```

```
Leu Pro Thr Ala Thr Leu Val Ala Gly Leu Ala Ala Val Ser Val His
     30                  35                  40

gag cca gcg caa ccc ctg gcg gtg gat tcc tat gcc atg gca gag gcc   195
Glu Pro Ala Gln Pro Leu Ala Val Asp Ser Tyr Ala Met Ala Glu Ala
 45                  50                  55                  60

gcc ggt tcc atg cgc acg gcc acg atc cgc gcc gcc acc agc gcc gcg   243
Ala Gly Ser Met Arg Thr Ala Thr Ile Arg Ala Ala Thr Ser Ala Ala
                 65                  70                  75

ctc acc cag gcc ggc gca tgc tcc aag ggt gat cta tta agc ttc atc   291
Leu Thr Gln Ala Gly Ala Cys Ser Lys Gly Asp Leu Leu Ser Phe Ile
             80                  85                  90

ggc ccg gag ata gct ctg gtc tcc gag gag ctc aac gac gcg cta tcg   339
Gly Pro Glu Ile Ala Leu Val Ser Glu Glu Leu Asn Asp Ala Leu Ser
         95                 100                 105

cgc acc gct tta agg ctt ctc gac ggc tcc agc gag caa att acc ctt   387
Arg Thr Ala Leu Arg Leu Leu Asp Gly Ser Ser Glu Gln Ile Thr Leu
    110                 115                 120

ctc ata gcg caa gac cgt cag tcc gcc ttc gac gaa gat gtt ttc cgc   435
Leu Ile Ala Gln Asp Arg Gln Ser Ala Phe Asp Glu Asp Val Phe Arg
125                 130                 135                 140

cgt ggc ctg gga act cac acg gat gtg gag atc acg gtc tat cct gct   483
Arg Gly Leu Gly Thr His Thr Asp Val Glu Ile Thr Val Tyr Pro Ala
                145                 150                 155

act gga atg gag aat ctg gta gag atc gga gtg gag tagccacatg        529
Thr Gly Met Glu Asn Leu Val Glu Ile Gly Val Glu
            160                 165

ttgggttggc atg                                                   542


<210> 344
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 344
Leu Leu Pro Asn Gly Leu Leu Thr Lys Arg Glu Leu Val Ser Ile Glu
  1               5                  10                  15

Arg Ser Ser His Ala Phe Glu Gln Ser Val Val Ile Leu Pro Thr Ala
            20                  25                  30

Thr Leu Val Ala Gly Leu Ala Ala Val Ser Val His Glu Pro Ala Gln
        35                  40                  45

Pro Leu Ala Val Asp Ser Tyr Ala Met Ala Glu Ala Ala Gly Ser Met
    50                  55                  60

Arg Thr Ala Thr Ile Arg Ala Ala Thr Ser Ala Ala Leu Thr Gln Ala
65                  70                  75                  80

Gly Ala Cys Ser Lys Gly Asp Leu Leu Ser Phe Ile Gly Pro Glu Ile
                85                  90                  95
```

```
Ala Leu Val Ser Glu Glu Leu Asn Asp Ala Leu Ser Arg Thr Ala Leu
            100                 105                 110

Arg Leu Leu Asp Gly Ser Ser Glu Gln Ile Thr Leu Leu Ile Ala Gln
        115                 120                 125

Asp Arg Gln Ser Ala Phe Asp Glu Asp Val Phe Arg Arg Gly Leu Gly
    130                 135                 140

Thr His Thr Asp Val Glu Ile Thr Val Tyr Pro Ala Thr Gly Met Glu
145                 150                 155                 160

Asn Leu Val Glu Ile Gly Val Glu
                165
```

<210> 345
<211> 1101
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1078)
<223> RXN00729

<400> 345

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ttcagcacag atcacccttt gccagctacc gacttagttt cgtaacacgt atagtgggag 60

gcgttttgcc agacgccaaa gaaagataat tggattacct atg agc gcc acc aac   115
                                              Met Ser Ala Thr Asn
                                                1               5

cct gat gcc cta gac gtg cag cac gtc tat ccc atc aag acg aaa aag   163
Pro Asp Ala Leu Asp Val Gln His Val Tyr Pro Ile Lys Thr Lys Lys
                10                  15                  20

act cca ctt gcg gtg att ttc aac atc att agc ggt ggt ttg att gga   211
Thr Pro Leu Ala Val Ile Phe Asn Ile Ile Ser Gly Gly Leu Ile Gly
            25                  30                  35

atg gcg gag ttg gtg cca gga att tcc ggc gga act gtc gct ttg gtt   259
Met Ala Glu Leu Val Pro Gly Ile Ser Gly Gly Thr Val Ala Leu Val
        40                  45                  50

ctt gga att tat gag cgc gca ctg cac aac ggt gat ctc ctc att gat   307
Leu Gly Ile Tyr Glu Arg Ala Leu His Asn Gly Asp Leu Leu Ile Asp
    55                  60                  65

ctg atc aag gtg ttg atc aag gac cgc tcg aag gtt aag gaa gct gcg   355
Leu Ile Lys Val Leu Ile Lys Asp Arg Ser Lys Val Lys Glu Ala Ala
70                  75                  80                  85

gcg aaa atc gac tgg tgg ttc ctc ggc gct atc ggc gtt ggc atg gtc   403
Ala Lys Ile Asp Trp Trp Phe Leu Gly Ala Ile Gly Val Gly Met Val
                90                  95                  100

gtg atg gtc ttc tcg atg tca tcg att ttg cat aca gtt gtt gag gac   451
Val Met Val Phe Ser Met Ser Ser Ile Leu His Thr Val Val Glu Asp
            105                 110                 115
```

```
tac cca gag atc act cgc ggt ctg ttc ctt gga atg gtt gcc gtg tct   499
Tyr Pro Glu Ile Thr Arg Gly Leu Phe Leu Gly Met Val Ala Val Ser
        120                 125                 130

atc ctt gtt ccg ttg gga atg atg gat atg cgg gat gcc aag aag cgc   547
Ile Leu Val Pro Leu Gly Met Met Asp Met Arg Asp Ala Lys Lys Arg
    135                 140                 145

ctc gca atc gtc atc ccg cta ttt ata atc tgc gcc atg ctg gga ttc   595
Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys Ala Met Leu Gly Phe
150                 155                 160                 165

ttt gga aca tcc ttc act agt gcg cct cgc acc gat cct tca ctg atc   643
Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr Asp Pro Ser Leu Ile
                170                 175                 180

ttt gtc ttc atc tgt gct gcg atc gct gtg tgt gct ctt gtt ctt cct   691
Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys Ala Leu Val Leu Pro
            185                 190                 195

ggt gtt tca gga tca ttc ttc ttg ctg gcg gtc ggt atg tac gcg cca   739
Gly Val Ser Gly Ser Phe Phe Leu Leu Ala Val Gly Met Tyr Ala Pro
        200                 205                 210

atc atg gaa tct ctg tcc aac cgt gac ttg tcg gtc atc ggc gtg ttc   787
Ile Met Glu Ser Leu Ser Asn Arg Asp Leu Ser Val Ile Gly Val Phe
    215                 220                 225

ttg ctt ggc gcg ctc acc ggt gtg atc ttg ttt gtg aag gtt ttg tct   835
Leu Leu Gly Ala Leu Thr Gly Val Ile Leu Phe Val Lys Val Leu Ser
230                 235                 240                 245

tat gtt ctc gag cac cac cgc acc atc acg ctg acc atc atg gct ggt   883
Tyr Val Leu Glu His His Arg Thr Ile Thr Leu Thr Ile Met Ala Gly
                250                 255                 260

ctc atg ctg ggt tca ctt cgt gcg ctg tgg cct tgg cag gac ggt gac   931
Leu Met Leu Gly Ser Leu Arg Ala Leu Trp Pro Trp Gln Asp Gly Asp
            265                 270                 275

gct aat cta ctt gct cct ggc gat aac gcc gtg atg att ttc agc atc   979
Ala Asn Leu Leu Ala Pro Gly Asp Asn Ala Val Met Ile Phe Ser Ile
        280                 285                 290

atc att ctt ggt ggc gcg att gtc gct gct ttg atg ttt gct gag cgt   1027
Ile Ile Leu Gly Gly Ala Ile Val Ala Ala Leu Met Phe Ala Glu Arg
    295                 300                 305

gtg tct tcc aag aac att gat tct gag acc gtg gca gaa gag cac ccg   1075
Val Ser Ser Lys Asn Ile Asp Ser Glu Thr Val Ala Glu Glu His Pro
310                 315                 320                 325

cgc taaataagaa ctccacaaag aaa                                    1101
Arg
```

<210> 346
<211> 326
<212> PRT

<213> Corynebacterium glutamicum

<400> 346

```
Met Ser Ala Thr Asn Pro Asp Ala Leu Asp Val Gln His Val Tyr Pro
  1               5                  10                  15

Ile Lys Thr Lys Lys Thr Pro Leu Ala Val Ile Phe Asn Ile Ile Ser
             20                  25                  30

Gly Gly Leu Ile Gly Met Ala Glu Leu Val Pro Gly Ile Ser Gly Gly
         35                  40                  45

Thr Val Ala Leu Val Leu Gly Ile Tyr Glu Arg Ala Leu His Asn Gly
     50                  55                  60

Asp Leu Leu Ile Asp Leu Ile Lys Val Leu Ile Lys Asp Arg Ser Lys
 65                  70                  75                  80

Val Lys Glu Ala Ala Ala Lys Ile Asp Trp Trp Phe Leu Gly Ala Ile
                 85                  90                  95

Gly Val Gly Met Val Val Met Val Phe Ser Met Ser Ser Ile Leu His
            100                 105                 110

Thr Val Val Glu Asp Tyr Pro Glu Ile Thr Arg Gly Leu Phe Leu Gly
        115                 120                 125

Met Val Ala Val Ser Ile Leu Val Pro Leu Gly Met Met Asp Met Arg
    130                 135                 140

Asp Ala Lys Lys Arg Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys
145                 150                 155                 160

Ala Met Leu Gly Phe Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr
                165                 170                 175

Asp Pro Ser Leu Ile Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys
            180                 185                 190

Ala Leu Val Leu Pro Gly Val Ser Gly Ser Phe Phe Leu Leu Ala Val
        195                 200                 205

Gly Met Tyr Ala Pro Ile Met Glu Ser Leu Ser Asn Arg Asp Leu Ser
    210                 215                 220

Val Ile Gly Val Phe Leu Leu Gly Ala Leu Thr Gly Val Ile Leu Phe
225                 230                 235                 240

Val Lys Val Leu Ser Tyr Val Leu Glu His His Arg Thr Ile Thr Leu
                245                 250                 255

Thr Ile Met Ala Gly Leu Met Leu Gly Ser Leu Arg Ala Leu Trp Pro
            260                 265                 270

Trp Gln Asp Gly Asp Ala Asn Leu Leu Ala Pro Gly Asp Asn Ala Val
        275                 280                 285

Met Ile Phe Ser Ile Ile Ile Leu Gly Gly Ala Ile Val Ala Ala Leu
    290                 295                 300

Met Phe Ala Glu Arg Val Ser Ser Lys Asn Ile Asp Ser Glu Thr Val
```

305 310 315 320

Ala Glu Glu His Pro Arg
325

<210> 347
<211> 665
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(642)
<223> FRXA00729

<400> 347

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aca gtt gtt gag gac tac caa gag ttc act cgc ggt ctg ttc ctt gga   48
Thr Val Val Glu Asp Tyr Gln Glu Phe Thr Arg Gly Leu Phe Leu Gly
  1               5                  10                  15

atg gtt gcc gtg tct atc ctt gtt ccg ttg gga atg atg gat atg cgg   96
Met Val Ala Val Ser Ile Leu Val Pro Leu Gly Met Met Asp Met Arg
             20                  25                  30

gat gcc aag aag cgc ctc gca atc gtc atc ccg cta ttt ata atc tgc   144
Asp Ala Lys Lys Arg Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys
         35                  40                  45

gcc atg ctg gga ttc ttt gga aca tcc ttc act agt gcg cct cgc acc   192
Ala Met Leu Gly Phe Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr
     50                  55                  60

gat cct tca ctg atc ttt gtc ttc atc tgt gct gcg atc gct gtg tgt   240
Asp Pro Ser Leu Ile Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys
 65                  70                  75                  80

gct ctt gtt ctt cct ggt gtt tca gga tca ttc ttc ttg ctg gcg gtc   288
Ala Leu Val Leu Pro Gly Val Ser Gly Ser Phe Phe Leu Leu Ala Val
                 85                  90                  95

ggt atg tac gcg cca atc atg gaa tct ctg tcc aac cgt gac ttg tcg   336
Gly Met Tyr Ala Pro Ile Met Glu Ser Leu Ser Asn Arg Asp Leu Ser
            100                 105                 110

gtc atc ggc gtg ttc ttg ctt ggc gcg ctc acc ggt gtg atc ttg ttt   384
Val Ile Gly Val Phe Leu Leu Gly Ala Leu Thr Gly Val Ile Leu Phe
        115                 120                 125

gtg aag gtt ttg tct tat gtt ctc gag cac cac cgc acc atc acg ctg   432
Val Lys Val Leu Ser Tyr Val Leu Glu His His Arg Thr Ile Thr Leu
    130                 135                 140

acc atc atg gct ggt ctc atg ctg ggt tca ctt cgt gcg ctg tgg cct   480
Thr Ile Met Ala Gly Leu Met Leu Gly Ser Leu Arg Ala Leu Trp Pro
145                 150                 155                 160

tgg cag gac ggt gac gct aat cta ctt gct cct ggc gat aac gcc gtg   528
Trp Gln Asp Gly Asp Ala Asn Leu Leu Ala Pro Gly Asp Asn Ala Val
                165                 170                 175
```

```
atg att ttc agc atc atc att ctt ggt ggc gcg att gtc gct gct ttg   576
Met Ile Phe Ser Ile Ile Ile Leu Gly Gly Ala Ile Val Ala Ala Leu
            180                 185                 190

atg ttt gct gag cgt gtg tct tcc aag aac att gat tct gag acc gtg   624
Met Phe Ala Glu Arg Val Ser Ser Lys Asn Ile Asp Ser Glu Thr Val
        195                 200                 205

gca gaa gag cac ccg cgc taaataagaa ctccacaaag aaa                 665
Ala Glu Glu His Pro Arg
    210
```

<210> 348
<211> 214
<212> PRT
<213> Corynebacterium glutamicum

<400> 348

```
Thr Val Val Glu Asp Tyr Gln Glu Phe Thr Arg Gly Leu Phe Leu Gly
  1               5                  10                  15

Met Val Ala Val Ser Ile Leu Val Pro Leu Gly Met Met Asp Met Arg
             20                  25                  30

Asp Ala Lys Lys Arg Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys
         35                  40                  45

Ala Met Leu Gly Phe Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr
     50                  55                  60

Asp Pro Ser Leu Ile Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys
 65                  70                  75                  80

Ala Leu Val Leu Pro Gly Val Ser Gly Ser Phe Phe Leu Leu Ala Val
                 85                  90                  95

Gly Met Tyr Ala Pro Ile Met Glu Ser Leu Ser Asn Arg Asp Leu Ser
            100                 105                 110

Val Ile Gly Val Phe Leu Leu Gly Ala Leu Thr Gly Val Ile Leu Phe
        115                 120                 125

Val Lys Val Leu Ser Tyr Val Leu Glu His His Arg Thr Ile Thr Leu
    130                 135                 140

Thr Ile Met Ala Gly Leu Met Leu Gly Ser Leu Arg Ala Leu Trp Pro
145                 150                 155                 160

Trp Gln Asp Gly Asp Ala Asn Leu Leu Ala Pro Gly Asp Asn Ala Val
                165                 170                 175

Met Ile Phe Ser Ile Ile Ile Leu Gly Gly Ala Ile Val Ala Ala Leu
            180                 185                 190

Met Phe Ala Glu Arg Val Ser Ser Lys Asn Ile Asp Ser Glu Thr Val
        195                 200                 205

Ala Glu Glu His Pro Arg
    210
```

<210> 349
<211> 706
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(706)
<223> FRXA02867

<400> 349
ttcagcacag atcacccttt gccagctacc gacttagttt cgtaacacgt atagtgggag 60

gcgttttgcc agacgccaaa gaaagataat tggattacct atg agc gcc acc aac 115
Met Ser Ala Thr Asn
1 5

cct gat gcc cta gac gtg cag cac gtc tat ccc atc aag acg aaa aag 163
Pro Asp Ala Leu Asp Val Gln His Val Tyr Pro Ile Lys Thr Lys Lys
10 15 20

act cca ctt gcg gtg att ttc aac atc att agc ggt ggt ttg att gga 211
Thr Pro Leu Ala Val Ile Phe Asn Ile Ile Ser Gly Gly Leu Ile Gly
25 30 35

atg gcg gag ttg gtg cca gga att tcc ggc gga act gtc gct ttg gtt 259
Met Ala Glu Leu Val Pro Gly Ile Ser Gly Gly Thr Val Ala Leu Val
40 45 50

ctt gga att tat gag cgc gca ctg cac aac ggt gat ctc ctc att gat 307
Leu Gly Ile Tyr Glu Arg Ala Leu His Asn Gly Asp Leu Leu Ile Asp
55 60 65

ctg atc aag gtg ttg atc aag gac cgc tcg aag gtt aag gaa gct gcg 355
Leu Ile Lys Val Leu Ile Lys Asp Arg Ser Lys Val Lys Glu Ala Ala
70 75 80 85

gcg aaa atc gac tgg tgg ttc ctc ggc gct atc ggc gtt ggc atg gtc 403
Ala Lys Ile Asp Trp Trp Phe Leu Gly Ala Ile Gly Val Gly Met Val
90 95 100

gtg atg gtc ttc tcg atg tca tcg att ttg cat aca gtt gtt gag gac 451
Val Met Val Phe Ser Met Ser Ser Ile Leu His Thr Val Val Glu Asp
105 110 115

tac cca gag atc act cgc ggt ctg ttc ctt gga atg gtt gcc gtg tct 499
Tyr Pro Glu Ile Thr Arg Gly Leu Phe Leu Gly Met Val Ala Val Ser
120 125 130

atc ctt gtt ccg ttg gga atg atg gat atg cgg gat gcc aag aag cgc 547
Ile Leu Val Pro Leu Gly Met Met Asp Met Arg Asp Ala Lys Lys Arg
135 140 145

ctc gca atc gtc atc ccg cta ttt ata atc tgc gcc atg ctg gga ttc 595
Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys Ala Met Leu Gly Phe
150 155 160 165

ttt gga aca tcc ttc act agt gcg cct cgc acc gat cct tca ctg atc 643
Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr Asp Pro Ser Leu Ile
170 175 180

```
ttt gtc ttc atc tgt gct gcg atc gct gtg tgt gct ctt gtt ctt cct   691
Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys Ala Leu Val Leu Pro
            185                 190                 195

ggt gtt cag gat cac                                               706
Gly Val Gln Asp His
        200
```

<210> 350
<211> 202
<212> PRT
<213> Corynebacterium glutamicum

<400> 350

```
Met Ser Ala Thr Asn Pro Asp Ala Leu Asp Val Gln His Val Tyr Pro
  1               5                  10                  15

Ile Lys Thr Lys Lys Thr Pro Leu Ala Val Ile Phe Asn Ile Ile Ser
             20                  25                  30

Gly Gly Leu Ile Gly Met Ala Glu Leu Val Pro Gly Ile Ser Gly Gly
         35                  40                  45

Thr Val Ala Leu Val Leu Gly Ile Tyr Glu Arg Ala Leu His Asn Gly
     50                  55                  60

Asp Leu Leu Ile Asp Leu Ile Lys Val Leu Ile Lys Asp Arg Ser Lys
 65                  70                  75                  80

Val Lys Glu Ala Ala Ala Lys Ile Asp Trp Trp Phe Leu Gly Ala Ile
                 85                  90                  95

Gly Val Gly Met Val Val Met Val Phe Ser Met Ser Ser Ile Leu His
            100                 105                 110

Thr Val Val Glu Asp Tyr Pro Glu Ile Thr Arg Gly Leu Phe Leu Gly
        115                 120                 125

Met Val Ala Val Ser Ile Leu Val Pro Leu Gly Met Met Asp Met Arg
    130                 135                 140

Asp Ala Lys Lys Arg Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys
145                 150                 155                 160

Ala Met Leu Gly Phe Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr
                165                 170                 175

Asp Pro Ser Leu Ile Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys
            180                 185                 190

Ala Leu Val Leu Pro Gly Val Gln Asp His
        195                 200
```

<210> 351
<211> 930
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(907)
<223> RXN00730

<400> 351
tggtgcaata accttaagtg aggctggatt ttgcgttggc aggcgctcgg gttttgtttt 60

atccggcatg ggctcgggag ggactttaaa ataaacagct atg tcg agc caa caa 115
Met Ser Ser Gln Gln
1 5

acg atc ttc atc att ttg ctc ttt gcc gca gtg att ctc att tcc ata 163
Thr Ile Phe Ile Ile Leu Leu Phe Ala Ala Val Ile Leu Ile Ser Ile
10 15 20

gta atg att aca gct gcc ttc aaa acc cgg aaa aag cgc ttt gcc gcg 211
Val Met Ile Thr Ala Ala Phe Lys Thr Arg Lys Lys Arg Phe Ala Ala
25 30 35

cgg gct gaa gga atg gcc aac cct aca att cct gcg cca act gtg ccg 259
Arg Ala Glu Gly Met Ala Asn Pro Thr Ile Pro Ala Pro Thr Val Pro
40 45 50

tgg cag cgc ttc gcc gga gca ctt gca gcc ttg tac gct agg cct gaa 307
Trp Gln Arg Phe Ala Gly Ala Leu Ala Ala Leu Tyr Ala Arg Pro Glu
55 60 65

tgg cac aag acc cgc gga gcg aaa cga gtg tac tca gct gaa cag act 355
Trp His Lys Thr Arg Gly Ala Lys Arg Val Tyr Ser Ala Glu Gln Thr
70 75 80 85

tat ttt ggg ttt gtc tca gca atg cca ctg ggg atg gtg caa aac atg 403
Tyr Phe Gly Phe Val Ser Ala Met Pro Leu Gly Met Val Gln Asn Met
90 95 100

ctg caa aca gac tgg ggt gtg aaa aag tct gag cat gca gtt gat cag 451
Leu Gln Thr Asp Trp Gly Val Lys Lys Ser Glu His Ala Val Asp Gln
105 110 115

ctt tct aaa gga gtg gaa gtg atc gtt ggg gta gcc gca ggc aac tgg 499
Leu Ser Lys Gly Val Glu Val Ile Val Gly Val Ala Ala Gly Asn Trp
120 125 130

cgt aaa aac gga gta tca ccc gca caa gtg gaa gag gca ggc cag cgg 547
Arg Lys Asn Gly Val Ser Pro Ala Gln Val Glu Glu Ala Gly Gln Arg
135 140 145

tta gca gct gaa gga ttg gct cat cca cac ttt gtt gta ttc caa aag 595
Leu Ala Ala Glu Gly Leu Ala His Pro His Phe Val Val Phe Gln Lys
150 155 160 165

cag ctt caa cag gca gat cca aat gca gaa tat gat ctc gat gtg ctc 643
Gln Leu Gln Gln Ala Asp Pro Asn Ala Glu Tyr Asp Leu Asp Val Leu
170 175 180

gca ttt gat atc gca cgc gta gcc aac ctc ctt cgc tgg gct gct tat 691
Ala Phe Asp Ile Ala Arg Val Ala Asn Leu Leu Arg Trp Ala Ala Tyr
185 190 195

aca gat ctg ttg ctc cct gca gaa gcc cgt tgg ttc caa gac cag ctg 739

```
Thr Asp Leu Leu Leu Pro Ala Glu Ala Arg Trp Phe Gln Asp Gln Leu
        200                 205                 210

gga att gcg gct gct gtg tcc ttt ggg agc tgg gaa gaa tac gga gag   787
Gly Ile Ala Ala Ala Val Ser Phe Gly Ser Trp Glu Glu Tyr Gly Glu
    215                 220                 225

cga tac gtc cgt gga cta cag aag aac ttc aag ggc gga aac aag cca   835
Arg Tyr Val Arg Gly Leu Gln Lys Asn Phe Lys Gly Gly Asn Lys Pro
230                 235                 240                 245

tat atc gaa gga gaa cgc tgg ctc aac act gag gct gaa agt cca tgg   883
Tyr Ile Glu Gly Glu Arg Trp Leu Asn Thr Glu Ala Glu Ser Pro Trp
                250                 255                 260

aag acc caa aag tgg att agc gcc taactgctca tgagctaagc ggc         930
Lys Thr Gln Lys Trp Ile Ser Ala
            265


<210> 352
<211> 269
<212> PRT
<213> Corynebacterium glutamicum

<400> 352
Met Ser Ser Gln Gln Thr Ile Phe Ile Ile Leu Leu Phe Ala Ala Val
  1               5                  10                  15

Ile Leu Ile Ser Ile Val Met Ile Thr Ala Ala Phe Lys Thr Arg Lys
             20                  25                  30

Lys Arg Phe Ala Ala Arg Ala Glu Gly Met Ala Asn Pro Thr Ile Pro
         35                  40                  45

Ala Pro Thr Val Pro Trp Gln Arg Phe Ala Gly Ala Leu Ala Ala Leu
     50                  55                  60

Tyr Ala Arg Pro Glu Trp His Lys Thr Arg Gly Ala Lys Arg Val Tyr
 65                  70                  75                  80

Ser Ala Glu Gln Thr Tyr Phe Gly Phe Val Ser Ala Met Pro Leu Gly
                 85                  90                  95

Met Val Gln Asn Met Leu Gln Thr Asp Trp Gly Val Lys Lys Ser Glu
            100                 105                 110

His Ala Val Asp Gln Leu Ser Lys Gly Val Glu Val Ile Val Gly Val
        115                 120                 125

Ala Ala Gly Asn Trp Arg Lys Asn Gly Val Ser Pro Ala Gln Val Glu
    130                 135                 140

Glu Ala Gly Gln Arg Leu Ala Ala Glu Gly Leu Ala His Pro His Phe
145                 150                 155                 160

Val Val Phe Gln Lys Gln Leu Gln Gln Ala Asp Pro Asn Ala Glu Tyr
                165                 170                 175

Asp Leu Asp Val Leu Ala Phe Asp Ile Ala Arg Val Ala Asn Leu Leu
            180                 185                 190
```

```
Arg Trp Ala Ala Tyr Thr Asp Leu Leu Leu Pro Ala Glu Ala Arg Trp
        195                 200                 205

Phe Gln Asp Gln Leu Gly Ile Ala Ala Ala Val Ser Phe Gly Ser Trp
    210                 215                 220

Glu Glu Tyr Gly Glu Arg Tyr Val Arg Gly Leu Gln Lys Asn Phe Lys
225                 230                 235                 240

Gly Gly Asn Lys Pro Tyr Ile Glu Gly Glu Arg Trp Leu Asn Thr Glu
                245                 250                 255

Ala Glu Ser Pro Trp Lys Thr Gln Lys Trp Ile Ser Ala
            260                 265


<210> 353
<211> 356
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(333)
<223> FRXA00730

<400> 353
cac ttt gtt gta ttc caa aag cag ctt caa cag gca gat cca aat gca   48
His Phe Val Val Phe Gln Lys Gln Leu Gln Gln Ala Asp Pro Asn Ala
  1               5                  10                  15

gaa tat gat ctc gat gtg ctc gca ttt gat atc gca cgc gta gcc aac   96
Glu Tyr Asp Leu Asp Val Leu Ala Phe Asp Ile Ala Arg Val Ala Asn
             20                  25                  30

ctc ctt cgc tgg gct gct tat aca gat ctg ttg ctc cct gca gaa gcc   144
Leu Leu Arg Trp Ala Ala Tyr Thr Asp Leu Leu Leu Pro Ala Glu Ala
         35                  40                  45

cgt tgg ttc caa gac cag ctg gga att gcg gct gct gtg tcc ttt ggg   192
Arg Trp Phe Gln Asp Gln Leu Gly Ile Ala Ala Ala Val Ser Phe Gly
     50                  55                  60

agc tgg gaa gaa tac gga gag cga tac gtc cgt gga cta cag aag aac   240
Ser Trp Glu Glu Tyr Gly Glu Arg Tyr Val Arg Gly Leu Gln Lys Asn
 65                  70                  75                  80

ttc aag ggc gga aac aag cca tat atc gaa gga gaa cgc tgg ctc aac   288
Phe Lys Gly Gly Asn Lys Pro Tyr Ile Glu Gly Glu Arg Trp Leu Asn
                85                  90                  95

act gag gct gaa agt cca tgg aag acc caa aag tgg att agc gcc       333
Thr Glu Ala Glu Ser Pro Trp Lys Thr Gln Lys Trp Ile Ser Ala
            100                 105                 110

taactgctca tgagctaagc ggc                                       356


<210> 354
<211> 111
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<212> PRT
<213> Corynebacterium glutamicum

<400> 354
His Phe Val Val Phe Gln Lys Gln Leu Gln Gln Ala Asp Pro Asn Ala
1 5 10 15

Glu Tyr Asp Leu Asp Val Leu Ala Phe Asp Ile Ala Arg Val Ala Asn
20 25 30

Leu Leu Arg Trp Ala Ala Tyr Thr Asp Leu Leu Leu Pro Ala Glu Ala
35 40 45

Arg Trp Phe Gln Asp Gln Leu Gly Ile Ala Ala Ala Val Ser Phe Gly
50 55 60

Ser Trp Glu Glu Tyr Gly Glu Arg Tyr Val Arg Gly Leu Gln Lys Asn
65 70 75 80

Phe Lys Gly Gly Asn Lys Pro Tyr Ile Glu Gly Glu Arg Trp Leu Asn
85 90 95

Thr Glu Ala Glu Ser Pro Trp Lys Thr Gln Lys Trp Ile Ser Ala
100 105 110

<210> 355
<211> 2619
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2596)
<223> RXN00731

<400> 355
ttgataccgt ggccggtgga cattccttcc aggtgtggcg cgtggcttta gcgaatactt 60

ttgattgggt tgccaagcgc ggcggattgc aggtttaaca atg aaa gac gct tca 115
Met Lys Asp Ala Ser
1 5

cag tcc tac tta tta ttc ggt ctg aga tgg ctg ggc agg tcc ctg cgt 163
Gln Ser Tyr Leu Leu Phe Gly Leu Arg Trp Leu Gly Arg Ser Leu Arg
10 15 20

ttc gca ccg tta agc ctg ctc atg atc gtt gtc atg cgg ggt ttg agg 211
Phe Ala Pro Leu Ser Leu Leu Met Ile Val Val Met Arg Gly Leu Arg
25 30 35

gaa gtg ttt ggc gcc gaa gat ccc gca aat agc tct ttg gta gac aac 259
Glu Val Phe Gly Ala Glu Asp Pro Ala Asn Ser Ser Leu Val Asp Asn
40 45 50

ctt ggg ctc acc ctg ccg tgg tct ctt aat gat ccg cat ttt ctc acc 307
Leu Gly Leu Thr Leu Pro Trp Ser Leu Asn Asp Pro His Phe Leu Thr
55 60 65

gca ggg ttt agc gct tcc acc acc aca gca gcg ctc atg tcc acg ttg 355
Ala Gly Phe Ser Ala Ser Thr Thr Thr Ala Ala Leu Met Ser Thr Leu

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 70                  75                  80                  85

tgg atc atc gtg ttt gcg gtg ccc tct gaa cgg att ctg ggc agc ctc   403
Trp Ile Ile Val Phe Ala Val Pro Ser Glu Arg Ile Leu Gly Ser Leu
                 90                  95                 100

aaa ttc gcg atc aca gca gcg ctt atc cac atc act tcc att ccg ctg   451
Lys Phe Ala Ile Thr Ala Ala Leu Ile His Ile Thr Ser Ile Pro Leu
            105                 110                 115

ggc atc ggc atc gcc cac ctc atc gaa gaa gcc gat ctc aac cgc tgg   499
Gly Ile Gly Ile Ala His Leu Ile Glu Glu Ala Asp Leu Asn Arg Trp
        120                 125                 130

ggc aac aac atg ttg gcc gat gtg ctg ctc acc cca gat ttc tgg gtc   547
Gly Asn Asn Met Leu Ala Asp Val Leu Leu Thr Pro Asp Phe Trp Val
    135                 140                 145

ttc ggc gtc gcc gct ttc gca tcc gcc tcc atg cca ctg ctc tgg cga   595
Phe Gly Val Ala Ala Phe Ala Ser Ala Ser Met Pro Leu Leu Trp Arg
150                 155                 160                 165

cgg cgc acc cga ttg ttc ctc ttt act atc acc ttg acg ctg ctg ctt   643
Arg Arg Thr Arg Leu Phe Leu Phe Thr Ile Thr Leu Thr Leu Leu Leu
                170                 175                 180

tat acg ggc acg ctt gcc gac gtc acc atg ctc acc gcg acc atc atc   691
Tyr Thr Gly Thr Leu Ala Asp Val Thr Met Leu Thr Ala Thr Ile Ile
            185                 190                 195

ggc acc gtt gcc ggc gag ttg aac agg cat cgg aaa acc cca ggt ggc   739
Gly Thr Val Ala Gly Glu Leu Asn Arg His Arg Lys Thr Pro Gly Gly
        200                 205                 210

cgc tgg ctt ccc ggt tcc ctc acc gtg cgt gaa gcg cgc att atg acg   787
Arg Trp Leu Pro Gly Ser Leu Thr Val Arg Glu Ala Arg Ile Met Thr
    215                 220                 225

gcc att ttg gtc act gcc gta gca gca ggt cca gtg ctt gct gcg ctt   835
Ala Ile Leu Val Thr Ala Val Ala Ala Gly Pro Val Leu Ala Ala Leu
230                 235                 240                 245

aat cca ctc acc cac ggc cct ttt tcc agt gca acg aaa ttg atc tgg   883
Asn Pro Leu Thr His Gly Pro Phe Ser Ser Ala Thr Lys Leu Ile Trp
                250                 255                 260

cag ccc ctt gtc act gaa gaa cac atg cat cac ctc tgc cac aca gac   931
Gln Pro Leu Val Thr Glu Glu His Met His His Leu Cys His Thr Asp
            265                 270                 275

agc acc tct gat gca tgc caa ggt gcg ctt gat cag ctc caa cag cac   979
Ser Thr Ser Asp Ala Cys Gln Gly Ala Leu Asp Gln Leu Gln Gln His
        280                 285                 290

ggt gtt ggc cct tcc gtt gcc aac ctg att cca ctg atc ctc acc gtg   1027
Gly Val Gly Pro Ser Val Ala Asn Leu Ile Pro Leu Ile Leu Thr Val
    295                 300                 305

gtc ctt gcg atg ggg ctt agc cgc gga cgt cga ctt gca tgg att ttg   1075
Val Leu Ala Met Gly Leu Ser Arg Gly Arg Arg Leu Ala Trp Ile Leu
310                 315                 320                 325
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gcg gtt ttg gcc cag ctc att tcc atc gca gtg ttg atg ttc cag ctg   1123
Ala Val Leu Ala Gln Leu Ile Ser Ile Ala Val Leu Met Phe Gln Leu
                330                 335                 340

acc aaa cta tcg gct gat tcc acc gat ctt cta tgg tca gtc aat gcc   1171
Thr Lys Leu Ser Ala Asp Ser Thr Asp Leu Leu Trp Ser Val Asn Ala
            345                 350                 355

ttt agc gtg atc gtt cct tgg ctg gtg gcg ctc gcc gtc ttg gtg ttt   1219
Phe Ser Val Ile Val Pro Trp Leu Val Ala Leu Ala Val Leu Val Phe
        360                 365                 370

tcc cgc cgt gca ttc cag gtg aag att gat acc acc cgg att tct aaa   1267
Ser Arg Arg Ala Phe Gln Val Lys Ile Asp Thr Thr Arg Ile Ser Lys
    375                 380                 385

tcc tta ggc gct ctc atg gtt aca tgg ttg gca acg gca gca ttg tgg   1315
Ser Leu Gly Ala Leu Met Val Thr Trp Leu Ala Thr Ala Ala Leu Trp
390                 395                 400                 405

atc ctt gcc aca ttg ttc ctg cca cac gca ttc cac cca cat cca aca   1363
Ile Leu Ala Thr Leu Phe Leu Pro His Ala Phe His Pro His Pro Thr
                410                 415                 420

ttg ggg ctg gct ttc aaa gaa ctc ccc ttc cgc tat ctc cca cca act   1411
Leu Gly Leu Ala Phe Lys Glu Leu Pro Phe Arg Tyr Leu Pro Pro Thr
            425                 430                 435

atc gaa acg gtg tta agc cat caa ctc ttc ccc aga agc cct gct ggg   1459
Ile Glu Thr Val Leu Ser His Gln Leu Phe Pro Arg Ser Pro Ala Gly
        440                 445                 450

tgg gca gtg ttt gaa tgg act gga acg cta ttc tgg ctg gtc gta gca   1507
Trp Ala Val Phe Glu Trp Thr Gly Thr Leu Phe Trp Leu Val Val Ala
    455                 460                 465

gca act ctt tat cat ctg ctc atg ggt gtg ccc agc aac aaa gcg cac   1555
Ala Thr Leu Tyr His Leu Leu Met Gly Val Pro Ser Asn Lys Ala His
470                 475                 480                 485

gag gac caa gaa aac gca gcg act ctc ctg cgc tct ggc agc ggc gat   1603
Glu Asp Gln Glu Asn Ala Ala Thr Leu Leu Arg Ser Gly Ser Gly Asp
                490                 495                 500

cac ttg tcc tgg atg acc att tgg ggt ggc aat acg tat tgg tgg gca   1651
His Leu Ser Trp Met Thr Ile Trp Gly Gly Asn Thr Tyr Trp Trp Ala
            505                 510                 515

cca gaa aat gca gga tat gtg gcc tac cgc gtg aaa agg ggc atc gca   1699
Pro Glu Asn Ala Gly Tyr Val Ala Tyr Arg Val Lys Arg Gly Ile Ala
        520                 525                 530

att aca ttg ggt gag cct att ctg ggt ccg gat tca tcc gtc tct aaa   1747
Ile Thr Leu Gly Glu Pro Ile Leu Gly Pro Asp Ser Ser Val Ser Lys
    535                 540                 545

gca gag ctg gcc gca cag ttt gaa gaa ttt gcc agc aac caa ggc tgg   1795
Ala Glu Leu Ala Ala Gln Phe Glu Glu Phe Ala Ser Asn Gln Gly Trp
550                 555                 560                 565
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att gtt gcg tgg tat tcc gtt tgt gaa gaa ttc tca aag gaa cgc atc   1843
Ile Val Ala Trp Tyr Ser Val Cys Glu Glu Phe Ser Lys Glu Arg Ile
                570                 575                 580

aac gct ggc cac cac aca ctt cgt gtg gct gag gaa gca gtc tta agc   1891
Asn Ala Gly His His Thr Leu Arg Val Ala Glu Glu Ala Val Leu Ser
            585                 590                 595

tca gct aat gcg gat ttc aaa ggt aag cac ttc caa aat gtc cgc acc   1939
Ser Ala Asn Ala Asp Phe Lys Gly Lys His Phe Gln Asn Val Arg Thr
        600                 605                 610

gcc cga aac cgc gcg gcc aaa gag ggc gta agt tcc atc tgg aca acc   1987
Ala Arg Asn Arg Ala Ala Lys Glu Gly Val Ser Ser Ile Trp Thr Thr
    615                 620                 625

tgg gct gat ttg agt gcc gaa atg cag cac aag atc atc acg ctg tcg   2035
Trp Ala Asp Leu Ser Ala Glu Met Gln His Lys Ile Ile Thr Leu Ser
630                 635                 640                 645

gaa gaa tgg gtc tct gat aaa gct ctg ccg gag atg ggc ttc acg ctt   2083
Glu Glu Trp Val Ser Asp Lys Ala Leu Pro Glu Met Gly Phe Thr Leu
                650                 655                 660

ggc act gtc aac gag ctc tca gat cca gat acc tat ctt ctt ctc gcg   2131
Gly Thr Val Asn Glu Leu Ser Asp Pro Asp Thr Tyr Leu Leu Leu Ala
            665                 670                 675

att gat gag gaa gag cat ctg cac ggt gtg acc agt tgg ttg ccg gtc   2179
Ile Asp Glu Glu Glu His Leu His Gly Val Thr Ser Trp Leu Pro Val
        680                 685                 690

tat gaa aaa gga cgc atc gtc ggc tac aca ctt gat gtg atg cgc cgt   2227
Tyr Glu Lys Gly Arg Ile Val Gly Tyr Thr Leu Asp Val Met Arg Arg
    695                 700                 705

gat ccg caa ggc ttt aaa tct gtc atc gag ttt ctc att tcc gag gcc   2275
Asp Pro Gln Gly Phe Lys Ser Val Ile Glu Phe Leu Ile Ser Glu Ala
710                 715                 720                 725

gtc gtt atc gca agg gat cac gat ctg gaa tgg atg tcg atg tcc ggc   2323
Val Val Ile Ala Arg Asp His Asp Leu Glu Trp Met Ser Met Ser Gly
                730                 735                 740

gct cct ttg agt acg ccc cca ggt gtg gcc gac gac ggc acc atc gga   2371
Ala Pro Leu Ser Thr Pro Pro Gly Val Ala Asp Asp Gly Thr Ile Gly
            745                 750                 755

caa att ttg gag ctt ttg ggc cga gca atg gag ccg ttc tac ggt ttc   2419
Gln Ile Leu Glu Leu Leu Gly Arg Ala Met Glu Pro Phe Tyr Gly Phe
        760                 765                 770

cgt tcc ctc gct gcg tcc aag aac aaa ttc cac cca gaa cac cac ggt   2467
Arg Ser Leu Ala Ala Ser Lys Asn Lys Phe His Pro Glu His His Gly
    775                 780                 785

tgg tac ttg tgt tac cgc gat gaa tta tcg tta cca agc att ggc ctt   2515
Trp Tyr Leu Cys Tyr Arg Asp Glu Leu Ser Leu Pro Ser Ile Gly Leu
790                 795                 800                 805

gcc gtt gct gcc tgc tac ctc aac gag ttt ccg ctg ccg aat tgg ctg   2563
```

```
Ala Val Ala Ala Cys Tyr Leu Asn Glu Phe Pro Leu Pro Asn Trp Leu
                810                 815                 820

aaa aag acc gcc act tcc gcc cca agc cac agc tagaaaaacg cgtaaccttg 2616
Lys Lys Thr Ala Thr Ser Ala Pro Ser His Ser
            825                 830

gtg                                                             2619


<210> 356
<211> 832
<212> PRT
<213> Corynebacterium glutamicum

<400> 356
Met Lys Asp Ala Ser Gln Ser Tyr Leu Leu Phe Gly Leu Arg Trp Leu
  1               5                  10                  15

Gly Arg Ser Leu Arg Phe Ala Pro Leu Ser Leu Leu Met Ile Val Val
            20                  25                  30

Met Arg Gly Leu Arg Glu Val Phe Gly Ala Glu Asp Pro Ala Asn Ser
         35                  40                  45

Ser Leu Val Asp Asn Leu Gly Leu Thr Leu Pro Trp Ser Leu Asn Asp
     50                  55                  60

Pro His Phe Leu Thr Ala Gly Phe Ser Ala Ser Thr Thr Thr Ala Ala
 65                  70                  75                  80

Leu Met Ser Thr Leu Trp Ile Ile Val Phe Ala Val Pro Ser Glu Arg
                85                  90                  95

Ile Leu Gly Ser Leu Lys Phe Ala Ile Thr Ala Ala Leu Ile His Ile
            100                 105                 110

Thr Ser Ile Pro Leu Gly Ile Gly Ile Ala His Leu Ile Glu Glu Ala
        115                 120                 125

Asp Leu Asn Arg Trp Gly Asn Asn Met Leu Ala Asp Val Leu Leu Thr
    130                 135                 140

Pro Asp Phe Trp Val Phe Gly Val Ala Ala Phe Ala Ser Ala Ser Met
145                 150                 155                 160

Pro Leu Leu Trp Arg Arg Arg Thr Arg Leu Phe Leu Phe Thr Ile Thr
                165                 170                 175

Leu Thr Leu Leu Leu Tyr Thr Gly Thr Leu Ala Asp Val Thr Met Leu
            180                 185                 190

Thr Ala Thr Ile Ile Gly Thr Val Ala Gly Glu Leu Asn Arg His Arg
        195                 200                 205

Lys Thr Pro Gly Gly Arg Trp Leu Pro Gly Ser Leu Thr Val Arg Glu
    210                 215                 220

Ala Arg Ile Met Thr Ala Ile Leu Val Thr Ala Val Ala Ala Gly Pro
225                 230                 235                 240
```

```
Val Leu Ala Ala Leu Asn Pro Leu Thr His Gly Pro Phe Ser Ser Ala
                245                 250                 255

Thr Lys Leu Ile Trp Gln Pro Leu Val Thr Glu Glu His Met His His
            260                 265                 270

Leu Cys His Thr Asp Ser Thr Ser Asp Ala Cys Gln Gly Ala Leu Asp
        275                 280                 285

Gln Leu Gln Gln His Gly Val Gly Pro Ser Val Ala Asn Leu Ile Pro
    290                 295                 300

Leu Ile Leu Thr Val Val Leu Ala Met Gly Leu Ser Arg Gly Arg Arg
305                 310                 315                 320

Leu Ala Trp Ile Leu Ala Val Leu Ala Gln Leu Ile Ser Ile Ala Val
                325                 330                 335

Leu Met Phe Gln Leu Thr Lys Leu Ser Ala Asp Ser Thr Asp Leu Leu
            340                 345                 350

Trp Ser Val Asn Ala Phe Ser Val Ile Val Pro Trp Leu Val Ala Leu
        355                 360                 365

Ala Val Leu Val Phe Ser Arg Arg Ala Phe Gln Val Lys Ile Asp Thr
    370                 375                 380

Thr Arg Ile Ser Lys Ser Leu Gly Ala Leu Met Val Thr Trp Leu Ala
385                 390                 395                 400

Thr Ala Ala Leu Trp Ile Leu Ala Thr Leu Phe Leu Pro His Ala Phe
                405                 410                 415

His Pro His Pro Thr Leu Gly Leu Ala Phe Lys Glu Leu Pro Phe Arg
            420                 425                 430

Tyr Leu Pro Pro Thr Ile Glu Thr Val Leu Ser His Gln Leu Phe Pro
        435                 440                 445

Arg Ser Pro Ala Gly Trp Ala Val Phe Glu Trp Thr Gly Thr Leu Phe
    450                 455                 460

Trp Leu Val Val Ala Ala Thr Leu Tyr His Leu Leu Met Gly Val Pro
465                 470                 475                 480

Ser Asn Lys Ala His Glu Asp Gln Glu Asn Ala Ala Thr Leu Leu Arg
                485                 490                 495

Ser Gly Ser Gly Asp His Leu Ser Trp Met Thr Ile Trp Gly Gly Asn
            500                 505                 510

Thr Tyr Trp Trp Ala Pro Glu Asn Ala Gly Tyr Val Ala Tyr Arg Val
        515                 520                 525

Lys Arg Gly Ile Ala Ile Thr Leu Gly Glu Pro Ile Leu Gly Pro Asp
    530                 535                 540

Ser Ser Val Ser Lys Ala Glu Leu Ala Ala Gln Phe Glu Glu Phe Ala
545                 550                 555                 560

Ser Asn Gln Gly Trp Ile Val Ala Trp Tyr Ser Val Cys Glu Glu Phe
```

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                565                 570                 575

Ser Lys Glu Arg Ile Asn Ala Gly His His Thr Leu Arg Val Ala Glu
            580                 585                 590

Glu Ala Val Leu Ser Ser Ala Asn Ala Asp Phe Lys Gly Lys His Phe
        595                 600                 605

Gln Asn Val Arg Thr Ala Arg Asn Arg Ala Ala Lys Glu Gly Val Ser
    610                 615                 620

Ser Ile Trp Thr Thr Trp Ala Asp Leu Ser Ala Glu Met Gln His Lys
625                 630                 635                 640

Ile Ile Thr Leu Ser Glu Glu Trp Val Ser Asp Lys Ala Leu Pro Glu
                645                 650                 655

Met Gly Phe Thr Leu Gly Thr Val Asn Glu Leu Ser Asp Pro Asp Thr
            660                 665                 670

Tyr Leu Leu Leu Ala Ile Asp Glu Glu Glu His Leu His Gly Val Thr
        675                 680                 685

Ser Trp Leu Pro Val Tyr Glu Lys Gly Arg Ile Val Gly Tyr Thr Leu
    690                 695                 700

Asp Val Met Arg Arg Asp Pro Gln Gly Phe Lys Ser Val Ile Glu Phe
705                 710                 715                 720

Leu Ile Ser Glu Ala Val Val Ile Ala Arg Asp His Asp Leu Glu Trp
                725                 730                 735

Met Ser Met Ser Gly Ala Pro Leu Ser Thr Pro Pro Gly Val Ala Asp
            740                 745                 750

Asp Gly Thr Ile Gly Gln Ile Leu Glu Leu Leu Gly Arg Ala Met Glu
        755                 760                 765

Pro Phe Tyr Gly Phe Arg Ser Leu Ala Ala Ser Lys Asn Lys Phe His
    770                 775                 780

Pro Glu His His Gly Trp Tyr Leu Cys Tyr Arg Asp Glu Leu Ser Leu
785                 790                 795                 800

Pro Ser Ile Gly Leu Ala Val Ala Ala Cys Tyr Leu Asn Glu Phe Pro
                805                 810                 815

Leu Pro Asn Trp Leu Lys Lys Thr Ala Thr Ser Ala Pro Ser His Ser
            820                 825                 830
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<210> 357
<211> 2495
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (1)..(2472)
<223> FRXA00731

<400> 357

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tta tta ttc ggt ctg aga tgg ctg ggc agg tcc ctg cgt ttc gca ccg   48
Leu Leu Phe Gly Leu Arg Trp Leu Gly Arg Ser Leu Arg Phe Ala Pro
  1               5                  10                  15

tta agc ctg ctc atg atc gtt gtc atg cgg ggt ttg agg gaa gtg ttt   96
Leu Ser Leu Leu Met Ile Val Val Met Arg Gly Leu Arg Glu Val Phe
             20                  25                  30

ggc gcc gaa gat ccc gca aat agc tct ttg gta gac aac ctt ggg ctc   144
Gly Ala Glu Asp Pro Ala Asn Ser Ser Leu Val Asp Asn Leu Gly Leu
         35                  40                  45

acc ctg ccg tgg tct ctt aat gat ccg cat ttt ctc acc gca ggg ttt   192
Thr Leu Pro Trp Ser Leu Asn Asp Pro His Phe Leu Thr Ala Gly Phe
     50                  55                  60

agc gct tcc acc acc aca gca gcg ctc atg tcc acg ttg tgg atc atc   240
Ser Ala Ser Thr Thr Thr Ala Ala Leu Met Ser Thr Leu Trp Ile Ile
 65                  70                  75                  80

gtg ttt gcg gtg ccc tct gaa cgg att ctg ggc agc ctc aaa ttc gcg   288
Val Phe Ala Val Pro Ser Glu Arg Ile Leu Gly Ser Leu Lys Phe Ala
                 85                  90                  95

atc aca gca gcg ctt atc cac atc act tcc att ccg ctg ggc atc ggc   336
Ile Thr Ala Ala Leu Ile His Ile Thr Ser Ile Pro Leu Gly Ile Gly
            100                 105                 110

atc gcc cac ctc atc gaa gaa gcc gat ctc aac cgc tgg ggc aac aac   384
Ile Ala His Leu Ile Glu Glu Ala Asp Leu Asn Arg Trp Gly Asn Asn
        115                 120                 125

atg ttg gcc gat gtg ctg ctc acc cca gat ttc tgg gtc ttc ggc gtc   432
Met Leu Ala Asp Val Leu Leu Thr Pro Asp Phe Trp Val Phe Gly Val
    130                 135                 140

gcc gct ttc gca tcc gcc tcc atg cca ctg ctc tgg cga cgg cgc acc   480
Ala Ala Phe Ala Ser Ala Ser Met Pro Leu Leu Trp Arg Arg Arg Thr
145                 150                 155                 160

cga ttg ttc ctc ttt act atc acc ttg acg ctg ctg ctt tat acg ggc   528
Arg Leu Phe Leu Phe Thr Ile Thr Leu Thr Leu Leu Leu Tyr Thr Gly
                165                 170                 175

acg ctt gcc gac gtc acc atg ctc acc gcg acc atc atc ggc acc gtt   576
Thr Leu Ala Asp Val Thr Met Leu Thr Ala Thr Ile Ile Gly Thr Val
            180                 185                 190

gcc ggc gag ttg aac agg cat cgg aaa acc cca ggt ggc cgc tgg ctt   624
Ala Gly Glu Leu Asn Arg His Arg Lys Thr Pro Gly Gly Arg Trp Leu
        195                 200                 205

ccc ggt tcc ctc acc gtg cgt gaa gcg cgc att atg acg gcc att ttg   672
Pro Gly Ser Leu Thr Val Arg Glu Ala Arg Ile Met Thr Ala Ile Leu
    210                 215                 220

gtc act gcc gta gca gca ggt cca gtg ctt gct gcg ctt aat cca ctc   720
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```
Val Thr Ala Val Ala Ala Gly Pro Val Leu Ala Ala Leu Asn Pro Leu
225                 230                 235                 240

acc cac ggc cct ttt tcc agt gca acg aaa ttg atc tgg cag ccc ctt   768
Thr His Gly Pro Phe Ser Ser Ala Thr Lys Leu Ile Trp Gln Pro Leu
                245                 250                 255

gtc act gaa gaa cac atg cat cac ctc tgc cac aca gac agc acc tct   816
Val Thr Glu Glu His Met His His Leu Cys His Thr Asp Ser Thr Ser
            260                 265                 270

gat gca tgc caa ggt gcg ctt gat cag ctc caa cag cac ggt gtt ggc   864
Asp Ala Cys Gln Gly Ala Leu Asp Gln Leu Gln Gln His Gly Val Gly
        275                 280                 285

cct tcc gtt gcc aac ctg att cca ctg atc ctc acc gtg gtc ctt gcg   912
Pro Ser Val Ala Asn Leu Ile Pro Leu Ile Leu Thr Val Val Leu Ala
    290                 295                 300

atg ggg ctt agc cgc gga cgt cga ctt gca tgg att ttg gcg gtt ttg   960
Met Gly Leu Ser Arg Gly Arg Arg Leu Ala Trp Ile Leu Ala Val Leu
305                 310                 315                 320

gcc cag ctc att tcc atc gca gtg ttg atg ttc cag ctg acc aaa cta  1008
Ala Gln Leu Ile Ser Ile Ala Val Leu Met Phe Gln Leu Thr Lys Leu
                325                 330                 335

tcg gct gat tcc acc gat ctt cta tgg tca gtc aat gcc ttt agc gtg  1056
Ser Ala Asp Ser Thr Asp Leu Leu Trp Ser Val Asn Ala Phe Ser Val
            340                 345                 350

atc gtt cct tgg ctg gtg gcg ctc gcc gtc ttg gtg ttt tcc cgc cgt  1104
Ile Val Pro Trp Leu Val Ala Leu Ala Val Leu Val Phe Ser Arg Arg
        355                 360                 365

gca ttc cag gtg aag att gat acc acc cgg att tct aaa tcc tta ggc  1152
Ala Phe Gln Val Lys Ile Asp Thr Thr Arg Ile Ser Lys Ser Leu Gly
    370                 375                 380

gct ctc atg gtt aca tgg ttg gca acg gca gca ttg tgg atc ctt gcc  1200
Ala Leu Met Val Thr Trp Leu Ala Thr Ala Ala Leu Trp Ile Leu Ala
385                 390                 395                 400

aca ttg ttc ctg cca cac gca ttc cac cca cat cca aca ttg ggg ctg  1248
Thr Leu Phe Leu Pro His Ala Phe His Pro His Pro Thr Leu Gly Leu
                405                 410                 415

gct ttc aaa gaa ctc ccc ttc cgc tat ctc cca cca act atc gaa acg  1296
Ala Phe Lys Glu Leu Pro Phe Arg Tyr Leu Pro Pro Thr Ile Glu Thr
            420                 425                 430

gtg tta agc cat caa ctc ttc ccc aga agc cct gct ggg tgg gca gtg  1344
Val Leu Ser His Gln Leu Phe Pro Arg Ser Pro Ala Gly Trp Ala Val
        435                 440                 445

ttt gaa tgg act gga acg cta ttc tgg ctg gtc gta gca gca act ctt  1392
Phe Glu Trp Thr Gly Thr Leu Phe Trp Leu Val Val Ala Ala Thr Leu
    450                 455                 460

tat cat ctg ctc atg ggt gtg ccc agc aac aaa gcg cac gag gac caa  1440
Tyr His Leu Leu Met Gly Val Pro Ser Asn Lys Ala His Glu Asp Gln
```

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465                 470                 475                 480

gaa aac gca gcg act ctc ctg cgc tct ggc agc ggc gat cac ttg tcc   1488
Glu Asn Ala Ala Thr Leu Leu Arg Ser Gly Ser Gly Asp His Leu Ser
                485                 490                 495

tgg atg acc att tgg ggt ggc aat acg tat tgg tgg gca cca gaa aat   1536
Trp Met Thr Ile Trp Gly Gly Asn Thr Tyr Trp Trp Ala Pro Glu Asn
            500                 505                 510

gca gga tat gtg gcc tac cgc gtg aaa agg ggc atc gca att aca ttg   1584
Ala Gly Tyr Val Ala Tyr Arg Val Lys Arg Gly Ile Ala Ile Thr Leu
        515                 520                 525

ggt gag cct att ctg ggt ccg gat tca tcc gtc tct aaa gca gag ctg   1632
Gly Glu Pro Ile Leu Gly Pro Asp Ser Ser Val Ser Lys Ala Glu Leu
    530                 535                 540

gcc gca cag ttt gaa gaa ttt gcc agc aac caa ggc tgg att gtt gcg   1680
Ala Ala Gln Phe Glu Glu Phe Ala Ser Asn Gln Gly Trp Ile Val Ala
545                 550                 555                 560

tgg tat tcc gtt tgt gaa gaa ttc tca aag gaa cgc atc aac gct ggc   1728
Trp Tyr Ser Val Cys Glu Glu Phe Ser Lys Glu Arg Ile Asn Ala Gly
                565                 570                 575

cac cac aca ctt cgt gtg gct gag gaa gca gtc tta agc tca gct aat   1776
His His Thr Leu Arg Val Ala Glu Glu Ala Val Leu Ser Ser Ala Asn
            580                 585                 590

gcg gat ttc aaa ggt aag cac ttc caa aat gtc cgc acc gcc cga aac   1824
Ala Asp Phe Lys Gly Lys His Phe Gln Asn Val Arg Thr Ala Arg Asn
        595                 600                 605

cgc gcg gcc aaa gag ggc gta agt tcc atc tgg aca acc tgg gct gat   1872
Arg Ala Ala Lys Glu Gly Val Ser Ser Ile Trp Thr Thr Trp Ala Asp
    610                 615                 620

ttg agt gcc gaa atg cag cac aag atc atc acg ctg tcg gaa gaa tgg   1920
Leu Ser Ala Glu Met Gln His Lys Ile Ile Thr Leu Ser Glu Glu Trp
625                 630                 635                 640

gtc tct gat aaa gct ctg ccg gag atg ggc ttc acg ctt ggc act gtc   1968
Val Ser Asp Lys Ala Leu Pro Glu Met Gly Phe Thr Leu Gly Thr Val
                645                 650                 655

aac gag ctc tca gat cca gat acc tat ctt ctt ctc gcg att gat gag   2016
Asn Glu Leu Ser Asp Pro Asp Thr Tyr Leu Leu Leu Ala Ile Asp Glu
            660                 665                 670

gaa gag cat ctg cac ggt gtg acc agt tgg ttg ccg gtc tat gaa aaa   2064
Glu Glu His Leu His Gly Val Thr Ser Trp Leu Pro Val Tyr Glu Lys
        675                 680                 685

gga cgc atc gtc ggc tac aca ctt gat gtg atg cgc cgt gat ccg caa   2112
Gly Arg Ile Val Gly Tyr Thr Leu Asp Val Met Arg Arg Asp Pro Gln
    690                 695                 700

ggc ttt aaa tct gtc atc gag ttt ctc att tcc gag gcc gtc gtt atc   2160
Gly Phe Lys Ser Val Ile Glu Phe Leu Ile Ser Glu Ala Val Val Ile
705                 710                 715                 720
```

```
gca agg gat cac gat ctg gaa tgg atg tcg atg tcc ggc gct cct ttg   2208
Ala Arg Asp His Asp Leu Glu Trp Met Ser Met Ser Gly Ala Pro Leu
                725                 730                 735

agt acg ccc cca ggt gtg gcc gac gac ggc acc atc gga caa att ttg   2256
Ser Thr Pro Pro Gly Val Ala Asp Asp Gly Thr Ile Gly Gln Ile Leu
            740                 745                 750

gag ctt ttg ggc cga gca atg gag ccg ttc tac ggt ttc cgt tcc ctc   2304
Glu Leu Leu Gly Arg Ala Met Glu Pro Phe Tyr Gly Phe Arg Ser Leu
        755                 760                 765

gct gcg tcc aag aac aaa ttc cac cca gaa cac cac ggt tgg tac ttg   2352
Ala Ala Ser Lys Asn Lys Phe His Pro Glu His His Gly Trp Tyr Leu
    770                 775                 780

tgt tac cgc gat gaa tta tcg tta cca agc att ggc ctt gcc gtt gct   2400
Cys Tyr Arg Asp Glu Leu Ser Leu Pro Ser Ile Gly Leu Ala Val Ala
785                 790                 795                 800

gcc tgc tac ctc aac gag ttt ccg ctg ccg aat tgg ctg aaa aag acc   2448
Ala Cys Tyr Leu Asn Glu Phe Pro Leu Pro Asn Trp Leu Lys Lys Thr
                805                 810                 815

gcc act tcc gcc cca agc cac agc tagaaaaacg cgtaaccttg gtg         2495
Ala Thr Ser Ala Pro Ser His Ser
            820
```

<210> 358
<211> 824
<212> PRT
<213> Corynebacterium glutamicum

<400> 358

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Leu Leu Phe Gly Leu Arg Trp Leu Gly Arg Ser Leu Arg Phe Ala Pro
  1               5                  10                  15

Leu Ser Leu Leu Met Ile Val Val Met Arg Gly Leu Arg Glu Val Phe
             20                  25                  30

Gly Ala Glu Asp Pro Ala Asn Ser Ser Leu Val Asp Asn Leu Gly Leu
         35                  40                  45

Thr Leu Pro Trp Ser Leu Asn Asp Pro His Phe Leu Thr Ala Gly Phe
     50                  55                  60

Ser Ala Ser Thr Thr Thr Ala Ala Leu Met Ser Thr Leu Trp Ile Ile
 65                  70                  75                  80

Val Phe Ala Val Pro Ser Glu Arg Ile Leu Gly Ser Leu Lys Phe Ala
                 85                  90                  95

Ile Thr Ala Ala Leu Ile His Ile Thr Ser Ile Pro Leu Gly Ile Gly
            100                 105                 110

Ile Ala His Leu Ile Glu Glu Ala Asp Leu Asn Arg Trp Gly Asn Asn
        115                 120                 125

Met Leu Ala Asp Val Leu Leu Thr Pro Asp Phe Trp Val Phe Gly Val
```

```
    130                 135                 140

Ala Ala Phe Ala Ser Ala Ser Met Pro Leu Leu Trp Arg Arg Arg Thr
145                 150                 155                 160

Arg Leu Phe Leu Phe Thr Ile Thr Leu Thr Leu Leu Leu Tyr Thr Gly
                165                 170                 175

Thr Leu Ala Asp Val Thr Met Leu Thr Ala Thr Ile Ile Gly Thr Val
            180                 185                 190

Ala Gly Glu Leu Asn Arg His Arg Lys Thr Pro Gly Gly Arg Trp Leu
        195                 200                 205

Pro Gly Ser Leu Thr Val Arg Glu Ala Arg Ile Met Thr Ala Ile Leu
    210                 215                 220

Val Thr Ala Val Ala Ala Gly Pro Val Leu Ala Ala Leu Asn Pro Leu
225                 230                 235                 240

Thr His Gly Pro Phe Ser Ser Ala Thr Lys Leu Ile Trp Gln Pro Leu
                245                 250                 255

Val Thr Glu Glu His Met His His Leu Cys His Thr Asp Ser Thr Ser
            260                 265                 270

Asp Ala Cys Gln Gly Ala Leu Asp Gln Leu Gln Gln His Gly Val Gly
        275                 280                 285

Pro Ser Val Ala Asn Leu Ile Pro Leu Ile Leu Thr Val Val Leu Ala
    290                 295                 300

Met Gly Leu Ser Arg Gly Arg Arg Leu Ala Trp Ile Leu Ala Val Leu
305                 310                 315                 320

Ala Gln Leu Ile Ser Ile Ala Val Leu Met Phe Gln Leu Thr Lys Leu
                325                 330                 335

Ser Ala Asp Ser Thr Asp Leu Leu Trp Ser Val Asn Ala Phe Ser Val
            340                 345                 350

Ile Val Pro Trp Leu Val Ala Leu Ala Val Leu Val Phe Ser Arg Arg
        355                 360                 365

Ala Phe Gln Val Lys Ile Asp Thr Thr Arg Ile Ser Lys Ser Leu Gly
    370                 375                 380

Ala Leu Met Val Thr Trp Leu Ala Thr Ala Ala Leu Trp Ile Leu Ala
385                 390                 395                 400

Thr Leu Phe Leu Pro His Ala Phe His Pro His Pro Thr Leu Gly Leu
                405                 410                 415

Ala Phe Lys Glu Leu Pro Phe Arg Tyr Leu Pro Pro Thr Ile Glu Thr
            420                 425                 430

Val Leu Ser His Gln Leu Phe Pro Arg Ser Pro Ala Gly Trp Ala Val
        435                 440                 445

Phe Glu Trp Thr Gly Thr Leu Phe Trp Leu Val Val Ala Ala Thr Leu
    450                 455                 460
```

```
Tyr His Leu Leu Met Gly Val Pro Ser Asn Lys Ala His Glu Asp Gln
465                 470                 475                 480

Glu Asn Ala Ala Thr Leu Leu Arg Ser Gly Ser Gly Asp His Leu Ser
                485                 490                 495

Trp Met Thr Ile Trp Gly Gly Asn Thr Tyr Trp Trp Ala Pro Glu Asn
            500                 505                 510

Ala Gly Tyr Val Ala Tyr Arg Val Lys Arg Gly Ile Ala Ile Thr Leu
        515                 520                 525

Gly Glu Pro Ile Leu Gly Pro Asp Ser Ser Val Ser Lys Ala Glu Leu
    530                 535                 540

Ala Ala Gln Phe Glu Glu Phe Ala Ser Asn Gln Gly Trp Ile Val Ala
545                 550                 555                 560

Trp Tyr Ser Val Cys Glu Glu Phe Ser Lys Glu Arg Ile Asn Ala Gly
                565                 570                 575

His His Thr Leu Arg Val Ala Glu Glu Ala Val Leu Ser Ser Ala Asn
            580                 585                 590

Ala Asp Phe Lys Gly Lys His Phe Gln Asn Val Arg Thr Ala Arg Asn
        595                 600                 605

Arg Ala Ala Lys Glu Gly Val Ser Ser Ile Trp Thr Thr Trp Ala Asp
    610                 615                 620

Leu Ser Ala Glu Met Gln His Lys Ile Ile Thr Leu Ser Glu Glu Trp
625                 630                 635                 640

Val Ser Asp Lys Ala Leu Pro Glu Met Gly Phe Thr Leu Gly Thr Val
                645                 650                 655

Asn Glu Leu Ser Asp Pro Asp Thr Tyr Leu Leu Leu Ala Ile Asp Glu
            660                 665                 670

Glu Glu His Leu His Gly Val Thr Ser Trp Leu Pro Val Tyr Glu Lys
        675                 680                 685

Gly Arg Ile Val Gly Tyr Thr Leu Asp Val Met Arg Arg Asp Pro Gln
    690                 695                 700

Gly Phe Lys Ser Val Ile Glu Phe Leu Ile Ser Glu Ala Val Val Ile
705                 710                 715                 720

Ala Arg Asp His Asp Leu Glu Trp Met Ser Met Ser Gly Ala Pro Leu
                725                 730                 735

Ser Thr Pro Pro Gly Val Ala Asp Asp Gly Thr Ile Gly Gln Ile Leu
            740                 745                 750

Glu Leu Leu Gly Arg Ala Met Glu Pro Phe Tyr Gly Phe Arg Ser Leu
        755                 760                 765

Ala Ala Ser Lys Asn Lys Phe His Pro Glu His His Gly Trp Tyr Leu
    770                 775                 780
```

```
Cys Tyr Arg Asp Glu Leu Ser Leu Pro Ser Ile Gly Leu Ala Val Ala
785                 790                 795                 800

Ala Cys Tyr Leu Asn Glu Phe Pro Leu Pro Asn Trp Leu Lys Lys Thr
                805                 810                 815

Ala Thr Ser Ala Pro Ser His Ser
            820


<210> 359
<211> 386
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(363)
<223> RXN00738

<400> 359
tgt caa gag gag acg gat ggc ttt ttt gat ttt ggg cgc gat atg cgg   48
Cys Gln Glu Glu Thr Asp Gly Phe Phe Asp Phe Gly Arg Asp Met Arg
  1               5                  10                  15

ccc ggt gag cgc cgg tcg tat ggc act ttg ctt aac gac gcc acg acg   96
Pro Gly Glu Arg Arg Ser Tyr Gly Thr Leu Leu Asn Asp Ala Thr Thr
             20                  25                  30

cag gtg tcg cac atc ctc ggc aat gcc ttc acc cga tct ggg ctc aac   144
Gln Val Ser His Ile Leu Gly Asn Ala Phe Thr Arg Ser Gly Leu Asn
         35                  40                  45

gct gag tac gcg aat ctt tat ggt cag gcg ttg gtg ggc atg gtg tcg   192
Ala Glu Tyr Ala Asn Leu Tyr Gly Gln Ala Leu Val Gly Met Val Ser
     50                  55                  60

atg acg gcg caa tgg tgg ttg gat gag cgc act ccg ccg aag gaa gaa   240
Met Thr Ala Gln Trp Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu
 65                  70                  75                  80

gtt gcc gca cat att gtt aat ctt tgt tgg aat ggt ttg acg ggg atg   288
Val Ala Ala His Ile Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met
                85                  90                  95

gaa gcc gat ccg aag tta act ccc atc agt tct gct gag ggt gcg att   336
Glu Ala Asp Pro Lys Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile
            100                 105                 110

ttt ggt caa gaa aag gag agt gaa gcg tgacacctat gctcgcgggg         383
Phe Gly Gln Glu Lys Glu Ser Glu Ala
        115                 120

ctg                                                               386


<210> 360
<211> 121
<212> PRT
<213> Corynebacterium glutamicum
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<400> 360
Cys Gln Glu Glu Thr Asp Gly Phe Phe Asp Phe Gly Arg Asp Met Arg
1 5 10 15

Pro Gly Glu Arg Arg Ser Tyr Gly Thr Leu Leu Asn Asp Ala Thr Thr
20 25 30

Gln Val Ser His Ile Leu Gly Asn Ala Phe Thr Arg Ser Gly Leu Asn
35 40 45

Ala Glu Tyr Ala Asn Leu Tyr Gly Gln Ala Leu Val Gly Met Val Ser
50 55 60

Met Thr Ala Gln Trp Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu
65 70 75 80

Val Ala Ala His Ile Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met
85 90 95

Glu Ala Asp Pro Lys Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile
100 105 110

Phe Gly Gln Glu Lys Glu Ser Glu Ala
115 120

<210> 361
<211> 388
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (78)..(365)
<223> FRXA00738

<400> 361
catgccccta ttagacggat ggctttttg attttgggcg cgatatgcgg cccggtgagc 60

gccggtcgta tggcactttg ctt aac gac gcc acg acg cag gtg tcg cac atc 113
Leu Leu Asn Asp Ala Thr Thr Gln Val Ser His Ile
1 5 10

ctc ggc aat gcc ttc acc cga tct ggg ctc aac gct gag tac gcg aat 161
Leu Gly Asn Ala Phe Thr Arg Ser Gly Leu Asn Ala Glu Tyr Ala Asn
15 20 25

ctt tat ggt cag gcg ttg gtg ggc atg gtg tcg atg acg gcg caa tgg 209
Leu Tyr Gly Gln Ala Leu Val Gly Met Val Ser Met Thr Ala Gln Trp
30 35 40

tgg ttg gat gag cgc act ccg ccg aag gaa gaa gtt gcc gca cat att 257
Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu Val Ala Ala His Ile
45 50 55 60

gtt aat ctt tgt tgg aat ggt ttg acg ggg atg gaa gcc gat ccg aag 305
Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met Glu Ala Asp Pro Lys
65 70 75

tta act ccc atc agt tct gct gag ggt gcg att ttt ggt caa gaa aag 353
Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile Phe Gly Gln Glu Lys

```
            80                  85                  90

gag agt gaa gcg tgacacctat gctcgcgggg ctg                          388
Glu Ser Glu Ala
         95


<210> 362
<211> 96
<212> PRT
<213> Corynebacterium glutamicum

<400> 362
Leu Leu Asn Asp Ala Thr Thr Gln Val Ser His Ile Leu Gly Asn Ala
  1               5                  10                  15

Phe Thr Arg Ser Gly Leu Asn Ala Glu Tyr Ala Asn Leu Tyr Gly Gln
             20                  25                  30

Ala Leu Val Gly Met Val Ser Met Thr Ala Gln Trp Trp Leu Asp Glu
         35                  40                  45

Arg Thr Pro Pro Lys Glu Glu Val Ala Ala His Ile Val Asn Leu Cys
     50                  55                  60

Trp Asn Gly Leu Thr Gly Met Glu Ala Asp Pro Lys Leu Thr Pro Ile
 65                  70                  75                  80

Ser Ser Ala Glu Gly Ala Ile Phe Gly Gln Glu Lys Glu Ser Glu Ala
                 85                  90                  95


<210> 363
<211> 561
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(538)
<223> RXN00750

<400> 363
tttaaacaaa agcgataaca atgaaccgat ggtgtctacg acagaaccga ctcccccacc 60

cactaacacc ccaccagaaa ataacacctc gaccgaacct atg gac tgg tcg atc   115
                                              Met Asp Trp Ser Ile
                                                1               5

att att aat gtg ctt gcc gtt gct act gtc gtg ata ctc acc ctt atc   163
Ile Ile Asn Val Leu Ala Val Ala Thr Val Val Ile Leu Thr Leu Ile
            10                  15                  20

atc gca gct gca tta tat agg ggt ttc aca cgc aac aaa ata aaa aaa   211
Ile Ala Ala Ala Leu Tyr Arg Gly Phe Thr Arg Asn Lys Ile Lys Lys
        25                  30                  35

ctt gaa gct ata cga gaa gcc cag caa cac gaa cgc gac aat ccc act   259
```

```
Leu Glu Ala Ile Arg Glu Ala Gln Gln His Glu Arg Asp Asn Pro Thr
         40                  45                  50

atc cgc att gct gat ctt cgc ggc atc atg gat act cac cac tac atc   307
Ile Arg Ile Ala Asp Leu Arg Gly Ile Met Asp Thr His His Tyr Ile
     55                  60                  65

tac acc gac gtc atg gtt aca cgt gca cat gaa ctc atg att act gca   355
Tyr Thr Asp Val Met Val Thr Arg Ala His Glu Leu Met Ile Thr Ala
 70                  75                  80                  85

ccc gca ttc ttt gat gtc act ctc ccc gaa gca gtg ctc tac gaa gat   403
Pro Ala Phe Phe Asp Val Thr Leu Pro Glu Ala Val Leu Tyr Glu Asp
                 90                  95                 100

act aaa cgt gct gct cat gat gcc ctt aac ggc tat aaa gac acc act   451
Thr Lys Arg Ala Ala His Asp Ala Leu Asn Gly Tyr Lys Asp Thr Thr
            105                 110                 115

gtc gct agt gca gag aag atc atg ctt gta gat gca gtc acc gca gca   499
Val Ala Ser Ala Glu Lys Ile Met Leu Val Asp Ala Val Thr Ala Ala
        120                 125                 130

tgg act ctc tat tcc aca aaa gca aac acc gga tcc acg tgatccgaga   548
Trp Thr Leu Tyr Ser Thr Lys Ala Asn Thr Gly Ser Thr
    135                 140                 145

gccgagtacc gct                                                  561
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CONFIDENTIAL

<210> 364
<211> 146
<212> PRT
<213> Corynebacterium glutamicum

<400> 364

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Met Asp Trp Ser Ile Ile Ile Asn Val Leu Ala Val Ala Thr Val Val
  1               5                  10                  15

Ile Leu Thr Leu Ile Ile Ala Ala Ala Leu Tyr Arg Gly Phe Thr Arg
             20                  25                  30

Asn Lys Ile Lys Lys Leu Glu Ala Ile Arg Glu Ala Gln Gln His Glu
         35                  40                  45

Arg Asp Asn Pro Thr Ile Arg Ile Ala Asp Leu Arg Gly Ile Met Asp
     50                  55                  60

Thr His His Tyr Ile Tyr Thr Asp Val Met Val Thr Arg Ala His Glu
 65                  70                  75                  80

Leu Met Ile Thr Ala Pro Ala Phe Phe Asp Val Thr Leu Pro Glu Ala
                 85                  90                  95

Val Leu Tyr Glu Asp Thr Lys Arg Ala Ala His Asp Ala Leu Asn Gly
            100                 105                 110

Tyr Lys Asp Thr Thr Val Ala Ser Ala Glu Lys Ile Met Leu Val Asp
        115                 120                 125

Ala Val Thr Ala Ala Trp Thr Leu Tyr Ser Thr Lys Ala Asn Thr Gly
```

```
    130                 135                 140

Ser Thr
145


<210> 365
<211> 561
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(538)
<223> FRXA00750

<400> 365
tttaaacaaa agcgataaca atgaaccgat ggtgtctacg acagaaccga ctcccccacc 60

cactaacacc ccaccagaaa ataacacctc gaccgaacct atg gac tgg tcg atc   115
                                              Met Asp Trp Ser Ile
                                                1               5

att att aat gtg ctt gcc gtt gct act gtc gtg ata ctc acc ctt atc   163
Ile Ile Asn Val Leu Ala Val Ala Thr Val Val Ile Leu Thr Leu Ile
                10                  15                  20

atc gca gct gca tta tat agg ggt ttc aca cgc aac aaa ata aaa aaa   211
Ile Ala Ala Ala Leu Tyr Arg Gly Phe Thr Arg Asn Lys Ile Lys Lys
            25                  30                  35

ctt gaa gct ata cga gaa gcc cag caa cac gaa cgc gac aat ccc act   259
Leu Glu Ala Ile Arg Glu Ala Gln Gln His Glu Arg Asp Asn Pro Thr
        40                  45                  50

atc cgc att gct gat ctt cgc ggc atc atg gat act cac cac tac atc   307
Ile Arg Ile Ala Asp Leu Arg Gly Ile Met Asp Thr His His Tyr Ile
    55                  60                  65

tac acc gac gtc atg gtt aca cgt gca cat gaa ctc atg att act gca   355
Tyr Thr Asp Val Met Val Thr Arg Ala His Glu Leu Met Ile Thr Ala
70                  75                  80                  85

ccc gca ttc ttt gat gtc act ctc ccc gaa gca gtg ctc tac gaa gat   403
Pro Ala Phe Phe Asp Val Thr Leu Pro Glu Ala Val Leu Tyr Glu Asp
                90                  95                 100

act aaa cgt gct gct cat gat gcc ctt aac ggc tat aaa gac acc act   451
Thr Lys Arg Ala Ala His Asp Ala Leu Asn Gly Tyr Lys Asp Thr Thr
            105                 110                 115

gtc gct agt gca gag aag atc atg ctt gta gat gca gtc acc gca gca   499
Val Ala Ser Ala Glu Lys Ile Met Leu Val Asp Ala Val Thr Ala Ala
        120                 125                 130

tgg act ctc tat tcc aca aaa gca aac acc gga tcc acg tgatccgaga    548
Trp Thr Leu Tyr Ser Thr Lys Ala Asn Thr Gly Ser Thr
    135                 140                 145

gccgagtacc gct                                                   561
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<210> 366
<211> 146
<212> PRT
<213> Corynebacterium glutamicum

<400> 366
Met Asp Trp Ser Ile Ile Ile Asn Val Leu Ala Val Ala Thr Val Val
1 5 10 15

Ile Leu Thr Leu Ile Ile Ala Ala Ala Leu Tyr Arg Gly Phe Thr Arg
20 25 30

Asn Lys Ile Lys Lys Leu Glu Ala Ile Arg Glu Ala Gln Gln His Glu
35 40 45

Arg Asp Asn Pro Thr Ile Arg Ile Ala Asp Leu Arg Gly Ile Met Asp
50 55 60

Thr His His Tyr Ile Tyr Thr Asp Val Met Val Thr Arg Ala His Glu
65 70 75 80

Leu Met Ile Thr Ala Pro Ala Phe Phe Asp Val Thr Leu Pro Glu Ala
85 90 95

Val Leu Tyr Glu Asp Thr Lys Arg Ala Ala His Asp Ala Leu Asn Gly
100 105 110

Tyr Lys Asp Thr Thr Val Ala Ser Ala Glu Lys Ile Met Leu Val Asp
115 120 125

Ala Val Thr Ala Ala Trp Thr Leu Tyr Ser Thr Lys Ala Asn Thr Gly
130 135 140

Ser Thr
145

<210> 367
<211> 999
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(976)
<223> RXN00762

<400> 367
gatgctgcga tggtcacaag tcgttttctg gatttttcca catctatatc tttaccccac 60

gttcctgcaa gagattcaaa cttggggcta acctggggac atg aat act tcc gat 115
Met Asn Thr Ser Asp
1 5

cgt att aaa agc act caa atc gcg ctg gat cgt gac ctc cgt gag cag 163
Arg Ile Lys Ser Thr Gln Ile Ala Leu Asp Arg Asp Leu Arg Glu Gln
10 15 20

gca cta ttg ctt ttg aag gag gtt cgc gca gtt gat ggc gtg gat gct 211
Ala Leu Leu Leu Leu Lys Glu Val Arg Ala Val Asp Gly Val Asp Ala

```
                25                  30                  35

tta tca gaa caa ttt gtc cgt ggg ctt gca gaa ccc gga ctt gtt cac   259
Leu Ser Glu Gln Phe Val Arg Gly Leu Ala Glu Pro Gly Leu Val His
         40                  45                  50

tcc cat tta ata gtc acg ctc aat agc gag ctg gtt ggc ctc gcg gcc   307
Ser His Leu Ile Val Thr Leu Asn Ser Glu Leu Val Gly Leu Ala Ala
     55                  60                  65

gcg gat gag gaa acc acg gaa ctg gct gtc cac ccg gcg cac agg cgt   355
Ala Asp Glu Glu Thr Thr Glu Leu Ala Val His Pro Ala His Arg Arg
 70                  75                  80                  85

cag gga atc ggt aag gcg ctt atc gac gcc gcc ccc acc tca tca atc   403
Gln Gly Ile Gly Lys Ala Leu Ile Asp Ala Ala Pro Thr Ser Ser Ile
                 90                  95                 100

tgg gcg cat gga aat aca gca ggt gca caa gcg ttg gca tcc acc ctg   451
Trp Ala His Gly Asn Thr Ala Gly Ala Gln Ala Leu Ala Ser Thr Leu
            105                 110                 115

cgt atg aag aag act cgc gag ctt ctg gtg atg gag att tcc gac agg   499
Arg Met Lys Lys Thr Arg Glu Leu Leu Val Met Glu Ile Ser Asp Arg
        120                 125                 130

gcg ctc gat gac tct gca gca tac aaa gat cca gat gga att aca cac   547
Ala Leu Asp Asp Ser Ala Ala Tyr Lys Asp Pro Asp Gly Ile Thr His
    135                 140                 145

agt agt ttg gcg aat gcc cct gtg gag aaa tca gta gct gag gct aaa   595
Ser Ser Leu Ala Asn Ala Pro Val Glu Lys Ser Val Ala Glu Ala Lys
150                 155                 160                 165

tgg ctt caa tcc aac aac gaa gca ttc gac tgg cat ccc gag cag ggc   643
Trp Leu Gln Ser Asn Asn Glu Ala Phe Asp Trp His Pro Glu Gln Gly
                170                 175                 180

gga tgg aca act cat cgg ttg gcg cag gct cag aaa gcc gat tgg tac   691
Gly Trp Thr Thr His Arg Leu Ala Gln Ala Gln Lys Ala Asp Trp Tyr
            185                 190                 195

aag gac tct gac gtg tta ttc ctc tgg gac ggc gaa gag atc gtt ggc   739
Lys Asp Ser Asp Val Leu Phe Leu Trp Asp Gly Glu Glu Ile Val Gly
        200                 205                 210

ttc cac tgg gta aag cag cac agt cca gaa tta caa gag att tac gta   787
Phe His Trp Val Lys Gln His Ser Pro Glu Leu Gln Glu Ile Tyr Val
    215                 220                 225

gtt ggc ctt tct tca gcc tac cgt ggt cgc ggc ttg gga gat ccg ctt   835
Val Gly Leu Ser Ser Ala Tyr Arg Gly Arg Gly Leu Gly Asp Pro Leu
230                 235                 240                 245

gtt cgc ctc gga ctg cat cac atg agg gct cat ggt gct cga aaa gtg   883
Val Arg Leu Gly Leu His His Met Arg Ala His Gly Ala Arg Lys Val
                250                 255                 260

att ctt tat gtg gaa gct ggc aac act ccg gca gtc gcg gca tac gaa   931
Ile Leu Tyr Val Glu Ala Gly Asn Thr Pro Ala Val Ala Ala Tyr Glu
            265                 270                 275
```

```
aaa ctg gga ttc act gtc gcg gaa agc cac gta gtt tac gaa aag       976
Lys Leu Gly Phe Thr Val Ala Glu Ser His Val Val Tyr Glu Lys
        280                 285                 290

taaaaaagag acttgctaaa aac                                        999


<210> 368
<211> 292
<212> PRT
<213> Corynebacterium glutamicum

<400> 368
Met Asn Thr Ser Asp Arg Ile Lys Ser Thr Gln Ile Ala Leu Asp Arg
  1               5                  10                  15

Asp Leu Arg Glu Gln Ala Leu Leu Leu Leu Lys Glu Val Arg Ala Val
             20                  25                  30

Asp Gly Val Asp Ala Leu Ser Glu Gln Phe Val Arg Gly Leu Ala Glu
         35                  40                  45

Pro Gly Leu Val His Ser His Leu Ile Val Thr Leu Asn Ser Glu Leu
     50                  55                  60

Val Gly Leu Ala Ala Ala Asp Glu Glu Thr Thr Glu Leu Ala Val His
 65                  70                  75                  80

Pro Ala His Arg Arg Gln Gly Ile Gly Lys Ala Leu Ile Asp Ala Ala
                 85                  90                  95

Pro Thr Ser Ser Ile Trp Ala His Gly Asn Thr Ala Gly Ala Gln Ala
            100                 105                 110

Leu Ala Ser Thr Leu Arg Met Lys Lys Thr Arg Glu Leu Leu Val Met
        115                 120                 125

Glu Ile Ser Asp Arg Ala Leu Asp Asp Ser Ala Ala Tyr Lys Asp Pro
    130                 135                 140

Asp Gly Ile Thr His Ser Ser Leu Ala Asn Ala Pro Val Glu Lys Ser
145                 150                 155                 160

Val Ala Glu Ala Lys Trp Leu Gln Ser Asn Asn Glu Ala Phe Asp Trp
                165                 170                 175

His Pro Glu Gln Gly Gly Trp Thr Thr His Arg Leu Ala Gln Ala Gln
            180                 185                 190

Lys Ala Asp Trp Tyr Lys Asp Ser Asp Val Leu Phe Leu Trp Asp Gly
        195                 200                 205

Glu Glu Ile Val Gly Phe His Trp Val Lys Gln His Ser Pro Glu Leu
    210                 215                 220

Gln Glu Ile Tyr Val Val Gly Leu Ser Ser Ala Tyr Arg Gly Arg Gly
225                 230                 235                 240

Leu Gly Asp Pro Leu Val Arg Leu Gly Leu His His Met Arg Ala His
                245                 250                 255
```

```
Gly Ala Arg Lys Val Ile Leu Tyr Val Glu Ala Gly Asn Thr Pro Ala
            260                 265                 270

Val Ala Ala Tyr Glu Lys Leu Gly Phe Thr Val Ala Glu Ser His Val
        275                 280                 285

Val Tyr Glu Lys
    290


<210> 369
<211> 1242
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1219)
<223> RXN00768

<400> 369
tcaagcgcca taacgcctga ttatgcacgg ttaaggcgca tctcgctcac tggtgctaac 60

cacttgcgct tttggaagga ataacccttc ctgtcagatt gtg ggt act atc gaa  115
                                          Val Gly Thr Ile Glu
                                            1               5

gac gtg gct aac gaa caa atc gag gtc gcg aac aac act gat cag att  163
Asp Val Ala Asn Glu Gln Ile Glu Val Ala Asn Asn Thr Asp Gln Ile
                10                  15                  20

cct gca gga tac aag tcc cct ctt ctt tct aga agt ggt gcg gca gaa  211
Pro Ala Gly Tyr Lys Ser Pro Leu Leu Ser Arg Ser Gly Ala Ala Glu
            25                  30                  35

gcg cag ggc gct gct gct caa gca ggt act gaa ggt gtc gcg tgg cat  259
Ala Gln Gly Ala Ala Ala Gln Ala Gly Thr Glu Gly Val Ala Trp His
        40                  45                  50

tac ggt tcc cct ctc gtc gag caa cgc atc ttc gaa act ggc acg ggc  307
Tyr Gly Ser Pro Leu Val Glu Gln Arg Ile Phe Glu Thr Gly Thr Gly
    55                  60                  65

tta gtt gac cgt tct aat cgc aag gtg atc aaa gtc gaa ggg cct gat  355
Leu Val Asp Arg Ser Asn Arg Lys Val Ile Lys Val Glu Gly Pro Asp
70                  75                  80                  85

gcc ccc acg ttc ctc aat aat att ttg tcc caa aag gtt gat tcc gtt  403
Ala Pro Thr Phe Leu Asn Asn Ile Leu Ser Gln Lys Val Asp Ser Val
                90                  95                  100

gaa aac ggc ttt act gcc ggt gcc ctg gat ttg gat gcg cag ggt cgt  451
Glu Asn Gly Phe Thr Ala Gly Ala Leu Asp Leu Asp Ala Gln Gly Arg
            105                 110                 115

att caa cac aca atg cag gta act gtc gtc gat ggg gtt ttc tac ctc  499
Ile Gln His Thr Met Gln Val Thr Val Val Asp Gly Val Phe Tyr Leu
        120                 125                 130

gac acg tcc gcg gcg gag ttt gat acc ctc atc ggt ttc ttg acc aag  547
```

```
Asp Thr Ser Ala Ala Glu Phe Asp Thr Leu Ile Gly Phe Leu Thr Lys
    135                 140                 145

atg att ttc tgg tcg gaa gtc acc gtc cag gaa gcc gat ctg gcg atc   595
Met Ile Phe Trp Ser Glu Val Thr Val Gln Glu Ala Asp Leu Ala Ile
150                 155                 160                 165

atc act ctg ctc ggc cag gaa att gcc ctt ccg gac gcg gtc ttt gcc   643
Ile Thr Leu Leu Gly Gln Glu Ile Ala Leu Pro Asp Ala Val Phe Ala
                170                 175                 180

cgt agg gtc gat tgg aat ggg cca tcg cgt atc gac gtc gcc atc cgg   691
Arg Arg Val Asp Trp Asn Gly Pro Ser Arg Ile Asp Val Ala Ile Arg
            185                 190                 195

cgt gaa aac ctg gag gag ggc gtc gac aag ctc tta gaa gct ggc gca   739
Arg Glu Asn Leu Glu Glu Gly Val Asp Lys Leu Leu Glu Ala Gly Ala
        200                 205                 210

aag ctc acc ggt ctc atg gct tac acg gcc gag cgc gtg aag gcg ttg   787
Lys Leu Thr Gly Leu Met Ala Tyr Thr Ala Glu Arg Val Lys Ala Leu
    215                 220                 225

gag ccc gct gcg ggc gtg gat ttg gat gat aag acc att ccc cat gaa   835
Glu Pro Ala Ala Gly Val Asp Leu Asp Asp Lys Thr Ile Pro His Glu
230                 235                 240                 245

atc ccc cat tgg att ggc cgt ggc gaa cat tta ggc gct gtg cat ttg   883
Ile Pro His Trp Ile Gly Arg Gly Glu His Leu Gly Ala Val His Leu
                250                 255                 260

acc aag ggt tgc tac cgc ggg cag gaa act gtc gcg cgc gtt gat aat   931
Thr Lys Gly Cys Tyr Arg Gly Gln Glu Thr Val Ala Arg Val Asp Asn
            265                 270                 275

ctt ggg cgt tcc ccg cgc gtg ctg gtt ctg ctt cat ctt gac ggt tcc   979
Leu Gly Arg Ser Pro Arg Val Leu Val Leu Leu His Leu Asp Gly Ser
        280                 285                 290

gca ccg ctg gat cct gtg act ggc gct gaa atc aag gcc ggt gcg cgc   1027
Ala Pro Leu Asp Pro Val Thr Gly Ala Glu Ile Lys Ala Gly Ala Arg
    295                 300                 305

acc gtt ggt cgt ctg ggc acc gtt gtc cat gac gcc gat tac ggg ccg   1075
Thr Val Gly Arg Leu Gly Thr Val Val His Asp Ala Asp Tyr Gly Pro
310                 315                 320                 325

atc gct ctc ggg ctg gtt aag cgc agc gct ttg gat aaa gaa ctt cac   1123
Ile Ala Leu Gly Leu Val Lys Arg Ser Ala Leu Asp Lys Glu Leu His
                330                 335                 340

atc gat gat gtc tct gta aac gtc gac cgc gat ctg ctt cct gcg gag   1171
Ile Asp Asp Val Ser Val Asn Val Asp Arg Asp Leu Leu Pro Ala Glu
            345                 350                 355

gaa agt gaa caa cgc gga cgc gca gcg atc aat aag ctc aag ggt ctt   1219
Glu Ser Glu Gln Arg Gly Arg Ala Ala Ile Asn Lys Leu Lys Gly Leu
        360                 365                 370

taactaaaac gatttatagc gaa                                        1242
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<210> 370
<211> 373
<212> PRT
<213> Corynebacterium glutamicum

<400> 370
Val Gly Thr Ile Glu Asp Val Ala Asn Glu Gln Ile Glu Val Ala Asn
1 5 10 15

Asn Thr Asp Gln Ile Pro Ala Gly Tyr Lys Ser Pro Leu Leu Ser Arg
20 25 30

Ser Gly Ala Ala Glu Ala Gln Gly Ala Ala Ala Gln Ala Gly Thr Glu
35 40 45

Gly Val Ala Trp His Tyr Gly Ser Pro Leu Val Glu Gln Arg Ile Phe
50 55 60

Glu Thr Gly Thr Gly Leu Val Asp Arg Ser Asn Arg Lys Val Ile Lys
65 70 75 80

Val Glu Gly Pro Asp Ala Pro Thr Phe Leu Asn Asn Ile Leu Ser Gln
85 90 95

Lys Val Asp Ser Val Glu Asn Gly Phe Thr Ala Gly Ala Leu Asp Leu
100 105 110

Asp Ala Gln Gly Arg Ile Gln His Thr Met Gln Val Thr Val Val Asp
115 120 125

Gly Val Phe Tyr Leu Asp Thr Ser Ala Ala Glu Phe Asp Thr Leu Ile
130 135 140

Gly Phe Leu Thr Lys Met Ile Phe Trp Ser Glu Val Thr Val Gln Glu
145 150 155 160

Ala Asp Leu Ala Ile Ile Thr Leu Leu Gly Gln Glu Ile Ala Leu Pro
165 170 175

Asp Ala Val Phe Ala Arg Arg Val Asp Trp Asn Gly Pro Ser Arg Ile
180 185 190

Asp Val Ala Ile Arg Arg Glu Asn Leu Glu Glu Gly Val Asp Lys Leu
195 200 205

Leu Glu Ala Gly Ala Lys Leu Thr Gly Leu Met Ala Tyr Thr Ala Glu
210 215 220

Arg Val Lys Ala Leu Glu Pro Ala Ala Gly Val Asp Leu Asp Asp Lys
225 230 235 240

Thr Ile Pro His Glu Ile Pro His Trp Ile Gly Arg Gly Glu His Leu
245 250 255

Gly Ala Val His Leu Thr Lys Gly Cys Tyr Arg Gly Gln Glu Thr Val
260 265 270

Ala Arg Val Asp Asn Leu Gly Arg Ser Pro Arg Val Leu Val Leu Leu
275 280 285

```
His Leu Asp Gly Ser Ala Pro Leu Asp Pro Val Thr Gly Ala Glu Ile
    290                 295                 300

Lys Ala Gly Ala Arg Thr Val Gly Arg Leu Gly Thr Val Val His Asp
305                 310                 315                 320

Ala Asp Tyr Gly Pro Ile Ala Leu Gly Leu Val Lys Arg Ser Ala Leu
                325                 330                 335

Asp Lys Glu Leu His Ile Asp Asp Val Ser Val Asn Val Asp Arg Asp
            340                 345                 350

Leu Leu Pro Ala Glu Glu Ser Glu Gln Arg Gly Arg Ala Ala Ile Asn
        355                 360                 365

Lys Leu Lys Gly Leu
    370
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<210> 371
<211> 567
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(544)
<223> FRXA00768

<400> 371

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gacgtcgcca tccggcgtga aaacctggag gagggcgtcg acaagctctt agaagctggc 60

gcaaagctca ccggtctcat ggcttacacg gcccgagcgc gtg aag gcg ttg gag   115
                                            Val Lys Ala Leu Glu
                                              1               5

ccc gct gcg ggc gtg gat ttg gat gat aag acc att ccc cat gaa atc   163
Pro Ala Ala Gly Val Asp Leu Asp Asp Lys Thr Ile Pro His Glu Ile
                 10                  15                  20

ccc cat tgg att ggc cgt ggc gaa cat tta ggc gct gtg cat ttg acc   211
Pro His Trp Ile Gly Arg Gly Glu His Leu Gly Ala Val His Leu Thr
             25                  30                  35

aag ggt tgc tac cgc ggg cag gaa act gtc gcg cgc gtt gat aat ctt   259
Lys Gly Cys Tyr Arg Gly Gln Glu Thr Val Ala Arg Val Asp Asn Leu
         40                  45                  50

ggg cgt tcc ccg cgc gtg ctg gtt ctg ctt cat ctt gac ggt tcc gca   307
Gly Arg Ser Pro Arg Val Leu Val Leu Leu His Leu Asp Gly Ser Ala
     55                  60                  65

ccg ctg gat cct gtg act ggc gct gaa atc aag gcc ggt gcg cgc acc   355
Pro Leu Asp Pro Val Thr Gly Ala Glu Ile Lys Ala Gly Ala Arg Thr
 70                  75                  80                  85

gtt ggt cgt ctg ggc acc gtt gtc cat gac gcc gat tac ggg ccg atc   403
Val Gly Arg Leu Gly Thr Val Val His Asp Ala Asp Tyr Gly Pro Ile
                 90                  95                 100

gct ctc ggg ctg gtt aag cgc agc gct ttg gat aaa gaa ctt cac atc   451
```

```
Ala Leu Gly Leu Val Lys Arg Ser Ala Leu Asp Lys Glu Leu His Ile
            105                 110                 115

gat gat gtc tct gta aac gtc gac cgc gat ctg ctt cct gcg gag gaa   499
Asp Asp Val Ser Val Asn Val Asp Arg Asp Leu Leu Pro Ala Glu Glu
        120                 125                 130

agt gaa caa cgc gga cgc gca gcg atc aat aag ctc aag ggt ctt       544
Ser Glu Gln Arg Gly Arg Ala Ala Ile Asn Lys Leu Lys Gly Leu
    135                 140                 145

taactaaaac gatttatagc gaa                                        567


<210> 372
<211> 148
<212> PRT
<213> Corynebacterium glutamicum

<400> 372
Val Lys Ala Leu Glu Pro Ala Ala Gly Val Asp Leu Asp Asp Lys Thr
  1               5                  10                  15

Ile Pro His Glu Ile Pro His Trp Ile Gly Arg Gly Glu His Leu Gly
             20                  25                  30

Ala Val His Leu Thr Lys Gly Cys Tyr Arg Gly Gln Glu Thr Val Ala
         35                  40                  45

Arg Val Asp Asn Leu Gly Arg Ser Pro Arg Val Leu Val Leu Leu His
     50                  55                  60

Leu Asp Gly Ser Ala Pro Leu Asp Pro Val Thr Gly Ala Glu Ile Lys
 65                  70                  75                  80

Ala Gly Ala Arg Thr Val Gly Arg Leu Gly Thr Val Val His Asp Ala
                 85                  90                  95

Asp Tyr Gly Pro Ile Ala Leu Gly Leu Val Lys Arg Ser Ala Leu Asp
            100                 105                 110

Lys Glu Leu His Ile Asp Asp Val Ser Val Asn Val Asp Arg Asp Leu
        115                 120                 125

Leu Pro Ala Glu Glu Ser Glu Gln Arg Gly Arg Ala Ala Ile Asn Lys
    130                 135                 140

Leu Lys Gly Leu
145


<210> 373
<211> 837
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(814)
<223> FRXA00767
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<400> 373
tcaagcgcca taacgcctga ttatgcacgg ttaaggcgca tctcgctcac tggtgctaac 60

cacttgcgct tttggaagga ataacccttc ctgtcagatt gtg ggt act atc gaa 115
Val Gly Thr Ile Glu
1 5

gac gtg gct aac gaa caa atc gag gtc gcg aac aac act gat cag att 163
Asp Val Ala Asn Glu Gln Ile Glu Val Ala Asn Asn Thr Asp Gln Ile
10 15 20

cct gca gga tac aag tcc cct ctt ctt tct aga agt ggt gcg gca gaa 211
Pro Ala Gly Tyr Lys Ser Pro Leu Leu Ser Arg Ser Gly Ala Ala Glu
25 30 35

gcg cag ggc gct gct gct caa gca ggt act gaa ggt gtc gcg tgg cat 259
Ala Gln Gly Ala Ala Ala Gln Ala Gly Thr Glu Gly Val Ala Trp His
40 45 50

tac ggt tcc cct ctc gtc gag caa cgc atc ttc gaa act ggc acg ggc 307
Tyr Gly Ser Pro Leu Val Glu Gln Arg Ile Phe Glu Thr Gly Thr Gly
55 60 65

tta gtt gac cgt tct aat cgc aag gtg atc aaa gtc gaa ggg cct gat 355
Leu Val Asp Arg Ser Asn Arg Lys Val Ile Lys Val Glu Gly Pro Asp
70 75 80 85

gcc ccc acg ttc ctc aat aat att ttg tcc caa aag gtt gat tcc gtt 403
Ala Pro Thr Phe Leu Asn Asn Ile Leu Ser Gln Lys Val Asp Ser Val
90 95 100

gaa aac ggc ttt act gcc ggt gcc ctg gat ttg gat gcg cag ggt cgt 451
Glu Asn Gly Phe Thr Ala Gly Ala Leu Asp Leu Asp Ala Gln Gly Arg
105 110 115

att caa cac aca atg cag gta act gtc gtc gat ggg gtt ttc tac ctc 499
Ile Gln His Thr Met Gln Val Thr Val Val Asp Gly Val Phe Tyr Leu
120 125 130

gac acg tcc gcg gcg gag ttt gat acc ctc atc ggt ttc ttg acc aag 547
Asp Thr Ser Ala Ala Glu Phe Asp Thr Leu Ile Gly Phe Leu Thr Lys
135 140 145

atg att ttc tgg tcg gaa gtc acc gtc cag gaa gcc gat ctg gcg atc 595
Met Ile Phe Trp Ser Glu Val Thr Val Gln Glu Ala Asp Leu Ala Ile
150 155 160 165

atc act ctg ctc ggc cag gaa att gcc ctt ccg gac gcg gtc ttt gcc 643
Ile Thr Leu Leu Gly Gln Glu Ile Ala Leu Pro Asp Ala Val Phe Ala
170 175 180

cgt agg gtc gat tgg aat ggg cca tcg cgt atc gac gtc gcc atc cgg 691
Arg Arg Val Asp Trp Asn Gly Pro Ser Arg Ile Asp Val Ala Ile Arg
185 190 195

cgt gaa aac ctg gag gag ggc gtc gac aag ctc tta gaa gct ggc gca 739
Arg Glu Asn Leu Glu Glu Gly Val Asp Lys Leu Leu Glu Ala Gly Ala
200 205 210

aag ctc acc ggt ctc atg gct tac acg gcc cga gcg cgt gaa ggc gtt 787
Lys Leu Thr Gly Leu Met Ala Tyr Thr Ala Arg Ala Arg Glu Gly Val

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    215                 220                 225

gga gcc cgc tgc ggg cgt gga ttt gga tgataagacc attccccatg          834
Gly Ala Arg Cys Gly Arg Gly Phe Gly
230                 235

aaa                                                                837


<210> 374
<211> 238
<212> PRT
<213> Corynebacterium glutamicum

<400> 374
Val Gly Thr Ile Glu Asp Val Ala Asn Glu Gln Ile Glu Val Ala Asn
  1               5                  10                  15

Asn Thr Asp Gln Ile Pro Ala Gly Tyr Lys Ser Pro Leu Leu Ser Arg
             20                  25                  30

Ser Gly Ala Ala Glu Ala Gln Gly Ala Ala Ala Gln Ala Gly Thr Glu
         35                  40                  45

Gly Val Ala Trp His Tyr Gly Ser Pro Leu Val Glu Gln Arg Ile Phe
     50                  55                  60

Glu Thr Gly Thr Gly Leu Val Asp Arg Ser Asn Arg Lys Val Ile Lys
 65                  70                  75                  80

Val Glu Gly Pro Asp Ala Pro Thr Phe Leu Asn Asn Ile Leu Ser Gln
                 85                  90                  95

Lys Val Asp Ser Val Glu Asn Gly Phe Thr Ala Gly Ala Leu Asp Leu
            100                 105                 110

Asp Ala Gln Gly Arg Ile Gln His Thr Met Gln Val Thr Val Val Asp
        115                 120                 125

Gly Val Phe Tyr Leu Asp Thr Ser Ala Ala Glu Phe Asp Thr Leu Ile
    130                 135                 140

Gly Phe Leu Thr Lys Met Ile Phe Trp Ser Glu Val Thr Val Gln Glu
145                 150                 155                 160

Ala Asp Leu Ala Ile Ile Thr Leu Leu Gly Gln Glu Ile Ala Leu Pro
                165                 170                 175

Asp Ala Val Phe Ala Arg Arg Val Asp Trp Asn Gly Pro Ser Arg Ile
            180                 185                 190

Asp Val Ala Ile Arg Arg Glu Asn Leu Glu Glu Gly Val Asp Lys Leu
        195                 200                 205

Leu Glu Ala Gly Ala Lys Leu Thr Gly Leu Met Ala Tyr Thr Ala Arg
    210                 215                 220

Ala Arg Glu Gly Val Gly Ala Arg Cys Gly Arg Gly Phe Gly
225                 230                 235
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<210> 375
<211> 336
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> RXN00769

<400> 375
ggctattgtg tctatcagga atacagttaa tacatcttga aaagcccatg ggccatccga 60

attcccagga tcggcccgct cactccaagg gggtcaggca atg ggt cgc ggt cgc 115
Met Gly Arg Gly Arg
1 5

gcg aag gca aaa cag acc aaa gtt gct cgc cag ttg aag tac agc tct 163
Ala Lys Ala Lys Gln Thr Lys Val Ala Arg Gln Leu Lys Tyr Ser Ser
10 15 20

cca gac atg gat ctc gat tcg ctg cag cgg gag ctg gct aac cag tct 211
Pro Asp Met Asp Leu Asp Ser Leu Gln Arg Glu Leu Ala Asn Gln Ser
25 30 35

cct agg cgt tcc tac tcc gat acc cct gat gat gag gac cag tac gca 259
Pro Arg Arg Ser Tyr Ser Asp Thr Pro Asp Asp Glu Asp Gln Tyr Ala
40 45 50

gag tat gcg gac tgg gat gag gac gac acc gac aat cgt gcc tac ggc 307
Glu Tyr Ala Asp Trp Asp Glu Asp Asp Thr Asp Asn Arg Ala Tyr Gly
55 60 65

aca aac tgatttcgtg tgtccttaac tct 336
Thr Asn
70

<210> 376
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 376
Met Gly Arg Gly Arg Ala Lys Ala Lys Gln Thr Lys Val Ala Arg Gln
1 5 10 15

Leu Lys Tyr Ser Ser Pro Asp Met Asp Leu Asp Ser Leu Gln Arg Glu
20 25 30

Leu Ala Asn Gln Ser Pro Arg Arg Ser Tyr Ser Asp Thr Pro Asp Asp
35 40 45

Glu Asp Gln Tyr Ala Glu Tyr Ala Asp Trp Asp Glu Asp Asp Thr Asp
50 55 60

Asn Arg Ala Tyr Gly Thr Asn
65 70

<210> 377

<211> 336
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> FRXA00769

<400> 377
ggctattgtg tctatcagga atacagttaa tacatcttga aaagcccatg ggccatccga 60

attcccagga tcggcccgct cactccaagg gggtcaggca atg ggt cgc ggt cgc 115
Met Gly Arg Gly Arg
1 5

gcg aag gca aaa cag acc aaa gtt gct cgc cag ttg aag tac agc tct 163
Ala Lys Ala Lys Gln Thr Lys Val Ala Arg Gln Leu Lys Tyr Ser Ser
10 15 20

cca gac atg gat ctc gat tcg ctg cag cgg gag ctg gct aac cag tct 211
Pro Asp Met Asp Leu Asp Ser Leu Gln Arg Glu Leu Ala Asn Gln Ser
25 30 35

cct agg cgt tcc tac tcc gat acc cct gat gat gag gac cag tac gca 259
Pro Arg Arg Ser Tyr Ser Asp Thr Pro Asp Asp Glu Asp Gln Tyr Ala
40 45 50

gag tat gcg gac tgg gat gag gac gac acc gac aat cgt gcc tac ggc 307
Glu Tyr Ala Asp Trp Asp Glu Asp Asp Thr Asp Asn Arg Ala Tyr Gly
55 60 65

aca aac tgatttcgtg tgtccttaac tct 336
Thr Asn
70

<210> 378
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 378
Met Gly Arg Gly Arg Ala Lys Ala Lys Gln Thr Lys Val Ala Arg Gln
1 5 10 15

Leu Lys Tyr Ser Ser Pro Asp Met Asp Leu Asp Ser Leu Gln Arg Glu
20 25 30

Leu Ala Asn Gln Ser Pro Arg Arg Ser Tyr Ser Asp Thr Pro Asp Asp
35 40 45

Glu Asp Gln Tyr Ala Glu Tyr Ala Asp Trp Asp Glu Asp Asp Thr Asp
50 55 60

Asn Arg Ala Tyr Gly Thr Asn
65 70

<210> 379
<211> 942

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(919)
<223> RXN00771

<400> 379
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tacccctgtt ttggagaatg ctccgagcca ggggtacttt tcttttcctc acacacagta 60

gctgctgaga aaaatgaaga ccttttgtta ggttgggagt atg acc aac cca tac   115
                                            Met Thr Asn Pro Tyr
                                              1               5

gag gcc ttc ata ccg ctc aag cat cgt acg ggg att gaa ccc gag cac   163
Glu Ala Phe Ile Pro Leu Lys His Arg Thr Gly Ile Glu Pro Glu His
                 10                  15                  20

acc ttt tgg gaa tgg gaa aac aaa agg gtt cac att gca agg aga cgt   211
Thr Phe Trp Glu Trp Glu Asn Lys Arg Val His Ile Ala Arg Arg Arg
             25                  30                  35

cga gaa gcg ccc gtc cgc gtt atc gtg gtg cat ggg cta ggc acc cat   259
Arg Glu Ala Pro Val Arg Val Ile Val Val His Gly Leu Gly Thr His
         40                  45                  50

agt ggc gcc ctc tgg ccc ctc gtc gcg gcc att gag ggc gcg gac ctc   307
Ser Gly Ala Leu Trp Pro Leu Val Ala Ala Ile Glu Gly Ala Asp Leu
     55                  60                  65

gcc gcg atc gac ctg cct aaa act ccg ctt tac gac gat tgg ctg cgc   355
Ala Ala Ile Asp Leu Pro Lys Thr Pro Leu Tyr Asp Asp Trp Leu Arg
 70                  75                  80                  85

ctt tta gaa tct ttc atc tcg tcc gaa gac gac ggt cgg cca ctc atc   403
Leu Leu Glu Ser Phe Ile Ser Ser Glu Asp Asp Gly Arg Pro Leu Ile
                 90                  95                 100

ctg atc ggt gca ggc acc gga ggc ttg ctt tgc gca gaa gct gca cac   451
Leu Ile Gly Ala Gly Thr Gly Gly Leu Leu Cys Ala Glu Ala Ala His
            105                 110                 115

cgc aca gga ctg gtc gca cac gtc att gcc acc tgc ctg ctc aac ccc   499
Arg Thr Gly Leu Val Ala His Val Ile Ala Thr Cys Leu Leu Asn Pro
        120                 125                 130

tcc gac cag ccg acg cgc cgg gca ctg ttc agg ttt tca ccg ctg act   547
Ser Asp Gln Pro Thr Arg Arg Ala Leu Phe Arg Phe Ser Pro Leu Thr
    135                 140                 145

cgg ttg atc caa ggc cgc ttg cgc aac cgc gaa att ccc gtg acc aga   595
Arg Leu Ile Gln Gly Arg Leu Arg Asn Arg Glu Ile Pro Val Thr Arg
150                 155                 160                 165

gtg ttg aac ttc agc aaa atc agc cgc agc cca gcc ctg agc aaa ttg   643
Val Leu Asn Phe Ser Lys Ile Ser Arg Ser Pro Ala Leu Ser Lys Leu
                170                 175                 180

tgc gcg gcc gat gaa ttt agc gga gca tcc aaa ata acc tgg ggt ttc   691
Cys Ala Ala Asp Glu Phe Ser Gly Ala Ser Lys Ile Thr Trp Gly Phe
```

```
            185                 190                 195

ctc gcg tca tat gtg caa cac aag gcc aaa ctg ggt gca gtt ccc gtc   739
Leu Ala Ser Tyr Val Gln His Lys Ala Lys Leu Gly Ala Val Pro Val
        200                 205                 210

act ctg atg cac cct gac cac gac ctt ctg act ccc gtt gag ctc agt   787
Thr Leu Met His Pro Asp His Asp Leu Leu Thr Pro Val Glu Leu Ser
    215                 220                 225

ctg cgt acg ctt tcg cgc ctc aaa gcg ccc act gac gtg gtt atg ctc   835
Leu Arg Thr Leu Ser Arg Leu Lys Ala Pro Thr Asp Val Val Met Leu
230                 235                 240                 245

aag gac tgc ggg cat ttt ccc atc gaa gaa ccc ggc ttc acc acc atg   883
Lys Asp Cys Gly His Phe Pro Ile Glu Glu Pro Gly Phe Thr Thr Met
                250                 255                 260

ctc gaa acc gtc aca tca gtt atc gcg cgg aat agt tagcgggcgc        929
Leu Glu Thr Val Thr Ser Val Ile Ala Arg Asn Ser
            265                 270

atgtggttgg gat                                                   942


<210> 380
<211> 273
<212> PRT
<213> Corynebacterium glutamicum

<400> 380
Met Thr Asn Pro Tyr Glu Ala Phe Ile Pro Leu Lys His Arg Thr Gly
  1               5                  10                  15

Ile Glu Pro Glu His Thr Phe Trp Glu Trp Glu Asn Lys Arg Val His
             20                  25                  30

Ile Ala Arg Arg Arg Arg Glu Ala Pro Val Arg Val Ile Val Val His
         35                  40                  45

Gly Leu Gly Thr His Ser Gly Ala Leu Trp Pro Leu Val Ala Ala Ile
     50                  55                  60

Glu Gly Ala Asp Leu Ala Ala Ile Asp Leu Pro Lys Thr Pro Leu Tyr
 65                  70                  75                  80

Asp Asp Trp Leu Arg Leu Leu Glu Ser Phe Ile Ser Ser Glu Asp Asp
                 85                  90                  95

Gly Arg Pro Leu Ile Leu Ile Gly Ala Gly Thr Gly Gly Leu Leu Cys
            100                 105                 110

Ala Glu Ala Ala His Arg Thr Gly Leu Val Ala His Val Ile Ala Thr
        115                 120                 125

Cys Leu Leu Asn Pro Ser Asp Gln Pro Thr Arg Arg Ala Leu Phe Arg
    130                 135                 140

Phe Ser Pro Leu Thr Arg Leu Ile Gln Gly Arg Leu Arg Asn Arg Glu
145                 150                 155                 160
```

```
Ile Pro Val Thr Arg Val Leu Asn Phe Ser Lys Ile Ser Arg Ser Pro
               165                 170                 175

Ala Leu Ser Lys Leu Cys Ala Ala Asp Glu Phe Ser Gly Ala Ser Lys
            180                 185                 190

Ile Thr Trp Gly Phe Leu Ala Ser Tyr Val Gln His Lys Ala Lys Leu
        195                 200                 205

Gly Ala Val Pro Val Thr Leu Met His Pro Asp His Asp Leu Leu Thr
    210                 215                 220

Pro Val Glu Leu Ser Leu Arg Thr Leu Ser Arg Leu Lys Ala Pro Thr
225                 230                 235                 240

Asp Val Val Met Leu Lys Asp Cys Gly His Phe Pro Ile Glu Glu Pro
                245                 250                 255

Gly Phe Thr Thr Met Leu Glu Thr Val Thr Ser Val Ile Ala Arg Asn
            260                 265                 270

Ser
```

0 0 0

```
ctt tta gaa tct ttc atc tcg tcc gaa gac gac ggt cgg cca ctc atc   403
Leu Leu Glu Ser Phe Ile Ser Ser Glu Asp Asp Gly Arg Pro Leu Ile
                 90                  95                 100

ctg atc ggt gca ggc acc gga ggc ttg ctt tgc gca gaa gct gca cac   451
Leu Ile Gly Ala Gly Thr Gly Gly Leu Leu Cys Ala Glu Ala Ala His
            105                 110                 115

cgc aca gga ctg gtc gca cac gtc att gcc acc tgc ctg ctc aac ccc   499
Arg Thr Gly Leu Val Ala His Val Ile Ala Thr Cys Leu Leu Asn Pro
        120                 125                 130

tcc gac cag ccg acg cgc cgg gca ctg ttc agg ttt tca ccg ctg act   547
Ser Asp Gln Pro Thr Arg Arg Ala Leu Phe Arg Phe Ser Pro Leu Thr
    135                 140                 145

cgg ttg atc caa ggc cgc ttg cgc aac cgc gaa att ccc gtg acc aga   595
Arg Leu Ile Gln Gly Arg Leu Arg Asn Arg Glu Ile Pro Val Thr Arg
150                 155                 160                 165

gtg ttg aac ttc agc aaa atc agc cgc agc cca gcc ctg agc aaa ttg   643
Val Leu Asn Phe Ser Lys Ile Ser Arg Ser Pro Ala Leu Ser Lys Leu
                170                 175                 180

tgc gcg gcc gat gaa ttt aac gga gca ttc aaa ata acc tgg ggt ttc   691
Cys Ala Ala Asp Glu Phe Asn Gly Ala Phe Lys Ile Thr Trp Gly Phe
            185                 190                 195

ctc gcg tca tat gtg caa cac aag gcc aaa ctg ggt gca gtt ccc ctc   739
Leu Ala Ser Tyr Val Gln His Lys Ala Lys Leu Gly Ala Val Pro Leu
        200                 205                 210

act ctg atg cac cct gac cac gac ctt ttt gac tcc cgt tgagctcaaa    788
Thr Leu Met His Pro Asp His Asp Leu Phe Asp Ser Arg
    215                 220                 225

tctgcgtacg ctt                                                   801
```

Confidential

<210> 382
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 382

```
Met Thr Asn Pro Tyr Glu Ala Phe Ile Pro Leu Lys His Arg Thr Gly
  1               5                  10                  15

Ile Glu Pro Glu His Thr Phe Trp Glu Trp Glu Asn Lys Arg Val His
             20                  25                  30

Ile Ala Arg Arg Arg Arg Glu Ala Pro Val Arg Val Ile Val Val His
         35                  40                  45

Gly Leu Gly Thr His Ser Gly Ala Leu Trp Pro Leu Val Ala Ala Ile
     50                  55                  60

Glu Gly Ala Asp Leu Ala Ala Ile Asp Leu Pro Lys Thr Pro Leu Tyr
 65                  70                  75                  80
```

```
Asp Asp Trp Leu Arg Leu Leu Glu Ser Phe Ile Ser Ser Glu Asp Asp
                 85                  90                  95

Gly Arg Pro Leu Ile Leu Ile Gly Ala Gly Thr Gly Gly Leu Leu Cys
            100                 105                 110

Ala Glu Ala Ala His Arg Thr Gly Leu Val Ala His Val Ile Ala Thr
        115                 120                 125

Cys Leu Leu Asn Pro Ser Asp Gln Pro Thr Arg Arg Ala Leu Phe Arg
    130                 135                 140

Phe Ser Pro Leu Thr Arg Leu Ile Gln Gly Arg Leu Arg Asn Arg Glu
145                 150                 155                 160

Ile Pro Val Thr Arg Val Leu Asn Phe Ser Lys Ile Ser Arg Ser Pro
                165                 170                 175

Ala Leu Ser Lys Leu Cys Ala Ala Asp Glu Phe Asn Gly Ala Phe Lys
            180                 185                 190

Ile Thr Trp Gly Phe Leu Ala Ser Tyr Val Gln His Lys Ala Lys Leu
        195                 200                 205

Gly Ala Val Pro Leu Thr Leu Met His Pro Asp His Asp Leu Phe Asp
    210                 215                 220

Ser Arg
225
```

Sequence Listing

<210> 383
<211> 680
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(657)
<223> RXN00785

<400> 383

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atc atc gct act ctc ggt gtg acc ttg ctg gtt gag gcc cgc gga tta   48
Ile Ile Ala Thr Leu Gly Val Thr Leu Leu Val Glu Ala Arg Gly Leu
  1               5                  10                  15

ttc ttg acg gtt gcg tcc att ccc att ctg ttt ggt att ttc aca cca   96
Phe Leu Thr Val Ala Ser Ile Pro Ile Leu Phe Gly Ile Phe Thr Pro
             20                  25                  30

ctg act tcg tgg ttt gtg tcc caa caa ggc gtg gct gcg aat gtg tcc   144
Leu Thr Ser Trp Phe Val Ser Gln Gln Gly Val Ala Ala Asn Val Ser
         35                  40                  45

cct ggt gtt tcc gtc acg gaa atc ctc acg gct gtt tat cct ttg gcg   192
Pro Gly Val Ser Val Thr Glu Ile Leu Thr Ala Val Tyr Pro Leu Ala
     50                  55                  60

cag ttg ttc ccc acc ctg atc atg gtc act ttg gtg gcg gca ttg atc   240
Gln Leu Phe Pro Thr Leu Ile Met Val Thr Leu Val Ala Ala Leu Ile
 65                  70                  75                  80
```

```
gct gtg gtg cgg att att ctg ctg cgc agg aac cag gaa tct cgt cag   288
Ala Val Val Arg Ile Ile Leu Leu Arg Arg Asn Gln Glu Ser Arg Gln
                 85                  90                  95

gtt tct ggg gaa ctt acc cgg cgc gcg cag cgt gag gct gag gaa gct   336
Val Ser Gly Glu Leu Thr Arg Arg Ala Gln Arg Glu Ala Glu Glu Ala
            100                 105                 110

aat cag aat gct gct cgt cgt gct cgc gca cag agc acg agg gta caa   384
Asn Gln Asn Ala Ala Arg Arg Ala Arg Ala Gln Ser Thr Arg Val Gln
        115                 120                 125

agt tct aaa aca cgt aac cgt cgc gcg caa cca acc ggc gat acc ggt   432
Ser Ser Lys Thr Arg Asn Arg Arg Ala Gln Pro Thr Gly Asp Thr Gly
    130                 135                 140

tca caa gtc acg gtt gat gag ttg atc agg cgt agc cag gag cgc cgg   480
Ser Gln Val Thr Val Asp Glu Leu Ile Arg Arg Ser Gln Glu Arg Arg
145                 150                 155                 160

caa act gtt gcg cag cgc caa act gag cgc ggt gtg ccg ttt act cca   528
Gln Thr Val Ala Gln Arg Gln Thr Glu Arg Gly Val Pro Phe Thr Pro
                165                 170                 175

act ccg ggt cct gtg gtg gcc ccc aag ccg cgc ccg agc gcc cct gag   576
Thr Pro Gly Pro Val Val Ala Pro Lys Pro Arg Pro Ser Ala Pro Glu
            180                 185                 190

gcg ccg gct cct acg gat gtg ggt gag cgt cga caa gca gcc cct aaa   624
Ala Pro Ala Pro Thr Asp Val Gly Glu Arg Arg Gln Ala Ala Pro Lys
        195                 200                 205

cgc cgc acc tcg ctc gac gat gat ctg tac agc taaaaaatcc ccgctcatgt 677
Arg Arg Thr Ser Leu Asp Asp Asp Leu Tyr Ser
    210                 215

ggc                                                               680
```

<210> 384
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

<400> 384

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Ile Ile Ala Thr Leu Gly Val Thr Leu Leu Val Glu Ala Arg Gly Leu
  1               5                  10                  15

Phe Leu Thr Val Ala Ser Ile Pro Ile Leu Phe Gly Ile Phe Thr Pro
             20                  25                  30

Leu Thr Ser Trp Phe Val Ser Gln Gln Gly Val Ala Ala Asn Val Ser
         35                  40                  45

Pro Gly Val Ser Val Thr Glu Ile Leu Thr Ala Val Tyr Pro Leu Ala
     50                  55                  60

Gln Leu Phe Pro Thr Leu Ile Met Val Thr Leu Val Ala Ala Leu Ile
 65                  70                  75                  80
```

```
Ala Val Val Arg Ile Ile Leu Leu Arg Arg Asn Gln Glu Ser Arg Gln
                 85                  90                  95

Val Ser Gly Glu Leu Thr Arg Arg Ala Gln Arg Glu Ala Glu Glu Ala
            100                 105                 110

Asn Gln Asn Ala Ala Arg Arg Ala Arg Ala Gln Ser Thr Arg Val Gln
        115                 120                 125

Ser Ser Lys Thr Arg Asn Arg Arg Ala Gln Pro Thr Gly Asp Thr Gly
    130                 135                 140

Ser Gln Val Thr Val Asp Glu Leu Ile Arg Arg Ser Gln Glu Arg Arg
145                 150                 155                 160

Gln Thr Val Ala Gln Arg Gln Thr Glu Arg Gly Val Pro Phe Thr Pro
                165                 170                 175

Thr Pro Gly Pro Val Val Ala Pro Lys Pro Arg Pro Ser Ala Pro Glu
            180                 185                 190

Ala Pro Ala Pro Thr Asp Val Gly Glu Arg Arg Gln Ala Ala Pro Lys
        195                 200                 205

Arg Arg Thr Ser Leu Asp Asp Asp Leu Tyr Ser
    210                 215


<210> 385
<211> 621
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(621)
<223> FRXA00785

<400> 385
atc atc gct act ctc ggt gtg acc ttg ctg gtt gag gcc cgc gga tta   48
Ile Ile Ala Thr Leu Gly Val Thr Leu Leu Val Glu Ala Arg Gly Leu
  1               5                  10                  15

ttc ttg acg gtt gcg tcc att ccc att ctg ttt ggt att ttc aca cca   96
Phe Leu Thr Val Ala Ser Ile Pro Ile Leu Phe Gly Ile Phe Thr Pro
             20                  25                  30

ctg act tcg tgg ttt gtg tcc caa caa ggc gtg gct gcg aat gtg tcc   144
Leu Thr Ser Trp Phe Val Ser Gln Gln Gly Val Ala Ala Asn Val Ser
         35                  40                  45

cct ggt gtt tcc gtc acg gaa atc ctc acg gct gtt tat cct ttg gcg   192
Pro Gly Val Ser Val Thr Glu Ile Leu Thr Ala Val Tyr Pro Leu Ala
     50                  55                  60

cag ttg ttc ccc acc ctg atc atg gtc act ttg gtg gcg gca ttg atc   240
Gln Leu Phe Pro Thr Leu Ile Met Val Thr Leu Val Ala Ala Leu Ile
 65                  70                  75                  80

gct gtg gtg cgg att att ctg ctg cgc agg aac cag gaa tct cgt cag   288
Ala Val Val Arg Ile Ile Leu Leu Arg Arg Asn Gln Glu Ser Arg Gln
```

```
                  85                  90                  95

gtt tct ggg gaa ctt acc cgg cgc gcg cag cgt gag gct gag gaa gct   336
Val Ser Gly Glu Leu Thr Arg Arg Ala Gln Arg Glu Ala Glu Glu Ala
            100                 105                 110

aat cag aat gct gct cgt cgt gct cgc gca cag agc acg agg gta caa   384
Asn Gln Asn Ala Ala Arg Arg Ala Arg Ala Gln Ser Thr Arg Val Gln
        115                 120                 125

agt tct aaa aca cgt aac cgt cgc gcg caa cca acc ggc gat acc ggt   432
Ser Ser Lys Thr Arg Asn Arg Arg Ala Gln Pro Thr Gly Asp Thr Gly
    130                 135                 140

tca caa gtc acg gtt gat gag ttg atc agg cgt agc cag gag cgc cgg   480
Ser Gln Val Thr Val Asp Glu Leu Ile Arg Arg Ser Gln Glu Arg Arg
145                 150                 155                 160

caa act gtt gcg cag cgc caa act gag cgc ggt gtg ccg ttt act cca   528
Gln Thr Val Ala Gln Arg Gln Thr Glu Arg Gly Val Pro Phe Thr Pro
                165                 170                 175

act ccg ggt cct gtg gtg gcc ccc aag ccg cgc ccg agc gcc cct gag   576
Thr Pro Gly Pro Val Val Ala Pro Lys Pro Arg Pro Ser Ala Pro Glu
            180                 185                 190

gcg ccg gct cct acg gat gtg ggt gag cgt cga caa gca gcc cct       621
Ala Pro Ala Pro Thr Asp Val Gly Glu Arg Arg Gln Ala Ala Pro
        195                 200                 205


<210> 386
<211> 207
<212> PRT
<213> Corynebacterium glutamicum

<400> 386
Ile Ile Ala Thr Leu Gly Val Thr Leu Leu Val Glu Ala Arg Gly Leu
  1               5                  10                  15

Phe Leu Thr Val Ala Ser Ile Pro Ile Leu Phe Gly Ile Phe Thr Pro
             20                  25                  30

Leu Thr Ser Trp Phe Val Ser Gln Gln Gly Val Ala Ala Asn Val Ser
         35                  40                  45

Pro Gly Val Ser Val Thr Glu Ile Leu Thr Ala Val Tyr Pro Leu Ala
     50                  55                  60

Gln Leu Phe Pro Thr Leu Ile Met Val Thr Leu Val Ala Ala Leu Ile
 65                  70                  75                  80

Ala Val Val Arg Ile Ile Leu Leu Arg Arg Asn Gln Glu Ser Arg Gln
                 85                  90                  95

Val Ser Gly Glu Leu Thr Arg Arg Ala Gln Arg Glu Ala Glu Glu Ala
            100                 105                 110

Asn Gln Asn Ala Ala Arg Arg Ala Arg Ala Gln Ser Thr Arg Val Gln
        115                 120                 125
```

```
Ser Ser Lys Thr Arg Asn Arg Arg Ala Gln Pro Thr Gly Asp Thr Gly
    130                 135                 140

Ser Gln Val Thr Val Asp Glu Leu Ile Arg Arg Ser Gln Glu Arg Arg
145                 150                 155                 160

Gln Thr Val Ala Gln Arg Gln Thr Glu Arg Gly Val Pro Phe Thr Pro
                165                 170                 175

Thr Pro Gly Pro Val Val Ala Pro Lys Pro Arg Pro Ser Ala Pro Glu
            180                 185                 190

Ala Pro Ala Pro Thr Asp Val Gly Glu Arg Arg Gln Ala Ala Pro
        195                 200                 205


<210> 387
<211> 651
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(628)
<223> RXN00795

<400> 387
tttggattct ggacacccaa aaggggttt cgtaccaaac tcgtgacata ctaggcgggt 60

ggctgagaaa cgaccgaaaa tttttgatgg cagtcgagac atg att atc tcg ttg   115
                                            Met Ile Ile Ser Leu
                                              1               5

gta gtc tcc gcg atc atc atg ttg gta gcg gtg gga ttc acg gga atg   163
Val Val Ser Ala Ile Ile Met Leu Val Ala Val Gly Phe Thr Gly Met
                 10                  15                  20

tgt tct ttc aat aca gga tcc cct gaa aat ggg cag gta cct gaa gtt   211
Cys Ser Phe Asn Thr Gly Ser Pro Glu Asn Gly Gln Val Pro Glu Val
             25                  30                  35

gat gct tcc act ttt atg tca atg gaa gcg cgc gca atg act gat cat   259
Asp Ala Ser Thr Phe Met Ser Met Glu Ala Arg Ala Met Thr Asp His
         40                  45                  50

gca act agg ttg ccg gaa act cct gaa ggc tgg acc aca aat tca gct   307
Ala Thr Arg Leu Pro Glu Thr Pro Glu Gly Trp Thr Thr Asn Ser Ala
     55                  60                  65

cga cgc acc atg gtg gat gac acc ccg gca tct gta gtt gga tat gtc   355
Arg Arg Thr Met Val Asp Asp Thr Pro Ala Ser Val Val Gly Tyr Val
 70                  75                  80                  85

acc gca gat gag ggc tat att cag ctc act caa act ggt gaa acc gtt   403
Thr Ala Asp Glu Gly Tyr Ile Gln Leu Thr Gln Thr Gly Glu Thr Val
                 90                  95                 100

gag gat gct gtg gct ggt tat gat act cgc tgg cgt gat ctt tct gag   451
Glu Asp Ala Val Ala Gly Tyr Asp Thr Arg Trp Arg Asp Leu Ser Glu
            105                 110                 115
```

```
tct tat gat ctt gat ggc cac gac gtg gga att tac acc tca cag gaa   499
Ser Tyr Asp Leu Asp Gly His Asp Val Gly Ile Tyr Thr Ser Gln Glu
        120                 125                 130

tct gat gtg cgt gat ctg cgt gtg atg gat ctg ggc gat gcc cgc gtc   547
Ser Asp Val Arg Asp Leu Arg Val Met Asp Leu Gly Asp Ala Arg Val
    135                 140                 145

atg gtc tcg ggt gct gct acc gat gaa gaa ttc aat gat ctg ctt cgc   595
Met Val Ser Gly Ala Ala Thr Asp Glu Glu Phe Asn Asp Leu Leu Arg
150                 155                 160                 165

gca gtt gcg aat tcg gag cca ctg cct acc aat taagaattgg tcgaaccacc 648
Ala Val Ala Asn Ser Glu Pro Leu Pro Thr Asn
                170                 175

aaa                                                               651


<210> 388
<211> 176
<212> PRT
<213> Corynebacterium glutamicum

<400> 388
Met Ile Ile Ser Leu Val Val Ser Ala Ile Ile Met Leu Val Ala Val
  1               5                  10                  15

Gly Phe Thr Gly Met Cys Ser Phe Asn Thr Gly Ser Pro Glu Asn Gly
             20                  25                  30

Gln Val Pro Glu Val Asp Ala Ser Thr Phe Met Ser Met Glu Ala Arg
         35                  40                  45

Ala Met Thr Asp His Ala Thr Arg Leu Pro Glu Thr Pro Glu Gly Trp
     50                  55                  60

Thr Thr Asn Ser Ala Arg Arg Thr Met Val Asp Asp Thr Pro Ala Ser
 65                  70                  75                  80

Val Val Gly Tyr Val Thr Ala Asp Glu Gly Tyr Ile Gln Leu Thr Gln
                 85                  90                  95

Thr Gly Glu Thr Val Glu Asp Ala Val Ala Gly Tyr Asp Thr Arg Trp
            100                 105                 110

Arg Asp Leu Ser Glu Ser Tyr Asp Leu Asp Gly His Asp Val Gly Ile
        115                 120                 125

Tyr Thr Ser Gln Glu Ser Asp Val Arg Asp Leu Arg Val Met Asp Leu
    130                 135                 140

Gly Asp Ala Arg Val Met Val Ser Gly Ala Ala Thr Asp Glu Glu Phe
145                 150                 155                 160

Asn Asp Leu Leu Arg Ala Val Ala Asn Ser Glu Pro Leu Pro Thr Asn
                165                 170                 175
```

<210> 389
<211> 651
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(628)
<223> FRXA00795

<400> 389
tttggattct ggacacccaa aaggggttt cgtaccaaac tcgtgacata ctaggcgggt 60

ggctgagaaa cgaccgaaaa tttttgatgg cagtcgagac atg att atc tcg ttg 115
Met Ile Ile Ser Leu
1 5

gta gtc tcc gcg atc atc atg ttg gta gcg gtg gga ttc acg gga atg 163
Val Val Ser Ala Ile Ile Met Leu Val Ala Val Gly Phe Thr Gly Met
10 15 20

tgt tct ttc aat aca gga tcc cct gaa aat ggg cag gta cct gaa gtt 211
Cys Ser Phe Asn Thr Gly Ser Pro Glu Asn Gly Gln Val Pro Glu Val
25 30 35

gat gct tcc act ttt atg tca atg gaa gcg cgc gca atg act gat cat 259
Asp Ala Ser Thr Phe Met Ser Met Glu Ala Arg Ala Met Thr Asp His
40 45 50

gca act agg ttg ccg gaa act cct gaa ggc tgg acc aca aat tca gct 307
Ala Thr Arg Leu Pro Glu Thr Pro Glu Gly Trp Thr Thr Asn Ser Ala
55 60 65

cga cgc acc atg gtg gat gac acc ccg gca tct gta gtt gga tat gtc 355
Arg Arg Thr Met Val Asp Asp Thr Pro Ala Ser Val Val Gly Tyr Val
70 75 80 85

acc gca gat gag ggc tat att cag ctc act caa act ggt gaa acc gtt 403
Thr Ala Asp Glu Gly Tyr Ile Gln Leu Thr Gln Thr Gly Glu Thr Val
90 95 100

gag gat gct gtg gct ggt tat gat act cgc tgg cgt gat ctt tct gag 451
Glu Asp Ala Val Ala Gly Tyr Asp Thr Arg Trp Arg Asp Leu Ser Glu
105 110 115

tct tat gat ctt gat ggc cac gac gtg gga att tac acc tca cag gaa 499
Ser Tyr Asp Leu Asp Gly His Asp Val Gly Ile Tyr Thr Ser Gln Glu
120 125 130

tct gat gtg cgt gat ctg cgt gtg atg gat ctg ggc gat gcc cgc gtc 547
Ser Asp Val Arg Asp Leu Arg Val Met Asp Leu Gly Asp Ala Arg Val
135 140 145

atg gtc tcg ggt gct gct acc gat gaa gaa ttc aat gat ctg ctt cgc 595
Met Val Ser Gly Ala Ala Thr Asp Glu Glu Phe Asn Asp Leu Leu Arg
150 155 160 165

gca gtt gcg aat tcg gag cca ctg cct acc aat taagaattgg tcgaaccacc 648
Ala Val Ala Asn Ser Glu Pro Leu Pro Thr Asn
170 175

aaa 651

<210> 390
<211> 176
<212> PRT
<213> Corynebacterium glutamicum

<400> 390

```
Met Ile Ile Ser Leu Val Val Ser Ala Ile Ile Met Leu Val Ala Val
  1               5                  10                  15

Gly Phe Thr Gly Met Cys Ser Phe Asn Thr Gly Ser Pro Glu Asn Gly
            20                  25                  30

Gln Val Pro Glu Val Asp Ala Ser Thr Phe Met Ser Met Glu Ala Arg
         35                  40                  45

Ala Met Thr Asp His Ala Thr Arg Leu Pro Glu Thr Pro Glu Gly Trp
     50                  55                  60

Thr Thr Asn Ser Ala Arg Arg Thr Met Val Asp Asp Thr Pro Ala Ser
 65                  70                  75                  80

Val Val Gly Tyr Val Thr Ala Asp Glu Gly Tyr Ile Gln Leu Thr Gln
                 85                  90                  95

Thr Gly Glu Thr Val Glu Asp Ala Val Ala Gly Tyr Asp Thr Arg Trp
            100                 105                 110

Arg Asp Leu Ser Glu Ser Tyr Asp Leu Asp Gly His Asp Val Gly Ile
        115                 120                 125

Tyr Thr Ser Gln Glu Ser Asp Val Arg Asp Leu Arg Val Met Asp Leu
    130                 135                 140

Gly Asp Ala Arg Val Met Val Ser Gly Ala Ala Thr Asp Glu Glu Phe
145                 150                 155                 160

Asn Asp Leu Leu Arg Ala Val Ala Asn Ser Glu Pro Leu Pro Thr Asn
                165                 170                 175
```

<210> 391
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> RXN00831

<400> 391

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agctccaaga aagtcagtgc tgtgcatggc tcggtgctgc tcatgctttt cggtgtttac 60

atgatgagca tgttcgcctg atttaggtag cctggtggga atg agt gca ctt gag   115
```

```
                                                    Met Ser Ala Leu Glu
                                                      1               5

aca ttg caa tgg cag gac tgg tca agc gtc tta att gtg gta gct cac   163
Thr Leu Gln Trp Gln Asp Trp Ser Ser Val Leu Ile Val Val Ala His
                 10                  15                  20

cca gat gat ccg gag tat ggg ctt tcc gcg gct gtt aaa gaa tgg aca   211
Pro Asp Asp Pro Glu Tyr Gly Leu Ser Ala Ala Val Lys Glu Trp Thr
             25                  30                  35

gac gcc ggg gtg gag gtg tct tac ctg ctg ctc acc cac ggg gag gca   259
Asp Ala Gly Val Glu Val Ser Tyr Leu Leu Leu Thr His Gly Glu Ala
         40                  45                  50

ggt atc caa ggt tta gac cct aaa gaa acc ggg tca ttg cgc gca gcg   307
Gly Ile Gln Gly Leu Asp Pro Lys Glu Thr Gly Ser Leu Arg Ala Ala
     55                  60                  65

gaa cag cgg gct gca tgt gat gtg gta gga gtt aga aat ctc acc att   355
Glu Gln Arg Ala Ala Cys Asp Val Val Gly Val Arg Asn Leu Thr Ile
 70                  75                  80                  85

ttg aat cac cca gat tcc atg ttg gtg tac aat ctg gta ctg cgc aaa   403
Leu Asn His Pro Asp Ser Met Leu Val Tyr Asn Leu Val Leu Arg Lys
                 90                  95                 100

gat att gct cgg gaa atc cgg atc cgt aaa cca aat gct gtg gtg gta   451
Asp Ile Ala Arg Glu Ile Arg Ile Arg Lys Pro Asn Ala Val Val Val
             105                 110                 115

tcc aat ttt gat gta gag gcc tac ggt ggt ttg aac cag gcg gat cac   499
Ser Asn Phe Asp Val Glu Ala Tyr Gly Gly Leu Asn Gln Ala Asp His
         120                 125                 130

cgc gtg gcg gga tta gcc gca att gat gcg acc cgc gat gcc gct aat   547
Arg Val Ala Gly Leu Ala Ala Ile Asp Ala Thr Arg Asp Ala Ala Asn
     135                 140                 145

ccg tgg gcg cag cca gag ctg ttg cag gag gat ctg cag ccg tgg gga   595
Pro Trp Ala Gln Pro Glu Leu Leu Gln Glu Asp Leu Gln Pro Trp Gly
150                 155                 160                 165

gct gaa gtc atc atc att gcc gga cac cca gag ccc acc cac acc atg   643
Ala Glu Val Ile Ile Ile Ala Gly His Pro Glu Pro Thr His Thr Met
                 170                 175                 180

gat ctg gct aaa gat tct gtt gat gcc gga gtt gca tcc ctt caa gct   691
Asp Leu Ala Lys Asp Ser Val Asp Ala Gly Val Ala Ser Leu Gln Ala
             185                 190                 195

cac aag gaa tac ttg gcc gct ctt cca gat ccc ccg aag ccg gag gag   739
His Lys Glu Tyr Leu Ala Ala Leu Pro Asp Pro Pro Lys Pro Glu Glu
         200                 205                 210

ttc att ccg gcg ttt ctc gag gta gag ggc ggt tac gca gcg gcc ttc   787
Phe Ile Pro Ala Phe Leu Glu Val Glu Gly Gly Tyr Ala Ala Ala Phe
     215                 220                 225

cga gtt ttc gga cgg taagcagggc gatacgtgat agg                     825
Arg Val Phe Gly Arg
```

230

<210> 392
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 392

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Met Ser Ala Leu Glu Thr Leu Gln Trp Gln Asp Trp Ser Ser Val Leu
  1               5                  10                  15

Ile Val Val Ala His Pro Asp Asp Pro Glu Tyr Gly Leu Ser Ala Ala
             20                  25                  30

Val Lys Glu Trp Thr Asp Ala Gly Val Glu Val Ser Tyr Leu Leu Leu
         35                  40                  45

Thr His Gly Glu Ala Gly Ile Gln Gly Leu Asp Pro Lys Glu Thr Gly
     50                  55                  60

Ser Leu Arg Ala Ala Glu Gln Arg Ala Ala Cys Asp Val Val Gly Val
 65                  70                  75                  80

Arg Asn Leu Thr Ile Leu Asn His Pro Asp Ser Met Leu Val Tyr Asn
                 85                  90                  95

Leu Val Leu Arg Lys Asp Ile Ala Arg Glu Ile Arg Ile Arg Lys Pro
            100                 105                 110

Asn Ala Val Val Val Ser Asn Phe Asp Val Glu Ala Tyr Gly Gly Leu
        115                 120                 125

Asn Gln Ala Asp His Arg Val Ala Gly Leu Ala Ala Ile Asp Ala Thr
    130                 135                 140

Arg Asp Ala Ala Asn Pro Trp Ala Gln Pro Glu Leu Leu Gln Glu Asp
145                 150                 155                 160

Leu Gln Pro Trp Gly Ala Glu Val Ile Ile Ile Ala Gly His Pro Glu
                165                 170                 175

Pro Thr His Thr Met Asp Leu Ala Lys Asp Ser Val Asp Ala Gly Val
            180                 185                 190

Ala Ser Leu Gln Ala His Lys Glu Tyr Leu Ala Ala Leu Pro Asp Pro
        195                 200                 205

Pro Lys Pro Glu Glu Phe Ile Pro Ala Phe Leu Glu Val Glu Gly Gly
    210                 215                 220

Tyr Ala Ala Ala Phe Arg Val Phe Gly Arg
225                 230
```

<210> 393
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(802)
<223> FRXA00831

<400> 393
agctccaaga aagtcagtgc tgtgcatggc tcggtgctgc tcatgctttt cggtgtttac 60

atgatgagca tgttcgcctg atttaggtag cctggtggga atg agt gca ctt gag 115
Met Ser Ala Leu Glu
1 5

aca ttg caa tgg cag gac tgg tca agc gtc tta att gtg gta gct cac 163
Thr Leu Gln Trp Gln Asp Trp Ser Ser Val Leu Ile Val Val Ala His
10 15 20

cca gat gat ccg gag tat ggg ctt tcc gcg gct gtt aaa gaa tgg aca 211
Pro Asp Asp Pro Glu Tyr Gly Leu Ser Ala Ala Val Lys Glu Trp Thr
25 30 35

gac gcc ggg gtg gag gtg tct tac ctg ctg ctc acc cac ggg gag gca 259
Asp Ala Gly Val Glu Val Ser Tyr Leu Leu Leu Thr His Gly Glu Ala
40 45 50

ggt atc caa ggt tta gac cct aaa gaa acc ggg tca ttg cgc gca gcg 307
Gly Ile Gln Gly Leu Asp Pro Lys Glu Thr Gly Ser Leu Arg Ala Ala
55 60 65

gaa cag cgg gct gca tgt gat gtg gta gga gtt aga aat ctc acc att 355
Glu Gln Arg Ala Ala Cys Asp Val Val Gly Val Arg Asn Leu Thr Ile
70 75 80 85

ttg aat cac cca gat tcc atg ttg gtg tac aat ctg gta ctg cgc aaa 403
Leu Asn His Pro Asp Ser Met Leu Val Tyr Asn Leu Val Leu Arg Lys
90 95 100

gat att gct cgg gaa atc cgg atc cgt aaa cca aat gct gtg gtg gta 451
Asp Ile Ala Arg Glu Ile Arg Ile Arg Lys Pro Asn Ala Val Val Val
105 110 115

tcc aat ttt gat gta gag gcc tac ggt ggt ttg aac cag gcg gat cac 499
Ser Asn Phe Asp Val Glu Ala Tyr Gly Gly Leu Asn Gln Ala Asp His
120 125 130

cgc gtg gcg gga tta gcc gca att gat gcg acc cgc gat gcc gct aat 547
Arg Val Ala Gly Leu Ala Ala Ile Asp Ala Thr Arg Asp Ala Ala Asn
135 140 145

ccg tgg gcg cag cca gag ctg ttg cag gag gat ctg cag ccg tgg gga 595
Pro Trp Ala Gln Pro Glu Leu Leu Gln Glu Asp Leu Gln Pro Trp Gly
150 155 160 165

gct gaa gtc atc atc att gcc gga cac cca gag ccc acc cac acc atg 643
Ala Glu Val Ile Ile Ile Ala Gly His Pro Glu Pro Thr His Thr Met
170 175 180

gat ctg gct aaa gat tct gtt gat gcc gga gtt gca tcc ctt caa gct 691
Asp Leu Ala Lys Asp Ser Val Asp Ala Gly Val Ala Ser Leu Gln Ala
185 190 195

cac aag gaa tac ttg gcc gct ctt cca gat ccc ccg aag ccg gag gag 739
His Lys Glu Tyr Leu Ala Ala Leu Pro Asp Pro Pro Lys Pro Glu Glu

```
        200                 205                 210

ttc att ccg gcg ttt ctc gag gta gag ggc ggt tac gca gcg gcc ttc   787
Phe Ile Pro Ala Phe Leu Glu Val Glu Gly Gly Tyr Ala Ala Ala Phe
    215                 220                 225

cga gtt ttc gga cgg taagcagggc gatacgtgat agg                     825
Arg Val Phe Gly Arg
230
```

<210> 394
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 394

```
Met Ser Ala Leu Glu Thr Leu Gln Trp Gln Asp Trp Ser Ser Val Leu
  1               5                  10                  15

Ile Val Val Ala His Pro Asp Asp Pro Glu Tyr Gly Leu Ser Ala Ala
             20                  25                  30

Val Lys Glu Trp Thr Asp Ala Gly Val Glu Val Ser Tyr Leu Leu Leu
         35                  40                  45

Thr His Gly Glu Ala Gly Ile Gln Gly Leu Asp Pro Lys Glu Thr Gly
     50                  55                  60

Ser Leu Arg Ala Ala Glu Gln Arg Ala Ala Cys Asp Val Val Gly Val
 65                  70                  75                  80

Arg Asn Leu Thr Ile Leu Asn His Pro Asp Ser Met Leu Val Tyr Asn
                 85                  90                  95

Leu Val Leu Arg Lys Asp Ile Ala Arg Glu Ile Arg Ile Arg Lys Pro
            100                 105                 110

Asn Ala Val Val Val Ser Asn Phe Asp Val Glu Ala Tyr Gly Gly Leu
        115                 120                 125

Asn Gln Ala Asp His Arg Val Ala Gly Leu Ala Ala Ile Asp Ala Thr
    130                 135                 140

Arg Asp Ala Ala Asn Pro Trp Ala Gln Pro Glu Leu Leu Gln Glu Asp
145                 150                 155                 160

Leu Gln Pro Trp Gly Ala Glu Val Ile Ile Ile Ala Gly His Pro Glu
                165                 170                 175

Pro Thr His Thr Met Asp Leu Ala Lys Asp Ser Val Asp Ala Gly Val
            180                 185                 190

Ala Ser Leu Gln Ala His Lys Glu Tyr Leu Ala Ala Leu Pro Asp Pro
        195                 200                 205

Pro Lys Pro Glu Glu Phe Ile Pro Ala Phe Leu Glu Val Glu Gly Gly
    210                 215                 220

Tyr Ala Ala Ala Phe Arg Val Phe Gly Arg
225                 230
```

<210> 395
<211> 1077
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1054)
<223> RXN00835

<400> 395
actgcaccag cgccaacgat cgcaattttc atacctgcta tcttgcctga gcacagataa 60

gatttgtaag cactacccct tctctacaaa ggagtcatca atg gcc ggt gga ttg 115
Met Ala Gly Gly Leu
1 5

gca gca cta tta gac gat gtc gca gca att act cga gcg gct gca gcc 163
Ala Ala Leu Leu Asp Asp Val Ala Ala Ile Thr Arg Ala Ala Ala Ala
10 15 20

agc ctc gat gat gtc acg gcg atg gct gga aaa acc agc gtt aaa gcc 211
Ser Leu Asp Asp Val Thr Ala Met Ala Gly Lys Thr Ser Val Lys Ala
25 30 35

gca ggc gtg gtt gta gat gac acg gca gtt acc ccg caa tat gtt caa 259
Ala Gly Val Val Val Asp Asp Thr Ala Val Thr Pro Gln Tyr Val Gln
40 45 50

ggt gtc aaa cct gca cgc gaa ctg ccc atg att tgg cgg atc gct aag 307
Gly Val Lys Pro Ala Arg Glu Leu Pro Met Ile Trp Arg Ile Ala Lys
55 60 65

ggc tct ttg gta aac aag atc atc atc att ttg ccc atc gcg ttg ctt 355
Gly Ser Leu Val Asn Lys Ile Ile Ile Ile Leu Pro Ile Ala Leu Leu
70 75 80 85

ctt tcc gcg ttt gct ccg tgg gct ctc aca cca att ttg atg ctg ggc 403
Leu Ser Ala Phe Ala Pro Trp Ala Leu Thr Pro Ile Leu Met Leu Gly
90 95 100

ggc tcc tac ctg tgc ttc gaa ggt gca gaa aag atc tgg cac tcc ctc 451
Gly Ser Tyr Leu Cys Phe Glu Gly Ala Glu Lys Ile Trp His Ser Leu
105 110 115

cac agg cgc atc aaa ggt gaa cag cac agc acc gaa ccc aag tcg cag 499
His Arg Arg Ile Lys Gly Glu Gln His Ser Thr Glu Pro Lys Ser Gln
120 125 130

gaa agc cca aag tca gag gat cag ctg gtc aaa agt gcc atc aca act 547
Glu Ser Pro Lys Ser Glu Asp Gln Leu Val Lys Ser Ala Ile Thr Thr
135 140 145

gac ctc atc ctt tcc gca gag atc atg gtt att tca ctc aat cag att 595
Asp Leu Ile Leu Ser Ala Glu Ile Met Val Ile Ser Leu Asn Gln Ile
150 155 160 165

gca gat caa act atc tgg atg cag gct gcg gtt ctt ttc gtc gta ggt 643
Ala Asp Gln Thr Ile Trp Met Gln Ala Ala Val Leu Phe Val Val Gly

```
                170                 175                 180

att ggc atc acc gcg ctc gtg tac ggc gta gtc ggt gtt ctt gtg aaa   691
Ile Gly Ile Thr Ala Leu Val Tyr Gly Val Val Gly Val Leu Val Lys
            185                 190                 195

atg gat gac gtc gga ctt aca ctt tca aag cgt gac tcc gca ggt atc   739
Met Asp Asp Val Gly Leu Thr Leu Ser Lys Arg Asp Ser Ala Gly Ile
        200                 205                 210

cag aaa ttt ggc cgc ggc ttg gtc aaa gcg atg ccc atc gtt ctt caa   787
Gln Lys Phe Gly Arg Gly Leu Val Lys Ala Met Pro Ile Val Leu Gln
    215                 220                 225

gtt att tct gtt gtc ggc gtt ttt gcc atg ctg tgg gtt ggt ggc cac   835
Val Ile Ser Val Val Gly Val Phe Ala Met Leu Trp Val Gly Gly His
230                 235                 240                 245

atc atg gtc gtt gga act gaa gag tta gga tgg gaa ctt ccc tac cac   883
Ile Met Val Val Gly Thr Glu Glu Leu Gly Trp Glu Leu Pro Tyr His
                250                 255                 260

ctt gtt cac gga cta gag tcc tgg gct aac ggt atc gga ggc agt gct   931
Leu Val His Gly Leu Glu Ser Trp Ala Asn Gly Ile Gly Gly Ser Ala
            265                 270                 275

ctg gga tgg gtt ggc aat act ttc ggg tca ctt gtg ttc ggc ctc att   979
Leu Gly Trp Val Gly Asn Thr Phe Gly Ser Leu Val Phe Gly Leu Ile
        280                 285                 290

tgg ggc gcg att atc acc gtt gtg gtc agt gtg atc aag aag ttc att   1027
Trp Gly Ala Ile Ile Thr Val Val Val Ser Val Ile Lys Lys Phe Ile
    295                 300                 305

cca cag cgt gcg caa aac tcg tct cat tagtggagag ttgttcgctg         1074
Pro Gln Arg Ala Gln Asn Ser Ser His
310                 315

taa                                                               1077
```

<210> 396
<211> 318
<212> PRT
<213> Corynebacterium glutamicum

<400> 396

```
Met Ala Gly Gly Leu Ala Ala Leu Leu Asp Asp Val Ala Ala Ile Thr
  1               5                  10                  15

Arg Ala Ala Ala Ala Ser Leu Asp Asp Val Thr Ala Met Ala Gly Lys
             20                  25                  30

Thr Ser Val Lys Ala Ala Gly Val Val Val Asp Asp Thr Ala Val Thr
         35                  40                  45

Pro Gln Tyr Val Gln Gly Val Lys Pro Ala Arg Glu Leu Pro Met Ile
     50                  55                  60

Trp Arg Ile Ala Lys Gly Ser Leu Val Asn Lys Ile Ile Ile Ile Leu
 65                  70                  75                  80
```

```
Pro Ile Ala Leu Leu Leu Ser Ala Phe Ala Pro Trp Ala Leu Thr Pro
                 85                  90                  95

Ile Leu Met Leu Gly Gly Ser Tyr Leu Cys Phe Glu Gly Ala Glu Lys
            100                 105                 110

Ile Trp His Ser Leu His Arg Arg Ile Lys Gly Glu Gln His Ser Thr
        115                 120                 125

Glu Pro Lys Ser Gln Glu Ser Pro Lys Ser Glu Asp Gln Leu Val Lys
    130                 135                 140

Ser Ala Ile Thr Thr Asp Leu Ile Leu Ser Ala Glu Ile Met Val Ile
145                 150                 155                 160

Ser Leu Asn Gln Ile Ala Asp Gln Thr Ile Trp Met Gln Ala Ala Val
                165                 170                 175

Leu Phe Val Val Gly Ile Gly Ile Thr Ala Leu Val Tyr Gly Val Val
            180                 185                 190

Gly Val Leu Val Lys Met Asp Asp Val Gly Leu Thr Leu Ser Lys Arg
        195                 200                 205

Asp Ser Ala Gly Ile Gln Lys Phe Gly Arg Gly Leu Val Lys Ala Met
    210                 215                 220

Pro Ile Val Leu Gln Val Ile Ser Val Val Gly Val Phe Ala Met Leu
225                 230                 235                 240

Trp Val Gly Gly His Ile Met Val Val Gly Thr Glu Glu Leu Gly Trp
                245                 250                 255

Glu Leu Pro Tyr His Leu Val His Gly Leu Glu Ser Trp Ala Asn Gly
            260                 265                 270

Ile Gly Gly Ser Ala Leu Gly Trp Val Gly Asn Thr Phe Gly Ser Leu
        275                 280                 285

Val Phe Gly Leu Ile Trp Gly Ala Ile Ile Thr Val Val Val Ser Val
    290                 295                 300

Ile Lys Lys Phe Ile Pro Gln Arg Ala Gln Asn Ser Ser His
305                 310                 315


<210> 397
<211> 713
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(690)
<223> FRXA00835

<400> 397
ttt gct ccg tgg gct ctc aca cca att ttg atg ctg ggc ggc tcc tac   48
Phe Ala Pro Trp Ala Leu Thr Pro Ile Leu Met Leu Gly Gly Ser Tyr
  1               5                  10                  15
```

```
ctg tgc ttc gaa ggt gca gaa aag atc tgg cac tcc ctc cac agg cgc   96
Leu Cys Phe Glu Gly Ala Glu Lys Ile Trp His Ser Leu His Arg Arg
            20                  25                  30

atc aaa ggt gaa cag cac agc acc gaa ccc aag tcg cag gaa agc cca  144
Ile Lys Gly Glu Gln His Ser Thr Glu Pro Lys Ser Gln Glu Ser Pro
        35                  40                  45

aag tca gag gat cag ctg gtc aaa agt gcc atc aca act gac ctc atc  192
Lys Ser Glu Asp Gln Leu Val Lys Ser Ala Ile Thr Thr Asp Leu Ile
    50                  55                  60

ctt tcc gca gag atc atg gtt att tca ctc aat cag att gca gat caa  240
Leu Ser Ala Glu Ile Met Val Ile Ser Leu Asn Gln Ile Ala Asp Gln
65                  70                  75                  80

act atc tgg atg cag gct gcg gtt ctt ttc gtc gta ggt att ggc atc  288
Thr Ile Trp Met Gln Ala Ala Val Leu Phe Val Val Gly Ile Gly Ile
                85                  90                  95

acc gcg ctc gtg tac ggc gta gtc ggt gtt ctt gtg aaa atg gat gac  336
Thr Ala Leu Val Tyr Gly Val Val Gly Val Leu Val Lys Met Asp Asp
            100                 105                 110

gtc gga ctt aca ctt tca aag cgt gac tcc gca ggt atc cag aaa ttt  384
Val Gly Leu Thr Leu Ser Lys Arg Asp Ser Ala Gly Ile Gln Lys Phe
        115                 120                 125

ggc cgc ggc ttg gtc aaa gcg atg ccc atc gtt ctt caa gtt att tct  432
Gly Arg Gly Leu Val Lys Ala Met Pro Ile Val Leu Gln Val Ile Ser
    130                 135                 140

gtt gtc ggc gtt ttt gcc atg ctg tgg gtt ggt ggc cac atc atg gtc  480
Val Val Gly Val Phe Ala Met Leu Trp Val Gly Gly His Ile Met Val
145                 150                 155                 160

gtt gga act gaa gag tta gga tgg gaa ctt ccc tac cac ctt gtt cac  528
Val Gly Thr Glu Glu Leu Gly Trp Glu Leu Pro Tyr His Leu Val His
                165                 170                 175

gga cta gag tcc tgg gct aac ggt atc gga ggc agt gct ctg gga tgg  576
Gly Leu Glu Ser Trp Ala Asn Gly Ile Gly Gly Ser Ala Leu Gly Trp
            180                 185                 190

gtt ggc aat act ttc ggg tca ctt gtg ttc ggc ctc att tgg ggc gcg  624
Val Gly Asn Thr Phe Gly Ser Leu Val Phe Gly Leu Ile Trp Gly Ala
        195                 200                 205

att atc acc gtt gtg gtc agt gtg atc aag aag ttc att cca cag cgt  672
Ile Ile Thr Val Val Val Ser Val Ile Lys Lys Phe Ile Pro Gln Arg
    210                 215                 220

gcg caa aac tcg tct cat tagtggagag ttgttcgctg taa                713
Ala Gln Asn Ser Ser His
225                 230
```

<210> 398
<211> 230
<212> PRT

<213> Corynebacterium glutamicum

<400> 398

```
Phe Ala Pro Trp Ala Leu Thr Pro Ile Leu Met Leu Gly Gly Ser Tyr
  1               5                  10                  15

Leu Cys Phe Glu Gly Ala Glu Lys Ile Trp His Ser Leu His Arg Arg
             20                  25                  30

Ile Lys Gly Glu Gln His Ser Thr Glu Pro Lys Ser Gln Glu Ser Pro
         35                  40                  45

Lys Ser Glu Asp Gln Leu Val Lys Ser Ala Ile Thr Thr Asp Leu Ile
     50                  55                  60

Leu Ser Ala Glu Ile Met Val Ile Ser Leu Asn Gln Ile Ala Asp Gln
 65                  70                  75                  80

Thr Ile Trp Met Gln Ala Ala Val Leu Phe Val Val Gly Ile Gly Ile
                 85                  90                  95

Thr Ala Leu Val Tyr Gly Val Val Gly Val Leu Val Lys Met Asp Asp
            100                 105                 110

Val Gly Leu Thr Leu Ser Lys Arg Asp Ser Ala Gly Ile Gln Lys Phe
        115                 120                 125

Gly Arg Gly Leu Val Lys Ala Met Pro Ile Val Leu Gln Val Ile Ser
    130                 135                 140

Val Val Gly Val Phe Ala Met Leu Trp Val Gly Gly His Ile Met Val
145                 150                 155                 160

Val Gly Thr Glu Glu Leu Gly Trp Glu Leu Pro Tyr His Leu Val His
                165                 170                 175

Gly Leu Glu Ser Trp Ala Asn Gly Ile Gly Gly Ser Ala Leu Gly Trp
            180                 185                 190

Val Gly Asn Thr Phe Gly Ser Leu Val Phe Gly Leu Ile Trp Gly Ala
        195                 200                 205

Ile Ile Thr Val Val Val Ser Val Ile Lys Lys Phe Ile Pro Gln Arg
    210                 215                 220

Ala Gln Asn Ser Ser His
225                 230
```

<210> 399
<211> 1816
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1816)
<223> RXN00836

<400> 399

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ggagagttgt tcgctgtaat ttcgctgtac agttaatatg acttttttact gtctcaatca 60
```

```
attcacaagt ttgcacgaaa tttaaggaaa ggagtgccca atg tat acc cat tca   115
                                             Met Tyr Thr His Ser
                                               1               5

aca ggc act cct cag ctt gat ttc gac ggt gac atc tat ccc ctt cac   163
Thr Gly Thr Pro Gln Leu Asp Phe Asp Gly Asp Ile Tyr Pro Leu His
                10                  15                  20

ctc ttc ttc tct gca cag act gcc caa cat ttc gct ctc gag cgc gtc   211
Leu Phe Phe Ser Ala Gln Thr Ala Gln His Phe Ala Leu Glu Arg Val
            25                  30                  35

aat tgg cat gtc tta cgc gct att gtg aaa cct gag caa ggc gaa ctc   259
Asn Trp His Val Leu Arg Ala Ile Val Lys Pro Glu Gln Gly Glu Leu
        40                  45                  50

atc gtc gaa gcg ctt ctc gca cca ata gaa tcc gca aca aaa atc ggt   307
Ile Val Glu Ala Leu Leu Ala Pro Ile Glu Ser Ala Thr Lys Ile Gly
    55                  60                  65

gtt tgg gtt caa gat gaa ttt ctc ggg gtg att gca gag tcc cag ttc   355
Val Trp Val Gln Asp Glu Phe Leu Gly Val Ile Ala Glu Ser Gln Phe
70                  75                  80                  85

ctg ttg aat tct caa ttg tct cga att ttt gcc tct ggc cac ctg att   403
Leu Leu Asn Ser Gln Leu Ser Arg Ile Phe Ala Ser Gly His Leu Ile
                90                  95                  100

tcc agc caa cta ctt ctc aca ccg agt aaa gga tct ctc gct tca gtt   451
Ser Ser Gln Leu Leu Leu Thr Pro Ser Lys Gly Ser Leu Ala Ser Val
            105                 110                 115

ctt ctt cca aac cta aaa ttc ggg ctc atc agc aat gat cct cca cga   499
Leu Leu Pro Asn Leu Lys Phe Gly Leu Ile Ser Asn Asp Pro Pro Arg
        120                 125                 130

gct gat tcc cac ctc tta ccg cta ggc aga atg tgg cgc gtt gag ccc   547
Ala Asp Ser His Leu Leu Pro Leu Gly Arg Met Trp Arg Val Glu Pro
    135                 140                 145

acc gtt cat gct ctg ttt gag gat ttc tca ctt ggc tcc acg att ctt   595
Thr Val His Ala Leu Phe Glu Asp Phe Ser Leu Gly Ser Thr Ile Leu
150                 155                 160                 165

ttt ggg ctg agg ctt gat tta gaa gcc cta att gtc tcc tat aac gga   643
Phe Gly Leu Arg Leu Asp Leu Glu Ala Leu Ile Val Ser Tyr Asn Gly
                170                 175                 180

ata gaa tgt ggc atc tta aac ttt gat gac gcc tca gca cta agc tct   691
Ile Glu Cys Gly Ile Leu Asn Phe Asp Asp Ala Ser Ala Leu Ser Ser
            185                 190                 195

gct gtg aaa ttc tca aat gca aat ggt ctc acc ccc acg gtg ctc ggc   739
Ala Val Lys Phe Ser Asn Ala Asn Gly Leu Thr Pro Thr Val Leu Gly
        200                 205                 210

cac gta gtc cgg gag aac ggt gaa aca tcc ttc gag att gac gtt ctc   787
His Val Val Arg Glu Asn Gly Glu Thr Ser Phe Glu Ile Asp Val Leu
    215                 220                 225
```

```
cca ctg gag ttg tgg tcg aag aag cag cat cgc ctt gag gtt tta aaa   835
Pro Leu Glu Leu Trp Ser Lys Lys Gln His Arg Leu Glu Val Leu Lys
230                 235                 240                 245

atc cct cgg ttg ata cct aaa gag gca gat tcc caa aat tat gtg aag   883
Ile Pro Arg Leu Ile Pro Lys Glu Ala Asp Ser Gln Asn Tyr Val Lys
                250                 255                 260

gcg aca gcg ctc ctt tca gac gag att ctg cga cca caa acg ctg tcc   931
Ala Thr Ala Leu Leu Ser Asp Glu Ile Leu Arg Pro Gln Thr Leu Ser
            265                 270                 275

aaa aag gca ctg tct ttg tcg gac acc gca gtt aag tac agc cct cat   979
Lys Lys Ala Leu Ser Leu Ser Asp Thr Ala Val Lys Tyr Ser Pro His
        280                 285                 290

gtt gct tgt ggc gtg ggg atg ttt agt ctt ttc gcc gtt att ccc ttt   1027
Val Ala Cys Gly Val Gly Met Phe Ser Leu Phe Ala Val Ile Pro Phe
    295                 300                 305

gac aag ttg agt gat cat agt gcg atg ctg ctc gca gtc att agc ttg   1075
Asp Lys Leu Ser Asp His Ser Ala Met Leu Leu Ala Val Ile Ser Leu
310                 315                 320                 325

atg ctt ttt gtg ctg gca tta gta att ctt ttc aag aga att cag tca   1123
Met Leu Phe Val Leu Ala Leu Val Ile Leu Phe Lys Arg Ile Gln Ser
                330                 335                 340

act aat act cag cgt tgg aac ttg gcc tcg tca gtc gga tta ctc gcg   1171
Thr Asn Thr Gln Arg Trp Asn Leu Ala Ser Ser Val Gly Leu Leu Ala
            345                 350                 355

aca ctt ccg att atc ata ttc ctg gtt gct gat aca ttg att cct cag   1219
Thr Leu Pro Ile Ile Ile Phe Leu Val Ala Asp Thr Leu Ile Pro Gln
        360                 365                 370

ggc agc ctg gaa aac cat gct caa ccc gac gta cag gta aca acg tta   1267
Gly Ser Leu Glu Asn His Ala Gln Pro Asp Val Gln Val Thr Thr Leu
    375                 380                 385

gct aac agg cgg cca agt tca cct acc tca ctg gac tca cta ggc gca   1315
Ala Asn Arg Arg Pro Ser Ser Pro Thr Ser Leu Asp Ser Leu Gly Ala
390                 395                 400                 405

ctg aat tca cca agt tcg ccg aat tcc ccg agc tca tca atg ctg caa   1363
Leu Asn Ser Pro Ser Ser Pro Asn Ser Pro Ser Ser Ser Met Leu Gln
                410                 415                 420

aac tct gaa atg ttc gcc tca cca ccg atc gcc tct ggg cag tca ccg   1411
Asn Ser Glu Met Phe Ala Ser Pro Pro Ile Ala Ser Gly Gln Ser Pro
            425                 430                 435

gtt tcg acg ttc cgc tca tgg cta gat cga tcc att ctg cca ctc aca   1459
Val Ser Thr Phe Arg Ser Trp Leu Asp Arg Ser Ile Leu Pro Leu Thr
        440                 445                 450

cga gaa aat tcc gct tca gaa agc gca gtg aca gct ctt gga ccg tcg   1507
Arg Glu Asn Ser Ala Ser Glu Ser Ala Val Thr Ala Leu Gly Pro Ser
    455                 460                 465

ata gtg cag cct gca tct gaa tcg att aca act cca gct caa acg tcg   1555
```

```
Ile Val Gln Pro Ala Ser Glu Ser Ile Thr Thr Pro Ala Gln Thr Ser
470                 475                 480                 485

caa agt cgc cac gca att gac gat ggt gac gac agt aaa acc tca acg   1603
Gln Ser Arg His Ala Ile Asp Asp Gly Asp Asp Ser Lys Thr Ser Thr
                490                 495                 500

gga aga cca gct ccc act act aac tcg ccg atc att gct ctt ccc cca   1651
Gly Arg Pro Ala Pro Thr Thr Asn Ser Pro Ile Ile Ala Leu Pro Pro
            505                 510                 515

acg tgg att atc ggg ccg gaa gat cca gaa tcc acc gac cct aca gca   1699
Thr Trp Ile Ile Gly Pro Glu Asp Pro Glu Ser Thr Asp Pro Thr Ala
        520                 525                 530

cca acc gag ccc acc gag cca agc gaa cct gtc gca acc gac gaa ccc   1747
Pro Thr Glu Pro Thr Glu Pro Ser Glu Pro Val Ala Thr Asp Glu Pro
    535                 540                 545

tca gag acc tct gaa caa act tca cct ctc tta gct cgc gac acc ccc   1795
Ser Glu Thr Ser Glu Gln Thr Ser Pro Leu Leu Ala Arg Asp Thr Pro
550                 555                 560                 565

gaa ctg aac cgg aaa caa ctg                                      1816
Glu Leu Asn Arg Lys Gln Leu
                570
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<210> 400
<211> 572
<212> PRT
<213> Corynebacterium glutamicum

<400> 400

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Met Tyr Thr His Ser Thr Gly Thr Pro Gln Leu Asp Phe Asp Gly Asp
  1               5                  10                  15

Ile Tyr Pro Leu His Leu Phe Phe Ser Ala Gln Thr Ala Gln His Phe
             20                  25                  30

Ala Leu Glu Arg Val Asn Trp His Val Leu Arg Ala Ile Val Lys Pro
         35                  40                  45

Glu Gln Gly Glu Leu Ile Val Glu Ala Leu Leu Ala Pro Ile Glu Ser
     50                  55                  60

Ala Thr Lys Ile Gly Val Trp Val Gln Asp Glu Phe Leu Gly Val Ile
 65                  70                  75                  80

Ala Glu Ser Gln Phe Leu Leu Asn Ser Gln Leu Ser Arg Ile Phe Ala
                 85                  90                  95

Ser Gly His Leu Ile Ser Ser Gln Leu Leu Leu Thr Pro Ser Lys Gly
            100                 105                 110

Ser Leu Ala Ser Val Leu Leu Pro Asn Leu Lys Phe Gly Leu Ile Ser
        115                 120                 125

Asn Asp Pro Pro Arg Ala Asp Ser His Leu Leu Pro Leu Gly Arg Met
    130                 135                 140
```

```
Trp Arg Val Glu Pro Thr Val His Ala Leu Phe Glu Asp Phe Ser Leu
145                 150                 155                 160

Gly Ser Thr Ile Leu Phe Gly Leu Arg Leu Asp Leu Glu Ala Leu Ile
                165                 170                 175

Val Ser Tyr Asn Gly Ile Glu Cys Gly Ile Leu Asn Phe Asp Asp Ala
            180                 185                 190

Ser Ala Leu Ser Ser Ala Val Lys Phe Ser Asn Ala Asn Gly Leu Thr
        195                 200                 205

Pro Thr Val Leu Gly His Val Val Arg Glu Asn Gly Glu Thr Ser Phe
    210                 215                 220

Glu Ile Asp Val Leu Pro Leu Glu Leu Trp Ser Lys Lys Gln His Arg
225                 230                 235                 240

Leu Glu Val Leu Lys Ile Pro Arg Leu Ile Pro Lys Glu Ala Asp Ser
                245                 250                 255

Gln Asn Tyr Val Lys Ala Thr Ala Leu Leu Ser Asp Glu Ile Leu Arg
            260                 265                 270

Pro Gln Thr Leu Ser Lys Lys Ala Leu Ser Leu Ser Asp Thr Ala Val
        275                 280                 285

Lys Tyr Ser Pro His Val Ala Cys Gly Val Gly Met Phe Ser Leu Phe
    290                 295                 300

Ala Val Ile Pro Phe Asp Lys Leu Ser Asp His Ser Ala Met Leu Leu
305                 310                 315                 320

Ala Val Ile Ser Leu Met Leu Phe Val Leu Ala Leu Val Ile Leu Phe
                325                 330                 335

Lys Arg Ile Gln Ser Thr Asn Thr Gln Arg Trp Asn Leu Ala Ser Ser
            340                 345                 350

Val Gly Leu Leu Ala Thr Leu Pro Ile Ile Ile Phe Leu Val Ala Asp
        355                 360                 365

Thr Leu Ile Pro Gln Gly Ser Leu Glu Asn His Ala Gln Pro Asp Val
    370                 375                 380

Gln Val Thr Thr Leu Ala Asn Arg Arg Pro Ser Ser Pro Thr Ser Leu
385                 390                 395                 400

Asp Ser Leu Gly Ala Leu Asn Ser Pro Ser Ser Pro Asn Ser Pro Ser
                405                 410                 415

Ser Ser Met Leu Gln Asn Ser Glu Met Phe Ala Ser Pro Pro Ile Ala
            420                 425                 430

Ser Gly Gln Ser Pro Val Ser Thr Phe Arg Ser Trp Leu Asp Arg Ser
        435                 440                 445

Ile Leu Pro Leu Thr Arg Glu Asn Ser Ala Ser Glu Ser Ala Val Thr
    450                 455                 460

Ala Leu Gly Pro Ser Ile Val Gln Pro Ala Ser Glu Ser Ile Thr Thr
```

```
465                 470                 475                 480

Pro Ala Gln Thr Ser Gln Ser Arg His Ala Ile Asp Asp Gly Asp Asp
                485                 490                 495

Ser Lys Thr Ser Thr Gly Arg Pro Ala Pro Thr Thr Asn Ser Pro Ile
            500                 505                 510

Ile Ala Leu Pro Pro Thr Trp Ile Ile Gly Pro Glu Asp Pro Glu Ser
        515                 520                 525

Thr Asp Pro Thr Ala Pro Thr Glu Pro Thr Glu Pro Ser Glu Pro Val
    530                 535                 540

Ala Thr Asp Glu Pro Ser Glu Thr Ser Glu Gln Thr Ser Pro Leu Leu
545                 550                 555                 560

Ala Arg Asp Thr Pro Glu Leu Asn Arg Lys Gln Leu
                565                 570
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Sequence Listing

<210> 401
<211> 1771
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1771)
<223> FRXA00836

<400> 401

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attcacaagt ttgcacgaaa tttaaggaaa ggagtgccca atg tat acc cat tca   115
                                              Met Tyr Thr His Ser
                                                1               5

aca ggc act cct cag ctt gat ttc gac ggt gac atc tat ccc ctt cac   163
Thr Gly Thr Pro Gln Leu Asp Phe Asp Gly Asp Ile Tyr Pro Leu His
                10                  15                  20

ctc ttc ttc tct gca cag act gcc caa cat ttc gct ctc gag cgc gtc   211
Leu Phe Phe Ser Ala Gln Thr Ala Gln His Phe Ala Leu Glu Arg Val
            25                  30                  35

aat tgg cat gtc tta cgc gct att gtg aaa cct gag caa ggc gaa ctc   259
Asn Trp His Val Leu Arg Ala Ile Val Lys Pro Glu Gln Gly Glu Leu
        40                  45                  50

atc gtc gaa gcg ctt ctc gca cca ata gaa tcc gca aca aaa atc ggt   307
Ile Val Glu Ala Leu Leu Ala Pro Ile Glu Ser Ala Thr Lys Ile Gly
    55                  60                  65

gtt tgg gtt caa gat gaa ttt ctc ggg gtg att gca gag tcc cag ttc   355
Val Trp Val Gln Asp Glu Phe Leu Gly Val Ile Ala Glu Ser Gln Phe
70                  75                  80                  85

ctg ttg aat tct caa ttg tct cga att ttt gcc tct ggc cac ctg att   403
Leu Leu Asn Ser Gln Leu Ser Arg Ile Phe Ala Ser Gly His Leu Ile
                90                  95                  100
```

```
tcc agc caa cta ctt ctc aca ccg agt aaa gga tct ctc gct tca gtt   451
Ser Ser Gln Leu Leu Leu Thr Pro Ser Lys Gly Ser Leu Ala Ser Val
            105                 110                 115

ctt ctt cca aac cta aaa ttc ggg ctc atc agc aat gat cct cca cga   499
Leu Leu Pro Asn Leu Lys Phe Gly Leu Ile Ser Asn Asp Pro Pro Arg
        120                 125                 130

gct gat tcc cac ctc tta ccg cta ggc aga atg tgg cgc gtt gag ccc   547
Ala Asp Ser His Leu Leu Pro Leu Gly Arg Met Trp Arg Val Glu Pro
    135                 140                 145

acc gtt cat gct ctg ttt gag gat ttc tca ctt ggc tcc acg att ctt   595
Thr Val His Ala Leu Phe Glu Asp Phe Ser Leu Gly Ser Thr Ile Leu
150                 155                 160                 165

ttt ggg ctg agg ctt gat tta gaa gcc cta att gtc tcc tat aac gga   643
Phe Gly Leu Arg Leu Asp Leu Glu Ala Leu Ile Val Ser Tyr Asn Gly
                170                 175                 180

ata gaa tgt ggc atc tta aac ttt gat gac gcc tca gca cta agc tct   691
Ile Glu Cys Gly Ile Leu Asn Phe Asp Asp Ala Ser Ala Leu Ser Ser
            185                 190                 195

gct gtg aaa ttc tca aat gca aat ggt ctc acc ccc acg gtg ctc ggc   739
Ala Val Lys Phe Ser Asn Ala Asn Gly Leu Thr Pro Thr Val Leu Gly
        200                 205                 210

cac gta gtc cgg gag aac ggt gaa aca tcc ttc gag att gac gtt ctc   787
His Val Val Arg Glu Asn Gly Glu Thr Ser Phe Glu Ile Asp Val Leu
    215                 220                 225

cca ctg gag ttg tgg tcg aag aag cag cat cgc ctt gag gtt tta aaa   835
Pro Leu Glu Leu Trp Ser Lys Lys Gln His Arg Leu Glu Val Leu Lys
230                 235                 240                 245

atc cct cgg ttg ata cct aaa gag gca gat tcc caa aat tat gtg aag   883
Ile Pro Arg Leu Ile Pro Lys Glu Ala Asp Ser Gln Asn Tyr Val Lys
                250                 255                 260

gcg aca gcg ctc ctt tca gac gag att ctg cga cca caa acg ctg tcc   931
Ala Thr Ala Leu Leu Ser Asp Glu Ile Leu Arg Pro Gln Thr Leu Ser
            265                 270                 275

aaa aag gca ctg tct ttg tcg gac acc gca gtt aag tac agc cct cat   979
Lys Lys Ala Leu Ser Leu Ser Asp Thr Ala Val Lys Tyr Ser Pro His
        280                 285                 290

gtt gct tgt ggc gtg ggg atg ttt agt ctt ttc gcc gtt att ccc ttt   1027
Val Ala Cys Gly Val Gly Met Phe Ser Leu Phe Ala Val Ile Pro Phe
    295                 300                 305

gac aag ttg agt gat cat agt gcg atg ctg ctc gca gtc att agc ttg   1075
Asp Lys Leu Ser Asp His Ser Ala Met Leu Leu Ala Val Ile Ser Leu
310                 315                 320                 325

atg ctt ttt gtg ctg gca tta gta att ctt ttc aag aga att cag tca   1123
Met Leu Phe Val Leu Ala Leu Val Ile Leu Phe Lys Arg Ile Gln Ser
                330                 335                 340
```

```
act aat act cag cgt tgg aac ttg gcc tcg tca gtc gga tta ctc gcg   1171
Thr Asn Thr Gln Arg Trp Asn Leu Ala Ser Ser Val Gly Leu Leu Ala
            345                 350                 355

aca ctt ccg att atc ata ttc ctg gtt gct gat aca ttg att cct cag   1219
Thr Leu Pro Ile Ile Ile Phe Leu Val Ala Asp Thr Leu Ile Pro Gln
        360                 365                 370

ggc agc ctg gaa aac cat gct caa ccc gac gta cag gta aca acg tta   1267
Gly Ser Leu Glu Asn His Ala Gln Pro Asp Val Gln Val Thr Thr Leu
    375                 380                 385

gct aac agg cgg cca agt tca cct acc tca ctg gac tca cta ggc gca   1315
Ala Asn Arg Arg Pro Ser Ser Pro Thr Ser Leu Asp Ser Leu Gly Ala
390                 395                 400                 405

ctg aat tca cca agt tcg ccg aat tcc ccg agc tca tca atg ctg caa   1363
Leu Asn Ser Pro Ser Ser Pro Asn Ser Pro Ser Ser Ser Met Leu Gln
                410                 415                 420

aac tct gaa atg ttc gcc tca cca ccg atc gcc tct ggg cag tca ccg   1411
Asn Ser Glu Met Phe Ala Ser Pro Pro Ile Ala Ser Gly Gln Ser Pro
            425                 430                 435

gtt tcg acg ttc cgc tca tgg cta gat cga tcc att ctg cca ctc aca   1459
Val Ser Thr Phe Arg Ser Trp Leu Asp Arg Ser Ile Leu Pro Leu Thr
        440                 445                 450

cga gaa aat tcc gct tca gaa agc gca gtg aca gct ctt gga ccg tcg   1507
Arg Glu Asn Ser Ala Ser Glu Ser Ala Val Thr Ala Leu Gly Pro Ser
    455                 460                 465

ata gtg cag cct gca tct gaa tcg att aca act cca gct caa acg tcg   1555
Ile Val Gln Pro Ala Ser Glu Ser Ile Thr Thr Pro Ala Gln Thr Ser
470                 475                 480                 485

caa agt cgc cac gca att gac gat ggt gac gac agt aaa acc tca acg   1603
Gln Ser Arg His Ala Ile Asp Asp Gly Asp Asp Ser Lys Thr Ser Thr
                490                 495                 500

gga aga cca gct ccc act act aac tcg ccg atc att gct ctt ccc cca   1651
Gly Arg Pro Ala Pro Thr Thr Asn Ser Pro Ile Ile Ala Leu Pro Pro
            505                 510                 515

acg tgg att atc ggg ccg gaa gat cca gaa tcc acc gac cct aca gca   1699
Thr Trp Ile Ile Gly Pro Glu Asp Pro Glu Ser Thr Asp Pro Thr Ala
        520                 525                 530

cca acc gag ccc acc gag cca agc gaa cct gtc gca acc gac gaa ccc   1747
Pro Thr Glu Pro Thr Glu Pro Ser Glu Pro Val Ala Thr Asp Glu Pro
    535                 540                 545

tca gag acc tct gaa caa act tca                                  1771
Ser Glu Thr Ser Glu Gln Thr Ser
550                 555
```

<210> 402
<211> 557
<212> PRT
<213> Corynebacterium glutamicum

<400> 402

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Met Tyr Thr His Ser Thr Gly Thr Pro Gln Leu Asp Phe Asp Gly Asp
 1               5                  10                  15

Ile Tyr Pro Leu His Leu Phe Phe Ser Ala Gln Thr Ala Gln His Phe
            20                  25                  30

Ala Leu Glu Arg Val Asn Trp His Val Leu Arg Ala Ile Val Lys Pro
        35                  40                  45

Glu Gln Gly Glu Leu Ile Val Glu Ala Leu Leu Ala Pro Ile Glu Ser
    50                  55                  60

Ala Thr Lys Ile Gly Val Trp Val Gln Asp Glu Phe Leu Gly Val Ile
65                  70                  75                  80

Ala Glu Ser Gln Phe Leu Leu Asn Ser Gln Leu Ser Arg Ile Phe Ala
                85                  90                  95

Ser Gly His Leu Ile Ser Ser Gln Leu Leu Leu Thr Pro Ser Lys Gly
            100                 105                 110

Ser Leu Ala Ser Val Leu Leu Pro Asn Leu Lys Phe Gly Leu Ile Ser
        115                 120                 125

Asn Asp Pro Pro Arg Ala Asp Ser His Leu Leu Pro Leu Gly Arg Met
    130                 135                 140

Trp Arg Val Glu Pro Thr Val His Ala Leu Phe Glu Asp Phe Ser Leu
145                 150                 155                 160

Gly Ser Thr Ile Leu Phe Gly Leu Arg Leu Asp Leu Glu Ala Leu Ile
                165                 170                 175

Val Ser Tyr Asn Gly Ile Glu Cys Gly Ile Leu Asn Phe Asp Asp Ala
            180                 185                 190

Ser Ala Leu Ser Ser Ala Val Lys Phe Ser Asn Ala Asn Gly Leu Thr
        195                 200                 205

Pro Thr Val Leu Gly His Val Val Arg Glu Asn Gly Glu Thr Ser Phe
    210                 215                 220

Glu Ile Asp Val Leu Pro Leu Glu Leu Trp Ser Lys Lys Gln His Arg
225                 230                 235                 240

Leu Glu Val Leu Lys Ile Pro Arg Leu Ile Pro Lys Glu Ala Asp Ser
                245                 250                 255

Gln Asn Tyr Val Lys Ala Thr Ala Leu Leu Ser Asp Glu Ile Leu Arg
            260                 265                 270

Pro Gln Thr Leu Ser Lys Lys Ala Leu Ser Leu Ser Asp Thr Ala Val
        275                 280                 285

Lys Tyr Ser Pro His Val Ala Cys Gly Val Gly Met Phe Ser Leu Phe
    290                 295                 300

Ala Val Ile Pro Phe Asp Lys Leu Ser Asp His Ser Ala Met Leu Leu
305                 310                 315                 320
```

```
Ala Val Ile Ser Leu Met Leu Phe Val Leu Ala Leu Val Ile Leu Phe
                325                 330                 335

Lys Arg Ile Gln Ser Thr Asn Thr Gln Arg Trp Asn Leu Ala Ser Ser
            340                 345                 350

Val Gly Leu Leu Ala Thr Leu Pro Ile Ile Ile Phe Leu Val Ala Asp
        355                 360                 365

Thr Leu Ile Pro Gln Gly Ser Leu Glu Asn His Ala Gln Pro Asp Val
    370                 375                 380

Gln Val Thr Thr Leu Ala Asn Arg Arg Pro Ser Ser Pro Thr Ser Leu
385                 390                 395                 400

Asp Ser Leu Gly Ala Leu Asn Ser Pro Ser Ser Pro Asn Ser Pro Ser
                405                 410                 415

Ser Ser Met Leu Gln Asn Ser Glu Met Phe Ala Ser Pro Pro Ile Ala
            420                 425                 430

Ser Gly Gln Ser Pro Val Ser Thr Phe Arg Ser Trp Leu Asp Arg Ser
        435                 440                 445

Ile Leu Pro Leu Thr Arg Glu Asn Ser Ala Ser Glu Ser Ala Val Thr
    450                 455                 460

Ala Leu Gly Pro Ser Ile Val Gln Pro Ala Ser Glu Ser Ile Thr Thr
465                 470                 475                 480

Pro Ala Gln Thr Ser Gln Ser Arg His Ala Ile Asp Asp Gly Asp Asp
                485                 490                 495

Ser Lys Thr Ser Thr Gly Arg Pro Ala Pro Thr Thr Asn Ser Pro Ile
            500                 505                 510

Ile Ala Leu Pro Pro Thr Trp Ile Ile Gly Pro Glu Asp Pro Glu Ser
        515                 520                 525

Thr Asp Pro Thr Ala Pro Thr Glu Pro Thr Glu Pro Ser Glu Pro Val
    530                 535                 540

Ala Thr Asp Glu Pro Ser Glu Thr Ser Glu Gln Thr Ser
545                 550                 555
```

<210> 403
<211> 837
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(814)
<223> RXN00840

<400> 403
gcgattaatg tgacaggagg aaaagaagtt aactgaagtt actaatgtga ctaaagttgt 60

tccctccgca ttgtctcgtt gaaaggtaag taaaactcaa gtg aca aag aca ctc 115

```
                                                    Val Thr Lys Thr Leu
                                                      1               5

ccc cga ctg ctt aca gtc gct gcc gct cta gcc att gca ctc ccg gca   163
Pro Arg Leu Leu Thr Val Ala Ala Ala Leu Ala Ile Ala Leu Pro Ala
                10                  15                  20

acc ccg gta gca tcg gct gtc aca cca gtt gaa caa gct ttc aac gcc   211
Thr Pro Val Ala Ser Ala Val Thr Pro Val Glu Gln Ala Phe Asn Ala
            25                  30                  35

tca tcg aat ctc tcc agc ggt ctc ccc gta gac caa tgg gga cgc ccc   259
Ser Ser Asn Leu Ser Ser Gly Leu Pro Val Asp Gln Trp Gly Arg Pro
        40                  45                  50

aac gag cag ttc cgc caa caa atc gaa cag gca gta aac caa ccg tgg   307
Asn Glu Gln Phe Arg Gln Gln Ile Glu Gln Ala Val Asn Gln Pro Trp
    55                  60                  65

gtc ccg cag gaa atc aag aac atc gtt tct cag gcc atg ggt ttt atc   355
Val Pro Gln Glu Ile Lys Asn Ile Val Ser Gln Ala Met Gly Phe Ile
70                  75                  80                  85

acc ggt gac ggc agc gaa ggt ggg gac att gaa atc ccc gac aac gca   403
Thr Gly Asp Gly Ser Glu Gly Gly Asp Ile Glu Ile Pro Asp Asn Ala
                90                  95                  100

cca cgc atc gcg cag ttc ttc tgg ccc acc cga tca gaa aac tgc atc   451
Pro Arg Ile Ala Gln Phe Phe Trp Pro Thr Arg Ser Glu Asn Cys Ile
            105                 110                 115

aac gga aat tct gca gcc gta gga tct gcc ttc gca gtt cca gga cca   499
Asn Gly Asn Ser Ala Ala Val Gly Ser Ala Phe Ala Val Pro Gly Pro
        120                 125                 130

gca gat ctc ccc ctc ccc ggc gca ggt gtc ggc caa acc tcc ttc gtg   547
Ala Asp Leu Pro Leu Pro Gly Ala Gly Val Gly Gln Thr Ser Phe Val
    135                 140                 145

ttc acc gca ctg gga act ggc ccc ctc gca gaa cag caa agc acc gca   595
Phe Thr Ala Leu Gly Thr Gly Pro Leu Ala Glu Gln Gln Ser Thr Ala
150                 155                 160                 165

atg act gtt caa tgg gca aac tta agc aac ttc acc cat ggc acc acg   643
Met Thr Val Gln Trp Ala Asn Leu Ser Asn Phe Thr His Gly Thr Thr
                170                 175                 180

acg ttg agc aac acc gga atc aac ccc gat ggc ccc tca acg att tcc   691
Thr Leu Ser Asn Thr Gly Ile Asn Pro Asp Gly Pro Ser Thr Ile Ser
            185                 190                 195

ggt gtg gca gac aca gga cgc ggc atc atc gtc gcc tcc atg tca ggc   739
Gly Val Ala Asp Thr Gly Arg Gly Ile Ile Val Ala Ser Met Ser Gly
        200                 205                 210

ggc ctc acc aca tcc acc gaa aac ggt tca gcg aac tgt aat ttc atc   787
Gly Leu Thr Thr Ser Thr Glu Asn Gly Ser Ala Asn Cys Asn Phe Ile
    215                 220                 225

ccg act gcc gtc gta ttc gat gtg agg taagaaaaca atgactgatc         834
Pro Thr Ala Val Val Phe Asp Val Arg
```

230 235

ttc 837

<210> 404
<211> 238
<212> PRT
<213> Corynebacterium glutamicum

<400> 404
Val Thr Lys Thr Leu Pro Arg Leu Leu Thr Val Ala Ala Ala Leu Ala
1 5 10 15

Ile Ala Leu Pro Ala Thr Pro Val Ala Ser Ala Val Thr Pro Val Glu
20 25 30

Gln Ala Phe Asn Ala Ser Ser Asn Leu Ser Ser Gly Leu Pro Val Asp
35 40 45

Gln Trp Gly Arg Pro Asn Glu Gln Phe Arg Gln Gln Ile Glu Gln Ala
50 55 60

Val Asn Gln Pro Trp Val Pro Gln Glu Ile Lys Asn Ile Val Ser Gln
65 70 75 80

Ala Met Gly Phe Ile Thr Gly Asp Gly Ser Glu Gly Gly Asp Ile Glu
85 90 95

Ile Pro Asp Asn Ala Pro Arg Ile Ala Gln Phe Phe Trp Pro Thr Arg
100 105 110

Ser Glu Asn Cys Ile Asn Gly Asn Ser Ala Ala Val Gly Ser Ala Phe
115 120 125

Ala Val Pro Gly Pro Ala Asp Leu Pro Leu Pro Gly Ala Gly Val Gly
130 135 140

Gln Thr Ser Phe Val Phe Thr Ala Leu Gly Thr Gly Pro Leu Ala Glu
145 150 155 160

Gln Gln Ser Thr Ala Met Thr Val Gln Trp Ala Asn Leu Ser Asn Phe
165 170 175

Thr His Gly Thr Thr Thr Leu Ser Asn Thr Gly Ile Asn Pro Asp Gly
180 185 190

Pro Ser Thr Ile Ser Gly Val Ala Asp Thr Gly Arg Gly Ile Ile Val
195 200 205

Ala Ser Met Ser Gly Gly Leu Thr Thr Ser Thr Glu Asn Gly Ser Ala
210 215 220

Asn Cys Asn Phe Ile Pro Thr Ala Val Val Phe Asp Val Arg
225 230 235

<210> 405
<211> 837
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(814)
<223> FRXA00840

<400> 405
gcgattaatg tgacaggagg aaaagaagtt aactgaagtt actaatgtga ctaaagttgt 60

tccctccgca ttgtctcgtt gaaaggtaag taaaactcaa gtg aca aag aca ctc 115
Val Thr Lys Thr Leu
1 5

ccc cga ctg ctt aca gtc gct gcc gct cta gcc att gca ctc ccg gca 163
Pro Arg Leu Leu Thr Val Ala Ala Ala Leu Ala Ile Ala Leu Pro Ala
10 15 20

acc ccg gta gca tcg gct gtc aca cca gtt gaa caa gct ttc aac gcc 211
Thr Pro Val Ala Ser Ala Val Thr Pro Val Glu Gln Ala Phe Asn Ala
25 30 35

tca tcg aat ctc tcc agc ggt ctc ccc gta gac caa tgg gga cgc ccc 259
Ser Ser Asn Leu Ser Ser Gly Leu Pro Val Asp Gln Trp Gly Arg Pro
40 45 50

aac gag cag ttc cgc caa caa atc gaa cag gca gta aac caa ccg tgg 307
Asn Glu Gln Phe Arg Gln Gln Ile Glu Gln Ala Val Asn Gln Pro Trp
55 60 65

gtc ccg cag gaa atc aag aac atc gtt tct cag gcc atg ggt ttt atc 355
Val Pro Gln Glu Ile Lys Asn Ile Val Ser Gln Ala Met Gly Phe Ile
70 75 80 85

acc ggt gac ggc agc gaa ggt ggg gac att gaa atc ccc gac aac gca 403
Thr Gly Asp Gly Ser Glu Gly Gly Asp Ile Glu Ile Pro Asp Asn Ala
90 95 100

cca cgc atc gcg cag ttc ttc tgg ccc acc cga tca gaa aac tgc atc 451
Pro Arg Ile Ala Gln Phe Phe Trp Pro Thr Arg Ser Glu Asn Cys Ile
105 110 115

aac gga aat tct gca gcc gta gga tct gcc ttc gca gtt cca gga cca 499
Asn Gly Asn Ser Ala Ala Val Gly Ser Ala Phe Ala Val Pro Gly Pro
120 125 130

gca gat ctc ccc ctc ccc ggc gca ggt gtc ggc caa acc tcc ttc gtg 547
Ala Asp Leu Pro Leu Pro Gly Ala Gly Val Gly Gln Thr Ser Phe Val
135 140 145

ttc acc gca ctg gga act ggc ccc ctc gca gaa cag caa agc acc gca 595
Phe Thr Ala Leu Gly Thr Gly Pro Leu Ala Glu Gln Gln Ser Thr Ala
150 155 160 165

atg act gtt caa tgg gca aac tta agc aac ttc acc cat ggc acc acg 643
Met Thr Val Gln Trp Ala Asn Leu Ser Asn Phe Thr His Gly Thr Thr
170 175 180

acg ttg agc aac acc gga atc aac ccc gat ggc ccc tca acg att tcc 691
Thr Leu Ser Asn Thr Gly Ile Asn Pro Asp Gly Pro Ser Thr Ile Ser
185 190 195

```
ggt gtg gca gac aca gga cgc ggc atc atc gtc gcc tcc atg tca ggc   739
Gly Val Ala Asp Thr Gly Arg Gly Ile Ile Val Ala Ser Met Ser Gly
        200                 205                 210

ggc ctc acc aca tcc acc gaa aac ggt tca gcg aac tgt aat ttc atc   787
Gly Leu Thr Thr Ser Thr Glu Asn Gly Ser Ala Asn Cys Asn Phe Ile
    215                 220                 225

ccg act gcc gtc gta ttc gat gtg agg taagaaaaca atgactgatc        834
Pro Thr Ala Val Val Phe Asp Val Arg
230                 235

ttc                                                              837
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<210> 406
<211> 238
<212> PRT
<213> Corynebacterium glutamicum

<400> 406

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Val Thr Lys Thr Leu Pro Arg Leu Leu Thr Val Ala Ala Ala Leu Ala
  1               5                  10                  15

Ile Ala Leu Pro Ala Thr Pro Val Ala Ser Ala Val Thr Pro Val Glu
            20                  25                  30

Gln Ala Phe Asn Ala Ser Ser Asn Leu Ser Ser Gly Leu Pro Val Asp
        35                  40                  45

Gln Trp Gly Arg Pro Asn Glu Gln Phe Arg Gln Gln Ile Glu Gln Ala
    50                  55                  60

Val Asn Gln Pro Trp Val Pro Gln Glu Ile Lys Asn Ile Val Ser Gln
65                  70                  75                  80

Ala Met Gly Phe Ile Thr Gly Asp Gly Ser Glu Gly Gly Asp Ile Glu
                85                  90                  95

Ile Pro Asp Asn Ala Pro Arg Ile Ala Gln Phe Phe Trp Pro Thr Arg
            100                 105                 110

Ser Glu Asn Cys Ile Asn Gly Asn Ser Ala Ala Val Gly Ser Ala Phe
        115                 120                 125

Ala Val Pro Gly Pro Ala Asp Leu Pro Leu Pro Gly Ala Gly Val Gly
    130                 135                 140

Gln Thr Ser Phe Val Phe Thr Ala Leu Gly Thr Gly Pro Leu Ala Glu
145                 150                 155                 160

Gln Gln Ser Thr Ala Met Thr Val Gln Trp Ala Asn Leu Ser Asn Phe
                165                 170                 175

Thr His Gly Thr Thr Thr Leu Ser Asn Thr Gly Ile Asn Pro Asp Gly
            180                 185                 190

Pro Ser Thr Ile Ser Gly Val Ala Asp Thr Gly Arg Gly Ile Ile Val
        195                 200                 205

Ala Ser Met Ser Gly Gly Leu Thr Thr Ser Thr Glu Asn Gly Ser Ala
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```
    210                 215                 220

Asn Cys Asn Phe Ile Pro Thr Ala Val Val Phe Asp Val Arg
225                 230                 235


<210> 407
<211> 660
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(637)
<223> RXN00841

<400> 407
gcctccatgt caggcggcct caccacatcc accgaaaacg gttcagcgaa ctgtaatttc 60

atcccgactg ccgtcgtatt cgatgtgagg taagaaaaca atg act gat ctt cat   115
                                            Met Thr Asp Leu His
                                              1               5

ccc gta aag cag gaa att ttc aac act gct gaa tcc ata aac aca gat   163
Pro Val Lys Gln Glu Ile Phe Asn Thr Ala Glu Ser Ile Asn Thr Asp
                 10                  15                  20

ccc aag ggg ttt ctc cgc gag gta gac acc ttc aaa gta acc gac ttc   211
Pro Lys Gly Phe Leu Arg Glu Val Asp Thr Phe Lys Val Thr Asp Phe
             25                  30                  35

ggc ctg tac atg gct cgt ggt gca aac cac ccc aag ttc gga tac ttg   259
Gly Leu Tyr Met Ala Arg Gly Ala Asn His Pro Lys Phe Gly Tyr Leu
         40                  45                  50

gaa agc tgg ctc ctc cca gaa ctt gga ttg cgt gcc aac att ttc cac   307
Glu Ser Trp Leu Leu Pro Glu Leu Gly Leu Arg Ala Asn Ile Phe His
     55                  60                  65

ttc cgc aaa ggc gtg gat gaa cgt cag gat tac tac atc gat gtc gct   355
Phe Arg Lys Gly Val Asp Glu Arg Gln Asp Tyr Tyr Ile Asp Val Ala
 70                  75                  80                  85

gaa att cgc gtc gaa gac aac atc tgg acc acc cgc gac ctc tac gtg   403
Glu Ile Arg Val Glu Asp Asn Ile Trp Thr Thr Arg Asp Leu Tyr Val
                 90                  95                 100

gat ctc atc tct gtc tgc gga gaa cca gta aca gtc atg gac atc gac   451
Asp Leu Ile Ser Val Cys Gly Glu Pro Val Thr Val Met Asp Ile Asp
            105                 110                 115

gaa cta gct gca gca acc tca gca ggg ctt atc act gca gat gac gct   499
Glu Leu Ala Ala Ala Thr Ser Ala Gly Leu Ile Thr Ala Asp Asp Ala
        120                 125                 130

gag cgc gca att gat gcc acc ttg aat gct gtt gaa gga atc acc cgc   547
Glu Arg Ala Ile Asp Ala Thr Leu Asn Ala Val Glu Gly Ile Thr Arg
    135                 140                 145

cac ggc gac gat cct atg cag tgg ctg cgc tcc aag gga atc gaa ctc   595
His Gly Asp Asp Pro Met Gln Trp Leu Arg Ser Lys Gly Ile Glu Leu
```

```
150                 155                 160                 165

acc tgg gct gac gcc agc cag gta gag ctc gtc cct gca gag          637
Thr Trp Ala Asp Ala Ser Gln Val Glu Leu Val Pro Ala Glu
                170                 175

taactacttc ctaaccgctg ctt                                        660


<210> 408
<211> 179
<212> PRT
<213> Corynebacterium glutamicum

<400> 408
Met Thr Asp Leu His Pro Val Lys Gln Glu Ile Phe Asn Thr Ala Glu
  1               5                  10                  15

Ser Ile Asn Thr Asp Pro Lys Gly Phe Leu Arg Glu Val Asp Thr Phe
             20                  25                  30

Lys Val Thr Asp Phe Gly Leu Tyr Met Ala Arg Gly Ala Asn His Pro
         35                  40                  45

Lys Phe Gly Tyr Leu Glu Ser Trp Leu Leu Pro Glu Leu Gly Leu Arg
     50                  55                  60

Ala Asn Ile Phe His Phe Arg Lys Gly Val Asp Glu Arg Gln Asp Tyr
 65                  70                  75                  80

Tyr Ile Asp Val Ala Glu Ile Arg Val Glu Asp Asn Ile Trp Thr Thr
                 85                  90                  95

Arg Asp Leu Tyr Val Asp Leu Ile Ser Val Cys Gly Glu Pro Val Thr
            100                 105                 110

Val Met Asp Ile Asp Glu Leu Ala Ala Ala Thr Ser Ala Gly Leu Ile
        115                 120                 125

Thr Ala Asp Asp Ala Glu Arg Ala Ile Asp Ala Thr Leu Asn Ala Val
    130                 135                 140

Glu Gly Ile Thr Arg His Gly Asp Asp Pro Met Gln Trp Leu Arg Ser
145                 150                 155                 160

Lys Gly Ile Glu Leu Thr Trp Ala Asp Ala Ser Gln Val Glu Leu Val
                165                 170                 175

Pro Ala Glu


<210> 409
<211> 660
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(637)
<223> FRXA00841
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<400> 409
gcctccatgt caggcggcct caccacatcc accgaaaacg gttcagcgaa ctgtaatttc 60

atcccgactg ccgtcgtatt cgatgtgagg taagaaaaca atg act gat ctt cat 115
Met Thr Asp Leu His
1 5

ccc gta aag cag gaa att ttc aac act gct gaa tcc ata aac aca gat 163
Pro Val Lys Gln Glu Ile Phe Asn Thr Ala Glu Ser Ile Asn Thr Asp
10 15 20

ccc aag ggg ttt ctc cgc gag gta gac acc ttc aaa gta acc gac ttc 211
Pro Lys Gly Phe Leu Arg Glu Val Asp Thr Phe Lys Val Thr Asp Phe
25 30 35

ggc ctg tac atg gct cgt ggt gca aac cac ccc aag ttc gga tac ttg 259
Gly Leu Tyr Met Ala Arg Gly Ala Asn His Pro Lys Phe Gly Tyr Leu
40 45 50

gaa agc tgg ctc ctc cca gaa ctt gga ttg cgt gcc aac att ttc cac 307
Glu Ser Trp Leu Leu Pro Glu Leu Gly Leu Arg Ala Asn Ile Phe His
55 60 65

ttc cgc aaa ggc gtg gat gaa cgt cag gat tac tac atc gat gtc gct 355
Phe Arg Lys Gly Val Asp Glu Arg Gln Asp Tyr Tyr Ile Asp Val Ala
70 75 80 85

gaa att cgc gtc gaa gac aac atc tgg acc acc cgc gac ctc tac gtg 403
Glu Ile Arg Val Glu Asp Asn Ile Trp Thr Thr Arg Asp Leu Tyr Val
90 95 100

gat ctc atc tct gtc tgc gga gaa cca gta aca gtc atg gac atc gac 451
Asp Leu Ile Ser Val Cys Gly Glu Pro Val Thr Val Met Asp Ile Asp
105 110 115

gaa cta gct gca gca acc tca gca ggg ctt atc act gca gat gac gct 499
Glu Leu Ala Ala Ala Thr Ser Ala Gly Leu Ile Thr Ala Asp Asp Ala
120 125 130

gag cgc gca att gat gcc acc ttg aat gct gtt gaa gga atc acc cgc 547
Glu Arg Ala Ile Asp Ala Thr Leu Asn Ala Val Glu Gly Ile Thr Arg
135 140 145

cac ggc gac gat cct atg cag tgg ctg cgc tcc aag gga atc gaa ctc 595
His Gly Asp Asp Pro Met Gln Trp Leu Arg Ser Lys Gly Ile Glu Leu
150 155 160 165

acc tgg gct gac gcc agc cag gta gag ctc gtc cct gca gag 637
Thr Trp Ala Asp Ala Ser Gln Val Glu Leu Val Pro Ala Glu
170 175

taactacttc ctaaccgctg ctt 660

<210> 410
<211> 179
<212> PRT
<213> Corynebacterium glutamicum

<400> 410

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Met Thr Asp Leu His Pro Val Lys Gln Glu Ile Phe Asn Thr Ala Glu
  1               5                  10                  15

Ser Ile Asn Thr Asp Pro Lys Gly Phe Leu Arg Glu Val Asp Thr Phe
             20                  25                  30

Lys Val Thr Asp Phe Gly Leu Tyr Met Ala Arg Gly Ala Asn His Pro
         35                  40                  45

Lys Phe Gly Tyr Leu Glu Ser Trp Leu Leu Pro Glu Leu Gly Leu Arg
     50                  55                  60

Ala Asn Ile Phe His Phe Arg Lys Gly Val Asp Glu Arg Gln Asp Tyr
 65                  70                  75                  80

Tyr Ile Asp Val Ala Glu Ile Arg Val Glu Asp Asn Ile Trp Thr Thr
                 85                  90                  95

Arg Asp Leu Tyr Val Asp Leu Ile Ser Val Cys Gly Glu Pro Val Thr
            100                 105                 110

Val Met Asp Ile Asp Glu Leu Ala Ala Ala Thr Ser Ala Gly Leu Ile
        115                 120                 125

Thr Ala Asp Asp Ala Glu Arg Ala Ile Asp Ala Thr Leu Asn Ala Val
    130                 135                 140

Glu Gly Ile Thr Arg His Gly Asp Asp Pro Met Gln Trp Leu Arg Ser
145                 150                 155                 160

Lys Gly Ile Glu Leu Thr Trp Ala Asp Ala Ser Gln Val Glu Leu Val
                165                 170                 175

Pro Ala Glu
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<210> 411
<211> 993
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(970)
<223> RXN00846

<400> 411

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ctgcgggaga ctcgggtaga agcgaaaaat aacggtatcc tcggggctgc ggatggctgg 60

cctgggggaa tttcaagtgc tgcaagttgg aggaaaaacg atg ttg aag aat gat   115
                                            Met Leu Lys Asn Asp
                                              1               5

ctg tct ggt gct cga gtt gta gct gtg cat gcg cac cct gac gat gag   163
Leu Ser Gly Ala Arg Val Val Ala Val His Ala His Pro Asp Asp Glu
                10                  15                  20

gcg att acc acc ggt ggt gtg ctt gcg gat ctt gct gct cgt ggc gcc   211
Ala Ile Thr Thr Gly Gly Val Leu Ala Asp Leu Ala Ala Arg Gly Ala
            25                  30                  35
```

```
gat gtc acg gta att acc tgc acg ttg ggc gag cag ggt gag gtt atc   259
Asp Val Thr Val Ile Thr Cys Thr Leu Gly Glu Gln Gly Glu Val Ile
         40                  45                  50

ggt gag aca ttc gcg cag cta gtc aac ggt gat gcg gat cag ctt ggc   307
Gly Glu Thr Phe Ala Gln Leu Val Asn Gly Asp Ala Asp Gln Leu Gly
     55                  60                  65

ggg ttt agg atc cat gag ctt tac gcc tcg ctg gag att ctg ggc gtg   355
Gly Phe Arg Ile His Glu Leu Tyr Ala Ser Leu Glu Ile Leu Gly Val
 70                  75                  80                  85

cgt ggc att cat ctg ggt ggc gct ggc tgc tgg agg gat tcc ggt atg   403
Arg Gly Ile His Leu Gly Gly Ala Gly Cys Trp Arg Asp Ser Gly Met
                 90                  95                 100

gtt ggt gat cct gca aat gag cat ccg cgt gcg ttt att cac tct ggt   451
Val Gly Asp Pro Ala Asn Glu His Pro Arg Ala Phe Ile His Ser Gly
            105                 110                 115

gac cgt gca gtg gag caa ttg aaa gaa ctt ctt gcg gaa ttg aag cca   499
Asp Arg Ala Val Glu Gln Leu Lys Glu Leu Leu Ala Glu Leu Lys Pro
        120                 125                 130

cat ctt ttg atc acc tat ggc cct gac ggc ggc tat ggg cac ccc gat   547
His Leu Leu Ile Thr Tyr Gly Pro Asp Gly Gly Tyr Gly His Pro Asp
    135                 140                 145

cac att cgt gcg cat gaa atc acc cac gca gca gcc ggc gag caa cgc   595
His Ile Arg Ala His Glu Ile Thr His Ala Ala Ala Gly Glu Gln Arg
150                 155                 160                 165

att ctg tgg gct gtg agc gac cgt gag gag ctc gag gac ggt cta aag   643
Ile Leu Trp Ala Val Ser Asp Arg Glu Glu Leu Glu Asp Gly Leu Lys
                170                 175                 180

gca atc act ggg ctt cct gaa ggt tgg ggc agg gga gag ctc tct gcg   691
Ala Ile Thr Gly Leu Pro Glu Gly Trp Gly Arg Gly Glu Leu Ser Ala
            185                 190                 195

gtc gat tcc gtg gac ctc tct gtt gag ctg aac gat gaa gtg tat gcc   739
Val Asp Ser Val Asp Leu Ser Val Glu Leu Asn Asp Glu Val Tyr Ala
        200                 205                 210

acc aag gtg gaa tcc atg cgc gcg cat gcg aca caa ttg tgg atc gct   787
Thr Lys Val Glu Ser Met Arg Ala His Ala Thr Gln Leu Trp Ile Ala
    215                 220                 225

gac ggt tcc gta tct cgc acc aac ccg gtt gcc gca cac gca gtg aca   835
Asp Gly Ser Val Ser Arg Thr Asn Pro Val Ala Ala His Ala Val Thr
230                 235                 240                 245

cag cag gac aat gtg aag gtg tgg gcg cta tct aat ttg att gca caa   883
Gln Gln Asp Asn Val Lys Val Trp Ala Leu Ser Asn Leu Ile Ala Gln
                250                 255                 260

ccc atc atg cgc cac gag cac tac caa ctc ggc gcc gga aca cca ctg   931
Pro Ile Met Arg His Glu His Tyr Gln Leu Gly Ala Gly Thr Pro Leu
            265                 270                 275
```

```
cct gaa ggt gca act gga gtg ctt gac gga ctg gag ttc tgacacggtt    980
Pro Glu Gly Ala Thr Gly Val Leu Asp Gly Leu Glu Phe
        280                 285                 290

atggcagaat cta                                                   993


<210> 412
<211> 290
<212> PRT
<213> Corynebacterium glutamicum

<400> 412
Met Leu Lys Asn Asp Leu Ser Gly Ala Arg Val Val Ala Val His Ala
  1               5                  10                  15

His Pro Asp Asp Glu Ala Ile Thr Thr Gly Gly Val Leu Ala Asp Leu
             20                  25                  30

Ala Ala Arg Gly Ala Asp Val Thr Val Ile Thr Cys Thr Leu Gly Glu
         35                  40                  45

Gln Gly Glu Val Ile Gly Glu Thr Phe Ala Gln Leu Val Asn Gly Asp
     50                  55                  60

Ala Asp Gln Leu Gly Gly Phe Arg Ile His Glu Leu Tyr Ala Ser Leu
 65                  70                  75                  80

Glu Ile Leu Gly Val Arg Gly Ile His Leu Gly Gly Ala Gly Cys Trp
                 85                  90                  95

Arg Asp Ser Gly Met Val Gly Asp Pro Ala Asn Glu His Pro Arg Ala
            100                 105                 110

Phe Ile His Ser Gly Asp Arg Ala Val Glu Gln Leu Lys Glu Leu Leu
        115                 120                 125

Ala Glu Leu Lys Pro His Leu Leu Ile Thr Tyr Gly Pro Asp Gly Gly
    130                 135                 140

Tyr Gly His Pro Asp His Ile Arg Ala His Glu Ile Thr His Ala Ala
145                 150                 155                 160

Ala Gly Glu Gln Arg Ile Leu Trp Ala Val Ser Asp Arg Glu Glu Leu
                165                 170                 175

Glu Asp Gly Leu Lys Ala Ile Thr Gly Leu Pro Glu Gly Trp Gly Arg
            180                 185                 190

Gly Glu Leu Ser Ala Val Asp Ser Val Asp Leu Ser Val Glu Leu Asn
        195                 200                 205

Asp Glu Val Tyr Ala Thr Lys Val Glu Ser Met Arg Ala His Ala Thr
    210                 215                 220

Gln Leu Trp Ile Ala Asp Gly Ser Val Ser Arg Thr Asn Pro Val Ala
225                 230                 235                 240

Ala His Ala Val Thr Gln Gln Asp Asn Val Lys Val Trp Ala Leu Ser
                245                 250                 255
```

```
Asn Leu Ile Ala Gln Pro Ile Met Arg His Glu His Tyr Gln Leu Gly
            260                 265                 270

Ala Gly Thr Pro Leu Pro Glu Gly Ala Thr Gly Val Leu Asp Gly Leu
        275                 280                 285

Glu Phe
    290


<210> 413
<211> 487
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(487)
<223> FRXA00846

<400> 413
ctgcgggaga ctcgggtaga agcgaaaaat aacggtatcc tcggggctgc ggatggctgg 60

cctgggggaa tttcaagtgc tgcaagttgg aggaaaaacg atg ttg aag aat gat   115
                                          Met Leu Lys Asn Asp
                                            1               5

ctg tct ggt gct cga gtt gta gct gtg cat gcg cac cct gac gat gag   163
Leu Ser Gly Ala Arg Val Val Ala Val His Ala His Pro Asp Asp Glu
                10                  15                  20

gcg att acc acc ggt ggt gtg ctt gcg gat ctt gct gct cgt ggc gcc   211
Ala Ile Thr Thr Gly Gly Val Leu Ala Asp Leu Ala Ala Arg Gly Ala
            25                  30                  35

gat gtc acg gta att acc tgc acg ttg ggc gag cag ggt gag gtt atc   259
Asp Val Thr Val Ile Thr Cys Thr Leu Gly Glu Gln Gly Glu Val Ile
        40                  45                  50

ggt gag aca ttc gcg cag cta gtc aac ggt gat gcg gat cag ctt ggc   307
Gly Glu Thr Phe Ala Gln Leu Val Asn Gly Asp Ala Asp Gln Leu Gly
    55                  60                  65

ggg ttt agg atc cat gag ctt tac gcc tcg ctg gag att ctg ggc gtg   355
Gly Phe Arg Ile His Glu Leu Tyr Ala Ser Leu Glu Ile Leu Gly Val
70                  75                  80                  85

cgt ggc att cat ctg ggt ggc gct ggc tgc tgg agg gat tcc ggt atg   403
Arg Gly Ile His Leu Gly Gly Ala Gly Cys Trp Arg Asp Ser Gly Met
                90                  95                  100

gtt ggt gat cct gca aat gag cat ccg cgt gcg ttt att cac tct ggt   451
Val Gly Asp Pro Ala Asn Glu His Pro Arg Ala Phe Ile His Ser Gly
            105                 110                 115

gac cgt gca gtg gag caa ttg aaa gaa ctt ctt gcg                   487
Asp Arg Ala Val Glu Gln Leu Lys Glu Leu Leu Ala
        120                 125


<210> 414
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<211> 129
<212> PRT
<213> Corynebacterium glutamicum

<400> 414
Met Leu Lys Asn Asp Leu Ser Gly Ala Arg Val Val Ala Val His Ala
1 5 10 15

His Pro Asp Asp Glu Ala Ile Thr Thr Gly Gly Val Leu Ala Asp Leu
20 25 30

Ala Ala Arg Gly Ala Asp Val Thr Val Ile Thr Cys Thr Leu Gly Glu
35 40 45

Gln Gly Glu Val Ile Gly Glu Thr Phe Ala Gln Leu Val Asn Gly Asp
50 55 60

Ala Asp Gln Leu Gly Gly Phe Arg Ile His Glu Leu Tyr Ala Ser Leu
65 70 75 80

Glu Ile Leu Gly Val Arg Gly Ile His Leu Gly Gly Ala Gly Cys Trp
85 90 95

Arg Asp Ser Gly Met Val Gly Asp Pro Ala Asn Glu His Pro Arg Ala
100 105 110

Phe Ile His Ser Gly Asp Arg Ala Val Glu Gln Leu Lys Glu Leu Leu
115 120 125

Ala

<210> 415
<211> 951
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(928)
<223> RXN00850

<400> 415
ggcagttgtg ccggtatacg tggcgtcatg gataatgatc gcataaatga atacagcgaa 60

attacctgtt tcagatattt aggaaggctc acttttcaac atg gct aat cca ttc 115
Met Ala Asn Pro Phe
1 5

tcc aag gca tgg aag tac ctc atg gcg ttg ttc gac tcc aag att gag 163
Ser Lys Ala Trp Lys Tyr Leu Met Ala Leu Phe Asp Ser Lys Ile Glu
10 15 20

gag aac gcg gat cct aag gta cag atc cag caa gcc atc gaa gat gct 211
Glu Asn Ala Asp Pro Lys Val Gln Ile Gln Gln Ala Ile Glu Asp Ala
25 30 35

cag cgc cag cat cag gag ctc tcc cag cag gca gca gct gtt att ggt 259
Gln Arg Gln His Gln Glu Leu Ser Gln Gln Ala Ala Ala Val Ile Gly
40 45 50

```
aac cag cgt cag ctt gaa atg cag ctg aac cgc cgt ctg gct gaa att   307
Asn Gln Arg Gln Leu Glu Met Gln Leu Asn Arg Arg Leu Ala Glu Ile
     55                  60                  65

gag aag ctg cag ggc aac acc cgc cag gct atc cag ctg gct gac aag   355
Glu Lys Leu Gln Gly Asn Thr Arg Gln Ala Ile Gln Leu Ala Asp Lys
 70                  75                  80                  85

gct cgc gct gac ggt gat gtc aag aag gct act gag tac gaa aac gcc   403
Ala Arg Ala Asp Gly Asp Val Lys Lys Ala Thr Glu Tyr Glu Asn Ala
                 90                  95                 100

gct gag gct ttc gct gca cag ctg gtt act gct gag cag tcc gtt gaa   451
Ala Glu Ala Phe Ala Ala Gln Leu Val Thr Ala Glu Gln Ser Val Glu
            105                 110                 115

gat acc aag cag ctc cac gac cag gct ctg cag cag gct gat cag gct   499
Asp Thr Lys Gln Leu His Asp Gln Ala Leu Gln Gln Ala Asp Gln Ala
        120                 125                 130

aag aag gct gtg gag cgt aac tcc atg gct ttg cag cag aag gtt gct   547
Lys Lys Ala Val Glu Arg Asn Ser Met Ala Leu Gln Gln Lys Val Ala
    135                 140                 145

gag cgc acc aag ctt ctg agc cag ctg gag cag gcg aag atg cag gaa   595
Glu Arg Thr Lys Leu Leu Ser Gln Leu Glu Gln Ala Lys Met Gln Glu
150                 155                 160                 165

aag gtt tcc gag tcc ctg aag tcc atg gat tct ttg acc tcc ggc agc   643
Lys Val Ser Glu Ser Leu Lys Ser Met Asp Ser Leu Thr Ser Gly Ser
                170                 175                 180

act cct aac ctg gat caa gtt cgt gag aag att gag cgt cgt tac gct   691
Thr Pro Asn Leu Asp Gln Val Arg Glu Lys Ile Glu Arg Arg Tyr Ala
            185                 190                 195

aac gcg ctt ggc cag gct gag ctt gcg tcc aac tct gtt gag ggc cgc   739
Asn Ala Leu Gly Gln Ala Glu Leu Ala Ser Asn Ser Val Glu Gly Arg
        200                 205                 210

atg gct gag gtt gag cag gct ggc gtt cag atg gct gga cac tcc cgc   787
Met Ala Glu Val Glu Gln Ala Gly Val Gln Met Ala Gly His Ser Arg
    215                 220                 225

ctt gag cag atc cgc gct gag atg gct ggt ggt tcc ctg acc gct ggt   835
Leu Glu Gln Ile Arg Ala Glu Met Ala Gly Gly Ser Leu Thr Ala Gly
230                 235                 240                 245

aac aag cag gag tcc att gag gct cct gca gcg ggc aac aac gtc act   883
Asn Lys Gln Glu Ser Ile Glu Ala Pro Ala Ala Gly Asn Asn Val Thr
                250                 255                 260

gat gac gca gtt gca cag cgc atg cgt gag ctg cgc ggc gag gct       928
Asp Asp Ala Val Ala Gln Arg Met Arg Glu Leu Arg Gly Glu Ala
            265                 270                 275

taaacctgcc acagcagact aaa                                        951
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<210> 416

<211> 276
<212> PRT
<213> Corynebacterium glutamicum

<400> 416

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Met Ala Asn Pro Phe Ser Lys Ala Trp Lys Tyr Leu Met Ala Leu Phe
  1               5                  10                  15

Asp Ser Lys Ile Glu Glu Asn Ala Asp Pro Lys Val Gln Ile Gln Gln
             20                  25                  30

Ala Ile Glu Asp Ala Gln Arg Gln His Gln Glu Leu Ser Gln Gln Ala
         35                  40                  45

Ala Ala Val Ile Gly Asn Gln Arg Gln Leu Glu Met Gln Leu Asn Arg
     50                  55                  60

Arg Leu Ala Glu Ile Glu Lys Leu Gln Gly Asn Thr Arg Gln Ala Ile
 65                  70                  75                  80

Gln Leu Ala Asp Lys Ala Arg Ala Asp Gly Asp Val Lys Lys Ala Thr
                 85                  90                  95

Glu Tyr Glu Asn Ala Ala Glu Ala Phe Ala Ala Gln Leu Val Thr Ala
            100                 105                 110

Glu Gln Ser Val Glu Asp Thr Lys Gln Leu His Asp Gln Ala Leu Gln
        115                 120                 125

Gln Ala Asp Gln Ala Lys Lys Ala Val Glu Arg Asn Ser Met Ala Leu
    130                 135                 140

Gln Gln Lys Val Ala Glu Arg Thr Lys Leu Leu Ser Gln Leu Glu Gln
145                 150                 155                 160

Ala Lys Met Gln Glu Lys Val Ser Glu Ser Leu Lys Ser Met Asp Ser
                165                 170                 175

Leu Thr Ser Gly Ser Thr Pro Asn Leu Asp Gln Val Arg Glu Lys Ile
            180                 185                 190

Glu Arg Arg Tyr Ala Asn Ala Leu Gly Gln Ala Glu Leu Ala Ser Asn
        195                 200                 205

Ser Val Glu Gly Arg Met Ala Glu Val Glu Gln Ala Gly Val Gln Met
    210                 215                 220

Ala Gly His Ser Arg Leu Glu Gln Ile Arg Ala Glu Met Ala Gly Gly
225                 230                 235                 240

Ser Leu Thr Ala Gly Asn Lys Gln Glu Ser Ile Glu Ala Pro Ala Ala
                245                 250                 255

Gly Asn Asn Val Thr Asp Asp Ala Val Ala Gln Arg Met Arg Glu Leu
            260                 265                 270

Arg Gly Glu Ala
        275
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<210> 417

<211> 336
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> RXN00854

<400> 417
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ggacacgtaa cttctgtgct tgcgctgtat tatcgtcccc atg cgt tta tcg gag 115
Met Arg Leu Ser Glu
1 5

ttt cgg caa ctc att gaa gat gaa ttc gga gaa gcc aaa ggg gag tgg 163
Phe Arg Gln Leu Ile Glu Asp Glu Phe Gly Glu Ala Lys Gly Glu Trp
10 15 20

att gca cac tcg cat gtg att ggt gcc ctc ggc gtc act gca gat gtt 211
Ile Ala His Ser His Val Ile Gly Ala Leu Gly Val Thr Ala Asp Val
25 30 35

gca gta gat acc ggg gtt gat ctg cgc gat gta tgg gaa caa ctg tgc 259
Ala Val Asp Thr Gly Val Asp Leu Arg Asp Val Trp Glu Gln Leu Cys
40 45 50

att gat ttc agt gtt ccc gaa gag cga cga ctt ggt aaa gat gaa cca 307
Ile Asp Phe Ser Val Pro Glu Glu Arg Arg Leu Gly Lys Asp Glu Pro
55 60 65

ggg ttc tagcttgttc gaggggttc gca 336
Gly Phe
70

<210> 418
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 418
Met Arg Leu Ser Glu Phe Arg Gln Leu Ile Glu Asp Glu Phe Gly Glu
1 5 10 15

Ala Lys Gly Glu Trp Ile Ala His Ser His Val Ile Gly Ala Leu Gly
20 25 30

Val Thr Ala Asp Val Ala Val Asp Thr Gly Val Asp Leu Arg Asp Val
35 40 45

Trp Glu Gln Leu Cys Ile Asp Phe Ser Val Pro Glu Glu Arg Arg Leu
50 55 60

Gly Lys Asp Glu Pro Gly Phe
65 70

<210> 419
<211> 336

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> FRXA00854

<400> 419
ttcatccgcc ctggaagacg gtcatgacgg ggacccttct tagggtcgct gtcggagatt 60

ggacacgtaa cttctgtgct tgcgctgtat tatcgtcccc atg cgt tta tcg gag 115
Met Arg Leu Ser Glu
1 5

ttt cgg caa ctc att gaa gat gaa ttc gga gaa gcc aaa ggg gag tgg 163
Phe Arg Gln Leu Ile Glu Asp Glu Phe Gly Glu Ala Lys Gly Glu Trp
10 15 20

att gca cac tcg cat gtg att ggt gcc ctc ggc gtc act gca gat gtt 211
Ile Ala His Ser His Val Ile Gly Ala Leu Gly Val Thr Ala Asp Val
25 30 35

gca gta gat acc ggg gtt gat ctg cgc gat gta tgg gaa caa ctg tgc 259
Ala Val Asp Thr Gly Val Asp Leu Arg Asp Val Trp Glu Gln Leu Cys
40 45 50

att gat ttc agt gtt ccc gaa gag cga cga ctt ggt aaa gat gaa cca 307
Ile Asp Phe Ser Val Pro Glu Glu Arg Arg Leu Gly Lys Asp Glu Pro
55 60 65

ggg ttc tagcttgttc gaggggttc gca 336
Gly Phe
70

<210> 420
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 420
Met Arg Leu Ser Glu Phe Arg Gln Leu Ile Glu Asp Glu Phe Gly Glu
1 5 10 15

Ala Lys Gly Glu Trp Ile Ala His Ser His Val Ile Gly Ala Leu Gly
20 25 30

Val Thr Ala Asp Val Ala Val Asp Thr Gly Val Asp Leu Arg Asp Val
35 40 45

Trp Glu Gln Leu Cys Ile Asp Phe Ser Val Pro Glu Glu Arg Arg Leu
50 55 60

Gly Lys Asp Glu Pro Gly Phe
65 70

<210> 421
<211> 408
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> RXN00855

<400> 421
taaaaacctc tcgacggacg aagcgccaca aaagcaagag aagaatataa gtgaaccaaa 60

ttccgtttag tgtacgtcta gacgcctaaa cttacctgtt atg act tat ttt gcc 115
Met Thr Tyr Phe Ala
1 5

gtg ctt tac aca tac aac cca gac agc gag aaa gtc gct gaa gtt cgt 163
Val Leu Tyr Thr Tyr Asn Pro Asp Ser Glu Lys Val Ala Glu Val Arg
10 15 20

acc gtc cac cgc gag ttc att gcc aac ctt cat gcg gag ggc aaa atc 211
Thr Val His Arg Glu Phe Ile Ala Asn Leu His Ala Glu Gly Lys Ile
25 30 35

gtt ggc tcc ggt cct ttc gtg gac ggc gac ggt ggc gcg ctg att gtc 259
Val Gly Ser Gly Pro Phe Val Asp Gly Asp Gly Gly Ala Leu Ile Val
40 45 50

atc aag ttg gaa gaa ggc tcc aac ctt gtt gat gct gaa acc ctg atg 307
Ile Lys Leu Glu Glu Gly Ser Asn Leu Val Asp Ala Glu Thr Leu Met
55 60 65

aac aat gat cca ttc cac gta gaa aac gtg ctg gac aac cgc gtc atc 355
Asn Asn Asp Pro Phe His Val Glu Asn Val Leu Asp Asn Arg Val Ile
70 75 80 85

cgt agc tgg aac cct gtg acc aaa gat ttc taggcaactt tttctttaac 405
Arg Ser Trp Asn Pro Val Thr Lys Asp Phe
90 95

aat 408

<210> 422
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 422
Met Thr Tyr Phe Ala Val Leu Tyr Thr Tyr Asn Pro Asp Ser Glu Lys
1 5 10 15

Val Ala Glu Val Arg Thr Val His Arg Glu Phe Ile Ala Asn Leu His
20 25 30

Ala Glu Gly Lys Ile Val Gly Ser Gly Pro Phe Val Asp Gly Asp Gly
35 40 45

Gly Ala Leu Ile Val Ile Lys Leu Glu Glu Gly Ser Asn Leu Val Asp
50 55 60

Ala Glu Thr Leu Met Asn Asn Asp Pro Phe His Val Glu Asn Val Leu
65 70 75 80

```
Asp Asn Arg Val Ile Arg Ser Trp Asn Pro Val Thr Lys Asp Phe
                 85                  90                  95


<210> 423
<211> 408
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> FRXA00855

<400> 423
taaaaacctc tcgacggacg aagcgccaca aaagcaagag aagaatataa gtgaaccaaa 60

ttccgtttag tgtacgtcta gacgcctaaa cttacctgtt atg act tat ttt gcc   115
                                          Met Thr Tyr Phe Ala
                                            1               5

gtg ctt tac aca tac aac cca gac agc gag aaa gtc gct gaa gtt cgt   163
Val Leu Tyr Thr Tyr Asn Pro Asp Ser Glu Lys Val Ala Glu Val Arg
                10                  15                  20

acc gtc cac cgc gag ttc att gcc aac ctt cat gcg gag ggc aaa atc   211
Thr Val His Arg Glu Phe Ile Ala Asn Leu His Ala Glu Gly Lys Ile
            25                  30                  35

gtt ggc tcc ggt cct ttc gtg gac ggc gac ggt ggc gcg ctg att gtc   259
Val Gly Ser Gly Pro Phe Val Asp Gly Asp Gly Gly Ala Leu Ile Val
        40                  45                  50

atc aag ttg gaa gaa ggc tcc aac ctt gtt gat gct gaa acc ctg atg   307
Ile Lys Leu Glu Glu Gly Ser Asn Leu Val Asp Ala Glu Thr Leu Met
    55                  60                  65

aac aat gat cca ttc cac gta gaa aac gtg ctg gac aac cgc gtc atc   355
Asn Asn Asp Pro Phe His Val Glu Asn Val Leu Asp Asn Arg Val Ile
70                  75                  80                  85

cgt agc tgg aac cct gtg acc aaa gat ttc taggcaactt tttctttaac     405
Arg Ser Trp Asn Pro Val Thr Lys Asp Phe
                90                  95

aat                                                               408


<210> 424
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 424
Met Thr Tyr Phe Ala Val Leu Tyr Thr Tyr Asn Pro Asp Ser Glu Lys
  1               5                  10                  15

Val Ala Glu Val Arg Thr Val His Arg Glu Phe Ile Ala Asn Leu His
            20                  25                  30
```

```
Ala Glu Gly Lys Ile Val Gly Ser Gly Pro Phe Val Asp Gly Asp Gly
         35                  40                  45

Gly Ala Leu Ile Val Ile Lys Leu Glu Glu Gly Ser Asn Leu Val Asp
     50                  55                  60

Ala Glu Thr Leu Met Asn Asn Asp Pro Phe His Val Glu Asn Val Leu
 65                  70                  75                  80

Asp Asn Arg Val Ile Arg Ser Trp Asn Pro Val Thr Lys Asp Phe
                 85                  90                  95


<210> 425
<211> 1044
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1021)
<223> RXN00869

<400> 425
gccaacaccg cgggtgcgct tgtggcgtcc cgtcttgaat gctccaccgc aatgcctact 60

accgatgagg tggaagcctc cctcaaccag aaagtctgat atg act cct ccg att   115
                                            Met Thr Pro Pro Ile
                                              1               5

atc tcc cca gag agc ttt gaa gcc cta agg cgg atg cgt gcg gct gaa   163
Ile Ser Pro Glu Ser Phe Glu Ala Leu Arg Arg Met Arg Ala Ala Glu
                 10                  15                  20

ccc acg atg gtg gcg gaa cgt ttc aag cag cgc cgt aag cgt gaa ctg   211
Pro Thr Met Val Ala Glu Arg Phe Lys Gln Arg Arg Lys Arg Glu Leu
             25                  30                  35

ctc ggt gag gac ggc aag ctg ttt atc gtg gct gcc gac cac cca gcg   259
Leu Gly Glu Asp Gly Lys Leu Phe Ile Val Ala Ala Asp His Pro Ala
         40                  45                  50

cgc ggc gca ctt gct gtt ggc gac aat gaa acc gcc atg gct aac cgc   307
Arg Gly Ala Leu Ala Val Gly Asp Asn Glu Thr Ala Met Ala Asn Arg
     55                  60                  65

tat gaa ctg ctc gaa cgc atg gct atc gca ctg tct cgc ccg ggt gtg   355
Tyr Glu Leu Leu Glu Arg Met Ala Ile Ala Leu Ser Arg Pro Gly Val
 70                  75                  80                  85

gat ggt gtg ctg gga act cca gac atc att gat gat ctg gcg gcg ctc   403
Asp Gly Val Leu Gly Thr Pro Asp Ile Ile Asp Asp Leu Ala Ala Leu
                 90                  95                 100

gga ctg ctc gat gac aag atc gtg gtt ggc tcc atg aac cgt ggt ggc   451
Gly Leu Leu Asp Asp Lys Ile Val Val Gly Ser Met Asn Arg Gly Gly
         105                 110                 115

ctg cgt ggc gct tcc ttt gaa atg gat gat cgc tac acc ggc tac aac   499
Leu Arg Gly Ala Ser Phe Glu Met Asp Asp Arg Tyr Thr Gly Tyr Asn
        120                 125                 130
```

```
gtg tcc tcc atg gtt gat cgt ggc gtg gat ttc gcg aaa acc cta gtg   547
Val Ser Ser Met Val Asp Arg Gly Val Asp Phe Ala Lys Thr Leu Val
    135                 140                 145

cgc atc aac ttg agc gac gcc gga acc gcc ccg acc ttg gaa gcc acc   595
Arg Ile Asn Leu Ser Asp Ala Gly Thr Ala Pro Thr Leu Glu Ala Thr
150                 155                 160                 165

gcg cat gca gtc aat gag gct gca gca gca cag ctg ccc atc atg ctc   643
Ala His Ala Val Asn Glu Ala Ala Ala Ala Gln Leu Pro Ile Met Leu
                170                 175                 180

gag ccg ttc atg agt aac tgg gta aac ggc aag gtg gtc aat gat ctt   691
Glu Pro Phe Met Ser Asn Trp Val Asn Gly Lys Val Val Asn Asp Leu
            185                 190                 195

tcc acc gat gca gtt atc caa tct gtc gcc att gct gct ggt ctg ggc   739
Ser Thr Asp Ala Val Ile Gln Ser Val Ala Ile Ala Ala Gly Leu Gly
        200                 205                 210

aat gat tct tcc tat acc tgg atg aag ctt cca gtg gtg gag gag atg   787
Asn Asp Ser Ser Tyr Thr Trp Met Lys Leu Pro Val Val Glu Glu Met
    215                 220                 225

gag cgc gtc atg gaa tcc acc acc atg cca acc ctg ttg ttg ggc ggc   835
Glu Arg Val Met Glu Ser Thr Thr Met Pro Thr Leu Leu Leu Gly Gly
230                 235                 240                 245

gaa ggc ggc aac gat cca gat gcc acc ttc gca tcc tgg gag cat gca   883
Glu Gly Gly Asn Asp Pro Asp Ala Thr Phe Ala Ser Trp Glu His Ala
                250                 255                 260

ctc acc ctg ccg ggt gtg cgt ggc ctg acc gtg gga cgc act ctg ctg   931
Leu Thr Leu Pro Gly Val Arg Gly Leu Thr Val Gly Arg Thr Leu Leu
            265                 270                 275

tat ccg caa gac ggc gat gtc gcc gcc gct gtt gat acc gca gcg cga   979
Tyr Pro Gln Asp Gly Asp Val Ala Ala Ala Val Asp Thr Ala Ala Arg
        280                 285                 290

ctt gtt cac aca gat att caa caa ttc act tcg cag agc att          1021
Leu Val His Thr Asp Ile Gln Gln Phe Thr Ser Gln Ser Ile
    295                 300                 305

taaggaattt acacacatgt ctg                                       1044
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<210> 426
<211> 307
<212> PRT
<213> Corynebacterium glutamicum

<400> 426

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Met Thr Pro Pro Ile Ile Ser Pro Glu Ser Phe Glu Ala Leu Arg Arg
  1               5                  10                  15

Met Arg Ala Ala Glu Pro Thr Met Val Ala Glu Arg Phe Lys Gln Arg
             20                  25                  30

Arg Lys Arg Glu Leu Leu Gly Glu Asp Gly Lys Leu Phe Ile Val Ala
```

```
          35                  40                  45

Ala Asp His Pro Ala Arg Gly Ala Leu Ala Val Gly Asp Asn Glu Thr
     50                  55                  60

Ala Met Ala Asn Arg Tyr Glu Leu Leu Glu Arg Met Ala Ile Ala Leu
 65                  70                  75                  80

Ser Arg Pro Gly Val Asp Gly Val Leu Gly Thr Pro Asp Ile Ile Asp
                 85                  90                  95

Asp Leu Ala Ala Leu Gly Leu Leu Asp Asp Lys Ile Val Val Gly Ser
            100                 105                 110

Met Asn Arg Gly Gly Leu Arg Gly Ala Ser Phe Glu Met Asp Asp Arg
        115                 120                 125

Tyr Thr Gly Tyr Asn Val Ser Ser Met Val Asp Arg Gly Val Asp Phe
    130                 135                 140

Ala Lys Thr Leu Val Arg Ile Asn Leu Ser Asp Ala Gly Thr Ala Pro
145                 150                 155                 160

Thr Leu Glu Ala Thr Ala His Ala Val Asn Glu Ala Ala Ala Ala Gln
                165                 170                 175

Leu Pro Ile Met Leu Glu Pro Phe Met Ser Asn Trp Val Asn Gly Lys
            180                 185                 190

Val Val Asn Asp Leu Ser Thr Asp Ala Val Ile Gln Ser Val Ala Ile
        195                 200                 205

Ala Ala Gly Leu Gly Asn Asp Ser Ser Tyr Thr Trp Met Lys Leu Pro
    210                 215                 220

Val Val Glu Glu Met Glu Arg Val Met Glu Ser Thr Thr Met Pro Thr
225                 230                 235                 240

Leu Leu Leu Gly Gly Glu Gly Gly Asn Asp Pro Asp Ala Thr Phe Ala
                245                 250                 255

Ser Trp Glu His Ala Leu Thr Leu Pro Gly Val Arg Gly Leu Thr Val
            260                 265                 270

Gly Arg Thr Leu Leu Tyr Pro Gln Asp Gly Asp Val Ala Ala Ala Val
        275                 280                 285

Asp Thr Ala Ala Arg Leu Val His Thr Asp Ile Gln Gln Phe Thr Ser
    290                 295                 300

Gln Ser Ile
305
```

<210> 427
<211> 815
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (1)..(792)
<223> FRXA00869

<400> 427

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ctg ttt atc gtg gct gcc gac cac cca gcg cgc ggc gca ctt gct gtt   48
Leu Phe Ile Val Ala Ala Asp His Pro Ala Arg Gly Ala Leu Ala Val
  1               5                  10                  15

ggc gac aat gaa ccc gcc atg gct aac cgc tat gaa ctg ctc gaa cgc   96
Gly Asp Asn Glu Pro Ala Met Ala Asn Arg Tyr Glu Leu Leu Glu Arg
             20                  25                  30

atg gct atc gca ctg tct cgc ccg ggt gtg gat ggt gtg ctg gga act   144
Met Ala Ile Ala Leu Ser Arg Pro Gly Val Asp Gly Val Leu Gly Thr
         35                  40                  45

cca gac atc att gat gat ctg gcg gcg ctc gga ctg ctc gat gac aag   192
Pro Asp Ile Ile Asp Asp Leu Ala Ala Leu Gly Leu Leu Asp Asp Lys
     50                  55                  60

atc gtg gtt ggc tcc atg aac cgt ggt ggc ctg cgt ggc gct tcc ttt   240
Ile Val Val Gly Ser Met Asn Arg Gly Gly Leu Arg Gly Ala Ser Phe
 65                  70                  75                  80

gaa atg gat gat cgc tac acc ggc tac aac gtg tcc tcc atg gtt gat   288
Glu Met Asp Asp Arg Tyr Thr Gly Tyr Asn Val Ser Ser Met Val Asp
                 85                  90                  95

cgt ggc gtg gat ttc gcg aaa acc cta gtg cgc atc aac ttg agc gac   336
Arg Gly Val Asp Phe Ala Lys Thr Leu Val Arg Ile Asn Leu Ser Asp
            100                 105                 110

gcc gga acc gcc ccg acc ttg gaa gcc acc gcg cat gca gtc aat gag   384
Ala Gly Thr Ala Pro Thr Leu Glu Ala Thr Ala His Ala Val Asn Glu
        115                 120                 125

gct gca gca gca cag ctg ccc atc atg ctc gag ccg ttc atg agt aac   432
Ala Ala Ala Ala Gln Leu Pro Ile Met Leu Glu Pro Phe Met Ser Asn
    130                 135                 140

tgg gta aac ggc aag gtg gtc aat gat ctt tcc acc gat gca gtt atc   480
Trp Val Asn Gly Lys Val Val Asn Asp Leu Ser Thr Asp Ala Val Ile
145                 150                 155                 160

caa tct gtc gcc att gct gct ggt ctg ggc aat gat tct tcc tat acc   528
Gln Ser Val Ala Ile Ala Ala Gly Leu Gly Asn Asp Ser Ser Tyr Thr
                165                 170                 175

tgg atg aag ctt cca gtg gtg gag gag atg gag cgc gtc atg gaa tcc   576
Trp Met Lys Leu Pro Val Val Glu Glu Met Glu Arg Val Met Glu Ser
            180                 185                 190

acc acc atg cca acc ctg ttg ttg ggc ggc gaa ggc ggc aac gat cca   624
Thr Thr Met Pro Thr Leu Leu Leu Gly Gly Glu Gly Gly Asn Asp Pro
        195                 200                 205

gat gcc acc ttc gca tcc tgg gag cat gca ctc acc ctg ccg ggt gtg   672
Asp Ala Thr Phe Ala Ser Trp Glu His Ala Leu Thr Leu Pro Gly Val
    210                 215                 220

cgt ggc ctg acc gtg gga cgc act ctg ctg tat ccg caa gac ggc gat   720
```

```
Arg Gly Leu Thr Val Gly Arg Thr Leu Leu Tyr Pro Gln Asp Gly Asp
225                 230                 235                 240

gtc gcc gcc gct gtt gat acc gca gcg cga ctt gtt cac aca gat att   768
Val Ala Ala Ala Val Asp Thr Ala Ala Arg Leu Val His Thr Asp Ile
                245                 250                 255

caa caa ttc act tcg cag agc att taaggaattt acacacatgt ctg         815
Gln Gln Phe Thr Ser Gln Ser Ile
            260


<210> 428
<211> 264
<212> PRT
<213> Corynebacterium glutamicum

<400> 428
Leu Phe Ile Val Ala Ala Asp His Pro Ala Arg Gly Ala Leu Ala Val
  1               5                  10                  15

Gly Asp Asn Glu Pro Ala Met Ala Asn Arg Tyr Glu Leu Leu Glu Arg
             20                  25                  30

Met Ala Ile Ala Leu Ser Arg Pro Gly Val Asp Gly Val Leu Gly Thr
         35                  40                  45

Pro Asp Ile Ile Asp Asp Leu Ala Ala Leu Gly Leu Leu Asp Asp Lys
     50                  55                  60

Ile Val Val Gly Ser Met Asn Arg Gly Gly Leu Arg Gly Ala Ser Phe
 65                  70                  75                  80

Glu Met Asp Asp Arg Tyr Thr Gly Tyr Asn Val Ser Ser Met Val Asp
                 85                  90                  95

Arg Gly Val Asp Phe Ala Lys Thr Leu Val Arg Ile Asn Leu Ser Asp
            100                 105                 110

Ala Gly Thr Ala Pro Thr Leu Glu Ala Thr Ala His Ala Val Asn Glu
        115                 120                 125

Ala Ala Ala Ala Gln Leu Pro Ile Met Leu Glu Pro Phe Met Ser Asn
    130                 135                 140

Trp Val Asn Gly Lys Val Val Asn Asp Leu Ser Thr Asp Ala Val Ile
145                 150                 155                 160

Gln Ser Val Ala Ile Ala Ala Gly Leu Gly Asn Asp Ser Ser Tyr Thr
                165                 170                 175

Trp Met Lys Leu Pro Val Val Glu Glu Met Glu Arg Val Met Glu Ser
            180                 185                 190

Thr Thr Met Pro Thr Leu Leu Leu Gly Gly Glu Gly Gly Asn Asp Pro
        195                 200                 205

Asp Ala Thr Phe Ala Ser Trp Glu His Ala Leu Thr Leu Pro Gly Val
    210                 215                 220

Arg Gly Leu Thr Val Gly Arg Thr Leu Leu Tyr Pro Gln Asp Gly Asp
```

```
225                 230                 235                 240

Val Ala Ala Ala Val Asp Thr Ala Ala Arg Leu Val His Thr Asp Ile
                245                 250                 255

Gln Gln Phe Thr Ser Gln Ser Ile
            260


<210> 429
<211> 753
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(730)
<223> RXN00915

<400> 429
cttggctgca ggtccaccat cagcacaggt ctttgacatg aacgtagctc gccgcgacgt 60

ttcttcagga ccttctctac ctggtgaggg tgagttctaa atg tcc gcc gcc tat   115
                                          Met Ser Ala Ala Tyr
                                            1               5

tcg cag gac acc att ttg acg gtg ttt ctg ggg agg ggt ctg acc gct   163
Ser Gln Asp Thr Ile Leu Thr Val Phe Leu Gly Arg Gly Leu Thr Ala
                10                  15                  20

gaa ggg atc cga cag acc cta gaa gac ttc gca gaa acc ggc cta gtc   211
Glu Gly Ile Arg Gln Thr Leu Glu Asp Phe Ala Glu Thr Gly Leu Val
            25                  30                  35

cgc aac ctg gtg tgg att gat gcc gat agt ttc cac gag tct tca tct   259
Arg Asn Leu Val Trp Ile Asp Ala Asp Ser Phe His Glu Ser Ser Ser
        40                  45                  50

gaa gtc acc cac ttg gca acc aac caa gac ggt ctt ccg gag ctt cag   307
Glu Val Thr His Leu Ala Thr Asn Gln Asp Gly Leu Pro Glu Leu Gln
    55                  60                  65

cga cga cct ttc aat gag ttg gtg tcc cgg tca cga acc acc aag ctt   355
Arg Arg Pro Phe Asn Glu Leu Val Ser Arg Ser Arg Thr Thr Lys Leu
70                  75                  80                  85

cac atc ggt gtc atc aac gtc att gat ggc agc gaa ggc atg ctt cat   403
His Ile Gly Val Ile Asn Val Ile Asp Gly Ser Glu Gly Met Leu His
                90                  95                  100

gca gaa gaa ctc aac cca ttg gtt ggg atc atc gac agt gtc tgt tca   451
Ala Glu Glu Leu Asn Pro Leu Val Gly Ile Ile Asp Ser Val Cys Ser
            105                 110                 115

cac cac caa att cac cga tcc aac gtg atg atc ggt gcg gtg gct gcc   499
His His Gln Ile His Arg Ser Asn Val Met Ile Gly Ala Val Ala Ala
        120                 125                 130

aca ctt gat gag gaa ctt cca att ctt cgt ggt tat gtg aac ctg atg   547
Thr Leu Asp Glu Glu Leu Pro Ile Leu Arg Gly Tyr Val Asn Leu Met
    135                 140                 145
```

```
ctg gca cct gaa gat agc cac agc cca ggc acc gca aca gtg acc tac   595
Leu Ala Pro Glu Asp Ser His Ser Pro Gly Thr Ala Thr Val Thr Tyr
150                 155                 160                 165

cgt cat ggt ttc agc gat cac cgt tta ccc tgc act gcg tgg cta ata   643
Arg His Gly Phe Ser Asp His Arg Leu Pro Cys Thr Ala Trp Leu Ile
                170                 175                 180

tcg cca gct tgt acg gac tgt ggg aag gca gca cat cca cac caa tcg   691
Ser Pro Ala Cys Thr Asp Cys Gly Lys Ala Ala His Pro His Gln Ser
            185                 190                 195

aac agc tcg tac ctg cga aag gtt cca gct ttc gtt tgg tgaggtcttt    740
Asn Ser Ser Tyr Leu Arg Lys Val Pro Ala Phe Val Trp
        200                 205                 210

ttacaggcga att                                                   753


<210> 430
<211> 210
<212> PRT
<213> Corynebacterium glutamicum

<400> 430
Met Ser Ala Ala Tyr Ser Gln Asp Thr Ile Leu Thr Val Phe Leu Gly
  1               5                  10                  15

Arg Gly Leu Thr Ala Glu Gly Ile Arg Gln Thr Leu Glu Asp Phe Ala
             20                  25                  30

Glu Thr Gly Leu Val Arg Asn Leu Val Trp Ile Asp Ala Asp Ser Phe
         35                  40                  45

His Glu Ser Ser Ser Glu Val Thr His Leu Ala Thr Asn Gln Asp Gly
     50                  55                  60

Leu Pro Glu Leu Gln Arg Arg Pro Phe Asn Glu Leu Val Ser Arg Ser
 65                  70                  75                  80

Arg Thr Thr Lys Leu His Ile Gly Val Ile Asn Val Ile Asp Gly Ser
                 85                  90                  95

Glu Gly Met Leu His Ala Glu Glu Leu Asn Pro Leu Val Gly Ile Ile
            100                 105                 110

Asp Ser Val Cys Ser His His Gln Ile His Arg Ser Asn Val Met Ile
        115                 120                 125

Gly Ala Val Ala Ala Thr Leu Asp Glu Glu Leu Pro Ile Leu Arg Gly
    130                 135                 140

Tyr Val Asn Leu Met Leu Ala Pro Glu Asp Ser His Ser Pro Gly Thr
145                 150                 155                 160

Ala Thr Val Thr Tyr Arg His Gly Phe Ser Asp His Arg Leu Pro Cys
                165                 170                 175

Thr Ala Trp Leu Ile Ser Pro Ala Cys Thr Asp Cys Gly Lys Ala Ala
            180                 185                 190
```

```
His Pro His Gln Ser Asn Ser Ser Tyr Leu Arg Lys Val Pro Ala Phe
        195                 200                 205

Val Trp
    210


<210> 431
<211> 610
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(610)
<223> FRXA00915

<400> 431
cttggctgca ggtccaccat cagcacaggt ctttgacatg aacgtagctc gccgcgacgt 60

ttcttcagga ccttctctac ctggtgaggg tgagttctaa atg tcc gcc gcc tat   115
                                            Met Ser Ala Ala Tyr
                                              1               5

tcg cag gac acc att ttg acg gtg ttt ctg ggg agg ggt ctg acc gct   163
Ser Gln Asp Thr Ile Leu Thr Val Phe Leu Gly Arg Gly Leu Thr Ala
                10                  15                  20

gaa ggg atc cga cag acc cta gaa gac ttc gca gaa acc ggc cta gtc   211
Glu Gly Ile Arg Gln Thr Leu Glu Asp Phe Ala Glu Thr Gly Leu Val
            25                  30                  35

cgc aac ctg gtg tgg att gat gcc gat agt ttc cac gag tct tca tct   259
Arg Asn Leu Val Trp Ile Asp Ala Asp Ser Phe His Glu Ser Ser Ser
        40                  45                  50

gaa gtc acc cac ttg gca acc aac caa gac ggt ctt ccg gag ctt cag   307
Glu Val Thr His Leu Ala Thr Asn Gln Asp Gly Leu Pro Glu Leu Gln
    55                  60                  65

cga cga cct ttc aat gag ttg gtg tcc cgg tca cga acc acc aag ctt   355
Arg Arg Pro Phe Asn Glu Leu Val Ser Arg Ser Arg Thr Thr Lys Leu
70                  75                  80                  85

cac atc ggt gtc atc aac gtc att gat ggc agc gaa ggc atg ctt cat   403
His Ile Gly Val Ile Asn Val Ile Asp Gly Ser Glu Gly Met Leu His
                90                  95                  100

gca gaa gaa ctc aac cca ttg gtt ggg atc atc gac agt gtc tgt tca   451
Ala Glu Glu Leu Asn Pro Leu Val Gly Ile Ile Asp Ser Val Cys Ser
            105                 110                 115

cac cac caa att cac cga tcc aac gtg atg atc ggt gcg gtg gct gcc   499
His His Gln Ile His Arg Ser Asn Val Met Ile Gly Ala Val Ala Ala
        120                 125                 130

aca ctt gat gag gaa ctt cca att ctt cgt ggt tat gtg aac ctg atg   547
Thr Leu Asp Glu Glu Leu Pro Ile Leu Arg Gly Tyr Val Asn Leu Met
    135                 140                 145
```

```
ctg gca cct gaa gat agc cac agc cca ggc acc gca aca gtg acc tac   595
Leu Ala Pro Glu Asp Ser His Ser Pro Gly Thr Ala Thr Val Thr Tyr
150                 155                 160                 165

cgt cat ggt ttc agc                                           610
Arg His Gly Phe Ser
                170
```

<210> 432
<211> 170
<212> PRT
<213> Corynebacterium glutamicum

<400> 432

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Met Ser Ala Ala Tyr Ser Gln Asp Thr Ile Leu Thr Val Phe Leu Gly
  1               5                  10                  15

Arg Gly Leu Thr Ala Glu Gly Ile Arg Gln Thr Leu Glu Asp Phe Ala
             20                  25                  30

Glu Thr Gly Leu Val Arg Asn Leu Val Trp Ile Asp Ala Asp Ser Phe
         35                  40                  45

His Glu Ser Ser Ser Glu Val Thr His Leu Ala Thr Asn Gln Asp Gly
     50                  55                  60

Leu Pro Glu Leu Gln Arg Arg Pro Phe Asn Glu Leu Val Ser Arg Ser
 65                  70                  75                  80

Arg Thr Thr Lys Leu His Ile Gly Val Ile Asn Val Ile Asp Gly Ser
                 85                  90                  95

Glu Gly Met Leu His Ala Glu Glu Leu Asn Pro Leu Val Gly Ile Ile
            100                 105                 110

Asp Ser Val Cys Ser His His Gln Ile His Arg Ser Asn Val Met Ile
        115                 120                 125

Gly Ala Val Ala Ala Thr Leu Asp Glu Glu Leu Pro Ile Leu Arg Gly
    130                 135                 140

Tyr Val Asn Leu Met Leu Ala Pro Glu Asp Ser His Ser Pro Gly Thr
145                 150                 155                 160

Ala Thr Val Thr Tyr Arg His Gly Phe Ser
                165                 170
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<210> 433
<211> 2802
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2779)
<223> RXN00917

<400> 433

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tgccgtggaa gaaagcgctc tttactgcga cagccgtcct attggtgttt gctgttgtgt 60
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ggtcggcctt ggatattgcc ctgtgggtag gaaagcagtc atg gtg aac acg ttg   115
                                              Met Val Asn Thr Leu
                                                1               5

aac tct aaa acc gtg aat gta ccc cgt ttt gcc aga ggc gtt gtt gct   163
Asn Ser Lys Thr Val Asn Val Pro Arg Phe Ala Arg Gly Val Val Ala
               10                  15                  20

gca gcc aca gcg cta ttt ttt ggc gct ttg gta agc ctc gcg cct agt   211
Ala Ala Thr Ala Leu Phe Phe Gly Ala Leu Val Ser Leu Ala Pro Ser
           25                  30                  35

gcg ttg gcg cag gaa cca cct gca gtt gag gcc gga gcg tca ggt tct   259
Ala Leu Ala Gln Glu Pro Pro Ala Val Glu Ala Gly Ala Ser Gly Ser
       40                  45                  50

ttg agc aac ctg ggt gcc tgc atc gct gat aaa ggc act ctt gat gtc   307
Leu Ser Asn Leu Gly Ala Cys Ile Ala Asp Lys Gly Thr Leu Asp Val
   55                  60                  65

atc atc atg atc gat gag aca gaa tcc ttg atc cat gaa gct cgt gac   355
Ile Ile Met Ile Asp Glu Thr Glu Ser Leu Ile His Glu Ala Arg Asp
70                  75                  80                  85

ggc gtg gtc aac gcc aat gaa cca ggc gcg gac gca cag cac cac cgt   403
Gly Val Val Asn Ala Asn Glu Pro Gly Ala Asp Ala Gln His His Arg
               90                  95                 100

gtt cct gca gca cag agc ttt gtg gat gag ctt cta gcc aag caa agc   451
Val Pro Ala Ala Gln Ser Phe Val Asp Glu Leu Leu Ala Lys Gln Ser
           105                 110                 115

gat ggt gat ctg aac acc cgc atc cgt gtt gct ggt ttc ggc cag acg   499
Asp Gly Asp Leu Asn Thr Arg Ile Arg Val Ala Gly Phe Gly Gln Thr
       120                 125                 130

tac aaa tct ggt gcc act gat cca gac aat tac gga gca tgg acg caa   547
Tyr Lys Ser Gly Ala Thr Asp Pro Asp Asn Tyr Gly Ala Trp Thr Gln
   135                 140                 145

cta gat gcc tcc acc gtt ggc gga gta caa gat gaa atc tcc cgc ttc   595
Leu Asp Ala Ser Thr Val Gly Gly Val Gln Asp Glu Ile Ser Arg Phe
150                 155                 160                 165

gct gac cgc acc cag gag cag tac acc aac tac gcc tcc gcg att gag   643
Ala Asp Arg Thr Gln Glu Gln Tyr Thr Asn Tyr Ala Ser Ala Ile Glu
               170                 175                 180

ggc gct tac cag gac ttc act agg tcc ggc tct gag gac gcc tgc cgc   691
Gly Ala Tyr Gln Asp Phe Thr Arg Ser Gly Ser Glu Asp Ala Cys Arg
           185                 190                 195

atg ctg gtg acc ttc acc gac ggc gca ctg acc gct caa gaa ggc gcc   739
Met Leu Val Thr Phe Thr Asp Gly Ala Leu Thr Ala Gln Glu Gly Ala
       200                 205                 210

gat gtt gca gaa gca gca ctg tgc gcg ccg ggt ggc gtc acc gat cga   787
Asp Val Ala Glu Ala Ala Leu Cys Ala Pro Gly Gly Val Thr Asp Arg
   215                 220                 225
```

```
ctg cgc agt gct ggc atc acc cac atc ggc atc ggt tta tcg gca cct   835
Leu Arg Ser Ala Gly Ile Thr His Ile Gly Ile Gly Leu Ser Ala Pro
230                 235                 240                 245

acc aac cca tct gat ttc agc ctg ctg cgc gga acc acc gca ggt ggc   883
Thr Asn Pro Ser Asp Phe Ser Leu Leu Arg Gly Thr Thr Ala Gly Gly
                250                 255                 260

gga aca tgt ggt gtc gaa cca gct aac ggt gca ttc ttc cca gca gat   931
Gly Thr Cys Gly Val Glu Pro Ala Asn Gly Ala Phe Phe Pro Ala Asp
            265                 270                 275

aac gtg ggc gga ctt ttc gca gca ttc cgt gaa gcc ctt gcg att ggt   979
Asn Val Gly Gly Leu Phe Ala Ala Phe Arg Glu Ala Leu Ala Ile Gly
        280                 285                 290

ggt gaa aca att ggt gaa acc cga gct ggt gat cct ttc agc ttc acc   1027
Gly Glu Thr Ile Gly Glu Thr Arg Ala Gly Asp Pro Phe Ser Phe Thr
    295                 300                 305

ctg gac aac tcg gtg aac tct gtg cgt ttc acc gcg atc gcc aag gat   1075
Leu Asp Asn Ser Val Asn Ser Val Arg Phe Thr Ala Ile Ala Lys Asp
310                 315                 320                 325

gat ctc ggc ccg aac gcc cac ttg gtg ctc acc gca ccc aac ggc gaa   1123
Asp Leu Gly Pro Asn Ala His Leu Val Leu Thr Ala Pro Asn Gly Glu
                330                 335                 340

acg gtt gag ctc aaa gat tct gga agc agc gtc gcc aac agc act gac   1171
Thr Val Glu Leu Lys Asp Ser Gly Ser Ser Val Ala Asn Ser Thr Asp
            345                 350                 355

gtg agt tgg gaa gcc gaa agc agc cca gta aaa atg gct gat ggt tcc   1219
Val Ser Trp Glu Ala Glu Ser Ser Pro Val Lys Met Ala Asp Gly Ser
        360                 365                 370

ctc aac ctg cag caa ggt ggg gat tgg aag ggt gtc tgg cag att cag   1267
Leu Asn Leu Gln Gln Gly Gly Asp Trp Lys Gly Val Trp Gln Ile Gln
    375                 380                 385

ttc caa gga att gat cct gca gcg gtt gat gga cgc gta ttc aac tca   1315
Phe Gln Gly Ile Asp Pro Ala Ala Val Asp Gly Arg Val Phe Asn Ser
390                 395                 400                 405

gtg gag atc cag cct gac ctc cag ctt gtg ttc agt ggc ggt gat tcg   1363
Val Glu Ile Gln Pro Asp Leu Gln Leu Val Phe Ser Gly Gly Asp Ser
                410                 415                 420

acg tca ggt gca ctt aac ctt cgc gat gat cag cag ctg aat atg cag   1411
Thr Ser Gly Ala Leu Asn Leu Arg Asp Asp Gln Gln Leu Asn Met Gln
            425                 430                 435

ctg gtg ggc cgt gat ggt cag cca cgc atc ctt gag ggg tcc gcg ctg   1459
Leu Val Gly Arg Asp Gly Gln Pro Arg Ile Leu Glu Gly Ser Ala Leu
        440                 445                 450

gtc gat ctt ggt ttc acc cgc gca gat acc ggc gag ttc gcc cct ttg   1507
Val Asp Leu Gly Phe Thr Arg Ala Asp Thr Gly Glu Phe Ala Pro Leu
    455                 460                 465

gct caa gga att gat att tct ggc ggc gaa tta agc ttc ccg ctg gat   1555
```

```
Ala Gln Gly Ile Asp Ile Ser Gly Gly Glu Leu Ser Phe Pro Leu Asp
470                 475                 480                 485

acg att tcg cag ctc cca gcc atc ggc acg gtg gaa gcg cgt acc acg   1603
Thr Ile Ser Gln Leu Pro Ala Ile Gly Thr Val Glu Ala Arg Thr Thr
                490                 495                 500

atc acc acc gca ggc gtc gat gat ctc ccc ggc acc acg ttg agc cca   1651
Ile Thr Thr Ala Gly Val Asp Asp Leu Pro Gly Thr Thr Leu Ser Pro
            505                 510                 515

att ctc aac acc acg cgc atc acc atc act cag cgc gat atg cct cag   1699
Ile Leu Asn Thr Thr Arg Ile Thr Ile Thr Gln Arg Asp Met Pro Gln
        520                 525                 530

ctg cca gcg tcg gtt cgc ttc aca gcg gat gag gac gtt gtt acc gta   1747
Leu Pro Ala Ser Val Arg Phe Thr Ala Asp Glu Asp Val Val Thr Val
    535                 540                 545

gac atc ccc atc acc ggc ccc ggc aag gta tgg att gca ccg gga acc   1795
Asp Ile Pro Ile Thr Gly Pro Gly Lys Val Trp Ile Ala Pro Gly Thr
550                 555                 560                 565

cag ctc agc gga gtg ctt cca gac ggc gtg gac ggc att gca gca tca   1843
Gln Leu Ser Gly Val Leu Pro Asp Gly Val Asp Gly Ile Ala Ala Ser
                570                 575                 580

agt act ttc gac agc cca gat aat gct ttg gtg ctc gga ctg gat gag   1891
Ser Thr Phe Asp Ser Pro Asp Asn Ala Leu Val Leu Gly Leu Asp Glu
            585                 590                 595

cag ggc acg att cct gtt gaa cta acc gtg agc gat ctt cgt gac gga   1939
Gln Gly Thr Ile Pro Val Glu Leu Thr Val Ser Asp Leu Arg Asp Gly
        600                 605                 610

ctg gtc aac ggc tcg att cca ctc cag atc tcc aac gct gag ggc gcc   1987
Leu Val Asn Gly Ser Ile Pro Leu Gln Ile Ser Asn Ala Glu Gly Ala
    615                 620                 625

aat gaa acc agc gtg gat ctg ccg aca gaa ggc acg ttg agc gtt ccc   2035
Asn Glu Thr Ser Val Asp Leu Pro Thr Glu Gly Thr Leu Ser Val Pro
630                 635                 640                 645

att aac gcc tcc act ttc gca ttg gca ttc att ttg gcc ctt gtg ctt   2083
Ile Asn Ala Ser Thr Phe Ala Leu Ala Phe Ile Leu Ala Leu Val Leu
                650                 655                 660

tcc ctc ctg att ccg ctg ctc att ttg tat att gtg cgt ttc ctc tcc   2131
Ser Leu Leu Ile Pro Leu Leu Ile Leu Tyr Ile Val Arg Phe Leu Ser
            665                 670                 675

gca aag gtt ccg tcc tct gcg atg agt ggc gtg cgc att cca gtg gaa   2179
Ala Lys Val Pro Ser Ser Ala Met Ser Gly Val Arg Ile Pro Val Glu
        680                 685                 690

ttc tcc ggt gaa gct ctg cgc tat gcg ggc agc act atg cct gat ctc   2227
Phe Ser Gly Glu Ala Leu Arg Tyr Ala Gly Ser Thr Met Pro Asp Leu
    695                 700                 705

gca tcg caa acc acc gcc acc aag cag gtc gtt gtt cat gga gac acc   2275
Ala Ser Gln Thr Thr Ala Thr Lys Gln Val Val Val His Gly Asp Thr
```

```
710                 715                 720                 725

ttc aat gtg gaa ggc cac aaa ctt aaa gtc cag cgc ttc cag ctg aac   2323
Phe Asn Val Glu Gly His Lys Leu Lys Val Gln Arg Phe Gln Leu Asn
                730                 735                 740

ccg att gcg tct cct gca gtg atc gtg cag acc gac ccg tcg atc agc   2371
Pro Ile Ala Ser Pro Ala Val Ile Val Gln Thr Asp Pro Ser Ile Ser
            745                 750                 755

ttc gac ggc aaa caa aag ggc aca caa gct aaa ctc ccg ctg gcg gtc   2419
Phe Asp Gly Lys Gln Lys Gly Thr Gln Ala Lys Leu Pro Leu Ala Val
        760                 765                 770

caa ggc agt tgg ttc ctc act gca agc ggc gct gac cct tcc aag atg   2467
Gln Gly Ser Trp Phe Leu Thr Ala Ser Gly Ala Asp Pro Ser Lys Met
    775                 780                 785

gaa ctc atc gcc ctg aca aac ctg ccg ctc gag cag ggc caa atc gac   2515
Glu Leu Ile Ala Leu Thr Asn Leu Pro Leu Glu Gln Gly Gln Ile Asp
790                 795                 800                 805

cgc atg atc gca ggt atc acc agc aaa gcc cct gat agg gca cgc gaa   2563
Arg Met Ile Ala Gly Ile Thr Ser Lys Ala Pro Asp Arg Ala Arg Glu
                810                 815                 820

cta caa aaa ttg ctt gac gac gcc gcg acc tcc cag ccc gca aag gtt   2611
Leu Gln Lys Leu Leu Asp Asp Ala Ala Thr Ser Gln Pro Ala Lys Val
            825                 830                 835

cca ccg cgc gcc cca gcc gcg cag ggc cac gtc gaa aag caa gct cct   2659
Pro Pro Arg Ala Pro Ala Ala Gln Gly His Val Glu Lys Gln Ala Pro
        840                 845                 850

agt ttt ggc act ggt tcc ggt ggt ggt ttc ggc tcc agc aat ggt gga   2707
Ser Phe Gly Thr Gly Ser Gly Gly Gly Phe Gly Ser Ser Asn Gly Gly
    855                 860                 865

ggc ttt ggc tcc ggt agc gga tcc aac gac aca aat ggt gga ttt ggt   2755
Gly Phe Gly Ser Gly Ser Gly Ser Asn Asp Thr Asn Gly Gly Phe Gly
870                 875                 880                 885

tcc agc ggc ggc ttc ggc gcg cga taacctgtaa cttgcgatta aaa         2802
Ser Ser Gly Gly Phe Gly Ala Arg
                890
```

<210> 434
<211> 893
<212> PRT
<213> Corynebacterium glutamicum

<400> 434

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Met Val Asn Thr Leu Asn Ser Lys Thr Val Asn Val Pro Arg Phe Ala
  1               5                  10                  15

Arg Gly Val Val Ala Ala Ala Thr Ala Leu Phe Phe Gly Ala Leu Val
             20                  25                  30

Ser Leu Ala Pro Ser Ala Leu Ala Gln Glu Pro Pro Ala Val Glu Ala
         35                  40                  45
```

```
Gly Ala Ser Gly Ser Leu Ser Asn Leu Gly Ala Cys Ile Ala Asp Lys
     50                  55                  60

Gly Thr Leu Asp Val Ile Ile Met Ile Asp Glu Thr Glu Ser Leu Ile
 65                  70                  75                  80

His Glu Ala Arg Asp Gly Val Val Asn Ala Asn Glu Pro Gly Ala Asp
                85                  90                  95

Ala Gln His His Arg Val Pro Ala Ala Gln Ser Phe Val Asp Glu Leu
            100                 105                 110

Leu Ala Lys Gln Ser Asp Gly Asp Leu Asn Thr Arg Ile Arg Val Ala
        115                 120                 125

Gly Phe Gly Gln Thr Tyr Lys Ser Gly Ala Thr Asp Pro Asp Asn Tyr
    130                 135                 140

Gly Ala Trp Thr Gln Leu Asp Ala Ser Thr Val Gly Gly Val Gln Asp
145                 150                 155                 160

Glu Ile Ser Arg Phe Ala Asp Arg Thr Gln Glu Gln Tyr Thr Asn Tyr
                165                 170                 175

Ala Ser Ala Ile Glu Gly Ala Tyr Gln Asp Phe Thr Arg Ser Gly Ser
            180                 185                 190

Glu Asp Ala Cys Arg Met Leu Val Thr Phe Thr Asp Gly Ala Leu Thr
        195                 200                 205

Ala Gln Glu Gly Ala Asp Val Ala Glu Ala Ala Leu Cys Ala Pro Gly
    210                 215                 220

Gly Val Thr Asp Arg Leu Arg Ser Ala Gly Ile Thr His Ile Gly Ile
225                 230                 235                 240

Gly Leu Ser Ala Pro Thr Asn Pro Ser Asp Phe Ser Leu Leu Arg Gly
                245                 250                 255

Thr Thr Ala Gly Gly Gly Thr Cys Gly Val Glu Pro Ala Asn Gly Ala
            260                 265                 270

Phe Phe Pro Ala Asp Asn Val Gly Gly Leu Phe Ala Ala Phe Arg Glu
        275                 280                 285

Ala Leu Ala Ile Gly Gly Glu Thr Ile Gly Glu Thr Arg Ala Gly Asp
    290                 295                 300

Pro Phe Ser Phe Thr Leu Asp Asn Ser Val Asn Ser Val Arg Phe Thr
305                 310                 315                 320

Ala Ile Ala Lys Asp Asp Leu Gly Pro Asn Ala His Leu Val Leu Thr
                325                 330                 335

Ala Pro Asn Gly Glu Thr Val Glu Leu Lys Asp Ser Gly Ser Ser Val
            340                 345                 350

Ala Asn Ser Thr Asp Val Ser Trp Glu Ala Glu Ser Ser Pro Val Lys
        355                 360                 365
```

```
Met Ala Asp Gly Ser Leu Asn Leu Gln Gln Gly Gly Asp Trp Lys Gly
    370                 375                 380

Val Trp Gln Ile Gln Phe Gln Gly Ile Asp Pro Ala Ala Val Asp Gly
385                 390                 395                 400

Arg Val Phe Asn Ser Val Glu Ile Gln Pro Asp Leu Gln Leu Val Phe
                405                 410                 415

Ser Gly Gly Asp Ser Thr Ser Gly Ala Leu Asn Leu Arg Asp Asp Gln
            420                 425                 430

Gln Leu Asn Met Gln Leu Val Gly Arg Asp Gly Gln Pro Arg Ile Leu
        435                 440                 445

Glu Gly Ser Ala Leu Val Asp Leu Gly Phe Thr Arg Ala Asp Thr Gly
    450                 455                 460

Glu Phe Ala Pro Leu Ala Gln Gly Ile Asp Ile Ser Gly Gly Glu Leu
465                 470                 475                 480

Ser Phe Pro Leu Asp Thr Ile Ser Gln Leu Pro Ala Ile Gly Thr Val
                485                 490                 495

Glu Ala Arg Thr Thr Ile Thr Thr Ala Gly Val Asp Asp Leu Pro Gly
            500                 505                 510

Thr Thr Leu Ser Pro Ile Leu Asn Thr Thr Arg Ile Thr Ile Thr Gln
        515                 520                 525

Arg Asp Met Pro Gln Leu Pro Ala Ser Val Arg Phe Thr Ala Asp Glu
    530                 535                 540

Asp Val Val Thr Val Asp Ile Pro Ile Thr Gly Pro Gly Lys Val Trp
545                 550                 555                 560

Ile Ala Pro Gly Thr Gln Leu Ser Gly Val Leu Pro Asp Gly Val Asp
                565                 570                 575

Gly Ile Ala Ala Ser Ser Thr Phe Asp Ser Pro Asp Asn Ala Leu Val
            580                 585                 590

Leu Gly Leu Asp Glu Gln Gly Thr Ile Pro Val Glu Leu Thr Val Ser
        595                 600                 605

Asp Leu Arg Asp Gly Leu Val Asn Gly Ser Ile Pro Leu Gln Ile Ser
    610                 615                 620

Asn Ala Glu Gly Ala Asn Glu Thr Ser Val Asp Leu Pro Thr Glu Gly
625                 630                 635                 640

Thr Leu Ser Val Pro Ile Asn Ala Ser Thr Phe Ala Leu Ala Phe Ile
                645                 650                 655

Leu Ala Leu Val Leu Ser Leu Leu Ile Pro Leu Leu Ile Leu Tyr Ile
            660                 665                 670

Val Arg Phe Leu Ser Ala Lys Val Pro Ser Ser Ala Met Ser Gly Val
        675                 680                 685

Arg Ile Pro Val Glu Phe Ser Gly Glu Ala Leu Arg Tyr Ala Gly Ser
```

```
    690                 695                 700

Thr Met Pro Asp Leu Ala Ser Gln Thr Thr Ala Thr Lys Gln Val Val
705                 710                 715                 720

Val His Gly Asp Thr Phe Asn Val Glu Gly His Lys Leu Lys Val Gln
                725                 730                 735

Arg Phe Gln Leu Asn Pro Ile Ala Ser Pro Ala Val Ile Val Gln Thr
            740                 745                 750

Asp Pro Ser Ile Ser Phe Asp Gly Lys Gln Lys Gly Thr Gln Ala Lys
        755                 760                 765

Leu Pro Leu Ala Val Gln Gly Ser Trp Phe Leu Thr Ala Ser Gly Ala
    770                 775                 780

Asp Pro Ser Lys Met Glu Leu Ile Ala Leu Thr Asn Leu Pro Leu Glu
785                 790                 795                 800

Gln Gly Gln Ile Asp Arg Met Ile Ala Gly Ile Thr Ser Lys Ala Pro
                805                 810                 815

Asp Arg Ala Arg Glu Leu Gln Lys Leu Leu Asp Asp Ala Ala Thr Ser
            820                 825                 830

Gln Pro Ala Lys Val Pro Pro Arg Ala Pro Ala Ala Gln Gly His Val
        835                 840                 845

Glu Lys Gln Ala Pro Ser Phe Gly Thr Gly Ser Gly Gly Gly Phe Gly
    850                 855                 860

Ser Ser Asn Gly Gly Gly Phe Gly Ser Gly Ser Gly Ser Asn Asp Thr
865                 870                 875                 880

Asn Gly Gly Phe Gly Ser Ser Gly Gly Phe Gly Ala Arg
                885                 890
```

<210> 435
<211> 1406
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1383)
<223> FRXA00917

<400> 435

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cag ctg aat atg cag ctg gtg ggc cgt gat ggt cag cca cgc atc ctt   48
Gln Leu Asn Met Gln Leu Val Gly Arg Asp Gly Gln Pro Arg Ile Leu
  1               5                  10                  15

gag ggg tcc gcg ctg gtc gat ctt ggt ttc acc cgc gca gat acc ggc   96
Glu Gly Ser Ala Leu Val Asp Leu Gly Phe Thr Arg Ala Asp Thr Gly
             20                  25                  30

gag ttc gcc cct ttg gct caa gga att gat att tct ggc ggc gaa tta   144
Glu Phe Ala Pro Leu Ala Gln Gly Ile Asp Ile Ser Gly Gly Glu Leu
         35                  40                  45
```

```
agc ttc ccg ctg gat acg att tcg cag ctc cca gcc atc ggc acg gtg   192
Ser Phe Pro Leu Asp Thr Ile Ser Gln Leu Pro Ala Ile Gly Thr Val
     50                  55                  60

gaa gcg cgt acc acg atc acc acc gca ggc gtc gat gat ctc ccc ggc   240
Glu Ala Arg Thr Thr Ile Thr Thr Ala Gly Val Asp Asp Leu Pro Gly
 65                  70                  75                  80

acc acg ttg agc cca att ctc aac acc acg cgc atc acc atc act cag   288
Thr Thr Leu Ser Pro Ile Leu Asn Thr Thr Arg Ile Thr Ile Thr Gln
                 85                  90                  95

cgc gat atg cct cag ctg cca gcg tcg gtt cgc ttc aca gcg gat gag   336
Arg Asp Met Pro Gln Leu Pro Ala Ser Val Arg Phe Thr Ala Asp Glu
            100                 105                 110

gac gtt gtt acc gta gac atc ccc atc acc ggc ccc ggc aag gta tgg   384
Asp Val Val Thr Val Asp Ile Pro Ile Thr Gly Pro Gly Lys Val Trp
        115                 120                 125

att gca ccg gga acc cag ctc agc gga gtg ctt cca gac ggc gtg gac   432
Ile Ala Pro Gly Thr Gln Leu Ser Gly Val Leu Pro Asp Gly Val Asp
    130                 135                 140

ggc att gca gca tca agt act ttc gac agc cca gat aat gct ttg gtg   480
Gly Ile Ala Ala Ser Ser Thr Phe Asp Ser Pro Asp Asn Ala Leu Val
145                 150                 155                 160

ctc gga ctg gat gag cag ggc acg att cct gtt gaa cta acc gtg agc   528
Leu Gly Leu Asp Glu Gln Gly Thr Ile Pro Val Glu Leu Thr Val Ser
                165                 170                 175

gat ctt cgt gac gga ctg gtc aac ggc tcg att cca ctc cag atc tcc   576
Asp Leu Arg Asp Gly Leu Val Asn Gly Ser Ile Pro Leu Gln Ile Ser
            180                 185                 190

aac gct gag ggc gcc aat gaa acc agc gtg gat ctg ccg aca gaa ggc   624
Asn Ala Glu Gly Ala Asn Glu Thr Ser Val Asp Leu Pro Thr Glu Gly
        195                 200                 205

acg ttg agc gtt ccc att aac gcc tcc act ttc gca ttg gca ttc att   672
Thr Leu Ser Val Pro Ile Asn Ala Ser Thr Phe Ala Leu Ala Phe Ile
    210                 215                 220

ttg gcc ctt gtg ctt tcc ctc ctg att ccg ctg ctc att ttg tat att   720
Leu Ala Leu Val Leu Ser Leu Leu Ile Pro Leu Leu Ile Leu Tyr Ile
225                 230                 235                 240

gtg cgt ttc ctc tcc gca aag gtt ccg tcc tct gcg atg agt ggc gtg   768
Val Arg Phe Leu Ser Ala Lys Val Pro Ser Ser Ala Met Ser Gly Val
                245                 250                 255

cgc att cca gtg gaa ttc tcc ggt gaa gct ctg cgc tat gcg ggc agc   816
Arg Ile Pro Val Glu Phe Ser Gly Glu Ala Leu Arg Tyr Ala Gly Ser
            260                 265                 270

act atg cct gat ctc gca tcg caa acc acc gcc acc aag cag gtc gtt   864
Thr Met Pro Asp Leu Ala Ser Gln Thr Thr Ala Thr Lys Gln Val Val
        275                 280                 285
```

```
gtt cat gga gac acc ttc aat gtg gaa ggc cac aaa ctt aaa gtc cag   912
Val His Gly Asp Thr Phe Asn Val Glu Gly His Lys Leu Lys Val Gln
    290                 295                 300

cgc ttc cag ctg aac ccg att gcg tct cct gca gtg atc gtg cag acc   960
Arg Phe Gln Leu Asn Pro Ile Ala Ser Pro Ala Val Ile Val Gln Thr
305                 310                 315                 320

gac ccg tcg atc agc ttc gac ggc aaa caa aag ggc aca caa gct aaa   1008
Asp Pro Ser Ile Ser Phe Asp Gly Lys Gln Lys Gly Thr Gln Ala Lys
                325                 330                 335

ctc ccg ctg gcg gtc caa ggc agt tgg ttc ctc act gca agc ggc gct   1056
Leu Pro Leu Ala Val Gln Gly Ser Trp Phe Leu Thr Ala Ser Gly Ala
            340                 345                 350

gac cct tcc aag atg gaa ctc atc gcc ctg aca aac ctg ccg ctc gag   1104
Asp Pro Ser Lys Met Glu Leu Ile Ala Leu Thr Asn Leu Pro Leu Glu
        355                 360                 365

cag ggc caa atc gac cgc atg atc gca ggt atc acc agc aaa gcc cct   1152
Gln Gly Gln Ile Asp Arg Met Ile Ala Gly Ile Thr Ser Lys Ala Pro
    370                 375                 380

gat agg gca cgc gaa cta caa aaa ttg ctt gac gac gcc gcg acc tcc   1200
Asp Arg Ala Arg Glu Leu Gln Lys Leu Leu Asp Asp Ala Ala Thr Ser
385                 390                 395                 400

cag ccc gca aag gtt cca ccg cgc gcc cca gcc gcg cag ggc cac gtc   1248
Gln Pro Ala Lys Val Pro Pro Arg Ala Pro Ala Ala Gln Gly His Val
                405                 410                 415

gaa aag caa gct cct agt ttt ggc act ggt tcc ggt ggt ggt ttc ggc   1296
Glu Lys Gln Ala Pro Ser Phe Gly Thr Gly Ser Gly Gly Gly Phe Gly
            420                 425                 430

tcc agc aat ggt gga ggc ttt ggc tcc ggt agc gga tcc aac gac aca   1344
Ser Ser Asn Gly Gly Gly Phe Gly Ser Gly Ser Gly Ser Asn Asp Thr
        435                 440                 445

aat ggt gga ttt ggt tcc agc ggc ggc ttc ggc gcg cga taacctgtaa   1393
Asn Gly Gly Phe Gly Ser Ser Gly Gly Phe Gly Ala Arg
    450                 455                 460

cttgcgatta aaa                                                  1406
```

<210> 436
<211> 461
<212> PRT
<213> Corynebacterium glutamicum

<400> 436

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Gln Leu Asn Met Gln Leu Val Gly Arg Asp Gly Gln Pro Arg Ile Leu
  1               5                  10                  15

Glu Gly Ser Ala Leu Val Asp Leu Gly Phe Thr Arg Ala Asp Thr Gly
             20                  25                  30

Glu Phe Ala Pro Leu Ala Gln Gly Ile Asp Ile Ser Gly Gly Glu Leu
         35                  40                  45
```

```
Ser Phe Pro Leu Asp Thr Ile Ser Gln Leu Pro Ala Ile Gly Thr Val
     50                  55                  60

Glu Ala Arg Thr Thr Ile Thr Thr Ala Gly Val Asp Asp Leu Pro Gly
 65                  70                  75                  80

Thr Thr Leu Ser Pro Ile Leu Asn Thr Thr Arg Ile Thr Ile Thr Gln
                 85                  90                  95

Arg Asp Met Pro Gln Leu Pro Ala Ser Val Arg Phe Thr Ala Asp Glu
            100                 105                 110

Asp Val Val Thr Val Asp Ile Pro Ile Thr Gly Pro Gly Lys Val Trp
        115                 120                 125

Ile Ala Pro Gly Thr Gln Leu Ser Gly Val Leu Pro Asp Gly Val Asp
    130                 135                 140

Gly Ile Ala Ala Ser Ser Thr Phe Asp Ser Pro Asp Asn Ala Leu Val
145                 150                 155                 160

Leu Gly Leu Asp Glu Gln Gly Thr Ile Pro Val Glu Leu Thr Val Ser
                165                 170                 175

Asp Leu Arg Asp Gly Leu Val Asn Gly Ser Ile Pro Leu Gln Ile Ser
            180                 185                 190

Asn Ala Glu Gly Ala Asn Glu Thr Ser Val Asp Leu Pro Thr Glu Gly
        195                 200                 205

Thr Leu Ser Val Pro Ile Asn Ala Ser Thr Phe Ala Leu Ala Phe Ile
    210                 215                 220

Leu Ala Leu Val Leu Ser Leu Leu Ile Pro Leu Leu Ile Leu Tyr Ile
225                 230                 235                 240

Val Arg Phe Leu Ser Ala Lys Val Pro Ser Ser Ala Met Ser Gly Val
                245                 250                 255

Arg Ile Pro Val Glu Phe Ser Gly Glu Ala Leu Arg Tyr Ala Gly Ser
            260                 265                 270

Thr Met Pro Asp Leu Ala Ser Gln Thr Thr Ala Thr Lys Gln Val Val
        275                 280                 285

Val His Gly Asp Thr Phe Asn Val Glu Gly His Lys Leu Lys Val Gln
    290                 295                 300

Arg Phe Gln Leu Asn Pro Ile Ala Ser Pro Ala Val Ile Val Gln Thr
305                 310                 315                 320

Asp Pro Ser Ile Ser Phe Asp Gly Lys Gln Lys Gly Thr Gln Ala Lys
                325                 330                 335

Leu Pro Leu Ala Val Gln Gly Ser Trp Phe Leu Thr Ala Ser Gly Ala
            340                 345                 350

Asp Pro Ser Lys Met Glu Leu Ile Ala Leu Thr Asn Leu Pro Leu Glu
        355                 360                 365
```

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Gln Gly Gln Ile Asp Arg Met Ile Ala Gly Ile Thr Ser Lys Ala Pro
    370                 375                 380

Asp Arg Ala Arg Glu Leu Gln Lys Leu Leu Asp Asp Ala Ala Thr Ser
385                 390                 395                 400

Gln Pro Ala Lys Val Pro Pro Arg Ala Pro Ala Ala Gln Gly His Val
                405                 410                 415

Glu Lys Gln Ala Pro Ser Phe Gly Thr Gly Ser Gly Gly Gly Phe Gly
            420                 425                 430

Ser Ser Asn Gly Gly Gly Phe Gly Ser Gly Ser Gly Ser Asn Asp Thr
        435                 440                 445

Asn Gly Gly Phe Gly Ser Ser Gly Gly Phe Gly Ala Arg
    450                 455                 460


<210> 437
<211> 536
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(513)
<223> RXN00921

<400> 437
cct gcg gca atc ctc ttg gac cat atc gtt ccg aac ttc agc aga gat   48
Pro Ala Ala Ile Leu Leu Asp His Ile Val Pro Asn Phe Ser Arg Asp
  1               5                  10                  15

cgg tct ttg cca gac atc gaa gac tgg acg aga agc gat gaa gct cag   96
Arg Ser Leu Pro Asp Ile Glu Asp Trp Thr Arg Ser Asp Glu Ala Gln
             20                  25                  30

cag atc ttt gca gga atc att gcg ggt gcg tct gtt caa act ggt aga   144
Gln Ile Phe Ala Gly Ile Ile Ala Gly Ala Ser Val Gln Thr Gly Arg
         35                  40                  45

agc cac ttc atg tgg gat ctt ttg cgg gcg tat ttt gga gtc gct ttg   192
Ser His Phe Met Trp Asp Leu Leu Arg Ala Tyr Phe Gly Val Ala Leu
     50                  55                  60

atc ggc gac gaa gat acc tac agg gct ttt act act ctc acg gtc gat   240
Ile Gly Asp Glu Asp Thr Tyr Arg Ala Phe Thr Thr Leu Thr Val Asp
 65                  70                  75                  80

tct gtt ctt agt ttc gtg cag tta act ctt caa gag ggc aga acg gaa   288
Ser Val Leu Ser Phe Val Gln Leu Thr Leu Gln Glu Gly Arg Thr Glu
                 85                  90                  95

gac att aga cga ttc gag aaa tat ggt gag cag att gcc cga gag gat   336
Asp Ile Arg Arg Phe Glu Lys Tyr Gly Glu Gln Ile Ala Arg Glu Asp
            100                 105                 110

ttg ccg tcg att ctc acc aat gct cga gca gta cag caa tat ctc ggc   384
Leu Pro Ser Ile Leu Thr Asn Ala Arg Ala Val Gln Gln Tyr Leu Gly
        115                 120                 125
```

```
tat atc gac caa gat atc atc aat aag aaa gtg tcc cgg tct agg gat   432
Tyr Ile Asp Gln Asp Ile Ile Asn Lys Lys Val Ser Arg Ser Arg Asp
    130                 135                 140

gtt aac cag att ttt act gag atg gcg cgc gct atc atc aga gca att   480
Val Asn Gln Ile Phe Thr Glu Met Ala Arg Ala Ile Ile Arg Ala Ile
145                 150                 155                 160

agc cgg aat aat att gga aag gac atg cgg tca tgaacgtgat tcgactggat 533
Ser Arg Asn Asn Ile Gly Lys Asp Met Arg Ser
                165                 170

tcc                                                               536
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<210> 438
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 438

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Pro Ala Ala Ile Leu Leu Asp His Ile Val Pro Asn Phe Ser Arg Asp
  1               5                  10                  15

Arg Ser Leu Pro Asp Ile Glu Asp Trp Thr Arg Ser Asp Glu Ala Gln
             20                  25                  30

Gln Ile Phe Ala Gly Ile Ile Ala Gly Ala Ser Val Gln Thr Gly Arg
         35                  40                  45

Ser His Phe Met Trp Asp Leu Leu Arg Ala Tyr Phe Gly Val Ala Leu
     50                  55                  60

Ile Gly Asp Glu Asp Thr Tyr Arg Ala Phe Thr Thr Leu Thr Val Asp
 65                  70                  75                  80

Ser Val Leu Ser Phe Val Gln Leu Thr Leu Gln Glu Gly Arg Thr Glu
                 85                  90                  95

Asp Ile Arg Arg Phe Glu Lys Tyr Gly Glu Gln Ile Ala Arg Glu Asp
            100                 105                 110

Leu Pro Ser Ile Leu Thr Asn Ala Arg Ala Val Gln Gln Tyr Leu Gly
        115                 120                 125

Tyr Ile Asp Gln Asp Ile Ile Asn Lys Lys Val Ser Arg Ser Arg Asp
    130                 135                 140

Val Asn Gln Ile Phe Thr Glu Met Ala Arg Ala Ile Ile Arg Ala Ile
145                 150                 155                 160

Ser Arg Asn Asn Ile Gly Lys Asp Met Arg Ser
                165                 170
```

<210> 439
<211> 2022
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1999)
<223> FRXA00921

<400> 439
tctgggaacg tggattggtg gaagcaggtg agttgcccgt ggccttgaga tggactcatg 60

tcacctacgc gtcctttaga ggaactgcag gtaggggtgg gtg gaa ggt gga act 115
Val Glu Gly Gly Thr
1 5

tgg tct gct cag gcc act aaa gaa gac ctc caa ttt atc gcg gag gtt 163
Trp Ser Ala Gln Ala Thr Lys Glu Asp Leu Gln Phe Ile Ala Glu Val
10 15 20

gcg ccc act cat att gaa acg gtg acc cct ttt gat gat ttc atc tca 211
Ala Pro Thr His Ile Glu Thr Val Thr Pro Phe Asp Asp Phe Ile Ser
25 30 35

tca gaa gat atc gat gcg ttg ccg agg agg ttt gag tac cgt cct ttg 259
Ser Glu Asp Ile Asp Ala Leu Pro Arg Arg Phe Glu Tyr Arg Pro Leu
40 45 50

gca ggc cga tcg ttg atc atg cag tct gtt cct gca ggt aaa gat gcc 307
Ala Gly Arg Ser Leu Ile Met Gln Ser Val Pro Ala Gly Lys Asp Ala
55 60 65

act gga cgt cca ggg aat gtg ttc acc cat gca gta ttt gat ggg gat 355
Thr Gly Arg Pro Gly Asn Val Phe Thr His Ala Val Phe Asp Gly Asp
70 75 80 85

cta gaa agc cca ctg gag tct gtt tat ccc att tcc ctg tac cgt tca 403
Leu Glu Ser Pro Leu Glu Ser Val Tyr Pro Ile Ser Leu Tyr Arg Ser
90 95 100

cct gat ttg ctg acc cct ttt cgt gca gcc gcg gtc aac gct gcc gag 451
Pro Asp Leu Leu Thr Pro Phe Arg Ala Ala Ala Val Asn Ala Ala Glu
105 110 115

ctc cct ttg gat gca ggc gag ccg aga att ggc ccc atc act gat ctg 499
Leu Pro Leu Asp Ala Gly Glu Pro Arg Ile Gly Pro Ile Thr Asp Leu
120 125 130

tcc ttg tcg tgg atg atg atc gac agc atg ttt ggc gat cgc aga cag 547
Ser Leu Ser Trp Met Met Ile Asp Ser Met Phe Gly Asp Arg Arg Gln
135 140 145

cag ttc tac cag ctt caa gat gct ctc caa gct gga gat aaa gct act 595
Gln Phe Tyr Gln Leu Gln Asp Ala Leu Gln Ala Gly Asp Lys Ala Thr
150 155 160 165

gtt ttg gtt ctg aac agc act aac gag gca gca tat tgg ctt caa gcg 643
Val Leu Val Leu Asn Ser Thr Asn Glu Ala Ala Tyr Trp Leu Gln Ala
170 175 180

ttg tct tct aca ttg act ccg aat gaa gcc cgg cgt ctg ttg cac ttc 691
Leu Ser Ser Thr Leu Thr Pro Asn Glu Ala Arg Arg Leu Leu His Phe
185 190 195

tca acc ttt gag cgt gct gct acc ttg cca gct cca gat aaa tca atg 739

```
Ser Thr Phe Glu Arg Ala Ala Thr Leu Pro Ala Pro Asp Lys Ser Met
        200                 205                 210

gag gct cgt tct ctg ttt gtg gtc cca gga att gat cgt gaa ttg ttg   787
Glu Ala Arg Ser Leu Phe Val Val Pro Gly Ile Asp Arg Glu Leu Leu
    215                 220                 225

gcg gag cat tca ggg att gtg att atc gat ccg gag att cca cag agc   835
Ala Glu His Ser Gly Ile Val Ile Ile Asp Pro Glu Ile Pro Gln Ser
230                 235                 240                 245

caa cct ttc ggc ccg cag gga tcc tgg tcc cga atg aca gaa ggg ctc   883
Gln Pro Phe Gly Pro Gln Gly Ser Trp Ser Arg Met Thr Glu Gly Leu
                250                 255                 260

ttc tcc gac ggt ttt gat gct gat gaa ctt gtc gca ggg ctg att cgt   931
Phe Ser Asp Gly Phe Asp Ala Asp Glu Leu Val Ala Gly Leu Ile Arg
            265                 270                 275

gcc aac gag aac ctg gat aat agc caa aag gaa ctc gct caa ttt gga   979
Ala Asn Glu Asn Leu Asp Asn Ser Gln Lys Glu Leu Ala Gln Phe Gly
        280                 285                 290

gac ggt tta gcg cga ttt atc cgg aat ggc cgt ttt tcc ggc acg cac   1027
Asp Gly Leu Ala Arg Phe Ile Arg Asn Gly Arg Phe Ser Gly Thr His
    295                 300                 305

ccg ctt cgc gta ctt gct gat cag cat atg ttt gga aag gtg cca gac   1075
Pro Leu Arg Val Leu Ala Asp Gln His Met Phe Gly Lys Val Pro Asp
310                 315                 320                 325

aag cca gca cct aag gtg gag cct gtc gct ccg gca cca aac ccc aat   1123
Lys Pro Ala Pro Lys Val Glu Pro Val Ala Pro Ala Pro Asn Pro Asn
                330                 335                 340

gca att tgg gcg cgt gca tct gag gta gtt cac aat cct cgg aga gca   1171
Ala Ile Trp Ala Arg Ala Ser Glu Val Val His Asn Pro Arg Arg Ala
            345                 350                 355

tca gaa tca caa gat tgg cca agt ctg agg cga ttg ccg gat agt cgg   1219
Ser Glu Ser Gln Asp Trp Pro Ser Leu Arg Arg Leu Pro Asp Ser Arg
        360                 365                 370

cgc agg atc atc aat atg tca gag cag gcg atc aac agc att gag aag   1267
Arg Arg Ile Ile Asn Met Ser Glu Gln Ala Ile Asn Ser Ile Glu Lys
    375                 380                 385

ctt cat gat tcg ccg gca cag gat ctt gtt gcc tat ttg gat ttc ctt   1315
Leu His Asp Ser Pro Ala Gln Asp Leu Val Ala Tyr Leu Asp Phe Leu
390                 395                 400                 405

ttg aaa act gag ctt gcg aca agc att aat gct tcg gat ccc ttt ttt   1363
Leu Lys Thr Glu Leu Ala Thr Ser Ile Asn Ala Ser Asp Pro Phe Phe
                410                 415                 420

cgg agt agt ttt tca gac ttt cca gcg atg gac aac tgg cga cac att   1411
Arg Ser Ser Phe Ser Asp Phe Pro Ala Met Asp Asn Trp Arg His Ile
            425                 430                 435

aag ttc acc gag gat gcg cac cct cgc ttg agg gaa cta ctc gtg gac   1459
Lys Phe Thr Glu Asp Ala His Pro Arg Leu Arg Glu Leu Leu Val Asp
```

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        440                 445                 450

gca gaa cgc gat gct agg aac aga gca cct gcg gca atc gtc ttg gac   1507
Ala Glu Arg Asp Ala Arg Asn Arg Ala Pro Ala Ala Ile Val Leu Asp
    455                 460                 465

cat atc gtt ccg aac ttc agc aga gat cgg tct ttg cca gac atc gaa   1555
His Ile Val Pro Asn Phe Ser Arg Asp Arg Ser Leu Pro Asp Ile Glu
470                 475                 480                 485

gac tgg acg aga agc gat gaa gct cag cag atc ttt gca gga atc att   1603
Asp Trp Thr Arg Ser Asp Glu Ala Gln Gln Ile Phe Ala Gly Ile Ile
                490                 495                 500

gcg ggt gcg tct gtt caa act ggt aga agc cac ttc atg tgg gat ctt   1651
Ala Gly Ala Ser Val Gln Thr Gly Arg Ser His Phe Met Trp Asp Leu
            505                 510                 515

ttg cgg gcg tat ttt gga gtc gct ttg atc ggc gac gaa gat acc tac   1699
Leu Arg Ala Tyr Phe Gly Val Ala Leu Ile Gly Asp Glu Asp Thr Tyr
        520                 525                 530

agg gct ttt act act ctc acg gtc gat tct gtt ctt agt ttc gtg cag   1747
Arg Ala Phe Thr Thr Leu Thr Val Asp Ser Val Leu Ser Phe Val Gln
    535                 540                 545

tta act ctt caa gag ggc aga acg gaa gac att aga cga ttc gag aaa   1795
Leu Thr Leu Gln Glu Gly Arg Thr Glu Asp Ile Arg Arg Phe Glu Lys
550                 555                 560                 565

tat ggt gag cag att gcc cga gag gat ttg ccg tcg att ctc acc aat   1843
Tyr Gly Glu Gln Ile Ala Arg Glu Asp Leu Pro Ser Ile Leu Thr Asn
                570                 575                 580

gct cga gca gta cag caa tat ctc ggc tat atc gac caa gat atc atc   1891
Ala Arg Ala Val Gln Gln Tyr Leu Gly Tyr Ile Asp Gln Asp Ile Ile
            585                 590                 595

aat aag aaa gtg tcc cgg tct agg gat gtt aac cag att ttt act gag   1939
Asn Lys Lys Val Ser Arg Ser Arg Asp Val Asn Gln Ile Phe Thr Glu
        600                 605                 610

atg gcg cgc gct atc atc aga gca att agc cgg aat aat att gga aag   1987
Met Ala Arg Ala Ile Ile Arg Ala Ile Ser Arg Asn Asn Ile Gly Lys
    615                 620                 625

gac atg cgg tca tgaacgtgat tcgactggat tcc                        2022
Asp Met Arg Ser
630
```

<210> 440
<211> 633
<212> PRT
<213> Corynebacterium glutamicum

<400> 440

```
Val Glu Gly Gly Thr Trp Ser Ala Gln Ala Thr Lys Glu Asp Leu Gln
  1               5                  10                  15

Phe Ile Ala Glu Val Ala Pro Thr His Ile Glu Thr Val Thr Pro Phe
```

```
                20                  25                  30

Asp Asp Phe Ile Ser Ser Glu Asp Ile Asp Ala Leu Pro Arg Arg Phe
          35                  40                  45

Glu Tyr Arg Pro Leu Ala Gly Arg Ser Leu Ile Met Gln Ser Val Pro
      50                  55                  60

Ala Gly Lys Asp Ala Thr Gly Arg Pro Gly Asn Val Phe Thr His Ala
 65                  70                  75                  80

Val Phe Asp Gly Asp Leu Glu Ser Pro Leu Glu Ser Val Tyr Pro Ile
                 85                  90                  95

Ser Leu Tyr Arg Ser Pro Asp Leu Leu Thr Pro Phe Arg Ala Ala Ala
            100                 105                 110

Val Asn Ala Ala Glu Leu Pro Leu Asp Ala Gly Glu Pro Arg Ile Gly
        115                 120                 125

Pro Ile Thr Asp Leu Ser Leu Ser Trp Met Met Ile Asp Ser Met Phe
    130                 135                 140

Gly Asp Arg Arg Gln Gln Phe Tyr Gln Leu Gln Asp Ala Leu Gln Ala
145                 150                 155                 160

Gly Asp Lys Ala Thr Val Leu Val Leu Asn Ser Thr Asn Glu Ala Ala
                165                 170                 175

Tyr Trp Leu Gln Ala Leu Ser Ser Thr Leu Thr Pro Asn Glu Ala Arg
            180                 185                 190

Arg Leu Leu His Phe Ser Thr Phe Glu Arg Ala Ala Thr Leu Pro Ala
        195                 200                 205

Pro Asp Lys Ser Met Glu Ala Arg Ser Leu Phe Val Val Pro Gly Ile
    210                 215                 220

Asp Arg Glu Leu Leu Ala Glu His Ser Gly Ile Val Ile Ile Asp Pro
225                 230                 235                 240

Glu Ile Pro Gln Ser Gln Pro Phe Gly Pro Gln Gly Ser Trp Ser Arg
                245                 250                 255

Met Thr Glu Gly Leu Phe Ser Asp Gly Phe Asp Ala Asp Glu Leu Val
            260                 265                 270

Ala Gly Leu Ile Arg Ala Asn Glu Asn Leu Asp Asn Ser Gln Lys Glu
        275                 280                 285

Leu Ala Gln Phe Gly Asp Gly Leu Ala Arg Phe Ile Arg Asn Gly Arg
    290                 295                 300

Phe Ser Gly Thr His Pro Leu Arg Val Leu Ala Asp Gln His Met Phe
305                 310                 315                 320

Gly Lys Val Pro Asp Lys Pro Ala Pro Lys Val Glu Pro Val Ala Pro
                325                 330                 335

Ala Pro Asn Pro Asn Ala Ile Trp Ala Arg Ala Ser Glu Val Val His
            340                 345                 350
```

```
Asn Pro Arg Arg Ala Ser Glu Ser Gln Asp Trp Pro Ser Leu Arg Arg
        355                 360                 365

Leu Pro Asp Ser Arg Arg Arg Ile Ile Asn Met Ser Glu Gln Ala Ile
    370                 375                 380

Asn Ser Ile Glu Lys Leu His Asp Ser Pro Ala Gln Asp Leu Val Ala
385                 390                 395                 400

Tyr Leu Asp Phe Leu Leu Lys Thr Glu Leu Ala Thr Ser Ile Asn Ala
                405                 410                 415

Ser Asp Pro Phe Phe Arg Ser Ser Phe Ser Asp Phe Pro Ala Met Asp
            420                 425                 430

Asn Trp Arg His Ile Lys Phe Thr Glu Asp Ala His Pro Arg Leu Arg
        435                 440                 445

Glu Leu Leu Val Asp Ala Glu Arg Asp Ala Arg Asn Arg Ala Pro Ala
    450                 455                 460

Ala Ile Val Leu Asp His Ile Val Pro Asn Phe Ser Arg Asp Arg Ser
465                 470                 475                 480

Leu Pro Asp Ile Glu Asp Trp Thr Arg Ser Asp Glu Ala Gln Gln Ile
                485                 490                 495

Phe Ala Gly Ile Ile Ala Gly Ala Ser Val Gln Thr Gly Arg Ser His
            500                 505                 510

Phe Met Trp Asp Leu Leu Arg Ala Tyr Phe Gly Val Ala Leu Ile Gly
        515                 520                 525

Asp Glu Asp Thr Tyr Arg Ala Phe Thr Thr Leu Thr Val Asp Ser Val
    530                 535                 540

Leu Ser Phe Val Gln Leu Thr Leu Gln Glu Gly Arg Thr Glu Asp Ile
545                 550                 555                 560

Arg Arg Phe Glu Lys Tyr Gly Glu Gln Ile Ala Arg Glu Asp Leu Pro
                565                 570                 575

Ser Ile Leu Thr Asn Ala Arg Ala Val Gln Gln Tyr Leu Gly Tyr Ile
            580                 585                 590

Asp Gln Asp Ile Ile Asn Lys Lys Val Ser Arg Ser Arg Asp Val Asn
        595                 600                 605

Gln Ile Phe Thr Glu Met Ala Arg Ala Ile Ile Arg Ala Ile Ser Arg
    610                 615                 620

Asn Asn Ile Gly Lys Asp Met Arg Ser
625                 630
```

<210> 441
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> RXN00943

<400> 441
taggtacgat cggacgagga gaaaaaatct gaaaacaatc cagtggccca cctcggctta 60

taaaactgga caacagtatt ttgattggag catcaccata atg atc cgc aaa ctt 115
Met Ile Arg Lys Leu
1 5

gct cga cca atg ctt gca tcg gtc tac gtc gca gat ggc gca gaa aca 163
Ala Arg Pro Met Leu Ala Ser Val Tyr Val Ala Asp Gly Ala Glu Thr
10 15 20

gta ttg aac acc agc gca cac gtc gaa ggc act cag gta gtt ctg gat 211
Val Leu Asn Thr Ser Ala His Val Glu Gly Thr Gln Val Val Leu Asp
25 30 35

cgt atc cgt tat gtg ctg ccc cgt aag tac gca aag cgc att tcc aga 259
Arg Ile Arg Tyr Val Leu Pro Arg Lys Tyr Ala Lys Arg Ile Ser Arg
40 45 50

gat cca gaa ttg gtc acc cgc gtc att ggc ggc acc aaa gtc ggt gcg 307
Asp Pro Glu Leu Val Thr Arg Val Ile Gly Gly Thr Lys Val Gly Ala
55 60 65

ggt tct ttg cta gct att ggt cgt gca cca cgc acc tct gca gct acc 355
Gly Ser Leu Leu Ala Ile Gly Arg Ala Pro Arg Thr Ser Ala Ala Thr
70 75 80 85

ctc gca atc ctg act atc cct aac atc ctg gct cgc aat gcg ttc tgg 403
Leu Ala Ile Leu Thr Ile Pro Asn Ile Leu Ala Arg Asn Ala Phe Trp
90 95 100

gaa acc cag gat gcg gat gaa aag cgt aac cgc cgc aac ggt ttc ctc 451
Glu Thr Gln Asp Ala Asp Glu Lys Arg Asn Arg Arg Asn Gly Phe Leu
105 110 115

acc aac att gcc ctg ctt ggt ggc ctg ttt atc act tct gtt gat act 499
Thr Asn Ile Ala Leu Leu Gly Gly Leu Phe Ile Thr Ser Val Asp Thr
120 125 130

gag ggc aag cct ggc gtg aag tgg cgt gca acc aat gct aca aag cgt 547
Glu Gly Lys Pro Gly Val Lys Trp Arg Ala Thr Asn Ala Thr Lys Arg
135 140 145

ggc aag aag cag ctg cag cag gca ctt cca acc aaa tct gag act gaa 595
Gly Lys Lys Gln Leu Gln Gln Ala Leu Pro Thr Lys Ser Glu Thr Glu
150 155 160 165

aag ttc ggt gag aag gcc tct gat tgg ttc aac gat act tct gac aag 643
Lys Phe Gly Glu Lys Ala Ser Asp Trp Phe Asn Asp Thr Ser Asp Lys
170 175 180

gtc acc gag tac gcg tac acc gct cag gat ttt gtc ggt gag aac aag 691
Val Thr Glu Tyr Ala Tyr Thr Ala Gln Asp Phe Val Gly Glu Asn Lys
185 190 195

gat gac tgg atc aag tcc gca acc gag act gct cac aag gtc gct gat 739

```
Asp Asp Trp Ile Lys Ser Ala Thr Glu Thr Ala His Lys Val Ala Asp
        200                 205                 210

act gtg agc gat tac gct cac aag gct acc tct tac ctt gag gag aac   787
Thr Val Ser Asp Tyr Ala His Lys Ala Thr Ser Tyr Leu Glu Glu Asn
    215                 220                 225

agc ggt gac tgg ctt gag gct gcg cag gct aac gcc aag act gct cgt   835
Ser Gly Asp Trp Leu Glu Ala Ala Gln Ala Asn Ala Lys Thr Ala Arg
230                 235                 240                 245

aag tct gca gtg aag gct gcc ggc aag gct cag gaa aag gct aac ttt   883
Lys Ser Ala Val Lys Ala Ala Gly Lys Ala Gln Glu Lys Ala Asn Phe
                250                 255                 260

gct ctt cag gtc gca gag gaa acc tct ggt cgc gcc aac aag aag gca   931
Ala Leu Gln Val Ala Glu Glu Thr Ser Gly Arg Ala Asn Lys Lys Ala
            265                 270                 275

act aag agc tac gac aag ctt cag aag cag gct gat aag gcc atc gat   979
Thr Lys Ser Tyr Asp Lys Leu Gln Lys Gln Ala Asp Lys Ala Ile Asp
        280                 285                 290

cgt gca cag aag aag ctg aag ggc atc gaa ctt taagtaactt cttcctgatt 1032
Arg Ala Gln Lys Lys Leu Lys Gly Ile Glu Leu
    295                 300

gag                                                               1035


<210> 442
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 442
Met Ile Arg Lys Leu Ala Arg Pro Met Leu Ala Ser Val Tyr Val Ala
  1               5                  10                  15

Asp Gly Ala Glu Thr Val Leu Asn Thr Ser Ala His Val Glu Gly Thr
             20                  25                  30

Gln Val Val Leu Asp Arg Ile Arg Tyr Val Leu Pro Arg Lys Tyr Ala
         35                  40                  45

Lys Arg Ile Ser Arg Asp Pro Glu Leu Val Thr Arg Val Ile Gly Gly
     50                  55                  60

Thr Lys Val Gly Ala Gly Ser Leu Leu Ala Ile Gly Arg Ala Pro Arg
 65                  70                  75                  80

Thr Ser Ala Ala Thr Leu Ala Ile Leu Thr Ile Pro Asn Ile Leu Ala
                 85                  90                  95

Arg Asn Ala Phe Trp Glu Thr Gln Asp Ala Asp Glu Lys Arg Asn Arg
            100                 105                 110

Arg Asn Gly Phe Leu Thr Asn Ile Ala Leu Leu Gly Gly Leu Phe Ile
        115                 120                 125

Thr Ser Val Asp Thr Glu Gly Lys Pro Gly Val Lys Trp Arg Ala Thr
```

```
    130                 135                 140

Asn Ala Thr Lys Arg Gly Lys Lys Gln Leu Gln Gln Ala Leu Pro Thr
145                 150                 155                 160

Lys Ser Glu Thr Glu Lys Phe Gly Glu Lys Ala Ser Asp Trp Phe Asn
                165                 170                 175

Asp Thr Ser Asp Lys Val Thr Glu Tyr Ala Tyr Thr Ala Gln Asp Phe
            180                 185                 190

Val Gly Glu Asn Lys Asp Asp Trp Ile Lys Ser Ala Thr Glu Thr Ala
        195                 200                 205

His Lys Val Ala Asp Thr Val Ser Asp Tyr Ala His Lys Ala Thr Ser
    210                 215                 220

Tyr Leu Glu Glu Asn Ser Gly Asp Trp Leu Glu Ala Ala Gln Ala Asn
225                 230                 235                 240

Ala Lys Thr Ala Arg Lys Ser Ala Val Lys Ala Ala Gly Lys Ala Gln
                245                 250                 255

Glu Lys Ala Asn Phe Ala Leu Gln Val Ala Glu Glu Thr Ser Gly Arg
            260                 265                 270

Ala Asn Lys Lys Ala Thr Lys Ser Tyr Asp Lys Leu Gln Lys Gln Ala
        275                 280                 285

Asp Lys Ala Ile Asp Arg Ala Gln Lys Lys Leu Lys Gly Ile Glu Leu
    290                 295                 300
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09850750.090705

<210> 443
<211> 530
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(507)
<223> FRXA00943

<400> 443

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aag cct ggc gtg aag tgg cgt gca acc aat gct aca aag cgt ggc aag   48
Lys Pro Gly Val Lys Trp Arg Ala Thr Asn Ala Thr Lys Arg Gly Lys
  1               5                  10                  15

aag cag ctg cag cag gca ctt tca acc aaa tct gag act gaa aag ttc   96
Lys Gln Leu Gln Gln Ala Leu Ser Thr Lys Ser Glu Thr Glu Lys Phe
             20                  25                  30

ggt gag aag gcc tct gat tgg ttc aac gat act tct gac aag gtc acc   144
Gly Glu Lys Ala Ser Asp Trp Phe Asn Asp Thr Ser Asp Lys Val Thr
         35                  40                  45

gag tac gcg tac acc gct cag gat ttt gtc ggt gag aac aag gat gac   192
Glu Tyr Ala Tyr Thr Ala Gln Asp Phe Val Gly Glu Asn Lys Asp Asp
```

```
     50                  55                  60

tgg atc aag tcc gca acc gag act gct cac aag gtc gct gat act gtg   240
Trp Ile Lys Ser Ala Thr Glu Thr Ala His Lys Val Ala Asp Thr Val
 65                  70                  75                  80

agc gat tac gct cac aag gct acc tct tac ctt gag gag aac agc ggt   288
Ser Asp Tyr Ala His Lys Ala Thr Ser Tyr Leu Glu Glu Asn Ser Gly
                85                  90                  95

gac tgg ctt gag gct gcg cag gct aac gcc aag act gct cgt aag tct   336
Asp Trp Leu Glu Ala Ala Gln Ala Asn Ala Lys Thr Ala Arg Lys Ser
            100                 105                 110

gca gtg aag gct gcc ggc aag gct cac gaa aag gct aac ttt gct ctt   384
Ala Val Lys Ala Ala Gly Lys Ala His Glu Lys Ala Asn Phe Ala Leu
        115                 120                 125

cag gtc gca gag gaa acc tct ggt cgc gcc aac aag aag gca act aag   432
Gln Val Ala Glu Glu Thr Ser Gly Arg Ala Asn Lys Lys Ala Thr Lys
    130                 135                 140

agc tac gac aag ctt cag aag cag gct gat aag gcc atc gat cgt gca   480
Ser Tyr Asp Lys Leu Gln Lys Gln Ala Asp Lys Ala Ile Asp Arg Ala
145                 150                 155                 160

cag aag aag ctg aag ggc atc gaa ctt taagtaactt cttcctgatt         527
Gln Lys Lys Leu Lys Gly Ile Glu Leu
                165

gag                                                               530


<210> 444
<211> 169
<212> PRT
<213> Corynebacterium glutamicum

<400> 444
Lys Pro Gly Val Lys Trp Arg Ala Thr Asn Ala Thr Lys Arg Gly Lys
  1               5                  10                  15

Lys Gln Leu Gln Gln Ala Leu Ser Thr Lys Ser Glu Thr Glu Lys Phe
            20                  25                  30

Gly Glu Lys Ala Ser Asp Trp Phe Asn Asp Thr Ser Asp Lys Val Thr
        35                  40                  45

Glu Tyr Ala Tyr Thr Ala Gln Asp Phe Val Gly Glu Asn Lys Asp Asp
    50                  55                  60

Trp Ile Lys Ser Ala Thr Glu Thr Ala His Lys Val Ala Asp Thr Val
 65                  70                  75                  80

Ser Asp Tyr Ala His Lys Ala Thr Ser Tyr Leu Glu Glu Asn Ser Gly
                85                  90                  95

Asp Trp Leu Glu Ala Ala Gln Ala Asn Ala Lys Thr Ala Arg Lys Ser
            100                 105                 110

Ala Val Lys Ala Ala Gly Lys Ala His Glu Lys Ala Asn Phe Ala Leu
```

```
        115                 120                 125

Gln Val Ala Glu Glu Thr Ser Gly Arg Ala Asn Lys Lys Ala Thr Lys
    130                 135                 140

Ser Tyr Asp Lys Leu Gln Lys Gln Ala Asp Lys Ala Ile Asp Arg Ala
145                 150                 155                 160

Gln Lys Lys Leu Lys Gly Ile Glu Leu
                165
```

<210> 445
<211> 316
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(316)
<223> FRXA02423

<400> 445

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taggtacgat cggacgagga gaaaaaatct gaaaacaatc cagtggccca cctcggctta 60

taaaactgga caacagtatt ttgattggag catcaccata atg atc cgc aaa ctt   115
                                            Met Ile Arg Lys Leu
                                              1               5

gct cga cca atg ctt gca tcg gtc tac gtc gca gat ggc gca gaa aca   163
Ala Arg Pro Met Leu Ala Ser Val Tyr Val Ala Asp Gly Ala Glu Thr
                  10                  15                  20

gta ttg aac acc agc gca cac gtc gaa ggc act cag gta gtt ctg gat   211
Val Leu Asn Thr Ser Ala His Val Glu Gly Thr Gln Val Val Leu Asp
              25                  30                  35

cgt atc cgt tat gtg ctg ccc cgt aag tac gca aag cgc att tcc aga   259
Arg Ile Arg Tyr Val Leu Pro Arg Lys Tyr Ala Lys Arg Ile Ser Arg
          40                  45                  50

gat cca gaa ttg gtc acc cgc gtc att ggc ggc acc aaa gtc tgt gcg   307
Asp Pro Glu Leu Val Thr Arg Val Ile Gly Gly Thr Lys Val Cys Ala
      55                  60                  65

ggt tct tgt                                                      316
Gly Ser Cys
 70
```

<210> 446
<211> 72
<212> PRT
<213> Corynebacterium glutamicum

<400> 446

```
Met Ile Arg Lys Leu Ala Arg Pro Met Leu Ala Ser Val Tyr Val Ala
  1               5                  10                  15

Asp Gly Ala Glu Thr Val Leu Asn Thr Ser Ala His Val Glu Gly Thr
             20                  25                  30
```

```
Gln Val Val Leu Asp Arg Ile Arg Tyr Val Leu Pro Arg Lys Tyr Ala
         35                  40                  45

Lys Arg Ile Ser Arg Asp Pro Glu Leu Val Thr Arg Val Ile Gly Gly
     50                  55                  60

Thr Lys Val Cys Ala Gly Ser Cys
 65                  70


<210> 447
<211> 1095
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1072)
<223> RXN00945

<400> 447
tcacagtacc acccacaagc cacaaggagg gtatggaggt gggcgtctaa agccaaattt 60

ttcccggtgt ttgaggcgat tgcaccgtac actaatgtgc atg ctt gaa cgc ctc   115
                                          Met Leu Glu Arg Leu
                                            1               5

aaa cgc cta gat ccg ctc att gtc ctc att gtg ctg gct gtc att gtg   163
Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val Leu Ala Val Ile Val
                 10                  15                  20

gcg atc atc att cca gtt cgc ggg gtt gct gcg gat tgg ttt gat gtc   211
Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala Asp Trp Phe Asp Val
             25                  30                  35

gcc gtc aag att gcc att gcg ctg ctg ttt ttt ctt tat ggt gcc cgc   259
Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe Leu Tyr Gly Ala Arg
         40                  45                  50

cta tcc acc caa gag gcg ctg aat ggt ctg aag cac tgg agg ctt cac   307
Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys His Trp Arg Leu His
     55                  60                  65

ctg act att ttg gcg atc act ttc gga ata ttc cca ctt atc ggc att   355
Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe Pro Leu Ile Gly Ile
 70                  75                  80                  85

ggg ctc gag ccg atg act gca ttt gtg tcg gaa gat att tat cgg gga   403
Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu Asp Ile Tyr Arg Gly
                 90                  95                 100

att ttg ttc ctc acg ctc gtt ccg tcc acc gtg cag tca tcg gtg gcg   451
Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val Gln Ser Ser Val Ala
            105                 110                 115

ttt acc tcg atc gct aaa ggc aac gta gct ggt gcg att gtg tcg gca   499
Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly Ala Ile Val Ser Ala
        120                 125                 130

tcg ctc tcc aac ctt gcg ggt gtt ttc ctc act ccg ctg ctg gtc atg   547
```

```
Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr Pro Leu Leu Val Met
    135                 140                 145

ctc atc atg tct gcg ggc ggg gga gtt cac gtg gat tcc cag gtc ttc   595
Leu Ile Met Ser Ala Gly Gly Gly Val His Val Asp Ser Gln Val Phe
150                 155                 160                 165

ctc gac att gcg att cag ctt ctg ctg ccg ttc atc ctc ggc cag gta   643
Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe Ile Leu Gly Gln Val
                170                 175                 180

tgt agg cgt tgg gtg aag aat ttt gcg gcc aac aaa gca aca aaa atc   691
Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn Lys Ala Thr Lys Ile
            185                 190                 195

gtg gac cgc ggc tcg atc gcg atg gtc gtg tac tcc gcg ttt tct gcc   739
Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr Ser Ala Phe Ser Ala
        200                 205                 210

ggc atg gtg gct ggc att tgg tcc act gtg agc gtt cta gag att atc   787
Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser Val Leu Glu Ile Ile
    215                 220                 225

tac ctc att gtt ttc gct att ctg ctg gtg atg gcc atg ctg tgg ttc   835
Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met Ala Met Leu Trp Phe
230                 235                 240                 245

acg ctg ttc atg gct aca cgc ctt gga ttt aac cgg gca gat tcc atc   883
Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn Arg Ala Asp Ser Ile
                250                 255                 260

gct att cag ttc tgc gga acc aag aaa tcc ctg gcc aca ggc ctc cca   931
Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu Ala Thr Gly Leu Pro
            265                 270                 275

atg gcg gca gtc atc ttc ggt ggc gcc aat atc ggc ctg ctc atc ttg   979
Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile Gly Leu Leu Ile Leu
        280                 285                 290

ccg ttg atg atc ttc cac caa gtc cag ctg atg att tgt gca tgg ctt   1027
Pro Leu Met Ile Phe His Gln Val Gln Leu Met Ile Cys Ala Trp Leu
    295                 300                 305

gca gct cgt tat ggt cgt gat gcg cag gaa cag aaa gcc aac gcc       1072
Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln Lys Ala Asn Ala
310                 315                 320

taaaagtcct cagtagctag cca                                       1095


<210> 448
<211> 324
<212> PRT
<213> Corynebacterium glutamicum

<400> 448
Met Leu Glu Arg Leu Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val
  1               5                  10                  15

Leu Ala Val Ile Val Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala
             20                  25                  30
```

```
Asp Trp Phe Asp Val Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe
         35                  40                  45

Leu Tyr Gly Ala Arg Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys
     50                  55                  60

His Trp Arg Leu His Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe
 65                  70                  75                  80

Pro Leu Ile Gly Ile Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu
                85                  90                  95

Asp Ile Tyr Arg Gly Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val
            100                 105                 110

Gln Ser Ser Val Ala Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly
        115                 120                 125

Ala Ile Val Ser Ala Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr
    130                 135                 140

Pro Leu Leu Val Met Leu Ile Met Ser Ala Gly Gly Gly Val His Val
145                 150                 155                 160

Asp Ser Gln Val Phe Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe
                165                 170                 175

Ile Leu Gly Gln Val Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn
            180                 185                 190

Lys Ala Thr Lys Ile Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr
        195                 200                 205

Ser Ala Phe Ser Ala Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser
    210                 215                 220

Val Leu Glu Ile Ile Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met
225                 230                 235                 240

Ala Met Leu Trp Phe Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn
                245                 250                 255

Arg Ala Asp Ser Ile Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu
            260                 265                 270

Ala Thr Gly Leu Pro Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile
        275                 280                 285

Gly Leu Leu Ile Leu Pro Leu Met Ile Phe His Gln Val Gln Leu Met
    290                 295                 300

Ile Cys Ala Trp Leu Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln
305                 310                 315                 320

Lys Ala Asn Ala
```

<210> 449
<211> 897

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> RXN00946

<400> 449
gggccggtgt gaataaaaca ccttccccaa atagacagca tggtctagat tagcttgaaa 60

cgaaagcgta cattcgcagc aactaacgga aagcacactc atg act cac act ctg 115
Met Thr His Thr Leu
1 5

cag gca act aat ccc ctt gat caa acc gct tgg cac gct tgg cat ttc 163
Gln Ala Thr Asn Pro Leu Asp Gln Thr Ala Trp His Ala Trp His Phe
10 15 20

tcc cga aac aaa gag gcc atc agc cgc acc ggc gcc acc agc ctg agt 211
Ser Arg Asn Lys Glu Ala Ile Ser Arg Thr Gly Ala Thr Ser Leu Ser
25 30 35

gcc aca gag tgg att agc gcc acc aca ctc aag gac gcg cac act ttt 259
Ala Thr Glu Trp Ile Ser Ala Thr Thr Leu Lys Asp Ala His Thr Phe
40 45 50

cct tca ctt ccc ggg cga tgg tat aaa cga ggc ggc ggg gta gtg gga 307
Pro Ser Leu Pro Gly Arg Trp Tyr Lys Arg Gly Gly Gly Val Val Gly
55 60 65

gca cat tta cca cca gct ttc gca aca act gga acg gtg caa ctg cgc 355
Ala His Leu Pro Pro Ala Phe Ala Thr Thr Gly Thr Val Gln Leu Arg
70 75 80 85

ccc ggt gag ctc ttg ata gcg gaa gat ttc acc ctc acc gtc att gaa 403
Pro Gly Glu Leu Leu Ile Ala Glu Asp Phe Thr Leu Thr Val Ile Glu
90 95 100

cgg ctt gga cag ttt gca ctt cag gtt ttt gat gca cgc aat ccg aag 451
Arg Leu Gly Gln Phe Ala Leu Gln Val Phe Asp Ala Arg Asn Pro Lys
105 110 115

cgt ttt gaa ttc cac tcc atc gca gct ttc cca ccg tcc gag gaa tgg 499
Arg Phe Glu Phe His Ser Ile Ala Ala Phe Pro Pro Ser Glu Glu Trp
120 125 130

cgg att gag gct cgc ttc ttc ccg gaa cct gac act gtt aac acc gct 547
Arg Ile Glu Ala Arg Phe Phe Pro Glu Pro Asp Thr Val Asn Thr Ala
135 140 145

gca gct gat gga gtt atc gtt gcc acg cct act gcg ggt tgg gtg cac 595
Ala Ala Asp Gly Val Ile Val Ala Thr Pro Thr Ala Gly Trp Val His
150 155 160 165

ttt ttg aag ggc cgt ctg gat tac cgt ctt cgt gta acc gtt cag aaa 643
Phe Leu Lys Gly Arg Leu Asp Tyr Arg Leu Arg Val Thr Val Gln Lys
170 175 180

aat aat cta cgg gca cta ttt agc gac aat tcc tcg acg ttg ggc gtt 691
Asn Asn Leu Arg Ala Leu Phe Ser Asp Asn Ser Ser Thr Leu Gly Val

```
            185                 190                 195

tat cag cat cgt ttt gtc gac atc cca cgc cct gat gcc gag gga aac   739
Tyr Gln His Arg Phe Val Asp Ile Pro Arg Pro Asp Ala Glu Gly Asn
        200                 205                 210

acc atc att gat ttc aac cgc gct tat ctt ccc cca aag gca ttg aac   787
Thr Ile Ile Asp Phe Asn Arg Ala Tyr Leu Pro Pro Lys Ala Leu Asn
    215                 220                 225

cga aag ttc ctg tgc cca tcg ccc agc ctg aac aac cac ctc aat ctc   835
Arg Lys Phe Leu Cys Pro Ser Pro Ser Leu Asn Asn His Leu Asn Leu
230                 235                 240                 245

acc gtg gag gca ggg gag aag tgg gtg gtt gct gga gga taatacttgc    884
Thr Val Glu Ala Gly Glu Lys Trp Val Val Ala Gly Gly
                250                 255

taaccgtcct aaa                                                   897


<210> 450
<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 450
Met Thr His Thr Leu Gln Ala Thr Asn Pro Leu Asp Gln Thr Ala Trp
  1               5                  10                  15

His Ala Trp His Phe Ser Arg Asn Lys Glu Ala Ile Ser Arg Thr Gly
             20                  25                  30

Ala Thr Ser Leu Ser Ala Thr Glu Trp Ile Ser Ala Thr Thr Leu Lys
         35                  40                  45

Asp Ala His Thr Phe Pro Ser Leu Pro Gly Arg Trp Tyr Lys Arg Gly
     50                  55                  60

Gly Gly Val Val Gly Ala His Leu Pro Pro Ala Phe Ala Thr Thr Gly
 65                  70                  75                  80

Thr Val Gln Leu Arg Pro Gly Glu Leu Leu Ile Ala Glu Asp Phe Thr
                 85                  90                  95

Leu Thr Val Ile Glu Arg Leu Gly Gln Phe Ala Leu Gln Val Phe Asp
            100                 105                 110

Ala Arg Asn Pro Lys Arg Phe Glu Phe His Ser Ile Ala Ala Phe Pro
        115                 120                 125

Pro Ser Glu Glu Trp Arg Ile Glu Ala Arg Phe Phe Pro Glu Pro Asp
    130                 135                 140

Thr Val Asn Thr Ala Ala Ala Asp Gly Val Ile Val Ala Thr Pro Thr
145                 150                 155                 160

Ala Gly Trp Val His Phe Leu Lys Gly Arg Leu Asp Tyr Arg Leu Arg
                165                 170                 175

Val Thr Val Gln Lys Asn Asn Leu Arg Ala Leu Phe Ser Asp Asn Ser
```

```
            180                 185                 190

Ser Thr Leu Gly Val Tyr Gln His Arg Phe Val Asp Ile Pro Arg Pro
        195                 200                 205

Asp Ala Glu Gly Asn Thr Ile Ile Asp Phe Asn Arg Ala Tyr Leu Pro
    210                 215                 220

Pro Lys Ala Leu Asn Arg Lys Phe Leu Cys Pro Ser Pro Ser Leu Asn
225                 230                 235                 240

Asn His Leu Asn Leu Thr Val Glu Ala Gly Glu Lys Trp Val Val Ala
                245                 250                 255

Gly Gly
```

<210> 451
<211> 897
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> FRXA00946

<400> 451

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gggccggtgt gaataaaaca ccttccccaa atagacagca tggtctagat tagcttgaaa 60

cgaaagcgta cattcgcagc aactaacgga aagcacactc atg act cac act ctg   115
                                              Met Thr His Thr Leu
                                                1               5

cag gca act aat ccc ctt gat caa acc gct tgg cac gct tgg cat ttc   163
Gln Ala Thr Asn Pro Leu Asp Gln Thr Ala Trp His Ala Trp His Phe
                10                  15                  20

tcc cga aac aaa gag gcc atc agc cgc acc ggc gcc acc agc ctg agt   211
Ser Arg Asn Lys Glu Ala Ile Ser Arg Thr Gly Ala Thr Ser Leu Ser
            25                  30                  35

gcc aca gag tgg att agc gcc acc aca ctc aag gac gcg cac act ttt   259
Ala Thr Glu Trp Ile Ser Ala Thr Thr Leu Lys Asp Ala His Thr Phe
        40                  45                  50

cct tca ctt ccc ggg cga tgg tat aaa cga ggc ggc ggg gta gtg gga   307
Pro Ser Leu Pro Gly Arg Trp Tyr Lys Arg Gly Gly Gly Val Val Gly
    55                  60                  65

gca cat tta cca cca gct ttc gca aca act gga acg gtg caa ctg cgc   355
Ala His Leu Pro Pro Ala Phe Ala Thr Thr Gly Thr Val Gln Leu Arg
70                  75                  80                  85

ccc ggt gag ctc ttg ata gcg gaa gat ttc acc ctc acc gtc att gaa   403
Pro Gly Glu Leu Leu Ile Ala Glu Asp Phe Thr Leu Thr Val Ile Glu
                90                  95                  100

cgg ctt gga cag ttt gca ctt cag gtt ttt gat gca cgc aat ccg aag   451
Arg Leu Gly Gln Phe Ala Leu Gln Val Phe Asp Ala Arg Asn Pro Lys
```

```
            105                 110                 115

cgt ttt gaa ttc cac tcc atc gca gct ttc cca ccg tcc gag gaa tgg   499
Arg Phe Glu Phe His Ser Ile Ala Ala Phe Pro Pro Ser Glu Glu Trp
        120                 125                 130

cgg att gag gct cgc ttc ttc ccg gaa cct gac act gtt aac acc gct   547
Arg Ile Glu Ala Arg Phe Phe Pro Glu Pro Asp Thr Val Asn Thr Ala
    135                 140                 145

gca gct gat gga gtt atc gtt gcc acg cct act gcg ggt tgg gtg cac   595
Ala Ala Asp Gly Val Ile Val Ala Thr Pro Thr Ala Gly Trp Val His
150                 155                 160                 165

ttt ttg aag ggc cgt ctg gat tac cgt ctt cgt gta acc gtt cag aaa   643
Phe Leu Lys Gly Arg Leu Asp Tyr Arg Leu Arg Val Thr Val Gln Lys
                170                 175                 180

aat aat cta cgg gca cta ttt agc gac aat tcc tcg acg ttg ggc gtt   691
Asn Asn Leu Arg Ala Leu Phe Ser Asp Asn Ser Ser Thr Leu Gly Val
            185                 190                 195

tat cag cat cgt ttt gtc gac atc cca cgc cct gat gcc gag gga aac   739
Tyr Gln His Arg Phe Val Asp Ile Pro Arg Pro Asp Ala Glu Gly Asn
        200                 205                 210

acc atc att gat ttc aac cgc gct tat ctt ccc cca aag gca ttg aac   787
Thr Ile Ile Asp Phe Asn Arg Ala Tyr Leu Pro Pro Lys Ala Leu Asn
    215                 220                 225

cga aag ttc ctg tgc cca tcg ccc agc ctg aac aac cac ctc aat ctc   835
Arg Lys Phe Leu Cys Pro Ser Pro Ser Leu Asn Asn His Leu Asn Leu
230                 235                 240                 245

acc gtg gag gca ggg gag aag tgg gtg gtt gct gga gga taatacttgc    884
Thr Val Glu Ala Gly Glu Lys Trp Val Val Ala Gly Gly
                250                 255

taaccgtcct aaa                                                   897


<210> 452
<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 452
Met Thr His Thr Leu Gln Ala Thr Asn Pro Leu Asp Gln Thr Ala Trp
  1               5                  10                  15

His Ala Trp His Phe Ser Arg Asn Lys Glu Ala Ile Ser Arg Thr Gly
             20                  25                  30

Ala Thr Ser Leu Ser Ala Thr Glu Trp Ile Ser Ala Thr Thr Leu Lys
         35                  40                  45

Asp Ala His Thr Phe Pro Ser Leu Pro Gly Arg Trp Tyr Lys Arg Gly
     50                  55                  60

Gly Gly Val Val Gly Ala His Leu Pro Pro Ala Phe Ala Thr Thr Gly
 65                  70                  75                  80
```

```
Thr Val Gln Leu Arg Pro Gly Glu Leu Leu Ile Ala Glu Asp Phe Thr
                 85                  90                  95

Leu Thr Val Ile Glu Arg Leu Gly Gln Phe Ala Leu Gln Val Phe Asp
            100                 105                 110

Ala Arg Asn Pro Lys Arg Phe Glu Phe His Ser Ile Ala Ala Phe Pro
        115                 120                 125

Pro Ser Glu Glu Trp Arg Ile Glu Ala Arg Phe Phe Pro Glu Pro Asp
    130                 135                 140

Thr Val Asn Thr Ala Ala Ala Asp Gly Val Ile Val Ala Thr Pro Thr
145                 150                 155                 160

Ala Gly Trp Val His Phe Leu Lys Gly Arg Leu Asp Tyr Arg Leu Arg
                165                 170                 175

Val Thr Val Gln Lys Asn Asn Leu Arg Ala Leu Phe Ser Asp Asn Ser
            180                 185                 190

Ser Thr Leu Gly Val Tyr Gln His Arg Phe Val Asp Ile Pro Arg Pro
        195                 200                 205

Asp Ala Glu Gly Asn Thr Ile Ile Asp Phe Asn Arg Ala Tyr Leu Pro
    210                 215                 220

Pro Lys Ala Leu Asn Arg Lys Phe Leu Cys Pro Ser Pro Ser Leu Asn
225                 230                 235                 240

Asn His Leu Asn Leu Thr Val Glu Ala Gly Glu Lys Trp Val Val Ala
                245                 250                 255

Gly Gly
```

<210> 453
<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (14)..(766)
<223> RXN00953

<400> 453

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cttgcattcc ccaatg gcg cca cca acg gta ggc aac tac atc atg cag tcc 52
               Met Ala Pro Pro Thr Val Gly Asn Tyr Ile Met Gln Ser
                 1               5                  10

ttc act caa ggt ctg cag ttc ggc gtt gca gtt gcc gtg att ctc ttt   100
Phe Thr Gln Gly Leu Gln Phe Gly Val Ala Val Ala Val Ile Leu Phe
     15                  20                  25

ggt gtc cgc acc att ctt ggt gaa ctg gtc ccc gca ttc caa ggt att   148
Gly Val Arg Thr Ile Leu Gly Glu Leu Val Pro Ala Phe Gln Gly Ile
 30                  35                  40                  45
```

```
gct gcg aag gtt gtt ccc gga gct atc ccc gca ttg gat gca ccg atc   196
Ala Ala Lys Val Val Pro Gly Ala Ile Pro Ala Leu Asp Ala Pro Ile
                 50                  55                  60

gtg ttc ccc tac gcg cag aac gcc gtt ctc att ggt ttc ttg tct tcc   244
Val Phe Pro Tyr Ala Gln Asn Ala Val Leu Ile Gly Phe Leu Ser Ser
            65                  70                  75

ttc gtc ggt ggc ttg gtt ggc ctg act gtt ctt gca tcg tgg ctg aac   292
Phe Val Gly Gly Leu Val Gly Leu Thr Val Leu Ala Ser Trp Leu Asn
         80                  85                  90

cca gct ttt ggt gtc gcg ttg att ctg cct ggt ttg gtc ccc cac ttc   340
Pro Ala Phe Gly Val Ala Leu Ile Leu Pro Gly Leu Val Pro His Phe
     95                 100                 105

ttc act ggt ggc gcg gcg ggc gtt tac ggt aat gcc acg ggt ggt cgt   388
Phe Thr Gly Gly Ala Ala Gly Val Tyr Gly Asn Ala Thr Gly Gly Arg
110                 115                 120                 125

cga gga gca gta ttt ggc gcc ttt gcc aac ggt ctt ctg att acc ttc   436
Arg Gly Ala Val Phe Gly Ala Phe Ala Asn Gly Leu Leu Ile Thr Phe
                130                 135                 140

ctc cct gct ttc ctg ctt ggt gtg ctt ggt tcc ttc ggg tca gag aac   484
Leu Pro Ala Phe Leu Leu Gly Val Leu Gly Ser Phe Gly Ser Glu Asn
            145                 150                 155

acc act ttc ggt gat gcg gac ttt ggt tgg ttc gga atc gtt gtt ggt   532
Thr Thr Phe Gly Asp Ala Asp Phe Gly Trp Phe Gly Ile Val Val Gly
        160                 165                 170

tct gca gcc aag gtg gaa ggt gct ggc ggg ctc atc ttg ttg ctc atc   580
Ser Ala Ala Lys Val Glu Gly Ala Gly Gly Leu Ile Leu Leu Leu Ile
    175                 180                 185

atc gca gcg gtt ctt ctg ggt ggc gcg atg gtc ttc cag aag cgc gtc   628
Ile Ala Ala Val Leu Leu Gly Gly Ala Met Val Phe Gln Lys Arg Val
190                 195                 200                 205

gtg aat ggg cac tgg gat cca gct ccc aac cgt gag cgc gtg gag aag   676
Val Asn Gly His Trp Asp Pro Ala Pro Asn Arg Glu Arg Val Glu Lys
                210                 215                 220

gcg gaa gct gat gcc act cca acg gct ggg gct cgg acc tac cct aag   724
Ala Glu Ala Asp Ala Thr Pro Thr Ala Gly Ala Arg Thr Tyr Pro Lys
            225                 230                 235

att gct cct ccg gcg ggc gct cct acc cca ccg gct cga agc           766
Ile Ala Pro Pro Ala Gly Ala Pro Thr Pro Pro Ala Arg Ser
        240                 245                 250

taagatctcc aaaaccctga gat                                        789
```

<210> 454
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

<400> 454

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Met Ala Pro Pro Thr Val Gly Asn Tyr Ile Met Gln Ser Phe Thr Gln
  1               5                  10                  15

Gly Leu Gln Phe Gly Val Ala Val Ala Val Ile Leu Phe Gly Val Arg
            20                  25                  30

Thr Ile Leu Gly Glu Leu Val Pro Ala Phe Gln Gly Ile Ala Ala Lys
        35                  40                  45

Val Val Pro Gly Ala Ile Pro Ala Leu Asp Ala Pro Ile Val Phe Pro
    50                  55                  60

Tyr Ala Gln Asn Ala Val Leu Ile Gly Phe Leu Ser Ser Phe Val Gly
65                  70                  75                  80

Gly Leu Val Gly Leu Thr Val Leu Ala Ser Trp Leu Asn Pro Ala Phe
                85                  90                  95

Gly Val Ala Leu Ile Leu Pro Gly Leu Val Pro His Phe Phe Thr Gly
            100                 105                 110

Gly Ala Ala Gly Val Tyr Gly Asn Ala Thr Gly Gly Arg Arg Gly Ala
        115                 120                 125

Val Phe Gly Ala Phe Ala Asn Gly Leu Leu Ile Thr Phe Leu Pro Ala
    130                 135                 140

Phe Leu Leu Gly Val Leu Gly Ser Phe Gly Ser Glu Asn Thr Thr Phe
145                 150                 155                 160

Gly Asp Ala Asp Phe Gly Trp Phe Gly Ile Val Val Gly Ser Ala Ala
                165                 170                 175

Lys Val Glu Gly Ala Gly Gly Leu Ile Leu Leu Leu Ile Ile Ala Ala
            180                 185                 190

Val Leu Leu Gly Gly Ala Met Val Phe Gln Lys Arg Val Val Asn Gly
        195                 200                 205

His Trp Asp Pro Ala Pro Asn Arg Glu Arg Val Glu Lys Ala Glu Ala
    210                 215                 220

Asp Ala Thr Pro Thr Ala Gly Ala Arg Thr Tyr Pro Lys Ile Ala Pro
225                 230                 235                 240

Pro Ala Gly Ala Pro Thr Pro Pro Ala Arg Ser
                245                 250
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<210> 455
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXN00959

<400> 455
tttggaggcg gagcatcata ccttttaatg tcaggatcgt gcagtgaaga attcaggatg 60

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aattactcgc tggaatattg gtggggatag agttgttgtt atg acg gtg atc gga   115
                                           Met Thr Val Ile Gly
                                             1               5

att att ctt ggc agc ctt ttt ggc gtt ctt gca gtc ctt ctc atc gtg   163
Ile Ile Leu Gly Ser Leu Phe Gly Val Leu Ala Val Leu Leu Ile Val
                10                  15                  20

gtt ggt gct ttg ggg tgg gcg gct aag ctc cct ggc aac ccg gtt gtg   211
Val Gly Ala Leu Gly Trp Ala Ala Lys Leu Pro Gly Asn Pro Val Val
            25                  30                  35

ggc att cgt gtc cct gag gtg cgt aaa tcc caa gaa ttg tgg gat atg   259
Gly Ile Arg Val Pro Glu Val Arg Lys Ser Gln Glu Leu Trp Asp Met
        40                  45                  50

gcg cac cgt gtc gct ggc ccg ttg tgg gtg ctg tcg gga gtt tcc ttt   307
Ala His Arg Val Ala Gly Pro Leu Trp Val Leu Ser Gly Val Ser Phe
    55                  60                  65

gtt att gca tcg cta gtt gcg ttt gtt gct tct ggt tgg atg tgg ctt   355
Val Ile Ala Ser Leu Val Ala Phe Val Ala Ser Gly Trp Met Trp Leu
70                  75                  80                  85

gtt gtg gcg ttg ggt gtt gag gct gcc atc gcg ttc att ggt atg ggt   403
Val Val Ala Leu Gly Val Glu Ala Ala Ile Ala Phe Ile Gly Met Gly
                90                  95                  100

gcg ggt atg gct gca cat act gtt gcg atg gtt gac gcg aag cgc att   451
Ala Gly Met Ala Ala His Thr Val Ala Met Val Asp Ala Lys Arg Ile
            105                 110                 115

cgc gaa acc ccg cag gcg cct gtt tcc gct gaa att gaa gag gcc ggt   499
Arg Glu Thr Pro Gln Ala Pro Val Ser Ala Glu Ile Glu Glu Ala Gly
        120                 125                 130

ggt gtg act att acc tct gcc gat tat caa caa gac tcc gct gaa tgc   547
Gly Val Thr Ile Thr Ser Ala Asp Tyr Gln Gln Asp Ser Ala Glu Cys
    135                 140                 145

ccc caa gat tgacttggat gcagtgcgta gag                             579
Pro Gln Asp
150
```

<210> 456
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 456

```
Met Thr Val Ile Gly Ile Ile Leu Gly Ser Leu Phe Gly Val Leu Ala
  1               5                  10                  15

Val Leu Leu Ile Val Val Gly Ala Leu Gly Trp Ala Ala Lys Leu Pro
            20                  25                  30

Gly Asn Pro Val Val Gly Ile Arg Val Pro Glu Val Arg Lys Ser Gln
        35                  40                  45
```

```
Glu Leu Trp Asp Met Ala His Arg Val Ala Gly Pro Leu Trp Val Leu
     50                  55                  60

Ser Gly Val Ser Phe Val Ile Ala Ser Leu Val Ala Phe Val Ala Ser
 65                  70                  75                  80

Gly Trp Met Trp Leu Val Val Ala Leu Gly Val Glu Ala Ala Ile Ala
                 85                  90                  95

Phe Ile Gly Met Gly Ala Gly Met Ala Ala His Thr Val Ala Met Val
            100                 105                 110

Asp Ala Lys Arg Ile Arg Glu Thr Pro Gln Ala Pro Val Ser Ala Glu
        115                 120                 125

Ile Glu Glu Ala Gly Gly Val Thr Ile Thr Ser Ala Asp Tyr Gln Gln
    130                 135                 140

Asp Ser Ala Glu Cys Pro Gln Asp
145                 150
```

<210> 457
<211> 427
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(427)
<223> FRXA00959

<400> 457

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tttggaggcg gagcatcata ccttttaatg tcaggatcgt gcagtgaaga attcaggatg 60

aattactcgc tggaatattg gtggggatag agttgttgtt atg acg gtg atc gga   115
                                          Met Thr Val Ile Gly
                                            1               5

att att ctt ggc agc ctt ttt ggc gtt ctt gca gtc ctt ctc atc gtg   163
Ile Ile Leu Gly Ser Leu Phe Gly Val Leu Ala Val Leu Leu Ile Val
                10                  15                  20

gtt ggt gct ttg ggg tgg gcg gct aag ctc cct ggc aac ccg gtt gtg   211
Val Gly Ala Leu Gly Trp Ala Ala Lys Leu Pro Gly Asn Pro Val Val
            25                  30                  35

ggc att cgt gtc cct gag gtg cgt aaa tcc caa gaa ttg tgg gat atg   259
Gly Ile Arg Val Pro Glu Val Arg Lys Ser Gln Glu Leu Trp Asp Met
        40                  45                  50

gcg cac cgt gtc gct ggc ccg ttg tgg gtg ctg tcg gga gtt tcc ttt   307
Ala His Arg Val Ala Gly Pro Leu Trp Val Leu Ser Gly Val Ser Phe
    55                  60                  65

gtt att gca tcg cta gtt gcg ttt gtt gct tct ggt tgg atg tgg ctt   355
Val Ile Ala Ser Leu Val Ala Phe Val Ala Ser Gly Trp Met Trp Leu
70                  75                  80                  85

gtt gtg gcg ttg ggt gtt gag gct gcc atc gcg ttc att ggt atg ggt   403
Val Val Ala Leu Gly Val Glu Ala Ala Ile Ala Phe Ile Gly Met Gly
```

```
                90                  95                  100

gcg ggt atg gct gcg cat act ggt                                    427
Ala Gly Met Ala Ala His Thr Gly
            105


<210> 458
<211> 109
<212> PRT
<213> Corynebacterium glutamicum

<400> 458
Met Thr Val Ile Gly Ile Ile Leu Gly Ser Leu Phe Gly Val Leu Ala
  1               5                  10                  15

Val Leu Leu Ile Val Val Gly Ala Leu Gly Trp Ala Ala Lys Leu Pro
             20                  25                  30

Gly Asn Pro Val Val Gly Ile Arg Val Pro Glu Val Arg Lys Ser Gln
         35                  40                  45

Glu Leu Trp Asp Met Ala His Arg Val Ala Gly Pro Leu Trp Val Leu
     50                  55                  60

Ser Gly Val Ser Phe Val Ile Ala Ser Leu Val Ala Phe Val Ala Ser
 65                  70                  75                  80

Gly Trp Met Trp Leu Val Val Ala Leu Gly Val Glu Ala Ala Ile Ala
                 85                  90                  95

Phe Ile Gly Met Gly Ala Gly Met Ala Ala His Thr Gly
            100                 105


<210> 459
<211> 960
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(937)
<223> RXN00963

<400> 459
ctggctctga cggcgtcgac ttgttctgct tctctgatac accaattttc gaggccctta 60

acctcgcacg tacttttact ccggaaggaa tctagaactt atg cgt ctt gca aca   115
                                        Met Arg Leu Ala Thr
                                          1               5

atc cgc acc aac ggc acc acc att gct gct cgt gtt gaa tct gaa aac   163
Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg Val Glu Ser Glu Asn
                 10                  15                  20

acc gct acc acc atc gag ggc ttt gcc aac gtc ggt gaa tta ctc cag   211
Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val Gly Glu Leu Leu Gln
             25                  30                  35

gaa tcc aac tgg cgc gag ctg gca gaa aac gct gct ggt gag gct gtg   259
```

```
Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala Ala Gly Glu Ala Val
         40                  45                  50

acc ttt gaa aac aag gag cta gat gca gta gtt cca gca cct aag aag   307
Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val Pro Ala Pro Lys Lys
     55                  60                  65

att gtg tgc gtc ggc ctt aac tac gcc aac cac att aaa gaa atg ggc   355
Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His Ile Lys Glu Met Gly
 70                  75                  80                  85

cgc gac ctc cct gat acc cca acc ctt ttt gtt aag ttc cct gac gcg   403
Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val Lys Phe Pro Asp Ala
                 90                  95                 100

ctc atc gga cct ttc gat gat gtt gtc gtt cca gag tgg gct aac aag   451
Leu Ile Gly Pro Phe Asp Asp Val Val Val Pro Glu Trp Ala Asn Lys
            105                 110                 115

gct ctc gac tgg gaa ggc gag atg gca gtt atc att ggc aag cgc gca   499
Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile Ile Gly Lys Arg Ala
        120                 125                 130

cgc cgt gtc aag cag gcc gat gct gct gag tac atc gct ggc tac gca   547
Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr Ile Ala Gly Tyr Ala
    135                 140                 145

gtg atg aac gat tac acc acc cgc gat ttc cag tac gca gca cct gca   595
Val Met Asn Asp Tyr Thr Thr Arg Asp Phe Gln Tyr Ala Ala Pro Ala
150                 155                 160                 165

aag act cca cag tgg cac cag ggc aag tct ttg gaa aag tcc gct ggc   643
Lys Thr Pro Gln Trp His Gln Gly Lys Ser Leu Glu Lys Ser Ala Gly
                170                 175                 180

ttc ggg cct tgg atg act acc cca gat tct ttt gag ttc ggc ggc gag   691
Phe Gly Pro Trp Met Thr Thr Pro Asp Ser Phe Glu Phe Gly Gly Glu
            185                 190                 195

ctg gca acc tac ctc gag ggc gag aag gta cag tcc acc cct acc aat   739
Leu Ala Thr Tyr Leu Glu Gly Glu Lys Val Gln Ser Thr Pro Thr Asn
        200                 205                 210

gac ctg gtc ttt agc cca gaa aag ctc atc gaa tac atc acc cac atc   787
Asp Leu Val Phe Ser Pro Glu Lys Leu Ile Glu Tyr Ile Thr His Ile
    215                 220                 225

tac cca ttg gat gct ggc gac gtc att gtc acc ggt acc cca ggc ggc   835
Tyr Pro Leu Asp Ala Gly Asp Val Ile Val Thr Gly Thr Pro Gly Gly
230                 235                 240                 245

gtt ggc cac gca cgt aac cca cag cgc tac atc ggt gac ggc gaa acc   883
Val Gly His Ala Arg Asn Pro Gln Arg Tyr Ile Gly Asp Gly Glu Thr
                250                 255                 260

gta aag gtt gag att gcg ggc ctc ggc ttc att gaa aac aag acg gtg   931
Val Lys Val Glu Ile Ala Gly Leu Gly Phe Ile Glu Asn Lys Thr Val
            265                 270                 275

ttt gaa taaatgacaa ctttccacga tct                                960
Phe Glu
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<210> 460
<211> 279
<212> PRT
<213> Corynebacterium glutamicum

<400> 460

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Met Arg Leu Ala Thr Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg
  1               5                  10                  15

Val Glu Ser Glu Asn Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val
             20                  25                  30

Gly Glu Leu Leu Gln Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala
         35                  40                  45

Ala Gly Glu Ala Val Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val
     50                  55                  60

Pro Ala Pro Lys Lys Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His
 65                  70                  75                  80

Ile Lys Glu Met Gly Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val
                 85                  90                  95

Lys Phe Pro Asp Ala Leu Ile Gly Pro Phe Asp Asp Val Val Val Pro
            100                 105                 110

Glu Trp Ala Asn Lys Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile
        115                 120                 125

Ile Gly Lys Arg Ala Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr
    130                 135                 140

Ile Ala Gly Tyr Ala Val Met Asn Asp Tyr Thr Thr Arg Asp Phe Gln
145                 150                 155                 160

Tyr Ala Ala Pro Ala Lys Thr Pro Gln Trp His Gln Gly Lys Ser Leu
                165                 170                 175

Glu Lys Ser Ala Gly Phe Gly Pro Trp Met Thr Thr Pro Asp Ser Phe
            180                 185                 190

Glu Phe Gly Gly Glu Leu Ala Thr Tyr Leu Glu Gly Glu Lys Val Gln
        195                 200                 205

Ser Thr Pro Thr Asn Asp Leu Val Phe Ser Pro Glu Lys Leu Ile Glu
    210                 215                 220

Tyr Ile Thr His Ile Tyr Pro Leu Asp Ala Gly Asp Val Ile Val Thr
225                 230                 235                 240

Gly Thr Pro Gly Gly Val Gly His Ala Arg Asn Pro Gln Arg Tyr Ile
                245                 250                 255

Gly Asp Gly Glu Thr Val Lys Val Glu Ile Ala Gly Leu Gly Phe Ile
            260                 265                 270

Glu Asn Lys Thr Val Phe Glu
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275

<210> 461
<211> 538
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(538)
<223> FRXA00963

<400> 461
ctggctctga cggcgtcgac ttgttctgct tctctgatac accaattttc gaggccctta 60

acctcgcacg tacttttact ccggaaggaa tctagaactt atg cgt ctt gca aca 115
Met Arg Leu Ala Thr
1 5

atc cgc acc aac ggc acc acc att gct gct cgt gtt gaa tct gaa aac 163
Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg Val Glu Ser Glu Asn
10 15 20

acc gct acc acc atc gag ggc ttt gcc aac gtc ggt gaa tta ctc cag 211
Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val Gly Glu Leu Leu Gln
25 30 35

gaa tcc aac tgg cgc gag ctg gca gaa aac gct gct ggt gag gct gtg 259
Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala Ala Gly Glu Ala Val
40 45 50

acc ttt gaa aac aag gag cta gat gca gta gtt cca gca cct aag aag 307
Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val Pro Ala Pro Lys Lys
55 60 65

att gtg tgc gtc ggc ctt aac tac gcc aac cac att aaa gaa atg ggc 355
Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His Ile Lys Glu Met Gly
70 75 80 85

cgc gac ctc cct gat acc cca acc ctt ttt gtt aag ttc cct gac gcg 403
Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val Lys Phe Pro Asp Ala
90 95 100

ctc atc gga cct ttc gat gat gtt gtc gtt cca gag tgg gct aac aag 451
Leu Ile Gly Pro Phe Asp Asp Val Val Val Pro Glu Trp Ala Asn Lys
105 110 115

gct ctc gac tgg gaa ggc gag atg gca gtt atc att ggc aag cgc gca 499
Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile Ile Gly Lys Arg Ala
120 125 130

cgc cgt gtc aag cag gcc gat gct gct gag tac atc gct 538
Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr Ile Ala
135 140 145

<210> 462
<211> 146
<212> PRT
<213> Corynebacterium glutamicum

<400> 462
Met Arg Leu Ala Thr Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg
1 5 10 15

Val Glu Ser Glu Asn Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val
20 25 30

Gly Glu Leu Leu Gln Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala
35 40 45

Ala Gly Glu Ala Val Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val
50 55 60

Pro Ala Pro Lys Lys Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His
65 70 75 80

Ile Lys Glu Met Gly Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val
85 90 95

Lys Phe Pro Asp Ala Leu Ile Gly Pro Phe Asp Asp Val Val Val Pro
100 105 110

Glu Trp Ala Asn Lys Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile
115 120 125

Ile Gly Lys Arg Ala Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr
130 135 140

Ile Ala
145

<210> 463
<211> 341
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(318)
<223> RXN00971

<400> 463
aaa gca ctt tcc atc gga acc cag tgg gca caa gtc atg ggc att aac 48
Lys Ala Leu Ser Ile Gly Thr Gln Trp Ala Gln Val Met Gly Ile Asn
1 5 10 15

cac gcc gaa gcc gaa gaa ctc gac gaa gcc ctc tcc ccg ctc att aac 96
His Ala Glu Ala Glu Glu Leu Asp Glu Ala Leu Ser Pro Leu Ile Asn
20 25 30

cgc ctc cgc gaa atg ggc ttt gac ccc acc gaa acc gaa gaa gca aac 144
Arg Leu Arg Glu Met Gly Phe Asp Pro Thr Glu Thr Glu Glu Ala Asn
35 40 45

tcc ctc gct cta cac agc tgc cca ttt gtg gtc aac gac aaa cgc cca 192
Ser Leu Ala Leu His Ser Cys Pro Phe Val Val Asn Asp Lys Arg Pro
50 55 60

tca gcc ttc gtc tgc gcc atc cac gcc gga ttc atc caa gaa agc ctc 240

```
Ser Ala Phe Val Cys Ala Ile His Ala Gly Phe Ile Gln Glu Ser Leu
 65                  70                  75                  80

ggt gaa aac aac cgc atc cag ctg gaa ctc aaa cca ctc aac gcg ccg   288
Gly Glu Asn Asn Arg Ile Gln Leu Glu Leu Lys Pro Leu Asn Ala Pro
                 85                  90                  95

ggc acc tgt aag gtt cac gtg ttc agc gaa taattgctgc actaataagg     338
Gly Thr Cys Lys Val His Val Phe Ser Glu
            100                 105

ccc                                                              341


<210> 464
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 464
Lys Ala Leu Ser Ile Gly Thr Gln Trp Ala Gln Val Met Gly Ile Asn
  1               5                  10                  15

His Ala Glu Ala Glu Glu Leu Asp Glu Ala Leu Ser Pro Leu Ile Asn
            20                  25                  30

Arg Leu Arg Glu Met Gly Phe Asp Pro Thr Glu Thr Glu Glu Ala Asn
        35                  40                  45

Ser Leu Ala Leu His Ser Cys Pro Phe Val Val Asn Asp Lys Arg Pro
    50                  55                  60

Ser Ala Phe Val Cys Ala Ile His Ala Gly Phe Ile Gln Glu Ser Leu
 65                  70                  75                  80

Gly Glu Asn Asn Arg Ile Gln Leu Glu Leu Lys Pro Leu Asn Ala Pro
                 85                  90                  95

Gly Thr Cys Lys Val His Val Phe Ser Glu
            100                 105


<210> 465
<211> 296
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(273)
<223> FRXA00971

<400> 465
aac cac gcc gaa gcc gaa gaa ctc gac gaa gcc ctc tcc ccg ctc att   48
Asn His Ala Glu Ala Glu Glu Leu Asp Glu Ala Leu Ser Pro Leu Ile
  1               5                  10                  15

aac cgc ctc cgc gaa atg ggc ttt gac ccc acc gaa acc gaa gaa gca   96
Asn Arg Leu Arg Glu Met Gly Phe Asp Pro Thr Glu Thr Glu Glu Ala
            20                  25                  30
```

```
aac tcc ctc gct cta cac agc tgc cca ttt gtg gtc aac gac aaa cgc   144
Asn Ser Leu Ala Leu His Ser Cys Pro Phe Val Val Asn Asp Lys Arg
         35                  40                  45

cca tca gcc ttc gtc tgc gcc atc cac gcc gga ttc atc caa gaa agc   192
Pro Ser Ala Phe Val Cys Ala Ile His Ala Gly Phe Ile Gln Glu Ser
     50                  55                  60

ctc ggt gaa aac aac cgc atc cag ctg gaa ctc aaa cca ctc aac gcg   240
Leu Gly Glu Asn Asn Arg Ile Gln Leu Glu Leu Lys Pro Leu Asn Ala
 65                  70                  75                  80

ccg ggc acc tgt aag gtt cac gtg ttc agc gaa taattgctgc actaataagg 293
Pro Gly Thr Cys Lys Val His Val Phe Ser Glu
                 85                  90

ccc                                                               296
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<210> 466
<211> 91
<212> PRT
<213> Corynebacterium glutamicum

<400> 466

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Asn His Ala Glu Ala Glu Glu Leu Asp Glu Ala Leu Ser Pro Leu Ile
  1               5                  10                  15

Asn Arg Leu Arg Glu Met Gly Phe Asp Pro Thr Glu Thr Glu Glu Ala
             20                  25                  30

Asn Ser Leu Ala Leu His Ser Cys Pro Phe Val Val Asn Asp Lys Arg
         35                  40                  45

Pro Ser Ala Phe Val Cys Ala Ile His Ala Gly Phe Ile Gln Glu Ser
     50                  55                  60

Leu Gly Glu Asn Asn Arg Ile Gln Leu Glu Leu Lys Pro Leu Asn Ala
 65                  70                  75                  80

Pro Gly Thr Cys Lys Val His Val Phe Ser Glu
                 85                  90
```

<210> 467
<211> 1503
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1480)
<223> RXN00991

<400> 467

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acttcaagga aagacggtcc caagagctaa aactccccca cggcacgcga agctgaacag 60

gctttcaccg cttctaaggg caacagctta aaccacgcta atg gac ata ctc ata   115
                                               Met Asp Ile Leu Ile
                                                 1               5
```

```
agc atc ctc tca ctg cta ggc ttc gtg ctt ctt acc gcg agc acc gga   163
Ser Ile Leu Ser Leu Leu Gly Phe Val Leu Leu Thr Ala Ser Thr Gly
                 10                  15                  20

cta ttc gtg gcc att gag ttc gca ctc acc ggc tta gaa aaa tcc act   211
Leu Phe Val Ala Ile Glu Phe Ala Leu Thr Gly Leu Glu Lys Ser Thr
            25                  30                  35

gta gaa aca cat gtg aag caa aaa ggc gac agc agc gcc cgc gca gtg   259
Val Glu Thr His Val Lys Gln Lys Gly Asp Ser Ser Ala Arg Ala Val
        40                  45                  50

cag agg gat cat caa aat ctg tcg ttc gtg ctc tct ggt gcc cag ctg   307
Gln Arg Asp His Gln Asn Leu Ser Phe Val Leu Ser Gly Ala Gln Leu
    55                  60                  65

ggc atc acg atc acg aca ctt gcc aca ggc ttc ctc gca gag ccg gtt   355
Gly Ile Thr Ile Thr Thr Leu Ala Thr Gly Phe Leu Ala Glu Pro Val
70                  75                  80                  85

ttg gcc aaa ttc ttc acc cca gca ctt gag ctg gtg gga tta aat gaa   403
Leu Ala Lys Phe Phe Thr Pro Ala Leu Glu Leu Val Gly Leu Asn Glu
                90                  95                  100

tca gca agc tcc gca gta gcc ctc atc atc gca ctg ttg gtg gca act   451
Ser Ala Ser Ser Ala Val Ala Leu Ile Ile Ala Leu Leu Val Ala Thr
            105                 110                 115

acc ctc tcc atg gtt ttt ggt gag ttg gtt ccc aaa aac tgg gcg atc   499
Thr Leu Ser Met Val Phe Gly Glu Leu Val Pro Lys Asn Trp Ala Ile
        120                 125                 130

acc aac ccg ttg ggc gtg gca cgt ttt gtt gtc cac cct gtc aat tgg   547
Thr Asn Pro Leu Gly Val Ala Arg Phe Val Val His Pro Val Asn Trp
    135                 140                 145

ttc aac atg gtt ctc aag ccg ttt att aac ggc atg aac aag tct gca   595
Phe Asn Met Val Leu Lys Pro Phe Ile Asn Gly Met Asn Lys Ser Ala
150                 155                 160                 165

aac ttt att gtc cgc aaa ctt ggt att gaa cca gcc gaa gag ctt gcc   643
Asn Phe Ile Val Arg Lys Leu Gly Ile Glu Pro Ala Glu Glu Leu Ala
                170                 175                 180

tct gcc cgt tcc tcc caa gag ctc acc gcc ttg gta cgc agc tcc gcg   691
Ser Ala Arg Ser Ser Gln Glu Leu Thr Ala Leu Val Arg Ser Ser Ala
            185                 190                 195

gaa agc ggc gga ctg gat caa aac acc gca gcg gtg atc aac cga tcc   739
Glu Ser Gly Gly Leu Asp Gln Asn Thr Ala Ala Val Ile Asn Arg Ser
        200                 205                 210

ctg cag ttc ggt gac gcc acc gct gat gaa ttc atg aca cct cgc tcc   787
Leu Gln Phe Gly Asp Ala Thr Ala Asp Glu Phe Met Thr Pro Arg Ser
    215                 220                 225

acc att gaa tca ttg cgt gcc aca gac acc gtc aat gat ttg atc gag   835
Thr Ile Glu Ser Leu Arg Ala Thr Asp Thr Val Asn Asp Leu Ile Glu
230                 235                 240                 245

ctt gcc ctg gaa acg ggt cac tcc cgc ttc cca gtc acc gaa ggc gac   883
```

```
Leu Ala Leu Glu Thr Gly His Ser Arg Phe Pro Val Thr Glu Gly Asp
                250                 255                 260

ttg gat gaa acc atc ggc atg gtc cac atc aag gac gca ttc tct gta   931
Leu Asp Glu Thr Ile Gly Met Val His Ile Lys Asp Ala Phe Ser Val
            265                 270                 275

gtg cag gca gaa cgc gcc acc acc atg gtg cgc gat cta gcc cgc aaa   979
Val Gln Ala Glu Arg Ala Thr Thr Met Val Arg Asp Leu Ala Arg Lys
        280                 285                 290

att cct gtg gta cca gcc agc ctt gac ggc gac tct gtc ctc aac gct   1027
Ile Pro Val Val Pro Ala Ser Leu Asp Gly Asp Ser Val Leu Asn Ala
    295                 300                 305

gtc cgc tcc gcc ggc tcc caa gtt att ttg gtt gcc gat gaa tac ggc   1075
Val Arg Ser Ala Gly Ser Gln Val Ile Leu Val Ala Asp Glu Tyr Gly
310                 315                 320                 325

gga acc gca ggc atg gtc acc atc gaa gac gtc gtg gag gaa atc ctc   1123
Gly Thr Ala Gly Met Val Thr Ile Glu Asp Val Val Glu Glu Ile Leu
                330                 335                 340

ggc gaa atc cac gat gag cac gac gac tcc gac gcc gaa cgc gat ttc   1171
Gly Glu Ile His Asp Glu His Asp Asp Ser Asp Ala Glu Arg Asp Phe
            345                 350                 355

caa caa ttc ggc gcc agc tgg gaa gtc tcc ggc ctg gtc cgc atc gat   1219
Gln Gln Phe Gly Ala Ser Trp Glu Val Ser Gly Leu Val Arg Ile Asp
        360                 365                 370

gaa ctc gaa aaa cgc gtc ggg tac gtc tcc cct gac ggc ccc tac gaa   1267
Glu Leu Glu Lys Arg Val Gly Tyr Val Ser Pro Asp Gly Pro Tyr Glu
    375                 380                 385

acc ctc ggc ggc ttg atc atg tac aca gtc ggc gcc att cct cgc gtc   1315
Thr Leu Gly Gly Leu Ile Met Tyr Thr Val Gly Ala Ile Pro Arg Val
390                 395                 400                 405

ggc gat gtc gcc cta ctc cca ctg acc gat acc cca acc atg gat gaa   1363
Gly Asp Val Ala Leu Leu Pro Leu Thr Asp Thr Pro Thr Met Asp Glu
                410                 415                 420

ttc gaa tcc ggc ttc tcc gga cgc tgg atc gca cga gta acg gtc atg   1411
Phe Glu Ser Gly Phe Ser Gly Arg Trp Ile Ala Arg Val Thr Val Met
            425                 430                 435

gaa gat cga cgc atc gac aaa gcc gtt ctc acc ccc atc acc cat gaa   1459
Glu Asp Arg Arg Ile Asp Lys Ala Val Leu Thr Pro Ile Thr His Glu
        440                 445                 450

gaa gca aag gag tac gaa aag tgagtatttg ggcaactgtc ctt             1503
Glu Ala Lys Glu Tyr Glu Lys
    455                 460
```

<210> 468
<211> 460
<212> PRT
<213> Corynebacterium glutamicum

<400> 468

```
Met Asp Ile Leu Ile Ser Ile Leu Ser Leu Leu Gly Phe Val Leu Leu
 1               5                  10                  15

Thr Ala Ser Thr Gly Leu Phe Val Ala Ile Glu Phe Ala Leu Thr Gly
            20                  25                  30

Leu Glu Lys Ser Thr Val Glu Thr His Val Lys Gln Lys Gly Asp Ser
        35                  40                  45

Ser Ala Arg Ala Val Gln Arg Asp His Gln Asn Leu Ser Phe Val Leu
    50                  55                  60

Ser Gly Ala Gln Leu Gly Ile Thr Ile Thr Thr Leu Ala Thr Gly Phe
65                  70                  75                  80

Leu Ala Glu Pro Val Leu Ala Lys Phe Phe Thr Pro Ala Leu Glu Leu
                85                  90                  95

Val Gly Leu Asn Glu Ser Ala Ser Ser Ala Val Ala Leu Ile Ile Ala
            100                 105                 110

Leu Leu Val Ala Thr Thr Leu Ser Met Val Phe Gly Glu Leu Val Pro
        115                 120                 125

Lys Asn Trp Ala Ile Thr Asn Pro Leu Gly Val Ala Arg Phe Val Val
    130                 135                 140

His Pro Val Asn Trp Phe Asn Met Val Leu Lys Pro Phe Ile Asn Gly
145                 150                 155                 160

Met Asn Lys Ser Ala Asn Phe Ile Val Arg Lys Leu Gly Ile Glu Pro
                165                 170                 175

Ala Glu Glu Leu Ala Ser Ala Arg Ser Ser Gln Glu Leu Thr Ala Leu
            180                 185                 190

Val Arg Ser Ser Ala Glu Ser Gly Gly Leu Asp Gln Asn Thr Ala Ala
        195                 200                 205

Val Ile Asn Arg Ser Leu Gln Phe Gly Asp Ala Thr Ala Asp Glu Phe
    210                 215                 220

Met Thr Pro Arg Ser Thr Ile Glu Ser Leu Arg Ala Thr Asp Thr Val
225                 230                 235                 240

Asn Asp Leu Ile Glu Leu Ala Leu Glu Thr Gly His Ser Arg Phe Pro
                245                 250                 255

Val Thr Glu Gly Asp Leu Asp Glu Thr Ile Gly Met Val His Ile Lys
            260                 265                 270

Asp Ala Phe Ser Val Val Gln Ala Glu Arg Ala Thr Thr Met Val Arg
        275                 280                 285

Asp Leu Ala Arg Lys Ile Pro Val Val Pro Ala Ser Leu Asp Gly Asp
    290                 295                 300

Ser Val Leu Asn Ala Val Arg Ser Ala Gly Ser Gln Val Ile Leu Val
305                 310                 315                 320
```

```
Ala Asp Glu Tyr Gly Gly Thr Ala Gly Met Val Thr Ile Glu Asp Val
                325                 330                 335

Val Glu Glu Ile Leu Gly Glu Ile His Asp Glu His Asp Asp Ser Asp
            340                 345                 350

Ala Glu Arg Asp Phe Gln Gln Phe Gly Ala Ser Trp Glu Val Ser Gly
        355                 360                 365

Leu Val Arg Ile Asp Glu Leu Glu Lys Arg Val Gly Tyr Val Ser Pro
    370                 375                 380

Asp Gly Pro Tyr Glu Thr Leu Gly Gly Leu Ile Met Tyr Thr Val Gly
385                 390                 395                 400

Ala Ile Pro Arg Val Gly Asp Val Ala Leu Leu Pro Leu Thr Asp Thr
                405                 410                 415

Pro Thr Met Asp Glu Phe Glu Ser Gly Phe Ser Gly Arg Trp Ile Ala
            420                 425                 430

Arg Val Thr Val Met Glu Asp Arg Arg Ile Asp Lys Ala Val Leu Thr
        435                 440                 445

Pro Ile Thr His Glu Glu Ala Lys Glu Tyr Glu Lys
    450                 455                 460
```

20050250234

<210> 469
<211> 1185
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1162)
<223> RXN01004

<400> 469

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ccggacgctg gatcgcacga gtaacggtca tggaagatcg acgcatcgac aaagccgttc 60

tcacccccat cacccatgaa gaagcaaagg agtacgaaaa gtg agt att tgg gca   115
                                            Val Ser Ile Trp Ala
                                              1               5

act gtc ctt cta att atc gtc ctt ctt tcc gcc aac gcc ttc ttc gtg   163
Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala Asn Ala Phe Phe Val
                  10                  15                  20

gcc gcg gag ttc gca ctg att tcc tcg cgc cgg gac cgc ctg gat tcc   211
Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg Asp Arg Leu Asp Ser
              25                  30                  35

ctg gta tcc cag ggt aaa aag gga gct gaa aag gtt ctc tac gca acc   259
Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys Val Leu Tyr Ala Thr
          40                  45                  50

gag cac ctc tcc atc atg ttg gcg ggc gct cag ttc ggt att acg gtc   307
Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln Phe Gly Ile Thr Val
      55                  60                  65
```

```
tgt tct ctg att ctg ggt aaa gtc gca gaa cct gcg atc gcc cac ttc   355
Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro Ala Ile Ala His Phe
 70                  75                  80                  85

att gag gtg cct ttc acc tcc tgg ggt gtt cca aat gat ttg atc cac   403
Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro Asn Asp Leu Ile His
                90                  95                 100

cca att tcc ttc gtc atc gca ctg gcg atc atc acc tgg ttg cac att   451
Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile Thr Trp Leu His Ile
            105                 110                 115

ctc ttt ggt gaa atg gtg cca aag aac atc gct att gct ggc cct gaa   499
Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala Ile Ala Gly Pro Glu
        120                 125                 130

acc tta ggc atg tgg ctt gct cca gtg ctc att gcg ttt gtg aag att   547
Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile Ala Phe Val Lys Ile
    135                 140                 145

acc cgc ccg ttg atc gag ttc atg aac tgg atc gcc cgt ctg acc ctt   595
Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile Ala Arg Leu Thr Leu
150                 155                 160                 165

cgc gcc ttt ggt gtg gag caa aaa aac gag ctg gat tcc acc gtg gac   643
Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu Asp Ser Thr Val Asp
                170                 175                 180

cca gag cag ctg gca tca atg att tcc gag tcc cgt tcc gaa ggc ctc   691
Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser Arg Ser Glu Gly Leu
            185                 190                 195

ctt gat gct gaa gag cac gcc cgc ctg tcc aag gcg ctg cgc tct gag   739
Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys Ala Leu Arg Ser Glu
        200                 205                 210

cag cgt tcc atc aag gaa ctg gtg att aag gat gag gac gtg cgc acg   787
Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp Glu Asp Val Arg Thr
    215                 220                 225

ctg gcg ttc ggt aaa tct ggc ccg acc ttg cac cag ttg gag gaa gca   835
Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His Gln Leu Glu Glu Ala
230                 235                 240                 245

gtc cgc gag acc ggt ttc tcc cgc ttc cct gtc acc ggc cgc gat gga   883
Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val Thr Gly Arg Asp Gly
                250                 255                 260

tcc tac ttg ggt tat atc cac atc aag gat att ttg cct cgt ctg gct   931
Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile Leu Pro Arg Leu Ala
            265                 270                 275

gat cct gag atg gat ccc tcc gag acc att ccg cgt tct gca ctg cgc   979
Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro Arg Ser Ala Leu Arg
        280                 285                 290

cct ttg agc aat gtg gat gcc gac ggc ctc atg gat gac gtc ttg gat  1027
Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met Asp Asp Val Leu Asp
    295                 300                 305

ttt atg cac tac cgc tcc gcg cac atg gct cag gtt cgc ctc aaa ggt  1075
```

```
Phe Met His Tyr Arg Ser Ala His Met Ala Gln Val Arg Leu Lys Gly
310                 315                 320                 325

gag ctt ctc ggc gtg att acg ctg gag gat ctc atc gaa gaa tac gtg   1123
Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu Ile Glu Glu Tyr Val
                330                 335                 340

ggc acc gtc aac gat tgg act cac gaa agc tcc gac gac tagaaatagt   1172
Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser Asp Asp
            345                 350

aactgtgttg gac                                                  1185


<210> 470
<211> 354
<212> PRT
<213> Corynebacterium glutamicum

<400> 470
Val Ser Ile Trp Ala Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala
  1               5                  10                  15

Asn Ala Phe Phe Val Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg
            20                  25                  30

Asp Arg Leu Asp Ser Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys
         35                  40                  45

Val Leu Tyr Ala Thr Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln
     50                  55                  60

Phe Gly Ile Thr Val Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro
 65                  70                  75                  80

Ala Ile Ala His Phe Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro
                85                  90                  95

Asn Asp Leu Ile His Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile
            100                 105                 110

Thr Trp Leu His Ile Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala
        115                 120                 125

Ile Ala Gly Pro Glu Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile
    130                 135                 140

Ala Phe Val Lys Ile Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile
145                 150                 155                 160

Ala Arg Leu Thr Leu Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu
                165                 170                 175

Asp Ser Thr Val Asp Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser
            180                 185                 190

Arg Ser Glu Gly Leu Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys
        195                 200                 205

Ala Leu Arg Ser Glu Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp
    210                 215                 220
```

```
Glu Asp Val Arg Thr Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His
225                 230                 235                 240

Gln Leu Glu Glu Ala Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val
                245                 250                 255

Thr Gly Arg Asp Gly Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile
            260                 265                 270

Leu Pro Arg Leu Ala Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro
        275                 280                 285

Arg Ser Ala Leu Arg Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met
    290                 295                 300

Asp Asp Val Leu Asp Phe Met His Tyr Arg Ser Ala His Met Ala Gln
305                 310                 315                 320

Val Arg Leu Lys Gly Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu
                325                 330                 335

Ile Glu Glu Tyr Val Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser
            340                 345                 350

Asp Asp
```

US 10,584,359 B2

<210> 471
<211> 771
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> RXN01016

<400> 471

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tgcccgtcga ggtgaacgcc caagaatagt tctctttcgt cgacttctca cgttgatacc 60

gctcggcatc atccaccaaa ttctccagcc gggtgaagca ttg ttg ccg tat gca   115
                                              Leu Leu Pro Tyr Ala
                                                1               5

ata gtc ggc ctg gtc att ttg ctg cca tcc tcc tgg ttg cct cgt tgg   163
Ile Val Gly Leu Val Ile Leu Leu Pro Ser Ser Trp Leu Pro Arg Trp
                10                  15                  20

gct gtc gca gtc ctt ggc gaa gtg tcg ctt gtg cca gcg gtg gtt ttc   211
Ala Val Ala Val Leu Gly Glu Val Ser Leu Val Pro Ala Val Val Phe
            25                  30                  35

ggt ggc ggg ttc ctg ctt atc ccc tca atg ttc ctg atc ggt tca gcg   259
Gly Gly Gly Phe Leu Leu Ile Pro Ser Met Phe Leu Ile Gly Ser Ala
        40                  45                  50

ctc gtt agg tat gga gta gtc gat cgg gca gag aac gca ccg cgg gct   307
Leu Val Arg Tyr Gly Val Val Asp Arg Ala Glu Asn Ala Pro Arg Ala
    55                  60                  65
```

```
atg gga gtc ttt ttc gcc gta agc gca gca atc gct ata cct acg ctg   355
Met Gly Val Phe Phe Ala Val Ser Ala Ala Ile Ala Ile Pro Thr Leu
 70                  75                  80                  85

atc atc cag gca cgt gac atc act tct tca ggc ttc tcg atc gtt tcc   403
Ile Ile Gln Ala Arg Asp Ile Thr Ser Ser Gly Phe Ser Ile Val Ser
                 90                  95                 100

aca gtg gcg gga ctc gcg ctt ggc ggc gtc tac att tct tta gtg ttg   451
Thr Val Ala Gly Leu Ala Leu Gly Gly Val Tyr Ile Ser Leu Val Leu
            105                 110                 115

ctg gcc ttg cat aca ccg att cgc ggt gca ctc gct gca gtt ttc gca   499
Leu Ala Leu His Thr Pro Ile Arg Gly Ala Leu Ala Ala Val Phe Ala
        120                 125                 130

cct tta ggg cgt atg gcg cta acc aac tac att ggt gca acg atc ctc   547
Pro Leu Gly Arg Met Ala Leu Thr Asn Tyr Ile Gly Ala Thr Ile Leu
    135                 140                 145

atg ctc att ggc ggg cta atc gtg gat ctt cca cac agc aca tca tgg   595
Met Leu Ile Gly Gly Leu Ile Val Asp Leu Pro His Ser Thr Ser Trp
150                 155                 160                 165

aca gct acg gtg ctc cta gct gcg ggt att ctc att att caa gag cta   643
Thr Ala Thr Val Leu Leu Ala Ala Gly Ile Leu Ile Ile Gln Glu Leu
                170                 175                 180

ctt tct gct tta tgg ttg cgc cac tac aca cag ggg cca ctt ggg tat   691
Leu Ser Ala Leu Trp Leu Arg His Tyr Thr Gln Gly Pro Leu Gly Tyr
            185                 190                 195

cta tgg cgt tgg gtg act tgg gga agc cgt tcc ccc ttc ctt acc cgt   739
Leu Trp Arg Trp Val Thr Trp Gly Ser Arg Ser Pro Phe Leu Thr Arg
        200                 205                 210

tcc gca tca tgacaggtac ggaagtgtcc tac                            771
Ser Ala Ser
    215
```

<210> 472
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 472

```
Leu Leu Pro Tyr Ala Ile Val Gly Leu Val Ile Leu Leu Pro Ser Ser
  1               5                  10                  15

Trp Leu Pro Arg Trp Ala Val Ala Val Leu Gly Glu Val Ser Leu Val
             20                  25                  30

Pro Ala Val Val Phe Gly Gly Gly Phe Leu Leu Ile Pro Ser Met Phe
         35                  40                  45

Leu Ile Gly Ser Ala Leu Val Arg Tyr Gly Val Val Asp Arg Ala Glu
     50                  55                  60

Asn Ala Pro Arg Ala Met Gly Val Phe Phe Ala Val Ser Ala Ala Ile
```

```
 65                  70                  75                  80

Ala Ile Pro Thr Leu Ile Ile Gln Ala Arg Asp Ile Thr Ser Ser Gly
                 85                  90                  95

Phe Ser Ile Val Ser Thr Val Ala Gly Leu Ala Leu Gly Gly Val Tyr
            100                 105                 110

Ile Ser Leu Val Leu Leu Ala Leu His Thr Pro Ile Arg Gly Ala Leu
        115                 120                 125

Ala Ala Val Phe Ala Pro Leu Gly Arg Met Ala Leu Thr Asn Tyr Ile
    130                 135                 140

Gly Ala Thr Ile Leu Met Leu Ile Gly Gly Leu Ile Val Asp Leu Pro
145                 150                 155                 160

His Ser Thr Ser Trp Thr Ala Thr Val Leu Leu Ala Ala Gly Ile Leu
                165                 170                 175

Ile Ile Gln Glu Leu Leu Ser Ala Leu Trp Leu Arg His Tyr Thr Gln
            180                 185                 190

Gly Pro Leu Gly Tyr Leu Trp Arg Trp Val Thr Trp Gly Ser Arg Ser
        195                 200                 205

Pro Phe Leu Thr Arg Ser Ala Ser
    210                 215


<210> 473
<211> 771
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> FRXA01016

<400> 473
tgcccgtcga ggtgaacgcc caagaatagt tctctttcgt cgacttctca cgttgatacc 60

gctcggcatc atccaccaaa ttctccagcc gggtgaagca ttg ttg ccg tat gca   115
                                              Leu Leu Pro Tyr Ala
                                                1               5

ata gtc ggc ctg gtc att ttg ctg cca tcc tcc tgg ttg cct cgt tgg   163
Ile Val Gly Leu Val Ile Leu Leu Pro Ser Ser Trp Leu Pro Arg Trp
                10                  15                  20

gct gtc gca gtc ctt ggc gaa gtg tcg ctt gtg cca gcg gtg gtt ttc   211
Ala Val Ala Val Leu Gly Glu Val Ser Leu Val Pro Ala Val Val Phe
            25                  30                  35

ggt ggc ggg ttc ctg ctt atc ccc tca atg ttc ctg atc ggt tca gcg   259
Gly Gly Gly Phe Leu Leu Ile Pro Ser Met Phe Leu Ile Gly Ser Ala
        40                  45                  50

ctc gtt agg tat gga gta gtc gat cgg gca gag aac gca ccg cgg gct   307
Leu Val Arg Tyr Gly Val Val Asp Arg Ala Glu Asn Ala Pro Arg Ala
```

```
     55                  60                  65

atg gga gtc ttt ttc gcc gta agc gca gca atc gct ata cct acg ctg   355
Met Gly Val Phe Phe Ala Val Ser Ala Ala Ile Ala Ile Pro Thr Leu
 70                  75                  80                  85

atc atc cag gca cgt gac atc act tct tca ggc ttc tcg atc gtt tcc   403
Ile Ile Gln Ala Arg Asp Ile Thr Ser Ser Gly Phe Ser Ile Val Ser
                 90                  95                 100

aca gtg gcg gga ctc gcg ctt ggc ggc gtc tac att tct tta gtg ttg   451
Thr Val Ala Gly Leu Ala Leu Gly Gly Val Tyr Ile Ser Leu Val Leu
            105                 110                 115

ctg gcc ttg cat aca ccg att cgc ggt gca ctc gct gca gtt ttc gca   499
Leu Ala Leu His Thr Pro Ile Arg Gly Ala Leu Ala Ala Val Phe Ala
        120                 125                 130

cct tta ggg cgt atg gcg cta acc aac tac att ggt gca acg atc ctc   547
Pro Leu Gly Arg Met Ala Leu Thr Asn Tyr Ile Gly Ala Thr Ile Leu
    135                 140                 145

atg ctc att ggc ggg cta atc gtg gat ctt cca cac agc aca tca tgg   595
Met Leu Ile Gly Gly Leu Ile Val Asp Leu Pro His Ser Thr Ser Trp
150                 155                 160                 165

aca gct acg gtg ctc cta gct gcg ggt att ctc att att caa gag cta   643
Thr Ala Thr Val Leu Leu Ala Ala Gly Ile Leu Ile Ile Gln Glu Leu
                170                 175                 180

ctt tct gct tta tgg ttg cgc cac tac aca cag ggg cca ctt ggg tat   691
Leu Ser Ala Leu Trp Leu Arg His Tyr Thr Gln Gly Pro Leu Gly Tyr
            185                 190                 195

cta tgg cgt tgg gtg act tgg gga agc cgt tcc ccc ttc ctt acc cgt   739
Leu Trp Arg Trp Val Thr Trp Gly Ser Arg Ser Pro Phe Leu Thr Arg
        200                 205                 210

tcc gca tca tgacaggtac ggaagtgtcc tac                            771
Ser Ala Ser
    215
```

Sequence Listing

<210> 474
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 474

```
Leu Leu Pro Tyr Ala Ile Val Gly Leu Val Ile Leu Leu Pro Ser Ser
  1               5                  10                  15

Trp Leu Pro Arg Trp Ala Val Ala Val Leu Gly Glu Val Ser Leu Val
             20                  25                  30

Pro Ala Val Val Phe Gly Gly Gly Phe Leu Leu Ile Pro Ser Met Phe
         35                  40                  45

Leu Ile Gly Ser Ala Leu Val Arg Tyr Gly Val Val Asp Arg Ala Glu
     50                  55                  60
```

```
Asn Ala Pro Arg Ala Met Gly Val Phe Phe Ala Val Ser Ala Ala Ile
 65                  70                  75                  80

Ala Ile Pro Thr Leu Ile Ile Gln Ala Arg Asp Ile Thr Ser Ser Gly
                85                  90                  95

Phe Ser Ile Val Ser Thr Val Ala Gly Leu Ala Leu Gly Gly Val Tyr
            100                 105                 110

Ile Ser Leu Val Leu Leu Ala Leu His Thr Pro Ile Arg Gly Ala Leu
        115                 120                 125

Ala Ala Val Phe Ala Pro Leu Gly Arg Met Ala Leu Thr Asn Tyr Ile
    130                 135                 140

Gly Ala Thr Ile Leu Met Leu Ile Gly Gly Leu Ile Val Asp Leu Pro
145                 150                 155                 160

His Ser Thr Ser Trp Thr Ala Thr Val Leu Leu Ala Ala Gly Ile Leu
                165                 170                 175

Ile Ile Gln Glu Leu Leu Ser Ala Leu Trp Leu Arg His Tyr Thr Gln
            180                 185                 190

Gly Pro Leu Gly Tyr Leu Trp Arg Trp Val Thr Trp Gly Ser Arg Ser
        195                 200                 205

Pro Phe Leu Thr Arg Ser Ala Ser
    210                 215


<210> 475
<211> 1101
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1078)
<223> RXN01023

<400> 475
aagcgaatcc gggaatgaaa gtgagtgcgc caaagtcaac tccttggttc aagtgtcagt 60

atttttctag tctatcgccc cacaggtagg ctcaggacac atg agt gcc gtg aac   115
                                            Met Ser Ala Val Asn
                                              1               5

agt gct ggt cgc cca gcc aac ggg gga att aac aaa acc ccc atg att   163
Ser Ala Gly Arg Pro Ala Asn Gly Gly Ile Asn Lys Thr Pro Met Ile
                10                  15                  20

att gcc cta gtg tta tct att gtg ttg gtt ttg gcg gtg ctg ttc ggc   211
Ile Ala Leu Val Leu Ser Ile Val Leu Val Leu Ala Val Leu Phe Gly
            25                  30                  35

gcc cga gtc ctc ctt ggc ccc gcc ggc cag caa cag ata gcc atg agt   259
Ala Arg Val Leu Leu Gly Pro Ala Gly Gln Gln Gln Ile Ala Met Ser
        40                  45                  50

ggg ctt ccc gcc cca gac gca gaa tct gct gag tgc gcc gca tta ctc   307
```

```
Gly Leu Pro Ala Pro Asp Ala Glu Ser Ala Glu Cys Ala Ala Leu Leu
     55                  60                  65

gag gat ctc ccc ggc gag gcc ttc ggg cac acc cgt gca gaa atc atg   355
Glu Asp Leu Pro Gly Glu Ala Phe Gly His Thr Arg Ala Glu Ile Met
 70                  75                  80                  85

gat cct gtt cca ccg ggc gct gcc gcc tgg tcc acc tca gac ctc gag   403
Asp Pro Val Pro Pro Gly Ala Ala Ala Trp Ser Thr Ser Asp Leu Glu
                 90                  95                 100

cgt gtg acg ctg cgt tgt ggc gtc gat atg cca ttc cag tac acc gcg   451
Arg Val Thr Leu Arg Cys Gly Val Asp Met Pro Phe Gln Tyr Thr Ala
            105                 110                 115

ctc gcc aac acc gtc gac gtc gac ggc acc acc tgg cta cct gtc tcc   499
Leu Ala Asn Thr Val Asp Val Asp Gly Thr Thr Trp Leu Pro Val Ser
        120                 125                 130

gac atg acc ccc ggc tcc tcc ctg gag acc tgg tac tcc gtc aac cgc   547
Asp Met Thr Pro Gly Ser Ser Leu Glu Thr Trp Tyr Ser Val Asn Arg
    135                 140                 145

ttc ccc gtc gtc gcc atc acc gcc gat gac atc agc acc gac agc gcc   595
Phe Pro Val Val Ala Ile Thr Ala Asp Asp Ile Ser Thr Asp Ser Ala
150                 155                 160                 165

gac aac ccc gtc gcc ccc ttc agc agc gcc gtc gac aag cta gaa aag   643
Asp Asn Pro Val Ala Pro Phe Ser Ser Ala Val Asp Lys Leu Glu Lys
                170                 175                 180

cgc gac ggc cag ccc ttc gac gcc cca ctt acc ggc ttg agc tca gcc   691
Arg Asp Gly Gln Pro Phe Asp Ala Pro Leu Thr Gly Leu Ser Ser Ala
            185                 190                 195

ggc acc aca tgc act tcg ctt ttc gac gcc ctc ccc cgc caa ctc gaa   739
Gly Thr Thr Cys Thr Ser Leu Phe Asp Ala Leu Pro Arg Gln Leu Glu
        200                 205                 210

gtc ggc ggc gac gac ggc aca acg tac gaa cgc atc gag gag gac cgc   787
Val Gly Gly Asp Asp Gly Thr Thr Tyr Glu Arg Ile Glu Glu Asp Arg
    215                 220                 225

atg cag gcc gcc gga tac tcc gac gac gca gtc gcg tgg gac acg ccg   835
Met Gln Ala Ala Gly Tyr Ser Asp Asp Ala Val Ala Trp Asp Thr Pro
230                 235                 240                 245

gga tta gaa ccc att gtg atc cgt tgc ggc gtg gag cct tct gag aac   883
Gly Leu Glu Pro Ile Val Ile Arg Cys Gly Val Glu Pro Ser Glu Asn
                250                 255                 260

tac gca gcc ggt gcc atg ttg cag cag atc gat gac atc ccg tgg ttc   931
Tyr Ala Ala Gly Ala Met Leu Gln Gln Ile Asp Asp Ile Pro Trp Phe
            265                 270                 275

gag gac acc att ttg gcc tcc ggt acc acc tcg tct acc tgg tat gcc   979
Glu Asp Thr Ile Leu Ala Ser Gly Thr Thr Ser Ser Thr Trp Tyr Ala
        280                 285                 290

ctt gga cgc gag atc gac atc gcc gtg tct ctg cct cag gct gct tcc   1027
Leu Gly Arg Glu Ile Asp Ile Ala Val Ser Leu Pro Gln Ala Ala Ser
```

```
    295                 300                 305

tct tcc ctg att act atc tcc ggt ttc att gaa gac acg gtt cct gcg   1075
Ser Ser Leu Ile Thr Ile Ser Gly Phe Ile Glu Asp Thr Val Pro Ala
310                 315                 320                 325

gaa taagacataa aaaatcgccc cac                                     1101
Glu
```

<210> 476
<211> 326
<212> PRT
<213> Corynebacterium glutamicum

<400> 476

```
Met Ser Ala Val Asn Ser Ala Gly Arg Pro Ala Asn Gly Gly Ile Asn
  1               5                  10                  15

Lys Thr Pro Met Ile Ile Ala Leu Val Leu Ser Ile Val Leu Val Leu
             20                  25                  30

Ala Val Leu Phe Gly Ala Arg Val Leu Leu Gly Pro Ala Gly Gln Gln
         35                  40                  45

Gln Ile Ala Met Ser Gly Leu Pro Ala Pro Asp Ala Glu Ser Ala Glu
     50                  55                  60

Cys Ala Ala Leu Leu Glu Asp Leu Pro Gly Glu Ala Phe Gly His Thr
 65                  70                  75                  80

Arg Ala Glu Ile Met Asp Pro Val Pro Pro Gly Ala Ala Ala Trp Ser
                 85                  90                  95

Thr Ser Asp Leu Glu Arg Val Thr Leu Arg Cys Gly Val Asp Met Pro
            100                 105                 110

Phe Gln Tyr Thr Ala Leu Ala Asn Thr Val Asp Val Asp Gly Thr Thr
        115                 120                 125

Trp Leu Pro Val Ser Asp Met Thr Pro Gly Ser Ser Leu Glu Thr Trp
    130                 135                 140

Tyr Ser Val Asn Arg Phe Pro Val Val Ala Ile Thr Ala Asp Asp Ile
145                 150                 155                 160

Ser Thr Asp Ser Ala Asp Asn Pro Val Ala Pro Phe Ser Ser Ala Val
                165                 170                 175

Asp Lys Leu Glu Lys Arg Asp Gly Gln Pro Phe Asp Ala Pro Leu Thr
            180                 185                 190

Gly Leu Ser Ser Ala Gly Thr Thr Cys Thr Ser Leu Phe Asp Ala Leu
        195                 200                 205

Pro Arg Gln Leu Glu Val Gly Gly Asp Asp Gly Thr Thr Tyr Glu Arg
    210                 215                 220

Ile Glu Glu Asp Arg Met Gln Ala Ala Gly Tyr Ser Asp Asp Ala Val
225                 230                 235                 240
```

```
Ala Trp Asp Thr Pro Gly Leu Glu Pro Ile Val Ile Arg Cys Gly Val
                245                 250                 255

Glu Pro Ser Glu Asn Tyr Ala Ala Gly Ala Met Leu Gln Gln Ile Asp
            260                 265                 270

Asp Ile Pro Trp Phe Glu Asp Thr Ile Leu Ala Ser Gly Thr Thr Ser
        275                 280                 285

Ser Thr Trp Tyr Ala Leu Gly Arg Glu Ile Asp Ile Ala Val Ser Leu
    290                 295                 300

Pro Gln Ala Ala Ser Ser Ser Leu Ile Thr Ile Ser Gly Phe Ile Glu
305                 310                 315                 320

Asp Thr Val Pro Ala Glu
                325
```

<210> 477
<211> 974
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(951)
<223> FRXA01023

<400> 477

```
cca gcc aac ggg gga att aac aaa acc ccc atg att att gcc cta gtg   48
Pro Ala Asn Gly Gly Ile Asn Lys Thr Pro Met Ile Ile Ala Leu Val
  1               5                  10                  15

tta tct att gtg ttg gtt ttg gcg gtg ctg ttc ggc gcc cga gtc ctc   96
Leu Ser Ile Val Leu Val Leu Ala Val Leu Phe Gly Ala Arg Val Leu
            20                  25                  30

ctt ggc ccc gcc ggc cag caa cag ata gcc atg agt ggg ctt ccc gcc   144
Leu Gly Pro Ala Gly Gln Gln Gln Ile Ala Met Ser Gly Leu Pro Ala
        35                  40                  45

cca gac gca gaa tct gct gag tgc gcc gca tta ctc gag gat ctc ccc   192
Pro Asp Ala Glu Ser Ala Glu Cys Ala Ala Leu Leu Glu Asp Leu Pro
    50                  55                  60

ggc gag gcc ttc ggg cac acc cgt gca gaa atc atg gat cct gtt cca   240
Gly Glu Ala Phe Gly His Thr Arg Ala Glu Ile Met Asp Pro Val Pro
65                  70                  75                  80

ccg ggc gct gcc gcc tgg tcc acc tca gac ctc gag cgt gtg acg ctg   288
Pro Gly Ala Ala Ala Trp Ser Thr Ser Asp Leu Glu Arg Val Thr Leu
                85                  90                  95

cgt tgt ggc gtc gat atg cca ttc cag tac acc gcg ctc gcc aac acc   336
Arg Cys Gly Val Asp Met Pro Phe Gln Tyr Thr Ala Leu Ala Asn Thr
            100                 105                 110

gtc gac gtc gac ggc acc acc tgg cta cct gtc tcc gac atg acc ccc   384
Val Asp Val Asp Gly Thr Thr Trp Leu Pro Val Ser Asp Met Thr Pro
```

```
        115                 120                 125

ggc tcc tcc ctg gag acc tgg tac tcc gtc aac cgc ttc ccc gtc gtc   432
Gly Ser Ser Leu Glu Thr Trp Tyr Ser Val Asn Arg Phe Pro Val Val
    130                 135                 140

gcc atc acc gcc gat gac atc agc acc gac agc gcc gac aac ccc gtc   480
Ala Ile Thr Ala Asp Asp Ile Ser Thr Asp Ser Ala Asp Asn Pro Val
145                 150                 155                 160

gac ccc ttc agc agc gcc gtc gac aag cta gaa aag cgc gac ggc cag   528
Asp Pro Phe Ser Ser Ala Val Asp Lys Leu Glu Lys Arg Asp Gly Gln
                165                 170                 175

ccc ttc gac gcc cca ctt acc ggc ttg agc tca gcc ggc acc aca tgc   576
Pro Phe Asp Ala Pro Leu Thr Gly Leu Ser Ser Ala Gly Thr Thr Cys
            180                 185                 190

act tcg ctt ttc gac gcc ctc ccc cgc caa ctc gaa gtc ggc ggc gac   624
Thr Ser Leu Phe Asp Ala Leu Pro Arg Gln Leu Glu Val Gly Gly Asp
        195                 200                 205

gac ggc aca acg tac gaa cgc atc gag gag gac cgc atg cag gcc gcc   672
Asp Gly Thr Thr Tyr Glu Arg Ile Glu Glu Asp Arg Met Gln Ala Ala
    210                 215                 220

gga tac tcc gac gac gca gtc gcg tgg gac acg ccg gga tta gaa ccc   720
Gly Tyr Ser Asp Asp Ala Val Ala Trp Asp Thr Pro Gly Leu Glu Pro
225                 230                 235                 240

att gtg atc cgt tgc ggc gtg gag cct tct gag aac tac gca gcc ggt   768
Ile Val Ile Arg Cys Gly Val Glu Pro Ser Glu Asn Tyr Ala Ala Gly
                245                 250                 255

gcc atg ttg cag cag atc gat gac atc ccg tgg ttc gag gac acc att   816
Ala Met Leu Gln Gln Ile Asp Asp Ile Pro Trp Phe Glu Asp Thr Ile
            260                 265                 270

ttg gcc tcc ggt acc acc tcg tct acc tgg tat gcc ctt gga cgc gag   864
Leu Ala Ser Gly Thr Thr Ser Ser Thr Trp Tyr Ala Leu Gly Arg Glu
        275                 280                 285

atc gac atc gcc gtg tct ctg cct cag gct gct tcc tct tcc ctg att   912
Ile Asp Ile Ala Val Ser Leu Pro Gln Ala Ala Ser Ser Ser Leu Ile
    290                 295                 300

act atc tcc ggt ttc att gaa gac acg gtt cct gcg gaa taagacataa   961
Thr Ile Ser Gly Phe Ile Glu Asp Thr Val Pro Ala Glu
305                 310                 315

aaaatcgccc cac                                                  974
```

<210> 478
<211> 317
<212> PRT
<213> Corynebacterium glutamicum

<400> 478

```
Pro Ala Asn Gly Gly Ile Asn Lys Thr Pro Met Ile Ile Ala Leu Val
  1               5                  10                  15
```

```
Leu Ser Ile Val Leu Val Leu Ala Val Leu Phe Gly Ala Arg Val Leu
            20                  25                  30

Leu Gly Pro Ala Gly Gln Gln Gln Ile Ala Met Ser Gly Leu Pro Ala
        35                  40                  45

Pro Asp Ala Glu Ser Ala Glu Cys Ala Ala Leu Leu Glu Asp Leu Pro
    50                  55                  60

Gly Glu Ala Phe Gly His Thr Arg Ala Glu Ile Met Asp Pro Val Pro
65                  70                  75                  80

Pro Gly Ala Ala Ala Trp Ser Thr Ser Asp Leu Glu Arg Val Thr Leu
                85                  90                  95

Arg Cys Gly Val Asp Met Pro Phe Gln Tyr Thr Ala Leu Ala Asn Thr
            100                 105                 110

Val Asp Val Asp Gly Thr Thr Trp Leu Pro Val Ser Asp Met Thr Pro
        115                 120                 125

Gly Ser Ser Leu Glu Thr Trp Tyr Ser Val Asn Arg Phe Pro Val Val
    130                 135                 140

Ala Ile Thr Ala Asp Asp Ile Ser Thr Asp Ser Ala Asp Asn Pro Val
145                 150                 155                 160

Asp Pro Phe Ser Ser Ala Val Asp Lys Leu Glu Lys Arg Asp Gly Gln
                165                 170                 175

Pro Phe Asp Ala Pro Leu Thr Gly Leu Ser Ser Ala Gly Thr Thr Cys
            180                 185                 190

Thr Ser Leu Phe Asp Ala Leu Pro Arg Gln Leu Glu Val Gly Gly Asp
        195                 200                 205

Asp Gly Thr Thr Tyr Glu Arg Ile Glu Glu Asp Arg Met Gln Ala Ala
    210                 215                 220

Gly Tyr Ser Asp Asp Ala Val Ala Trp Asp Thr Pro Gly Leu Glu Pro
225                 230                 235                 240

Ile Val Ile Arg Cys Gly Val Glu Pro Ser Glu Asn Tyr Ala Ala Gly
                245                 250                 255

Ala Met Leu Gln Gln Ile Asp Asp Ile Pro Trp Phe Glu Asp Thr Ile
            260                 265                 270

Leu Ala Ser Gly Thr Thr Ser Ser Thr Trp Tyr Ala Leu Gly Arg Glu
        275                 280                 285

Ile Asp Ile Ala Val Ser Leu Pro Gln Ala Ala Ser Ser Ser Leu Ile
    290                 295                 300

Thr Ile Ser Gly Phe Ile Glu Asp Thr Val Pro Ala Glu
305                 310                 315
```

<210> 479
<211> 2172

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2149)
<223> RXN01028

<400> 479
cgcaagcagc tgcactatat tcaggcattt taccgtgcct gggacccatc aacgccgctt 60

caatgacgct gacccagcgg tgacccatcc gcatctcaca gtg atc tac cca ccg 115
Val Ile Tyr Pro Pro
1 5

ctc acc cct gca tcc gaa gag aaa ttc aac aag atc acc tca gtc gct 163
Leu Thr Pro Ala Ser Glu Glu Lys Phe Asn Lys Ile Thr Ser Val Ala
10 15 20

gct gtg agc aag cgc cca acc acc ctg ccg tat ttc cgt gca gat ggt 211
Ala Val Ser Lys Arg Pro Thr Thr Leu Pro Tyr Phe Arg Ala Asp Gly
25 30 35

tca cct act cgt ggc ttt gct aac ttc tcc aca gga ggt att cac ggt 259
Ser Pro Thr Arg Gly Phe Ala Asn Phe Ser Thr Gly Gly Ile His Gly
40 45 50

gcg gaa tac aac gaa gat cgt ttt gac cat gat caa gat cta cac aca 307
Ala Glu Tyr Asn Glu Asp Arg Phe Asp His Asp Gln Asp Leu His Thr
55 60 65

gtg gca acc cgt gaa ttc ttc gcc att ctt gat gcg aca tta gcg gct 355
Val Ala Thr Arg Glu Phe Phe Ala Ile Leu Asp Ala Thr Leu Ala Ala
70 75 80 85

ctc tac gca gcc cac caa gcc gaa cct gaa tcg gcg gac tac cag att 403
Leu Tyr Ala Ala His Gln Ala Glu Pro Glu Ser Ala Asp Tyr Gln Ile
90 95 100

gca caa gac gca ctc gcc tgg gca aag aat gta ctt agc gat caa aaa 451
Ala Gln Asp Ala Leu Ala Trp Ala Lys Asn Val Leu Ser Asp Gln Lys
105 110 115

ctc atc gct aag tcg cct cag tta tac aac ccc gaa acc ggg gtc acc 499
Leu Ile Ala Lys Ser Pro Gln Leu Tyr Asn Pro Glu Thr Gly Val Thr
120 125 130

tat gag tgg gag ttt gtc gct caa gca gca tgg tgg att cgc aac aaa 547
Tyr Glu Trp Glu Phe Val Ala Gln Ala Ala Trp Trp Ile Arg Asn Lys
135 140 145

ccg gtt gag gtt att tta cca aca ggt gaa tca atg acc gta aaa cac 595
Pro Val Glu Val Ile Leu Pro Thr Gly Glu Ser Met Thr Val Lys His
150 155 160 165

aaa tct gta ttg gca tct gcg tcc tac cca ctc cga gac aac gtg gcg 643
Lys Ser Val Leu Ala Ser Ala Ser Tyr Pro Leu Arg Asp Asn Val Ala
170 175 180

tac tgg cgt agc gaa ccc aaa aca cca cag ctg ttt ccc gta gca aaa 691
Tyr Trp Arg Ser Glu Pro Lys Thr Pro Gln Leu Phe Pro Val Ala Lys

```
                185                 190                 195

tct ggt ggt tcc tcg ctt gag aag aag tac aac tac acc tct gtg ggt   739
Ser Gly Gly Ser Ser Leu Glu Lys Lys Tyr Asn Tyr Thr Ser Val Gly
        200                 205                 210

act gct att cac gag gac ttt agc agt tac tat ccg ctc ttg ctc acc   787
Thr Ala Ile His Glu Asp Phe Ser Ser Tyr Tyr Pro Leu Leu Leu Thr
    215                 220                 225

aat atg gct gca ttt acc aat gct gac tta ggt att gat gag aaa acc   835
Asn Met Ala Ala Phe Thr Asn Ala Asp Leu Gly Ile Asp Glu Lys Thr
230                 235                 240                 245

ggg cgc cct cgt gac cgc tac cgt gaa atc tac gaa caa aaa gag atc   883
Gly Arg Pro Arg Asp Arg Tyr Arg Glu Ile Tyr Glu Gln Lys Glu Ile
                250                 255                 260

tat ggc gca cag cgc aaa gac ccc tcc att gat gaa gaa aca aag caa   931
Tyr Gly Ala Gln Arg Lys Asp Pro Ser Ile Asp Glu Glu Thr Lys Gln
            265                 270                 275

cgt cta ggg att ttg cgc gaa ggt acc aag ttg att ctt aac tcg gcc   979
Arg Leu Gly Ile Leu Arg Glu Gly Thr Lys Leu Ile Leu Asn Ser Ala
        280                 285                 290

acc ggt gct gct gat gct ggt cac gac acc ccg atc ctc atg aac aat  1027
Thr Gly Ala Ala Asp Ala Gly His Asp Thr Pro Ile Leu Met Asn Asn
    295                 300                 305

cgc gtt att gcc atg agg att att ggg cag cta ttt tct tgg aga att  1075
Arg Val Ile Ala Met Arg Ile Ile Gly Gln Leu Phe Ser Trp Arg Ile
310                 315                 320                 325

ggg caa gct caa tca ctg gct ggt gca acg att att tcc act aac act  1123
Gly Gln Ala Gln Ser Leu Ala Gly Ala Thr Ile Ile Ser Thr Asn Thr
                330                 335                 340

gat ggc ctg tat tcc gta ctc gat atg ggg act aac cag cgc gtt ctt  1171
Asp Gly Leu Tyr Ser Val Leu Asp Met Gly Thr Asn Gln Arg Val Leu
            345                 350                 355

gat gaa cac gct aca gcc atc ggt gtg caa att gag cct gaa gaa ctg  1219
Asp Glu His Ala Thr Ala Ile Gly Val Gln Ile Glu Pro Glu Glu Leu
        360                 365                 370

gat att gtc tcc aag gat tcc aac tca cgt gcc gaa ttt ctc ggc aat  1267
Asp Ile Val Ser Lys Asp Ser Asn Ser Arg Ala Glu Phe Leu Gly Asn
    375                 380                 385

ggc tac atc aat gcg gcc ggt gac ttg gcg tgt tgg gat gga ccc aac  1315
Gly Tyr Ile Asn Ala Ala Gly Asp Leu Ala Cys Trp Asp Gly Pro Asn
390                 395                 400                 405

tct cgg aac tca cta gat cac ccg gcc ttt gtt gac cat gtg ctg gtg  1363
Ser Arg Asn Ser Leu Asp His Pro Ala Phe Val Asp His Val Leu Val
                410                 415                 420

aag tat ttc cag ctc gtc gtc aac aac act gtg cca gag att cca gaa  1411
Lys Tyr Phe Gln Leu Val Val Asn Asn Thr Val Pro Glu Ile Pro Glu
            425                 430                 435
```

```
aca cct gag ctt gag ggt gta ccg ctg gct ctt gat caa ccc atg aac   1459
Thr Pro Glu Leu Glu Gly Val Pro Leu Ala Leu Asp Gln Pro Met Asn
        440                 445                 450

cgc cac gaa gtc tcg aag att gtc gcc act atg cac aag gaa ttc gag   1507
Arg His Glu Val Ser Lys Ile Val Ala Thr Met His Lys Glu Phe Glu
    455                 460                 465

ccg aaa aag ctg ctg tcg ttt tac caa aac att ttg gcc tct tca cgc   1555
Pro Lys Lys Leu Leu Ser Phe Tyr Gln Asn Ile Leu Ala Ser Ser Arg
470                 475                 480                 485

ggt tct aat acc ttc cta ttc tct gtc ccc tat atc cct gca aca gaa   1603
Gly Ser Asn Thr Phe Leu Phe Ser Val Pro Tyr Ile Pro Ala Thr Glu
                490                 495                 500

gga gaa gaa acc cac cct gca aca gat acc agc act att gcg aca cca   1651
Gly Glu Glu Thr His Pro Ala Thr Asp Thr Ser Thr Ile Ala Thr Pro
            505                 510                 515

acc ttg agc ttt gat gct tat ggt aat aag gcc gag gtc atg ccg act   1699
Thr Leu Ser Phe Asp Ala Tyr Gly Asn Lys Ala Glu Val Met Pro Thr
        520                 525                 530

caa tcc act gtg gat aag cgc gtg ccc tct ttg ctg cag tat tac acg   1747
Gln Ser Thr Val Asp Lys Arg Val Pro Ser Leu Leu Gln Tyr Tyr Thr
    535                 540                 545

cgt aca ttc cat gtg cga caa gat acg cag cag gct gtc ttt gat gtt   1795
Arg Thr Phe His Val Arg Gln Asp Thr Gln Gln Ala Val Phe Asp Val
550                 555                 560                 565

att ggc gcc aac ccc gtg ctc atc gcc gca gca aaa gct gca tcc ata   1843
Ile Gly Ala Asn Pro Val Leu Ile Ala Ala Ala Lys Ala Ala Ser Ile
                570                 575                 580

tca ccg gct tct gct gat tca cgt aga aag aag ggc ctg gcc tcc acc   1891
Ser Pro Ala Ser Ala Asp Ser Arg Arg Lys Lys Gly Leu Ala Ser Thr
            585                 590                 595

aac gct gac cca gta gcc aag cat gta cta gaa att gca gga gct gat   1939
Asn Ala Asp Pro Val Ala Lys His Val Leu Glu Ile Ala Gly Ala Asp
        600                 605                 610

gtg gaa tcg ctg cgc cat gaa aag gat ctc aag gtc acc aag cac act   1987
Val Glu Ser Leu Arg His Glu Lys Asp Leu Lys Val Thr Lys His Thr
    615                 620                 625

ggc caa gac cca gca ctg cct gtc gtg gtc ttt aac caa acc att tgg   2035
Gly Gln Asp Pro Ala Leu Pro Val Val Val Phe Asn Gln Thr Ile Trp
630                 635                 640                 645

cat aac ccc aac gac gat gtg att aat gca tta ctg ggc gct att gac   2083
His Asn Pro Asn Asp Asp Val Ile Asn Ala Leu Leu Gly Ala Ile Asp
                650                 655                 660

cag gat gcc tac att gac atg gcg atc tcg tcc tac aac aag tcc tgg   2131
Gln Asp Ala Tyr Ile Asp Met Ala Ile Ser Ser Tyr Asn Lys Ser Trp
            665                 670                 675
```

```
cac aac att atc ccg gct taactaccgc tgggtagacc cct                2172
His Asn Ile Ile Pro Ala
        680
```

<210> 480
<211> 683
<212> PRT
<213> Corynebacterium glutamicum

<400> 480

```
Val Ile Tyr Pro Pro Leu Thr Pro Ala Ser Glu Glu Lys Phe Asn Lys
  1               5                  10                  15

Ile Thr Ser Val Ala Ala Val Ser Lys Arg Pro Thr Thr Leu Pro Tyr
             20                  25                  30

Phe Arg Ala Asp Gly Ser Pro Thr Arg Gly Phe Ala Asn Phe Ser Thr
         35                  40                  45

Gly Gly Ile His Gly Ala Glu Tyr Asn Glu Asp Arg Phe Asp His Asp
     50                  55                  60

Gln Asp Leu His Thr Val Ala Thr Arg Glu Phe Phe Ala Ile Leu Asp
 65                  70                  75                  80

Ala Thr Leu Ala Ala Leu Tyr Ala Ala His Gln Ala Glu Pro Glu Ser
                 85                  90                  95

Ala Asp Tyr Gln Ile Ala Gln Asp Ala Leu Ala Trp Ala Lys Asn Val
            100                 105                 110

Leu Ser Asp Gln Lys Leu Ile Ala Lys Ser Pro Gln Leu Tyr Asn Pro
        115                 120                 125

Glu Thr Gly Val Thr Tyr Glu Trp Glu Phe Val Ala Gln Ala Ala Trp
    130                 135                 140

Trp Ile Arg Asn Lys Pro Val Glu Val Ile Leu Pro Thr Gly Glu Ser
145                 150                 155                 160

Met Thr Val Lys His Lys Ser Val Leu Ala Ser Ala Ser Tyr Pro Leu
                165                 170                 175

Arg Asp Asn Val Ala Tyr Trp Arg Ser Glu Pro Lys Thr Pro Gln Leu
            180                 185                 190

Phe Pro Val Ala Lys Ser Gly Gly Ser Ser Leu Glu Lys Lys Tyr Asn
        195                 200                 205

Tyr Thr Ser Val Gly Thr Ala Ile His Glu Asp Phe Ser Ser Tyr Tyr
    210                 215                 220

Pro Leu Leu Leu Thr Asn Met Ala Ala Phe Thr Asn Ala Asp Leu Gly
225                 230                 235                 240

Ile Asp Glu Lys Thr Gly Arg Pro Arg Asp Arg Tyr Arg Glu Ile Tyr
                245                 250                 255

Glu Gln Lys Glu Ile Tyr Gly Ala Gln Arg Lys Asp Pro Ser Ile Asp
            260                 265                 270
```

```
Glu Glu Thr Lys Gln Arg Leu Gly Ile Leu Arg Glu Gly Thr Lys Leu
        275                 280                 285

Ile Leu Asn Ser Ala Thr Gly Ala Ala Asp Ala Gly His Asp Thr Pro
    290                 295                 300

Ile Leu Met Asn Asn Arg Val Ile Ala Met Arg Ile Ile Gly Gln Leu
305                 310                 315                 320

Phe Ser Trp Arg Ile Gly Gln Ala Gln Ser Leu Ala Gly Ala Thr Ile
                325                 330                 335

Ile Ser Thr Asn Thr Asp Gly Leu Tyr Ser Val Leu Asp Met Gly Thr
            340                 345                 350

Asn Gln Arg Val Leu Asp Glu His Ala Thr Ala Ile Gly Val Gln Ile
        355                 360                 365

Glu Pro Glu Glu Leu Asp Ile Val Ser Lys Asp Ser Asn Ser Arg Ala
    370                 375                 380

Glu Phe Leu Gly Asn Gly Tyr Ile Asn Ala Ala Gly Asp Leu Ala Cys
385                 390                 395                 400

Trp Asp Gly Pro Asn Ser Arg Asn Ser Leu Asp His Pro Ala Phe Val
                405                 410                 415

Asp His Val Leu Val Lys Tyr Phe Gln Leu Val Val Asn Asn Thr Val
            420                 425                 430

Pro Glu Ile Pro Glu Thr Pro Glu Leu Glu Gly Val Pro Leu Ala Leu
        435                 440                 445

Asp Gln Pro Met Asn Arg His Glu Val Ser Lys Ile Val Ala Thr Met
    450                 455                 460

His Lys Glu Phe Glu Pro Lys Lys Leu Leu Ser Phe Tyr Gln Asn Ile
465                 470                 475                 480

Leu Ala Ser Ser Arg Gly Ser Asn Thr Phe Leu Phe Ser Val Pro Tyr
                485                 490                 495

Ile Pro Ala Thr Glu Gly Glu Glu Thr His Pro Ala Thr Asp Thr Ser
            500                 505                 510

Thr Ile Ala Thr Pro Thr Leu Ser Phe Asp Ala Tyr Gly Asn Lys Ala
        515                 520                 525

Glu Val Met Pro Thr Gln Ser Thr Val Asp Lys Arg Val Pro Ser Leu
    530                 535                 540

Leu Gln Tyr Tyr Thr Arg Thr Phe His Val Arg Gln Asp Thr Gln Gln
545                 550                 555                 560

Ala Val Phe Asp Val Ile Gly Ala Asn Pro Val Leu Ile Ala Ala Ala
                565                 570                 575

Lys Ala Ala Ser Ile Ser Pro Ala Ser Ala Asp Ser Arg Arg Lys Lys
            580                 585                 590
```

```
Gly Leu Ala Ser Thr Asn Ala Asp Pro Val Ala Lys His Val Leu Glu
        595                 600                 605

Ile Ala Gly Ala Asp Val Glu Ser Leu Arg His Glu Lys Asp Leu Lys
    610                 615                 620

Val Thr Lys His Thr Gly Gln Asp Pro Ala Leu Pro Val Val Val Phe
625                 630                 635                 640

Asn Gln Thr Ile Trp His Asn Pro Asn Asp Asp Val Ile Asn Ala Leu
                645                 650                 655

Leu Gly Ala Ile Asp Gln Asp Ala Tyr Ile Asp Met Ala Ile Ser Ser
            660                 665                 670

Tyr Asn Lys Ser Trp His Asn Ile Ile Pro Ala
        675                 680


<210> 481
<211> 647
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(624)
<223> FRXA01028

<400> 481
ttt tac caa aac att ttg gcc tct tca cgc ggt tct aat acc ttc cta   48
Phe Tyr Gln Asn Ile Leu Ala Ser Ser Arg Gly Ser Asn Thr Phe Leu
  1               5                  10                  15

ttc tct gtc ccc tat atc cct gca aca gaa gga gaa gaa acc cac cct   96
Phe Ser Val Pro Tyr Ile Pro Ala Thr Glu Gly Glu Glu Thr His Pro
            20                  25                  30

gca aca gat acc agc act att gcg aca cca acc ttg agc ttt gat gct   144
Ala Thr Asp Thr Ser Thr Ile Ala Thr Pro Thr Leu Ser Phe Asp Ala
        35                  40                  45

tat ggt aat aag gcc gag gtc atg ccg act caa tcc act gtg gat aag   192
Tyr Gly Asn Lys Ala Glu Val Met Pro Thr Gln Ser Thr Val Asp Lys
    50                  55                  60

cgc gtg ccc tct ttg ctg cag tat tac acg cgt aca ttc cat gtg cga   240
Arg Val Pro Ser Leu Leu Gln Tyr Tyr Thr Arg Thr Phe His Val Arg
65                  70                  75                  80

caa gat acg cag cag gct gtc ttt gat gtt att ggc gcc aac ccc gtg   288
Gln Asp Thr Gln Gln Ala Val Phe Asp Val Ile Gly Ala Asn Pro Val
                85                  90                  95

ctc atc gcc gca gca aaa gct gca tcc ata tca ccg gct tct gct gat   336
Leu Ile Ala Ala Ala Lys Ala Ala Ser Ile Ser Pro Ala Ser Ala Asp
            100                 105                 110

tca cgt aga aag aag ggc ctg gcc tcc acc aac gct gac cca gta gcc   384
Ser Arg Arg Lys Lys Gly Leu Ala Ser Thr Asn Ala Asp Pro Val Ala
        115                 120                 125
```

```
aag cat gta cta gaa att gca gga gct gat gtg gaa tcg ctg cgc cat   432
Lys His Val Leu Glu Ile Ala Gly Ala Asp Val Glu Ser Leu Arg His
    130                 135                 140

gaa aag gat ctc aag gtc acc aag cac act ggc caa gac cca gca ctg   480
Glu Lys Asp Leu Lys Val Thr Lys His Thr Gly Gln Asp Pro Ala Leu
145                 150                 155                 160

cct gtc gtg gtc ttt aac caa acc att tgg cat aac ccc aac gac gat   528
Pro Val Val Val Phe Asn Gln Thr Ile Trp His Asn Pro Asn Asp Asp
                165                 170                 175

gtg att aat gca tta ctg ggc gct att gac cag gat gcc tac att gac   576
Val Ile Asn Ala Leu Leu Gly Ala Ile Asp Gln Asp Ala Tyr Ile Asp
            180                 185                 190

atg gcg atc tcg tcc tac aac aag tcc tgg cac aac att atc ccg gct   624
Met Ala Ile Ser Ser Tyr Asn Lys Ser Trp His Asn Ile Ile Pro Ala
        195                 200                 205

taactaccgc tgggtagacc cct                                        647
```

<210> 482
<211> 208
<212> PRT
<213> Corynebacterium glutamicum

<400> 482

```
Phe Tyr Gln Asn Ile Leu Ala Ser Ser Arg Gly Ser Asn Thr Phe Leu
  1               5                  10                  15

Phe Ser Val Pro Tyr Ile Pro Ala Thr Glu Gly Glu Glu Thr His Pro
             20                  25                  30

Ala Thr Asp Thr Ser Thr Ile Ala Thr Pro Thr Leu Ser Phe Asp Ala
         35                  40                  45

Tyr Gly Asn Lys Ala Glu Val Met Pro Thr Gln Ser Thr Val Asp Lys
     50                  55                  60

Arg Val Pro Ser Leu Leu Gln Tyr Tyr Thr Arg Thr Phe His Val Arg
 65                  70                  75                  80

Gln Asp Thr Gln Gln Ala Val Phe Asp Val Ile Gly Ala Asn Pro Val
                 85                  90                  95

Leu Ile Ala Ala Ala Lys Ala Ala Ser Ile Ser Pro Ala Ser Ala Asp
            100                 105                 110

Ser Arg Arg Lys Lys Gly Leu Ala Ser Thr Asn Ala Asp Pro Val Ala
        115                 120                 125

Lys His Val Leu Glu Ile Ala Gly Ala Asp Val Glu Ser Leu Arg His
    130                 135                 140

Glu Lys Asp Leu Lys Val Thr Lys His Thr Gly Gln Asp Pro Ala Leu
145                 150                 155                 160

Pro Val Val Val Phe Asn Gln Thr Ile Trp His Asn Pro Asn Asp Asp
```

```
                165                 170                 175

Val Ile Asn Ala Leu Leu Gly Ala Ile Asp Gln Asp Ala Tyr Ile Asp
            180                 185                 190

Met Ala Ile Ser Ser Tyr Asn Lys Ser Trp His Asn Ile Ile Pro Ala
        195                 200                 205
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<210> 483
<211> 1230
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1230)
<223> FRXA01812

<400> 483

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agc ttc aat gac gtt gac cca gcg gtg acc cat ccg cat ctc aca gtg   48
Ser Phe Asn Asp Val Asp Pro Ala Val Thr His Pro His Leu Thr Val
  1               5                  10                  15

atc tac cca ccg ctc acc cct gca tcc gaa gag aaa ttc aac aag atc   96
Ile Tyr Pro Pro Leu Thr Pro Ala Ser Glu Glu Lys Phe Asn Lys Ile
             20                  25                  30

acc tca gtc gct gct gtg agc aag cgc cca acc acc ctg ccg tat ttc  144
Thr Ser Val Ala Ala Val Ser Lys Arg Pro Thr Thr Leu Pro Tyr Phe
         35                  40                  45

cgt gca gat ggt tca cct act cgt ggc ttt gct aac ttc tcc aca gga  192
Arg Ala Asp Gly Ser Pro Thr Arg Gly Phe Ala Asn Phe Ser Thr Gly
     50                  55                  60

ggt att cac ggt gcg gaa tac aac gaa gat cgt ttt gac cat gat caa  240
Gly Ile His Gly Ala Glu Tyr Asn Glu Asp Arg Phe Asp His Asp Gln
 65                  70                  75                  80

gat cta cac aca gtg gca acc cgt gaa ttc ttc gcc att ctt gat gcg  288
Asp Leu His Thr Val Ala Thr Arg Glu Phe Phe Ala Ile Leu Asp Ala
                 85                  90                  95

aca tta gcg gct ctc tac gca gcc cac caa gcc gaa cct gaa tcg gcg  336
Thr Leu Ala Ala Leu Tyr Ala Ala His Gln Ala Glu Pro Glu Ser Ala
            100                 105                 110

gac tac cag att gca caa gac gca ctc gcc tgg gca aag aat gta ctt  384
Asp Tyr Gln Ile Ala Gln Asp Ala Leu Ala Trp Ala Lys Asn Val Leu
        115                 120                 125

agc gat caa aaa ctc atc gct aag tcg cct cag tta tac aac ccc gaa  432
Ser Asp Gln Lys Leu Ile Ala Lys Ser Pro Gln Leu Tyr Asn Pro Glu
    130                 135                 140

acc ggg gtc acc tat gag tgg gag ttt gtc gct caa gca gca tgg tgg  480
Thr Gly Val Thr Tyr Glu Trp Glu Phe Val Ala Gln Ala Ala Trp Trp
```

```
145                 150                 155                 160

att cgc aac aaa ccg gtt gag gtt att tta cca aca ggt gaa tca atg   528
Ile Arg Asn Lys Pro Val Glu Val Ile Leu Pro Thr Gly Glu Ser Met
                165                 170                 175

acc gta aaa cac aaa tct gta ttg gca tct gcg tcc tac cca ctc cga   576
Thr Val Lys His Lys Ser Val Leu Ala Ser Ala Ser Tyr Pro Leu Arg
            180                 185                 190

gac aac gtg gcg tac tgg cgt agc gaa ccc aaa aca cca cag ctg ttt   624
Asp Asn Val Ala Tyr Trp Arg Ser Glu Pro Lys Thr Pro Gln Leu Phe
        195                 200                 205

ccc gta gca aaa tct ggt ggt tcc tcg ctt gag aag aag tac aac tac   672
Pro Val Ala Lys Ser Gly Gly Ser Ser Leu Glu Lys Lys Tyr Asn Tyr
    210                 215                 220

acc tct gtg ggt act gct att cac gag gac ttt agc agt tac tat ccg   720
Thr Ser Val Gly Thr Ala Ile His Glu Asp Phe Ser Ser Tyr Tyr Pro
225                 230                 235                 240

ctc ttg ctc acc aat atg gct gca ttt acc aat gct gac tta ggt att   768
Leu Leu Leu Thr Asn Met Ala Ala Phe Thr Asn Ala Asp Leu Gly Ile
                245                 250                 255

gat gag aaa acc ggg cgc cct cgt gac cgc tac cgt gaa atc tac gaa   816
Asp Glu Lys Thr Gly Arg Pro Arg Asp Arg Tyr Arg Glu Ile Tyr Glu
            260                 265                 270

caa aaa gag atc tat ggc gca cag cgc aaa gac ccc tcc att gat gaa   864
Gln Lys Glu Ile Tyr Gly Ala Gln Arg Lys Asp Pro Ser Ile Asp Glu
        275                 280                 285

gaa aca aag caa cgt cta ggg att ttg cgc gaa ggt acc aag ttg att   912
Glu Thr Lys Gln Arg Leu Gly Ile Leu Arg Glu Gly Thr Lys Leu Ile
    290                 295                 300

ctt aac tcg gcc acc ggt gct gct gat gct ggt cac gac acc ccg atc   960
Leu Asn Ser Ala Thr Gly Ala Ala Asp Ala Gly His Asp Thr Pro Ile
305                 310                 315                 320

ctc atg aac aat cgc gtt att gcc atg agg att att ggg cag cta ttt  1008
Leu Met Asn Asn Arg Val Ile Ala Met Arg Ile Ile Gly Gln Leu Phe
                325                 330                 335

tct tgg aga att ggg caa gct caa tca ctg gct ggt gca acg att att  1056
Ser Trp Arg Ile Gly Gln Ala Gln Ser Leu Ala Gly Ala Thr Ile Ile
            340                 345                 350

tcc act aac act gat ggc ctg tat tcc gta ctc gat atg ggg act aac  1104
Ser Thr Asn Thr Asp Gly Leu Tyr Ser Val Leu Asp Met Gly Thr Asn
        355                 360                 365

cag cgc gtt ctt gat gaa cac gct aca gcc atc ggt gtg caa att gag  1152
Gln Arg Val Leu Asp Glu His Ala Thr Ala Ile Gly Val Gln Ile Glu
    370                 375                 380

cct gaa gaa ctg gat att gtc tcc aag gat tcc aac tca cgt gcc gaa  1200
Pro Glu Glu Leu Asp Ile Val Ser Lys Asp Ser Asn Ser Arg Ala Glu
385                 390                 395                 400
```

```
ttt ctc ggc aat ggc tac atc aat gcg gcc                                  1230
Phe Leu Gly Asn Gly Tyr Ile Asn Ala Ala
                405                 410


<210> 484
<211> 410
<212> PRT
<213> Corynebacterium glutamicum

<400> 484
Ser Phe Asn Asp Val Asp Pro Ala Val Thr His Pro His Leu Thr Val
  1               5                  10                  15

Ile Tyr Pro Pro Leu Thr Pro Ala Ser Glu Glu Lys Phe Asn Lys Ile
             20                  25                  30

Thr Ser Val Ala Ala Val Ser Lys Arg Pro Thr Thr Leu Pro Tyr Phe
         35                  40                  45

Arg Ala Asp Gly Ser Pro Thr Arg Gly Phe Ala Asn Phe Ser Thr Gly
     50                  55                  60

Gly Ile His Gly Ala Glu Tyr Asn Glu Asp Arg Phe Asp His Asp Gln
 65                  70                  75                  80

Asp Leu His Thr Val Ala Thr Arg Glu Phe Phe Ala Ile Leu Asp Ala
                 85                  90                  95

Thr Leu Ala Ala Leu Tyr Ala Ala His Gln Ala Glu Pro Glu Ser Ala
            100                 105                 110

Asp Tyr Gln Ile Ala Gln Asp Ala Leu Ala Trp Ala Lys Asn Val Leu
        115                 120                 125

Ser Asp Gln Lys Leu Ile Ala Lys Ser Pro Gln Leu Tyr Asn Pro Glu
    130                 135                 140

Thr Gly Val Thr Tyr Glu Trp Glu Phe Val Ala Gln Ala Ala Trp Trp
145                 150                 155                 160

Ile Arg Asn Lys Pro Val Glu Val Ile Leu Pro Thr Gly Glu Ser Met
                165                 170                 175

Thr Val Lys His Lys Ser Val Leu Ala Ser Ala Ser Tyr Pro Leu Arg
            180                 185                 190

Asp Asn Val Ala Tyr Trp Arg Ser Glu Pro Lys Thr Pro Gln Leu Phe
        195                 200                 205

Pro Val Ala Lys Ser Gly Gly Ser Ser Leu Glu Lys Lys Tyr Asn Tyr
    210                 215                 220

Thr Ser Val Gly Thr Ala Ile His Glu Asp Phe Ser Ser Tyr Tyr Pro
225                 230                 235                 240

Leu Leu Leu Thr Asn Met Ala Ala Phe Thr Asn Ala Asp Leu Gly Ile
                245                 250                 255

Asp Glu Lys Thr Gly Arg Pro Arg Asp Arg Tyr Arg Glu Ile Tyr Glu
```

```
            260                 265                 270

Gln Lys Glu Ile Tyr Gly Ala Gln Arg Lys Asp Pro Ser Ile Asp Glu
        275                 280                 285

Glu Thr Lys Gln Arg Leu Gly Ile Leu Arg Glu Gly Thr Lys Leu Ile
    290                 295                 300

Leu Asn Ser Ala Thr Gly Ala Ala Asp Ala Gly His Asp Thr Pro Ile
305                 310                 315                 320

Leu Met Asn Asn Arg Val Ile Ala Met Arg Ile Ile Gly Gln Leu Phe
                325                 330                 335

Ser Trp Arg Ile Gly Gln Ala Gln Ser Leu Ala Gly Ala Thr Ile Ile
            340                 345                 350

Ser Thr Asn Thr Asp Gly Leu Tyr Ser Val Leu Asp Met Gly Thr Asn
        355                 360                 365

Gln Arg Val Leu Asp Glu His Ala Thr Ala Ile Gly Val Gln Ile Glu
    370                 375                 380

Pro Glu Glu Leu Asp Ile Val Ser Lys Asp Ser Asn Ser Arg Ala Glu
385                 390                 395                 400

Phe Leu Gly Asn Gly Tyr Ile Asn Ala Ala
                405                 410


<210> 485
<211> 837
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(814)
<223> RXN01069

<400> 485
tcctaagctc tcttgagtac ctgagacctt ctcagcaaaa cacaaagtgc cttcacccaa 60

cctggggtgg aggcactttc tcattgctaa ggtgtgcatc gtg aac gat tta ccg   115
                                            Val Asn Asp Leu Pro
                                              1               5

aac cta cca aag ctg ccc ttc aac tgg aca tgg gtg ctg gca act gtt   163
Asn Leu Pro Lys Leu Pro Phe Asn Trp Thr Trp Val Leu Ala Thr Val
                  10                  15                  20

gcc acg aca gtg gtg ttg gcg ggt att ggt ttg tat gtg tat tac ccg   211
Ala Thr Thr Val Val Leu Ala Gly Ile Gly Leu Tyr Val Tyr Tyr Pro
              25                  30                  35

tcg ttg cca gat cct atg ccg gtg cat tgg aat gga tcc ggg gag gcg   259
Ser Leu Pro Asp Pro Met Pro Val His Trp Asn Gly Ser Gly Glu Ala
          40                  45                  50

gat aat tgg acg cct aaa tcg gtg ggt tcg ttt ctt tca ctg att ttg   307
Asp Asn Trp Thr Pro Lys Ser Val Gly Ser Phe Leu Ser Leu Ile Leu
```

```
     55                  60                  65

ata ggg cca ggc att att ttg ctg acc ctg tcg ggt atg cag gcg ttg   355
Ile Gly Pro Gly Ile Ile Leu Leu Thr Leu Ser Gly Met Gln Ala Leu
 70                  75                  80                  85

ctg acc atg cag tct gga gtg atc acg caa cgc ggt ggg gcg aaa tcg   403
Leu Thr Met Gln Ser Gly Val Ile Thr Gln Arg Gly Gly Ala Lys Ser
                90                  95                 100

gcg aat gaa gcg cac cgg cag tgg gaa acc tac aag gca aca agc atg   451
Ala Asn Glu Ala His Arg Gln Trp Glu Thr Tyr Lys Ala Thr Ser Met
            105                 110                 115

cac atg ggt tgg tac atg ttt gtg ctc aac gct ttg att ttg gtg atg   499
His Met Gly Trp Tyr Met Phe Val Leu Asn Ala Leu Ile Leu Val Met
        120                 125                 130

atc ctc aat gag ttc cgc cca aac cct ctg cct ggt gga ttt atc atc   547
Ile Leu Asn Glu Phe Arg Pro Asn Pro Leu Pro Gly Gly Phe Ile Ile
    135                 140                 145

ggg ctt att gga att att gct gcc acg att gtc ctg ttg gtt ctg att   595
Gly Leu Ile Gly Ile Ile Ala Ala Thr Ile Val Leu Leu Val Leu Ile
150                 155                 160                 165

gga aaa aca acc acg agt ttg gca aag aaa tac ccc atg cct gac caa   643
Gly Lys Thr Thr Thr Ser Leu Ala Lys Lys Tyr Pro Met Pro Asp Gln
                170                 175                 180

gat gga aag acg tgg ggg att ttc tac aac gat ccg gac gat aat cgg   691
Asp Gly Lys Thr Trp Gly Ile Phe Tyr Asn Asp Pro Asp Asp Asn Arg
            185                 190                 195

atc tta gtg gac acc ggg atg ggg atg aat tac acg ttt aac att gcc   739
Ile Leu Val Asp Thr Gly Met Gly Met Asn Tyr Thr Phe Asn Ile Ala
        200                 205                 210

cat acg tgg ggc aag atc ttc gcg gtt ttg atc ttc gcg gtg cca gta   787
His Thr Trp Gly Lys Ile Phe Ala Val Leu Ile Phe Ala Val Pro Val
    215                 220                 225

ctc atc gtt tta tta acc gtt ctc ctt taacctcgat ccaccgatgt         834
Leu Ile Val Leu Leu Thr Val Leu Leu
230                 235

gcc                                                               837


<210> 486
<211> 238
<212> PRT
<213> Corynebacterium glutamicum

<400> 486
Val Asn Asp Leu Pro Asn Leu Pro Lys Leu Pro Phe Asn Trp Thr Trp
  1               5                  10                  15

Val Leu Ala Thr Val Ala Thr Thr Val Val Leu Ala Gly Ile Gly Leu
             20                  25                  30
```

```
Tyr Val Tyr Tyr Pro Ser Leu Pro Asp Pro Met Pro Val His Trp Asn
         35                  40                  45

Gly Ser Gly Glu Ala Asp Asn Trp Thr Pro Lys Ser Val Gly Ser Phe
     50                  55                  60

Leu Ser Leu Ile Leu Ile Gly Pro Gly Ile Ile Leu Leu Thr Leu Ser
 65                  70                  75                  80

Gly Met Gln Ala Leu Leu Thr Met Gln Ser Gly Val Ile Thr Gln Arg
                 85                  90                  95

Gly Gly Ala Lys Ser Ala Asn Glu Ala His Arg Gln Trp Glu Thr Tyr
            100                 105                 110

Lys Ala Thr Ser Met His Met Gly Trp Tyr Met Phe Val Leu Asn Ala
        115                 120                 125

Leu Ile Leu Val Met Ile Leu Asn Glu Phe Arg Pro Asn Pro Leu Pro
    130                 135                 140

Gly Gly Phe Ile Ile Gly Leu Ile Gly Ile Ile Ala Ala Thr Ile Val
145                 150                 155                 160

Leu Leu Val Leu Ile Gly Lys Thr Thr Thr Ser Leu Ala Lys Lys Tyr
                165                 170                 175

Pro Met Pro Asp Gln Asp Gly Lys Thr Trp Gly Ile Phe Tyr Asn Asp
            180                 185                 190

Pro Asp Asp Asn Arg Ile Leu Val Asp Thr Gly Met Gly Met Asn Tyr
        195                 200                 205

Thr Phe Asn Ile Ala His Thr Trp Gly Lys Ile Phe Ala Val Leu Ile
    210                 215                 220

Phe Ala Val Pro Val Leu Ile Val Leu Leu Thr Val Leu Leu
225                 230                 235
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Doc Code = 0000000000

<210> 487
<211> 703
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> FRXA01069

<400> 487

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tcctaagctc tcttgagtac ctgagacctt ctcagcaaaa cacaaagtgc cttcacccaa 60

cctggggtgg aggcactttc tcattgctaa ggtgtgcatc gtg aac gat tta ccg   115
                                            Val Asn Asp Leu Pro
                                              1               5

aac cta cca aag ctg ccc ttc aac tgg aca tgg gtg ctg gca act gtt   163
Asn Leu Pro Lys Leu Pro Phe Asn Trp Thr Trp Val Leu Ala Thr Val
                10                  15                  20
```

```
gcc acg aca gtg gtg ttg gcg ggt att ggt ttg tat gtg tat tac ccg   211
Ala Thr Thr Val Val Leu Ala Gly Ile Gly Leu Tyr Val Tyr Tyr Pro
            25                  30                  35

tcg ttg cca gat cct atg ccg gtg cat tgg aat gga tcc ggg gag gcg   259
Ser Leu Pro Asp Pro Met Pro Val His Trp Asn Gly Ser Gly Glu Ala
        40                  45                  50

gat aat tgg acg cct aaa tcg gtg ggt tcg ttt ctt tca ctg att ttg   307
Asp Asn Trp Thr Pro Lys Ser Val Gly Ser Phe Leu Ser Leu Ile Leu
    55                  60                  65

ata ggg cca ggc att att ttg ctg acc ctg tcg ggt atg cag gcg ttg   355
Ile Gly Pro Gly Ile Ile Leu Leu Thr Leu Ser Gly Met Gln Ala Leu
70                  75                  80                  85

ctg acc atg cag tct gga gtg atc acg caa cgc ggt ggg gcg aaa tcg   403
Leu Thr Met Gln Ser Gly Val Ile Thr Gln Arg Gly Gly Ala Lys Ser
                90                  95                  100

gcg aat gaa gcg cac cgg cag tgg gaa acc tac aag gca aca agc atg   451
Ala Asn Glu Ala His Arg Gln Trp Glu Thr Tyr Lys Ala Thr Ser Met
            105                 110                 115

cac atg ggt tgg tac atg ttt gtg ctc aac gct ttg att ttg gtg atg   499
His Met Gly Trp Tyr Met Phe Val Leu Asn Ala Leu Ile Leu Val Met
        120                 125                 130

atc ctc aat gag ttc cgc cca aac cct ctg cct ggt gga ttt atc atc   547
Ile Leu Asn Glu Phe Arg Pro Asn Pro Leu Pro Gly Gly Phe Ile Ile
    135                 140                 145

ggg ctt att gga att att gct gcc acg att gtc ctg ttg gtt ctg att   595
Gly Leu Ile Gly Ile Ile Ala Ala Thr Ile Val Leu Leu Val Leu Ile
150                 155                 160                 165

gga aaa aca acc acg agt ttg gca aag aaa tac ccc atg cct gac caa   643
Gly Lys Thr Thr Thr Ser Leu Ala Lys Lys Tyr Pro Met Pro Asp Gln
                170                 175                 180

gat gga aag acg tgg ggg att ttc tac aac gat ccg gac gat aat cgg   691
Asp Gly Lys Thr Trp Gly Ile Phe Tyr Asn Asp Pro Asp Asp Asn Arg
            185                 190                 195

atc tta gtg gac                                                  703
Ile Leu Val Asp
        200
```

CONFIDENTIAL

<210> 488
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 488

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Val Asn Asp Leu Pro Asn Leu Pro Lys Leu Pro Phe Asn Trp Thr Trp
  1               5                  10                  15

Val Leu Ala Thr Val Ala Thr Thr Val Val Leu Ala Gly Ile Gly Leu
            20                  25                  30
```

```
Tyr Val Tyr Tyr Pro Ser Leu Pro Asp Pro Met Pro Val His Trp Asn
         35                  40                  45

Gly Ser Gly Glu Ala Asp Asn Trp Thr Pro Lys Ser Val Gly Ser Phe
     50                  55                  60

Leu Ser Leu Ile Leu Ile Gly Pro Gly Ile Ile Leu Leu Thr Leu Ser
 65                  70                  75                  80

Gly Met Gln Ala Leu Leu Thr Met Gln Ser Gly Val Ile Thr Gln Arg
                 85                  90                  95

Gly Gly Ala Lys Ser Ala Asn Glu Ala His Arg Gln Trp Glu Thr Tyr
            100                 105                 110

Lys Ala Thr Ser Met His Met Gly Trp Tyr Met Phe Val Leu Asn Ala
        115                 120                 125

Leu Ile Leu Val Met Ile Leu Asn Glu Phe Arg Pro Asn Pro Leu Pro
    130                 135                 140

Gly Gly Phe Ile Ile Gly Leu Ile Gly Ile Ile Ala Ala Thr Ile Val
145                 150                 155                 160

Leu Leu Val Leu Ile Gly Lys Thr Thr Thr Ser Leu Ala Lys Lys Tyr
                165                 170                 175

Pro Met Pro Asp Gln Asp Gly Lys Thr Trp Gly Ile Phe Tyr Asn Asp
            180                 185                 190

Pro Asp Asp Asn Arg Ile Leu Val Asp
        195                 200
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US 2004/0265956 A1

<210> 489
<211> 2187
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2164)
<223> RXN01071

<400> 489

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cacctgaatt ggctgaggga gaggcaccga ctggcaccga agaggtgctt gcctcgaagg 60

cgggcgctga ggcgaatggc ctggagtagg ggaccagatc ttg gtc gtg gac tcc   115
                                              Leu Val Val Asp Ser
                                                1               5

agt ggc cgc tac aac gtc acc atc aca ggc ctg acc acc act gag acg   163
Ser Gly Arg Tyr Asn Val Thr Ile Thr Gly Leu Thr Thr Thr Glu Thr
                10                  15                  20

gat tcg gcc acc gcg ctg aac ctg cag atg tcg gaa gct ggc tac ctg   211
Asp Ser Ala Thr Ala Leu Asn Leu Gln Met Ser Glu Ala Gly Tyr Leu
            25                  30                  35

gag cgt tac acc gac ggg gct acc gtc ccc agc gtc atg ctg tcg gct   259
Glu Arg Tyr Thr Asp Gly Ala Thr Val Pro Ser Val Met Leu Ser Ala
```

```
         40                  45                  50

gca gat ggc acc acg cct caa gag ctt gtc gac gcc ctc gct gcc gaa   307
Ala Asp Gly Thr Thr Pro Gln Glu Leu Val Asp Ala Leu Ala Ala Glu
     55                  60                  65

ctt gga tcg aac ttt gat gta gaa acc ggc gaa gcg cta gtc gag cag   355
Leu Gly Ser Asn Phe Asp Val Glu Thr Gly Glu Ala Leu Val Glu Gln
 70                  75                  80                  85

gct aca gga atg atc acg cag gcc ttg agc ttc gtg cag tac ttc ctc   403
Ala Thr Gly Met Ile Thr Gln Ala Leu Ser Phe Val Gln Tyr Phe Leu
                 90                  95                 100

gtt gcc ttc ggt ctc att gca ctg ctg gtt ggt acc ttc atc atc gcg   451
Val Ala Phe Gly Leu Ile Ala Leu Leu Val Gly Thr Phe Ile Ile Ala
            105                 110                 115

aat acc ttc tcc atg att gtg gct cag cgc atg cgt gag ttc gct ctc   499
Asn Thr Phe Ser Met Ile Val Ala Gln Arg Met Arg Glu Phe Ala Leu
        120                 125                 130

ctg cga gcc ctg ggt gcg gcg cca gga cag atc act cgc tct gtg gtg   547
Leu Arg Ala Leu Gly Ala Ala Pro Gly Gln Ile Thr Arg Ser Val Val
    135                 140                 145

ctg gaa gca acc atc gtt ggc ctc ttc ggc tct gct ctt ggt gtg ctg   595
Leu Glu Ala Thr Ile Val Gly Leu Phe Gly Ser Ala Leu Gly Val Leu
150                 155                 160                 165

ggt ggt atg ggc ctc gta gcg atc att tca gct gtc ctc aat aac ctg   643
Gly Gly Met Gly Leu Val Ala Ile Ile Ser Ala Val Leu Asn Asn Leu
                170                 175                 180

ggc atg ccg atg gga tcc agc gtt ggc ttg act cct tct gca gtg gtt   691
Gly Met Pro Met Gly Ser Ser Val Gly Leu Thr Pro Ser Ala Val Val
            185                 190                 195

acc gcg ctc gta ttg ggc acc gtt gtc acc att gtg agc gcg tgg gct   739
Thr Ala Leu Val Leu Gly Thr Val Val Thr Ile Val Ser Ala Trp Ala
        200                 205                 210

ccg gct cgt cgt gca ggt gag gtt aag cct gtt gaa gcg atg cgc aac   787
Pro Ala Arg Arg Ala Gly Glu Val Lys Pro Val Glu Ala Met Arg Asn
    215                 220                 225

atg gaa acc acc act atg cgt tcc atg atg ggg cgc acg atc acc ggt   835
Met Glu Thr Thr Thr Met Arg Ser Met Met Gly Arg Thr Ile Thr Gly
230                 235                 240                 245

ggc atc gtt cta gca ctc ggc atc atc ttt gcg att gcc ggt gcg atg   883
Gly Ile Val Leu Ala Leu Gly Ile Ile Phe Ala Ile Ala Gly Ala Met
                250                 255                 260

atg act gat tct tcc acc gct act cgt tcc atc ctg gtg ggc att ggt   931
Met Thr Asp Ser Ser Thr Ala Thr Arg Ser Ile Leu Val Gly Ile Gly
            265                 270                 275

gca ctg ttt gtc atc gtg ggt acg ttc ctc ttc tca cca gcg ctc tcc   979
Ala Leu Phe Val Ile Val Gly Thr Phe Leu Phe Ser Pro Ala Leu Ser
        280                 285                 290
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atg cct gtg gtg ggt ggc ctg ggc aag gtt atc ggt gca ccg ttt ggc   1027
Met Pro Val Val Gly Gly Leu Gly Lys Val Ile Gly Ala Pro Phe Gly
    295                 300                 305

agc gtt gga agc ctt gct gcg acc aac tcc aag cga aac cct cgc cgt   1075
Ser Val Gly Ser Leu Ala Ala Thr Asn Ser Lys Arg Asn Pro Arg Arg
310                 315                 320                 325

acc gca act aca gcg ttc gca ctg acg ttg ggc att gcc tta gtg act   1123
Thr Ala Thr Thr Ala Phe Ala Leu Thr Leu Gly Ile Ala Leu Val Thr
                330                 335                 340

gca att ggc atg ctt tct gca acc atg aag gac gca gtc tcc gac atg   1171
Ala Ile Gly Met Leu Ser Ala Thr Met Lys Asp Ala Val Ser Asp Met
            345                 350                 355

atg gcg gag cag tac acc gca gat tac atc ctg cag gga cca acc aac   1219
Met Ala Glu Gln Tyr Thr Ala Asp Tyr Ile Leu Gln Gly Pro Thr Asn
        360                 365                 370

ggt tcc atc acc atg ccg aag gaa tct gtc aat gat gtt cgc gat gct   1267
Gly Ser Ile Thr Met Pro Lys Glu Ser Val Asn Asp Val Arg Asp Ala
    375                 380                 385

gag ggc gtt gcc gat gtc gtg ctc gtt tcc atg aac tct gcc tcg gtg   1315
Glu Gly Val Ala Asp Val Val Leu Val Ser Met Asn Ser Ala Ser Val
390                 395                 400                 405

aac ggt cag gct tca tac agc cag ctg ggc cag tct gta acc ttt gtc   1363
Asn Gly Gln Ala Ser Tyr Ser Gln Leu Gly Gln Ser Val Thr Phe Val
                410                 415                 420

gct gac ggc gac ctg agc aag gtc atc agc aca gaa agc att gat ggc   1411
Ala Asp Gly Asp Leu Ser Lys Val Ile Ser Thr Glu Ser Ile Asp Gly
            425                 430                 435

tcc ctc gac ttg agc aac cca ggt gtt gtg act aac cag acg ttt gct   1459
Ser Leu Asp Leu Ser Asn Pro Gly Val Val Thr Asn Gln Thr Phe Ala
        440                 445                 450

gat gaa aac ggc tgg gca gta ggc gat act ctg cag ctt gaa tca atg   1507
Asp Glu Asn Gly Trp Ala Val Gly Asp Thr Leu Gln Leu Glu Ser Met
    455                 460                 465

ggg cag acc atc ggc gat atc gag ttg atc ggt acc ttc acc gga aac   1555
Gly Gln Thr Ile Gly Asp Ile Glu Leu Ile Gly Thr Phe Thr Gly Asn
470                 475                 480                 485

gac gcc atc gga aat atg atc atc tcc gaa agt tcc ttg gct gat aca   1603
Asp Ala Ile Gly Asn Met Ile Ile Ser Glu Ser Ser Leu Ala Asp Thr
                490                 495                 500

cca gcg gca gac act gct gtt cct cag atg atg ctg gtg gta ggc gaa   1651
Pro Ala Ala Asp Thr Ala Val Pro Gln Met Met Leu Val Val Gly Glu
            505                 510                 515

gaa ggc ttt gat aag gaa caa ctg cgc acc aac ttg gaa gac gca gtc   1699
Glu Gly Phe Asp Lys Glu Gln Leu Arg Thr Asn Leu Glu Asp Ala Val
        520                 525                 530
```

```
gct gat tac att gtc atc tct gtg aaa tca gca acc gag ttc gct ggt   1747
Ala Asp Tyr Ile Val Ile Ser Val Lys Ser Ala Thr Glu Phe Ala Gly
    535                 540                 545

gaa acg gtt gcg atg atc gac acc atg atg aac att ctg tac gcg ctg   1795
Glu Thr Val Ala Met Ile Asp Thr Met Met Asn Ile Leu Tyr Ala Leu
550                 555                 560                 565

ctt gct ctg tct gtc att gtt gcc atc atc ggc atc atc aac acc ctg   1843
Leu Ala Leu Ser Val Ile Val Ala Ile Ile Gly Ile Ile Asn Thr Leu
                570                 575                 580

gca ctg aat gtg atc gag cgt cgc cag gag atc ggt atg ctc cgc gca   1891
Ala Leu Asn Val Ile Glu Arg Arg Gln Glu Ile Gly Met Leu Arg Ala
            585                 590                 595

gtt ggc gtg aag cgc gga cag gtc cgc acc atg atc acc tta gaa tct   1939
Val Gly Val Lys Arg Gly Gln Val Arg Thr Met Ile Thr Leu Glu Ser
        600                 605                 610

gtt cag atc gcc atc tac ggt gct gtg att ggt atc gcg att ggt ctt   1987
Val Gln Ile Ala Ile Tyr Gly Ala Val Ile Gly Ile Ala Ile Gly Leu
    615                 620                 625

ggt ctg ggc tgg gcc ttt gtg aca gtg atg tca ggc gaa gga cta gac   2035
Gly Leu Gly Trp Ala Phe Val Thr Val Met Ser Gly Glu Gly Leu Asp
630                 635                 640                 645

gct gcg gtt agt atc ccg tgg ggt cag gtc gga ctg atg ctt gtt ggt   2083
Ala Ala Val Ser Ile Pro Trp Gly Gln Val Gly Leu Met Leu Val Gly
                650                 655                 660

tcc gct gta gtc ggt gtt atc gcc gcg ctg tgg ccg gca gtc aag gca   2131
Ser Ala Val Val Gly Val Ile Ala Ala Leu Trp Pro Ala Val Lys Ala
            665                 670                 675

tct agg aca cca cct ttg gat gcg att acc gac tagttttagc ggcagttgaa 2184
Ser Arg Thr Pro Pro Leu Asp Ala Ile Thr Asp
        680                 685

tca                                                               2187
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<210> 490
<211> 688
<212> PRT
<213> Corynebacterium glutamicum

<400> 490

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Leu Val Val Asp Ser Ser Gly Arg Tyr Asn Val Thr Ile Thr Gly Leu
  1               5                  10                  15

Thr Thr Thr Glu Thr Asp Ser Ala Thr Ala Leu Asn Leu Gln Met Ser
             20                  25                  30

Glu Ala Gly Tyr Leu Glu Arg Tyr Thr Asp Gly Ala Thr Val Pro Ser
         35                  40                  45

Val Met Leu Ser Ala Ala Asp Gly Thr Thr Pro Gln Glu Leu Val Asp
     50                  55                  60
```

```
Ala Leu Ala Ala Glu Leu Gly Ser Asn Phe Asp Val Glu Thr Gly Glu
 65                  70                  75                  80

Ala Leu Val Glu Gln Ala Thr Gly Met Ile Thr Gln Ala Leu Ser Phe
                85                  90                  95

Val Gln Tyr Phe Leu Val Ala Phe Gly Leu Ile Ala Leu Leu Val Gly
            100                 105                 110

Thr Phe Ile Ile Ala Asn Thr Phe Ser Met Ile Val Ala Gln Arg Met
        115                 120                 125

Arg Glu Phe Ala Leu Leu Arg Ala Leu Gly Ala Ala Pro Gly Gln Ile
    130                 135                 140

Thr Arg Ser Val Val Leu Glu Ala Thr Ile Val Gly Leu Phe Gly Ser
145                 150                 155                 160

Ala Leu Gly Val Leu Gly Gly Met Gly Leu Val Ala Ile Ile Ser Ala
                165                 170                 175

Val Leu Asn Asn Leu Gly Met Pro Met Gly Ser Ser Val Gly Leu Thr
            180                 185                 190

Pro Ser Ala Val Val Thr Ala Leu Val Leu Gly Thr Val Val Thr Ile
        195                 200                 205

Val Ser Ala Trp Ala Pro Ala Arg Arg Ala Gly Glu Val Lys Pro Val
    210                 215                 220

Glu Ala Met Arg Asn Met Glu Thr Thr Thr Met Arg Ser Met Met Gly
225                 230                 235                 240

Arg Thr Ile Thr Gly Gly Ile Val Leu Ala Leu Gly Ile Ile Phe Ala
                245                 250                 255

Ile Ala Gly Ala Met Met Thr Asp Ser Ser Thr Ala Thr Arg Ser Ile
            260                 265                 270

Leu Val Gly Ile Gly Ala Leu Phe Val Ile Val Gly Thr Phe Leu Phe
        275                 280                 285

Ser Pro Ala Leu Ser Met Pro Val Val Gly Gly Leu Gly Lys Val Ile
    290                 295                 300

Gly Ala Pro Phe Gly Ser Val Gly Ser Leu Ala Ala Thr Asn Ser Lys
305                 310                 315                 320

Arg Asn Pro Arg Arg Thr Ala Thr Thr Ala Phe Ala Leu Thr Leu Gly
                325                 330                 335

Ile Ala Leu Val Thr Ala Ile Gly Met Leu Ser Ala Thr Met Lys Asp
            340                 345                 350

Ala Val Ser Asp Met Met Ala Glu Gln Tyr Thr Ala Asp Tyr Ile Leu
        355                 360                 365

Gln Gly Pro Thr Asn Gly Ser Ile Thr Met Pro Lys Glu Ser Val Asn
    370                 375                 380

Asp Val Arg Asp Ala Glu Gly Val Ala Asp Val Val Leu Val Ser Met
```

385 390 395 400

Asn Ser Ala Ser Val Asn Gly Gln Ala Ser Tyr Ser Gln Leu Gly Gln
405 410 415

Ser Val Thr Phe Val Ala Asp Gly Asp Leu Ser Lys Val Ile Ser Thr
420 425 430

Glu Ser Ile Asp Gly Ser Leu Asp Leu Ser Asn Pro Gly Val Val Thr
435 440 445

Asn Gln Thr Phe Ala Asp Glu Asn Gly Trp Ala Val Gly Asp Thr Leu
450 455 460

Gln Leu Glu Ser Met Gly Gln Thr Ile Gly Asp Ile Glu Leu Ile Gly
465 470 475 480

Thr Phe Thr Gly Asn Asp Ala Ile Gly Asn Met Ile Ile Ser Glu Ser
485 490 495

Ser Leu Ala Asp Thr Pro Ala Ala Asp Thr Ala Val Pro Gln Met Met
500 505 510

Leu Val Val Gly Glu Glu Gly Phe Asp Lys Glu Gln Leu Arg Thr Asn
515 520 525

Leu Glu Asp Ala Val Ala Asp Tyr Ile Val Ile Ser Val Lys Ser Ala
530 535 540

Thr Glu Phe Ala Gly Glu Thr Val Ala Met Ile Asp Thr Met Met Asn
545 550 555 560

Ile Leu Tyr Ala Leu Leu Ala Leu Ser Val Ile Val Ala Ile Ile Gly
565 570 575

Ile Ile Asn Thr Leu Ala Leu Asn Val Ile Glu Arg Arg Gln Glu Ile
580 585 590

Gly Met Leu Arg Ala Val Gly Val Lys Arg Gly Gln Val Arg Thr Met
595 600 605

Ile Thr Leu Glu Ser Val Gln Ile Ala Ile Tyr Gly Ala Val Ile Gly
610 615 620

Ile Ala Ile Gly Leu Gly Leu Gly Trp Ala Phe Val Thr Val Met Ser
625 630 635 640

Gly Glu Gly Leu Asp Ala Ala Val Ser Ile Pro Trp Gly Gln Val Gly
645 650 655

Leu Met Leu Val Gly Ser Ala Val Val Gly Val Ile Ala Ala Leu Trp
660 665 670

Pro Ala Val Lys Ala Ser Arg Thr Pro Pro Leu Asp Ala Ile Thr Asp
675 680 685

<210> 491

<211> 1726
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1726)
<223> FRXA02898

<400> 491
cacctgaatt ggctgaggga gaggcaccga ctggcaccga agaggtgctt gcctcgaagg 60

cgggcgctga ggcgaatggc ctggagtagg ggaccagatc ttg gtc gtg gac tcc 115
Leu Val Val Asp Ser
1 5

agt ggc cgc tac aac gtc acc atc aca ggc ctg acc acc act gag acg 163
Ser Gly Arg Tyr Asn Val Thr Ile Thr Gly Leu Thr Thr Thr Glu Thr
10 15 20

gat tcg gcc acc gcg ctg aac ctg cag atg tcg gaa gct ggc tac ctg 211
Asp Ser Ala Thr Ala Leu Asn Leu Gln Met Ser Glu Ala Gly Tyr Leu
25 30 35

gag cgt tac acc gac ggg gct acc gtc ccc agc gtc atg ctg tcg gct 259
Glu Arg Tyr Thr Asp Gly Ala Thr Val Pro Ser Val Met Leu Ser Ala
40 45 50

gca gat ggc acc acg cct caa gag ctt gtc gac gcc ctc gct gcc gaa 307
Ala Asp Gly Thr Thr Pro Gln Glu Leu Val Asp Ala Leu Ala Ala Glu
55 60 65

ctt gga tcg aac ttt gat gta gaa acc ggc gaa gcg cta gtc gag cag 355
Leu Gly Ser Asn Phe Asp Val Glu Thr Gly Glu Ala Leu Val Glu Gln
70 75 80 85

gct aca gga atg atc acg cag gcc ttg agc ttc gtg cag tac ttc ctc 403
Ala Thr Gly Met Ile Thr Gln Ala Leu Ser Phe Val Gln Tyr Phe Leu
90 95 100

gtt gcc ttc ggt ctc att gca ctg ctg gtt ggt acc ttc atc atc gcg 451
Val Ala Phe Gly Leu Ile Ala Leu Leu Val Gly Thr Phe Ile Ile Ala
105 110 115

aat acc ttc tcc atg att gtg gct cag cgc atg cgt gag ttc gct ctc 499
Asn Thr Phe Ser Met Ile Val Ala Gln Arg Met Arg Glu Phe Ala Leu
120 125 130

ctg cga gcc ctg ggt gcg gcg cca gga cag atc act cgc tct gtg gtg 547
Leu Arg Ala Leu Gly Ala Ala Pro Gly Gln Ile Thr Arg Ser Val Val
135 140 145

ctg gaa gca acc atc gtt ggc ctc ttc ggc tct gct ctt ggt gtg ctg 595
Leu Glu Ala Thr Ile Val Gly Leu Phe Gly Ser Ala Leu Gly Val Leu
150 155 160 165

ggt ggt atg ggc ctc gta gcg atc att tca gct gtc ctc aat aac ctg 643
Gly Gly Met Gly Leu Val Ala Ile Ile Ser Ala Val Leu Asn Asn Leu
170 175 180

ggc atg ccg atg gga tcc agc gtt ggc ttg act cct tct gca gtg gtt 691

```
Gly Met Pro Met Gly Ser Ser Val Gly Leu Thr Pro Ser Ala Val Val
          185                 190                 195

acc gcg ctc gta ttg ggc acc gtt gtc acc att gtg agc gcg tgg gct   739
Thr Ala Leu Val Leu Gly Thr Val Val Thr Ile Val Ser Ala Trp Ala
        200                 205                 210

ccg gct cgt cgt gca ggt gag gtt aag cct gtt gaa gcg atg cgc aac   787
Pro Ala Arg Arg Ala Gly Glu Val Lys Pro Val Glu Ala Met Arg Asn
    215                 220                 225

atg gaa acc acc act atg cgt tcc atg atg ggg cgc acg atc acc ggt   835
Met Glu Thr Thr Thr Met Arg Ser Met Met Gly Arg Thr Ile Thr Gly
230                 235                 240                 245

ggc atc gtt cta gca ctc ggc atc atc ttt gcg att gcc ggt gcg atg   883
Gly Ile Val Leu Ala Leu Gly Ile Ile Phe Ala Ile Ala Gly Ala Met
                250                 255                 260

atg act gat tct tcc acc gct act cgt tcc atc ctg gtg ggc att ggt   931
Met Thr Asp Ser Ser Thr Ala Thr Arg Ser Ile Leu Val Gly Ile Gly
            265                 270                 275

gca ctg ttt gtc atc gtg ggt acg ttc ctc ttc tca cca gcg ctc tcc   979
Ala Leu Phe Val Ile Val Gly Thr Phe Leu Phe Ser Pro Ala Leu Ser
        280                 285                 290

atg cct gtg gtg ggt ggc ctg ggc aag gtt atc ggt gca ccg ttt ggc   1027
Met Pro Val Val Gly Gly Leu Gly Lys Val Ile Gly Ala Pro Phe Gly
    295                 300                 305

agc gtt gga agc ctt gct gcg acc aac tcc aag cga aac cct cgc cgt   1075
Ser Val Gly Ser Leu Ala Ala Thr Asn Ser Lys Arg Asn Pro Arg Arg
310                 315                 320                 325

acc gca act aca gcg ttc gca ctg acg ttg ggc att gcc tta gtg act   1123
Thr Ala Thr Thr Ala Phe Ala Leu Thr Leu Gly Ile Ala Leu Val Thr
                330                 335                 340

gca att ggc atg ctt tct gca acc atg aag gac gca gtc tcc gac atg   1171
Ala Ile Gly Met Leu Ser Ala Thr Met Lys Asp Ala Val Ser Asp Met
            345                 350                 355

atg gcg gag cag tac acc gca gat tac atc ctg cag gga cca acc aac   1219
Met Ala Glu Gln Tyr Thr Ala Asp Tyr Ile Leu Gln Gly Pro Thr Asn
        360                 365                 370

ggt tcc atc acc atg ccg aag gaa tct gtc aat gat gtt cgc gat gct   1267
Gly Ser Ile Thr Met Pro Lys Glu Ser Val Asn Asp Val Arg Asp Ala
    375                 380                 385

gag ggc gtt gcc gat gtc gtg ctc gtt tcc atg aac tct gcc tcg gtg   1315
Glu Gly Val Ala Asp Val Val Leu Val Ser Met Asn Ser Ala Ser Val
390                 395                 400                 405

aac ggt cag gct tca tac agc cag ctg ggc cag tct gta acc ttt gtc   1363
Asn Gly Gln Ala Ser Tyr Ser Gln Leu Gly Gln Ser Val Thr Phe Val
                410                 415                 420

gct gac ggc gac ctg agc aag gtc atc agc aca gaa agc att gat ggc   1411
Ala Asp Gly Asp Leu Ser Lys Val Ile Ser Thr Glu Ser Ile Asp Gly
```

```
            425                 430                 435

tcc ctc gac ttg agc aac cca ggt gtt gtg act aac cag acg ttt gct   1459
Ser Leu Asp Leu Ser Asn Pro Gly Val Val Thr Asn Gln Thr Phe Ala
        440                 445                 450

gat gaa aac ggc tgg gca gta ggc gat act ctg cag ctt gaa tca atg   1507
Asp Glu Asn Gly Trp Ala Val Gly Asp Thr Leu Gln Leu Glu Ser Met
    455                 460                 465

ggg cag acc atc ggc gat atc gag ttg atc ggt acc ttc acc gga aac   1555
Gly Gln Thr Ile Gly Asp Ile Glu Leu Ile Gly Thr Phe Thr Gly Asn
470                 475                 480                 485

gac gcc atc gga aat atg atc atc tcc gaa agt tcc ttg gct gat aca   1603
Asp Ala Ile Gly Asn Met Ile Ile Ser Glu Ser Ser Leu Ala Asp Thr
                490                 495                 500

cca gcg gca gac act gct gtt cct cag atg atg ctg gtg gta ggc gaa   1651
Pro Ala Ala Asp Thr Ala Val Pro Gln Met Met Leu Val Val Gly Glu
            505                 510                 515

gaa ggc ttt gat aag gaa caa ctg cgc acc aac ttg gaa gac gca gtc   1699
Glu Gly Phe Asp Lys Glu Gln Leu Arg Thr Asn Leu Glu Asp Ala Val
        520                 525                 530

gct gat tac att gtc atc tct gtg aaa                              1726
Ala Asp Tyr Ile Val Ile Ser Val Lys
    535                 540
```

Sequence Listing Page 590 of 1000

<210> 492
<211> 542
<212> PRT
<213> Corynebacterium glutamicum

<400> 492

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Leu Val Val Asp Ser Ser Gly Arg Tyr Asn Val Thr Ile Thr Gly Leu
  1               5                  10                  15

Thr Thr Thr Glu Thr Asp Ser Ala Thr Ala Leu Asn Leu Gln Met Ser
             20                  25                  30

Glu Ala Gly Tyr Leu Glu Arg Tyr Thr Asp Gly Ala Thr Val Pro Ser
         35                  40                  45

Val Met Leu Ser Ala Ala Asp Gly Thr Thr Pro Gln Glu Leu Val Asp
     50                  55                  60

Ala Leu Ala Ala Glu Leu Gly Ser Asn Phe Asp Val Glu Thr Gly Glu
 65                  70                  75                  80

Ala Leu Val Glu Gln Ala Thr Gly Met Ile Thr Gln Ala Leu Ser Phe
                 85                  90                  95

Val Gln Tyr Phe Leu Val Ala Phe Gly Leu Ile Ala Leu Leu Val Gly
            100                 105                 110

Thr Phe Ile Ile Ala Asn Thr Phe Ser Met Ile Val Ala Gln Arg Met
        115                 120                 125
```

```
Arg Glu Phe Ala Leu Leu Arg Ala Leu Gly Ala Ala Pro Gly Gln Ile
    130                 135                 140

Thr Arg Ser Val Val Leu Glu Ala Thr Ile Val Gly Leu Phe Gly Ser
145                 150                 155                 160

Ala Leu Gly Val Leu Gly Gly Met Gly Leu Val Ala Ile Ile Ser Ala
                165                 170                 175

Val Leu Asn Asn Leu Gly Met Pro Met Gly Ser Ser Val Gly Leu Thr
            180                 185                 190

Pro Ser Ala Val Val Thr Ala Leu Val Leu Gly Thr Val Val Thr Ile
        195                 200                 205

Val Ser Ala Trp Ala Pro Ala Arg Arg Ala Gly Glu Val Lys Pro Val
    210                 215                 220

Glu Ala Met Arg Asn Met Glu Thr Thr Thr Met Arg Ser Met Met Gly
225                 230                 235                 240

Arg Thr Ile Thr Gly Gly Ile Val Leu Ala Leu Gly Ile Ile Phe Ala
                245                 250                 255

Ile Ala Gly Ala Met Met Thr Asp Ser Ser Thr Ala Thr Arg Ser Ile
            260                 265                 270

Leu Val Gly Ile Gly Ala Leu Phe Val Ile Val Gly Thr Phe Leu Phe
        275                 280                 285

Ser Pro Ala Leu Ser Met Pro Val Val Gly Gly Leu Gly Lys Val Ile
    290                 295                 300

Gly Ala Pro Phe Gly Ser Val Gly Ser Leu Ala Ala Thr Asn Ser Lys
305                 310                 315                 320

Arg Asn Pro Arg Arg Thr Ala Thr Thr Ala Phe Ala Leu Thr Leu Gly
                325                 330                 335

Ile Ala Leu Val Thr Ala Ile Gly Met Leu Ser Ala Thr Met Lys Asp
            340                 345                 350

Ala Val Ser Asp Met Met Ala Glu Gln Tyr Thr Ala Asp Tyr Ile Leu
        355                 360                 365

Gln Gly Pro Thr Asn Gly Ser Ile Thr Met Pro Lys Glu Ser Val Asn
    370                 375                 380

Asp Val Arg Asp Ala Glu Gly Val Ala Asp Val Val Leu Val Ser Met
385                 390                 395                 400

Asn Ser Ala Ser Val Asn Gly Gln Ala Ser Tyr Ser Gln Leu Gly Gln
                405                 410                 415

Ser Val Thr Phe Val Ala Asp Gly Asp Leu Ser Lys Val Ile Ser Thr
            420                 425                 430

Glu Ser Ile Asp Gly Ser Leu Asp Leu Ser Asn Pro Gly Val Val Thr
        435                 440                 445

Asn Gln Thr Phe Ala Asp Glu Asn Gly Trp Ala Val Gly Asp Thr Leu
```

```
    450                 455                 460

Gln Leu Glu Ser Met Gly Gln Thr Ile Gly Asp Ile Glu Leu Ile Gly
465                 470                 475                 480

Thr Phe Thr Gly Asn Asp Ala Ile Gly Asn Met Ile Ile Ser Glu Ser
                485                 490                 495

Ser Leu Ala Asp Thr Pro Ala Ala Asp Thr Ala Val Pro Gln Met Met
            500                 505                 510

Leu Val Val Gly Glu Glu Gly Phe Asp Lys Glu Gln Leu Arg Thr Asn
        515                 520                 525

Leu Glu Asp Ala Val Ala Asp Tyr Ile Val Ile Ser Val Lys
    530                 535                 540


<210> 493
<211> 410
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(387)
<223> FRXA01071

<400> 493
aac att ctg tac gcg ctg ctt gct ctg tct gtc att gtt gcc atc atc   48
Asn Ile Leu Tyr Ala Leu Leu Ala Leu Ser Val Ile Val Ala Ile Ile
  1               5                  10                  15

ggc atc atc aac acc ctg gca ctg aat gtg atc gag cgt cgc cag gag   96
Gly Ile Ile Asn Thr Leu Ala Leu Asn Val Ile Glu Arg Arg Gln Glu
             20                  25                  30

atc ggt atg ctc cgc gca gtt ggc gtg aag cgc gga cag gtc cgc acc   144
Ile Gly Met Leu Arg Ala Val Gly Val Lys Arg Gly Gln Val Arg Thr
         35                  40                  45

atg atc acc tta gaa tct gtt cag atc gcc atc tac ggt gct gtg att   192
Met Ile Thr Leu Glu Ser Val Gln Ile Ala Ile Tyr Gly Ala Val Ile
     50                  55                  60

ggt atc gcg att ggt ctt ggt ctg ggc tgg gcc ttt gtg aca gtg atg   240
Gly Ile Ala Ile Gly Leu Gly Leu Gly Trp Ala Phe Val Thr Val Met
 65                  70                  75                  80

tca ggc gaa gga cta gac gct gcg gtt agt atc ccg tgg ggt cag gtc   288
Ser Gly Glu Gly Leu Asp Ala Ala Val Ser Ile Pro Trp Gly Gln Val
                 85                  90                  95

gga ctg atg ctt gtt ggt tcc gct gta gtc ggt gtt atc gcc gcg ctg   336
Gly Leu Met Leu Val Gly Ser Ala Val Val Gly Val Ile Ala Ala Leu
            100                 105                 110

tgg ccg gca gtc aag gca tct agg aca cca cct ttg gat gcg att acc   384
Trp Pro Ala Val Lys Ala Ser Arg Thr Pro Pro Leu Asp Ala Ile Thr
        115                 120                 125
```

```
gac tagttttagc ggcagttgaa tca                                          410
Asp
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<210> 494
<211> 129
<212> PRT
<213> Corynebacterium glutamicum

<400> 494

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Asn Ile Leu Tyr Ala Leu Leu Ala Leu Ser Val Ile Val Ala Ile Ile
  1               5                  10                  15

Gly Ile Ile Asn Thr Leu Ala Leu Asn Val Ile Glu Arg Arg Gln Glu
             20                  25                  30

Ile Gly Met Leu Arg Ala Val Gly Val Lys Arg Gly Gln Val Arg Thr
         35                  40                  45

Met Ile Thr Leu Glu Ser Val Gln Ile Ala Ile Tyr Gly Ala Val Ile
     50                  55                  60

Gly Ile Ala Ile Gly Leu Gly Leu Gly Trp Ala Phe Val Thr Val Met
 65                  70                  75                  80

Ser Gly Glu Gly Leu Asp Ala Ala Val Ser Ile Pro Trp Gly Gln Val
                 85                  90                  95

Gly Leu Met Leu Val Gly Ser Ala Val Val Gly Val Ile Ala Ala Leu
            100                 105                 110

Trp Pro Ala Val Lys Ala Ser Arg Thr Pro Pro Leu Asp Ala Ile Thr
        115                 120                 125

Asp
```

<210> 495
<211> 534
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> RXN01075

<400> 495

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gcggtgcgtg ttcattagca ggtcaagcgc gtaattgagg gctagactgg ttagtaccgg 60

atattctttt tttctttagt ttgtgggagt ggagataact atg gac aat cca gtc   115
                                               Met Asp Asn Pro Val
                                                 1               5

aac atc ctc aat gag cag gaa gct ttg gag cgc ctg cag tcg gtg tct   163
Asn Ile Leu Asn Glu Gln Glu Ala Leu Glu Arg Leu Gln Ser Val Ser
                 10                  15                  20

ctt ggt cgc gtg gtg gtt cgt cgc agc gat gag atg gac att ttc ccg   211
```

```
Leu Gly Arg Val Val Val Arg Arg Ser Asp Glu Met Asp Ile Phe Pro
           25                  30                  35

gtg aac ttc att gtg gat aag ggc gca att tac att cgt aca gct gag   259
Val Asn Phe Ile Val Asp Lys Gly Ala Ile Tyr Ile Arg Thr Ala Glu
        40                  45                  50

ggc aac aag ttg ttc agc atg aat ctc aac cac gat gtg ctc ttt gaa   307
Gly Asn Lys Leu Phe Ser Met Asn Leu Asn His Asp Val Leu Phe Glu
     55                  60                  65

gcc gat gag gtc aag gac gga aag gcc tgg tcc gtg gtg gtt cgt gcg   355
Ala Asp Glu Val Lys Asp Gly Lys Ala Trp Ser Val Val Val Arg Ala
 70                  75                  80                  85

acc gca gag att gtg cgc aag ctg gat gag atc gct act gcc gac act   403
Thr Ala Glu Ile Val Arg Lys Leu Asp Glu Ile Ala Thr Ala Asp Thr
                90                  95                 100

ttg gag ttg aag cct tgg att cca acc ctg aag tcc aac ttt gcc cgt   451
Leu Glu Leu Lys Pro Trp Ile Pro Thr Leu Lys Ser Asn Phe Ala Arg
            105                 110                 115

att gtt ccg aat gaa atc act ggg cgg gag ttc acc ctc ggc gag gag   499
Ile Val Pro Asn Glu Ile Thr Gly Arg Glu Phe Thr Leu Gly Glu Glu
        120                 125                 130

cct gag cgc tac tagctttgcc acatttcact aaa                        534
Pro Glu Arg Tyr
    135
```

<210> 496
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 496

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Met Asp Asn Pro Val Asn Ile Leu Asn Glu Gln Glu Ala Leu Glu Arg
  1               5                  10                  15

Leu Gln Ser Val Ser Leu Gly Arg Val Val Val Arg Arg Ser Asp Glu
            20                  25                  30

Met Asp Ile Phe Pro Val Asn Phe Ile Val Asp Lys Gly Ala Ile Tyr
        35                  40                  45

Ile Arg Thr Ala Glu Gly Asn Lys Leu Phe Ser Met Asn Leu Asn His
     50                  55                  60

Asp Val Leu Phe Glu Ala Asp Glu Val Lys Asp Gly Lys Ala Trp Ser
 65                  70                  75                  80

Val Val Val Arg Ala Thr Ala Glu Ile Val Arg Lys Leu Asp Glu Ile
                85                  90                  95

Ala Thr Ala Asp Thr Leu Glu Leu Lys Pro Trp Ile Pro Thr Leu Lys
            100                 105                 110

Ser Asn Phe Ala Arg Ile Val Pro Asn Glu Ile Thr Gly Arg Glu Phe
        115                 120                 125
```

```
Thr Leu Gly Glu Glu Pro Glu Arg Tyr
    130                 135


<210> 497
<211> 534
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> FRXA01075

<400> 497
gcggtgcgtg ttcattagca ggtcaagcgc gtaattgagg gctagactgg ttagtaccgg 60

atattctttt tttctttagt ttgtgggagt ggagataact atg gac aat cca gtc   115
                                            Met Asp Asn Pro Val
                                              1               5

aac atc ctc aat gag cag gaa gct ttg gag cgc ctg cag tcg gtg tct   163
Asn Ile Leu Asn Glu Gln Glu Ala Leu Glu Arg Leu Gln Ser Val Ser
                 10                  15                  20

ctt ggt cgc gtg gtg gtt cgt cgc agc gat gag atg gac att ttc ccg   211
Leu Gly Arg Val Val Val Arg Arg Ser Asp Glu Met Asp Ile Phe Pro
             25                  30                  35

gtg aac ttc att gtg gat aag ggc gca att tac att cgt aca gct gag   259
Val Asn Phe Ile Val Asp Lys Gly Ala Ile Tyr Ile Arg Thr Ala Glu
         40                  45                  50

ggc aac aag ttg ttc agc atg aat ctc aac cac gat gtg ctc ttt gaa   307
Gly Asn Lys Leu Phe Ser Met Asn Leu Asn His Asp Val Leu Phe Glu
     55                  60                  65

gcc gat gag gtc aag gac gga aag gcc tgg tcc gtg gtg gtt cgt gcg   355
Ala Asp Glu Val Lys Asp Gly Lys Ala Trp Ser Val Val Val Arg Ala
 70                  75                  80                  85

acc gca gag att gtg cgc aag ctg gat gag atc gct act gcc gac act   403
Thr Ala Glu Ile Val Arg Lys Leu Asp Glu Ile Ala Thr Ala Asp Thr
                 90                  95                 100

ttg gag ttg aag cct tgg att cca acc ctg aag tcc aac ttt gcc cgt   451
Leu Glu Leu Lys Pro Trp Ile Pro Thr Leu Lys Ser Asn Phe Ala Arg
            105                 110                 115

att gtt ccg aat gaa atc act ggg cgg gag ttc acc ctc ggc gag gag   499
Ile Val Pro Asn Glu Ile Thr Gly Arg Glu Phe Thr Leu Gly Glu Glu
        120                 125                 130

cct gag cgc tac tagctttgcc acatttcact aaa                        534
Pro Glu Arg Tyr
    135


<210> 498
<211> 137
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<212> PRT
<213> Corynebacterium glutamicum

<400> 498
Met Asp Asn Pro Val Asn Ile Leu Asn Glu Gln Glu Ala Leu Glu Arg
1 5 10 15

Leu Gln Ser Val Ser Leu Gly Arg Val Val Val Arg Arg Ser Asp Glu
20 25 30

Met Asp Ile Phe Pro Val Asn Phe Ile Val Asp Lys Gly Ala Ile Tyr
35 40 45

Ile Arg Thr Ala Glu Gly Asn Lys Leu Phe Ser Met Asn Leu Asn His
50 55 60

Asp Val Leu Phe Glu Ala Asp Glu Val Lys Asp Gly Lys Ala Trp Ser
65 70 75 80

Val Val Val Arg Ala Thr Ala Glu Ile Val Arg Lys Leu Asp Glu Ile
85 90 95

Ala Thr Ala Asp Thr Leu Glu Leu Lys Pro Trp Ile Pro Thr Leu Lys
100 105 110

Ser Asn Phe Ala Arg Ile Val Pro Asn Glu Ile Thr Gly Arg Glu Phe
115 120 125

Thr Leu Gly Glu Glu Pro Glu Arg Tyr
130 135

<210> 499
<211> 1137
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1114)
<223> RXN01128

<400> 499
attcgagtac aaataaattt gagaacaaaa agatgggggg aaatatgtta aagtgcgtta 60

tattgcttta gcgaaagtaa cttccatgca tcaacgttcg atg agc ttc act ttc 115
Met Ser Phe Thr Phe
1 5

att cgt act ttt ttc gta ctt ttt ggc atc acg ttg tta gtg tca tgc 163
Ile Arg Thr Phe Phe Val Leu Phe Gly Ile Thr Leu Leu Val Ser Cys
10 15 20

gtt cca gag cct cct gac tcc tac act aaa gaa tcc act gtg ctg cgg 211
Val Pro Glu Pro Pro Asp Ser Tyr Thr Lys Glu Ser Thr Val Leu Arg
25 30 35

tat cag gtc tct gat ttc aat cta aac ttc gtg gaa tta gca gtt gcg 259
Tyr Gln Val Ser Asp Phe Asn Leu Asn Phe Val Glu Leu Ala Val Ala
40 45 50

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ctt ggg tat ttg aac aac att gag ctc caa gta gtc gga tct gta caa   307
Leu Gly Tyr Leu Asn Asn Ile Glu Leu Gln Val Val Gly Ser Val Gln
     55                  60                  65

ggc ggc gtt gag tcc att gaa tcg ctc aaa aag gat gac att gac ttc   355
Gly Gly Val Glu Ser Ile Glu Ser Leu Lys Lys Asp Asp Ile Asp Phe
 70                  75                  80                  85

gcg gca gtc ccc ttc att ggc ctt gtt gca gga gag ata gcc acc ggt   403
Ala Ala Val Pro Phe Ile Gly Leu Val Ala Gly Glu Ile Ala Thr Gly
                 90                  95                 100

gcg ccc atc aaa gca gtg gcc gca agt tac gga att tcc cac gat tct   451
Ala Pro Ile Lys Ala Val Ala Ala Ser Tyr Gly Ile Ser His Asp Ser
            105                 110                 115

tct tct gca ctt cta gtc ctt aaa gac agt gag ata cac gaa gtg cac   499
Ser Ser Ala Leu Leu Val Leu Lys Asp Ser Glu Ile His Glu Val His
        120                 125                 130

gat ctc att ggc aaa aca gtt ggc ata aac acc ctc ggt gct ctg gga   547
Asp Leu Ile Gly Lys Thr Val Gly Ile Asn Thr Leu Gly Ala Leu Gly
    135                 140                 145

tct gcg atg gtt gag cgt cat cta ttc gac gcc ggt ctc acc gaa cct   595
Ser Ala Met Val Glu Arg His Leu Phe Asp Ala Gly Leu Thr Glu Pro
150                 155                 160                 165

gag atc gtg agc gtc act caa cgt gca tta ccc ggt gag tac tta gaa   643
Glu Ile Val Ser Val Thr Gln Arg Ala Leu Pro Gly Glu Tyr Leu Glu
                170                 175                 180

caa cgc ctc tac cag ggg caa gtt gat gca att tgg gtc acc gat agc   691
Gln Arg Leu Tyr Gln Gly Gln Val Asp Ala Ile Trp Val Thr Asp Ser
            185                 190                 195

gct aaa cac caa gcg ctt gaa act gga gat ttt cgg atc ttg gca gag   739
Ala Lys His Gln Ala Leu Glu Thr Gly Asp Phe Arg Ile Leu Ala Glu
        200                 205                 210

gat tca gac ctt gtg cag gaa ctc aac act ggc tgc atg gtg gtg tcg   787
Asp Ser Asp Leu Val Gln Glu Leu Asn Thr Gly Cys Met Val Val Ser
    215                 220                 225

caa aaa ctc atc gac gag cac ccc gca gtg gtt gga gaa tta gtg gat   835
Gln Lys Leu Ile Asp Glu His Pro Ala Val Val Gly Glu Leu Val Asp
230                 235                 240                 245

gga gta gct cag gca atc gag ttt gaa cga tcc cac tcc cct gaa gaa   883
Gly Val Ala Gln Ala Ile Glu Phe Glu Arg Ser His Ser Pro Glu Glu
                250                 255                 260

gtg cgc gaa gtt tat ttc aac tac ctc gaa gcc cat ggt cag agt gat   931
Val Arg Glu Val Tyr Phe Asn Tyr Leu Glu Ala His Gly Gln Ser Asp
            265                 270                 275

aga ata tcc agc ttt aga tat tgg gag cat tcg ggc atc gca acc cga   979
Arg Ile Ser Ser Phe Arg Tyr Trp Glu His Ser Gly Ile Ala Thr Arg
        280                 285                 290

ggt gga gtg ctc agt gat agg gag ttc agc atg tgg tcc cac tgg att   1027
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```
Gly Gly Val Leu Ser Asp Arg Glu Phe Ser Met Trp Ser His Trp Ile
    295                 300                 305

gac cgc caa tac gac gtc ccc gat atc aat cca gca agt att tac acc   1075
Asp Arg Gln Tyr Asp Val Pro Asp Ile Asn Pro Ala Ser Ile Tyr Thr
310                 315                 320                 325

aac caa ttc aac cca tac cga aaa gta aac ccc tcg cca taaaaggcaa    1124
Asn Gln Phe Asn Pro Tyr Arg Lys Val Asn Pro Ser Pro
                330                 335

gggggtcggc gtt                                                   1137


<210> 500
<211> 338
<212> PRT
<213> Corynebacterium glutamicum

<400> 500
Met Ser Phe Thr Phe Ile Arg Thr Phe Phe Val Leu Phe Gly Ile Thr
  1               5                  10                  15

Leu Leu Val Ser Cys Val Pro Glu Pro Pro Asp Ser Tyr Thr Lys Glu
            20                  25                  30

Ser Thr Val Leu Arg Tyr Gln Val Ser Asp Phe Asn Leu Asn Phe Val
        35                  40                  45

Glu Leu Ala Val Ala Leu Gly Tyr Leu Asn Asn Ile Glu Leu Gln Val
    50                  55                  60

Val Gly Ser Val Gln Gly Gly Val Glu Ser Ile Glu Ser Leu Lys Lys
65                  70                  75                  80

Asp Asp Ile Asp Phe Ala Ala Val Pro Phe Ile Gly Leu Val Ala Gly
                85                  90                  95

Glu Ile Ala Thr Gly Ala Pro Ile Lys Ala Val Ala Ala Ser Tyr Gly
            100                 105                 110

Ile Ser His Asp Ser Ser Ser Ala Leu Leu Val Leu Lys Asp Ser Glu
        115                 120                 125

Ile His Glu Val His Asp Leu Ile Gly Lys Thr Val Gly Ile Asn Thr
    130                 135                 140

Leu Gly Ala Leu Gly Ser Ala Met Val Glu Arg His Leu Phe Asp Ala
145                 150                 155                 160

Gly Leu Thr Glu Pro Glu Ile Val Ser Val Thr Gln Arg Ala Leu Pro
                165                 170                 175

Gly Glu Tyr Leu Glu Gln Arg Leu Tyr Gln Gly Gln Val Asp Ala Ile
            180                 185                 190

Trp Val Thr Asp Ser Ala Lys His Gln Ala Leu Glu Thr Gly Asp Phe
        195                 200                 205

Arg Ile Leu Ala Glu Asp Ser Asp Leu Val Gln Glu Leu Asn Thr Gly
    210                 215                 220
```

```
Cys Met Val Val Ser Gln Lys Leu Ile Asp Glu His Pro Ala Val Val
225                 230                 235                 240

Gly Glu Leu Val Asp Gly Val Ala Gln Ala Ile Glu Phe Glu Arg Ser
                245                 250                 255

His Ser Pro Glu Glu Val Arg Glu Val Tyr Phe Asn Tyr Leu Glu Ala
            260                 265                 270

His Gly Gln Ser Asp Arg Ile Ser Ser Phe Arg Tyr Trp Glu His Ser
        275                 280                 285

Gly Ile Ala Thr Arg Gly Gly Val Leu Ser Asp Arg Glu Phe Ser Met
    290                 295                 300

Trp Ser His Trp Ile Asp Arg Gln Tyr Asp Val Pro Asp Ile Asn Pro
305                 310                 315                 320

Ala Ser Ile Tyr Thr Asn Gln Phe Asn Pro Tyr Arg Lys Val Asn Pro
                325                 330                 335

Ser Pro
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<210> 501
<211> 1137
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1114)
<223> FRXA01128

<400> 501
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tattgcttta gcgaaagtaa cttccatgca tcaacgttcg atg agc ttc act ttc   115
                                            Met Ser Phe Thr Phe
                                              1               5

att cgt act ttt ttc gta ctt ttt ggc atc acg ttg tta gtg tca tgc   163
Ile Arg Thr Phe Phe Val Leu Phe Gly Ile Thr Leu Leu Val Ser Cys
                  10                  15                  20

gtt cca gag cct cct gac tcc tac act aaa gaa tcc act gtg ctg cgg   211
Val Pro Glu Pro Pro Asp Ser Tyr Thr Lys Glu Ser Thr Val Leu Arg
              25                  30                  35

tat cag gtc tct gat ttc aat cta aac ttc gtg gaa tta gca gtt gcg   259
Tyr Gln Val Ser Asp Phe Asn Leu Asn Phe Val Glu Leu Ala Val Ala
          40                  45                  50

ctt ggg tat ttg aac aac att gag ctc caa gta gtc gga tct gta caa   307
Leu Gly Tyr Leu Asn Asn Ile Glu Leu Gln Val Val Gly Ser Val Gln
      55                  60                  65

ggc ggc gtt gag tcc att gaa tcg ctc aaa aag gat gac att gac ttc   355
Gly Gly Val Glu Ser Ile Glu Ser Leu Lys Lys Asp Asp Ile Asp Phe
```

```
 70                  75                  80                  85

gcg gca gtc ccc ttc att ggc ctt gtt gca gga gag ata gcc acc ggt   403
Ala Ala Val Pro Phe Ile Gly Leu Val Ala Gly Glu Ile Ala Thr Gly
                 90                  95                 100

gcg ccc atc aaa gca gtg gcc gca agt tac gga att tcc cac gat tct   451
Ala Pro Ile Lys Ala Val Ala Ala Ser Tyr Gly Ile Ser His Asp Ser
            105                 110                 115

tct tct gca ctt cta gtc ctt aaa gac agt gag ata cac gaa gtg cac   499
Ser Ser Ala Leu Leu Val Leu Lys Asp Ser Glu Ile His Glu Val His
        120                 125                 130

gat ctc att ggc aaa aca gtt ggc ata aac acc ctc ggt gct ctg gga   547
Asp Leu Ile Gly Lys Thr Val Gly Ile Asn Thr Leu Gly Ala Leu Gly
    135                 140                 145

tct gcg atg gtt gag cgt cat cta ttc gac gcc ggt ctc acc gaa cct   595
Ser Ala Met Val Glu Arg His Leu Phe Asp Ala Gly Leu Thr Glu Pro
150                 155                 160                 165

gag atc gtg agc gtc act caa cgt gca tta ccc ggt gag tac tta gaa   643
Glu Ile Val Ser Val Thr Gln Arg Ala Leu Pro Gly Glu Tyr Leu Glu
                170                 175                 180

caa cgc ctc tac cag ggg caa gtt gat gca att tgg gtc acc gat agc   691
Gln Arg Leu Tyr Gln Gly Gln Val Asp Ala Ile Trp Val Thr Asp Ser
            185                 190                 195

gct aaa cac caa gcg ctt gaa act gga gat ttt cgg atc ttg gca gag   739
Ala Lys His Gln Ala Leu Glu Thr Gly Asp Phe Arg Ile Leu Ala Glu
        200                 205                 210

gat tca gac ctt gtg cag gaa ctc aac act ggc tgc atg gtg gtg tcg   787
Asp Ser Asp Leu Val Gln Glu Leu Asn Thr Gly Cys Met Val Val Ser
    215                 220                 225

caa aaa ctc atc gac gag cac ccc gca gtg gtt gga gaa tta gtg gat   835
Gln Lys Leu Ile Asp Glu His Pro Ala Val Val Gly Glu Leu Val Asp
230                 235                 240                 245

gga gta gct cag gca atc gag ttt gaa cga tcc cac tcc cct gaa gaa   883
Gly Val Ala Gln Ala Ile Glu Phe Glu Arg Ser His Ser Pro Glu Glu
                250                 255                 260

gtg cgc gaa gtt tat ttc aac tac ctc gaa gcc cat ggt cag agt gat   931
Val Arg Glu Val Tyr Phe Asn Tyr Leu Glu Ala His Gly Gln Ser Asp
            265                 270                 275

aga ata tcc agc ttt aga tat tgg gag cat tcg ggc atc gca acc cga   979
Arg Ile Ser Ser Phe Arg Tyr Trp Glu His Ser Gly Ile Ala Thr Arg
        280                 285                 290

ggt gga gtg ctc agt gat agg gag ttc agc atg tgg tcc cac tgg att   1027
Gly Gly Val Leu Ser Asp Arg Glu Phe Ser Met Trp Ser His Trp Ile
    295                 300                 305

gac cgc caa tac gac gtc ccc gat atc aat cca gca agt att tac acc   1075
Asp Arg Gln Tyr Asp Val Pro Asp Ile Asn Pro Ala Ser Ile Tyr Thr
310                 315                 320                 325
```

```
aac caa ttc aac cca tac cga aaa gta aac ccc tcg cca taaaaggcaa    1124
Asn Gln Phe Asn Pro Tyr Arg Lys Val Asn Pro Ser Pro
                330                 335

gggggtcggc gtt                                                  1137
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<210> 502
<211> 338
<212> PRT
<213> Corynebacterium glutamicum

<400> 502

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Met Ser Phe Thr Phe Ile Arg Thr Phe Phe Val Leu Phe Gly Ile Thr
  1               5                  10                  15

Leu Leu Val Ser Cys Val Pro Glu Pro Pro Asp Ser Tyr Thr Lys Glu
             20                  25                  30

Ser Thr Val Leu Arg Tyr Gln Val Ser Asp Phe Asn Leu Asn Phe Val
         35                  40                  45

Glu Leu Ala Val Ala Leu Gly Tyr Leu Asn Asn Ile Glu Leu Gln Val
     50                  55                  60

Val Gly Ser Val Gln Gly Gly Val Glu Ser Ile Glu Ser Leu Lys Lys
 65                  70                  75                  80

Asp Asp Ile Asp Phe Ala Ala Val Pro Phe Ile Gly Leu Val Ala Gly
                 85                  90                  95

Glu Ile Ala Thr Gly Ala Pro Ile Lys Ala Val Ala Ala Ser Tyr Gly
            100                 105                 110

Ile Ser His Asp Ser Ser Ser Ala Leu Leu Val Leu Lys Asp Ser Glu
        115                 120                 125

Ile His Glu Val His Asp Leu Ile Gly Lys Thr Val Gly Ile Asn Thr
    130                 135                 140

Leu Gly Ala Leu Gly Ser Ala Met Val Glu Arg His Leu Phe Asp Ala
145                 150                 155                 160

Gly Leu Thr Glu Pro Glu Ile Val Ser Val Thr Gln Arg Ala Leu Pro
                165                 170                 175

Gly Glu Tyr Leu Glu Gln Arg Leu Tyr Gln Gly Gln Val Asp Ala Ile
            180                 185                 190

Trp Val Thr Asp Ser Ala Lys His Gln Ala Leu Glu Thr Gly Asp Phe
        195                 200                 205

Arg Ile Leu Ala Glu Asp Ser Asp Leu Val Gln Glu Leu Asn Thr Gly
    210                 215                 220

Cys Met Val Val Ser Gln Lys Leu Ile Asp Glu His Pro Ala Val Val
225                 230                 235                 240

Gly Glu Leu Val Asp Gly Val Ala Gln Ala Ile Glu Phe Glu Arg Ser
                245                 250                 255
```

```
His Ser Pro Glu Glu Val Arg Glu Val Tyr Phe Asn Tyr Leu Glu Ala
            260                 265                 270

His Gly Gln Ser Asp Arg Ile Ser Ser Phe Arg Tyr Trp Glu His Ser
        275                 280                 285

Gly Ile Ala Thr Arg Gly Gly Val Leu Ser Asp Arg Glu Phe Ser Met
    290                 295                 300

Trp Ser His Trp Ile Asp Arg Gln Tyr Asp Val Pro Asp Ile Asn Pro
305                 310                 315                 320

Ala Ser Ile Tyr Thr Asn Gln Phe Asn Pro Tyr Arg Lys Val Asn Pro
                325                 330                 335

Ser Pro
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<210> 503
<211> 871
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(871)
<223> RXN01134

<400> 503

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gatatcttga acttgacgct ggctgaatac attcctgctg ccgatgaaat gatcaagggc 60

ttcgacgagg cggctgaatt cctgcgtcag cgatgcattt ttg agt ctc gac cag   115
                                          Leu Ser Leu Asp Gln
                                            1               5

gtt cca tac acc gcg cag att gtt cca ctg gcc gtg atc ctc acc ctg   163
Val Pro Tyr Thr Ala Gln Ile Val Pro Leu Ala Val Ile Leu Thr Leu
                10                  15                  20

ctt gat gca gaa gaa atg gcc acc gca cgt tca tgg gat cgt ttg aat   211
Leu Asp Ala Glu Glu Met Ala Thr Ala Arg Ser Trp Asp Arg Leu Asn
            25                  30                  35

cag tgg ttc tgg agc ggt gtc ttg ggt gag ctt tat ggc tcg cct gct   259
Gln Trp Phe Trp Ser Gly Val Leu Gly Glu Leu Tyr Gly Ser Pro Ala
        40                  45                  50

gtg atc gca cgt tcc ggt cgc gat acc gat caa gtt gct gcg tgg att   307
Val Ile Ala Arg Ser Gly Arg Asp Thr Asp Gln Val Ala Ala Trp Ile
    55                  60                  65

cgt gaa ggt gcc ggc gaa act gcg gtt gtg cca aag act att cgc gat   355
Arg Glu Gly Ala Gly Glu Thr Ala Val Val Pro Lys Thr Ile Arg Asp
70                  75                  80                  85

acc gtt ttc cac gaa tca cgt ctt ctc agt gca acc caa gac acc gga   403
Thr Val Phe His Glu Ser Arg Leu Leu Ser Ala Thr Gln Asp Thr Gly
                90                  95                  100
```

```
gtg tgg aag ggt atc ttc gca ctg ctc atg ggc agg gga gca cgc gac   451
Val Trp Lys Gly Ile Phe Ala Leu Leu Met Gly Arg Gly Ala Arg Asp
            105                 110                 115

tgg cgc acc gga cag cag ttt gat cgc tgg act ttt gat gag ctg ggt   499
Trp Arg Thr Gly Gln Gln Phe Asp Arg Trp Thr Phe Asp Glu Leu Gly
        120                 125                 130

tgc aat ttc cac cag att ttc ccc acc aaa tgg tgc aag gaa cgc ggc   547
Cys Asn Phe His Gln Ile Phe Pro Thr Lys Trp Cys Lys Glu Arg Gly
    135                 140                 145

atc gat cct gtc ctt acg gaa tca gta ctg aac cgc acc ccg atg ggt   595
Ile Asp Pro Val Leu Thr Glu Ser Val Leu Asn Arg Thr Pro Met Gly
150                 155                 160                 165

cgc cgt acc gaa gta gtc atc ggc gat acc cct cca tcc cgc tac ctg   643
Arg Arg Thr Glu Val Val Ile Gly Asp Thr Pro Pro Ser Arg Tyr Leu
                170                 175                 180

tct cgt gtt caa tcc aag tcg ctc atg ggt gat gag gaa ttc gat cag   691
Ser Arg Val Gln Ser Lys Ser Leu Met Gly Asp Glu Glu Phe Asp Gln
            185                 190                 195

atg ctg gat acc cac ctg ctc agc gcg gaa gac ctg cac agt tcc aac   739
Met Leu Asp Thr His Leu Leu Ser Ala Glu Asp Leu His Ser Ser Asn
        200                 205                 210

acc acg cac ttc ttt gct tct cga cgc acc aac ttc atc gac atg gtc   787
Thr Thr His Phe Phe Ala Ser Arg Arg Thr Asn Phe Ile Asp Met Val
    215                 220                 225

gag gat gcc atc ggt aaa gcg gtg atc agg gac gtc aac gag tca gat   835
Glu Asp Ala Ile Gly Lys Ala Val Ile Arg Asp Val Asn Glu Ser Asp
230                 235                 240                 245

ctc acc ggt gga cac gat ggt ccc tcg gta cac ggg                   871
Leu Thr Gly Gly His Asp Gly Pro Ser Val His Gly
                250                 255
```

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<210> 504
<211> 257
<212> PRT
<213> Corynebacterium glutamicum

<400> 504

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Leu Ser Leu Asp Gln Val Pro Tyr Thr Ala Gln Ile Val Pro Leu Ala
  1               5                  10                  15

Val Ile Leu Thr Leu Leu Asp Ala Glu Glu Met Ala Thr Ala Arg Ser
            20                  25                  30

Trp Asp Arg Leu Asn Gln Trp Phe Trp Ser Gly Val Leu Gly Glu Leu
        35                  40                  45

Tyr Gly Ser Pro Ala Val Ile Ala Arg Ser Gly Arg Asp Thr Asp Gln
    50                  55                  60

Val Ala Ala Trp Ile Arg Glu Gly Ala Gly Glu Thr Ala Val Val Pro
65                  70                  75                  80
```

```
Lys Thr Ile Arg Asp Thr Val Phe His Glu Ser Arg Leu Leu Ser Ala
                 85                  90                  95

Thr Gln Asp Thr Gly Val Trp Lys Gly Ile Phe Ala Leu Leu Met Gly
            100                 105                 110

Arg Gly Ala Arg Asp Trp Arg Thr Gly Gln Gln Phe Asp Arg Trp Thr
        115                 120                 125

Phe Asp Glu Leu Gly Cys Asn Phe His Gln Ile Phe Pro Thr Lys Trp
    130                 135                 140

Cys Lys Glu Arg Gly Ile Asp Pro Val Leu Thr Glu Ser Val Leu Asn
145                 150                 155                 160

Arg Thr Pro Met Gly Arg Arg Thr Glu Val Val Ile Gly Asp Thr Pro
                165                 170                 175

Pro Ser Arg Tyr Leu Ser Arg Val Gln Ser Lys Ser Leu Met Gly Asp
            180                 185                 190

Glu Glu Phe Asp Gln Met Leu Asp Thr His Leu Leu Ser Ala Glu Asp
        195                 200                 205

Leu His Ser Ser Asn Thr Thr His Phe Phe Ala Ser Arg Arg Thr Asn
    210                 215                 220

Phe Ile Asp Met Val Glu Asp Ala Ile Gly Lys Ala Val Ile Arg Asp
225                 230                 235                 240

Val Asn Glu Ser Asp Leu Thr Gly Gly His Asp Gly Pro Ser Val His
                245                 250                 255

Gly
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US-09-505-505

<210> 505
<211> 459
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(459)
<223> FRXA01134

<400> 505

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agt gca acc caa gac acc gga gtg tgg aag ggt atc ttc gca ctg ctc   48
Ser Ala Thr Gln Asp Thr Gly Val Trp Lys Gly Ile Phe Ala Leu Leu
  1               5                  10                  15

atg ggc agg gga gca cgc gac tgg cgc acc gga cag cag ttt gat cgc   96
Met Gly Arg Gly Ala Arg Asp Trp Arg Thr Gly Gln Gln Phe Asp Arg
             20                  25                  30

tgg act ttt gat gag ctg ggt tgc aat ttc cac cag att ttc ccc acc   144
Trp Thr Phe Asp Glu Leu Gly Cys Asn Phe His Gln Ile Phe Pro Thr
         35                  40                  45
```

```
aaa tgg tgc aag gaa cgc ggc atc gat cct gtc ctt acg gaa tca gta   192
Lys Trp Cys Lys Glu Arg Gly Ile Asp Pro Val Leu Thr Glu Ser Val
     50                  55                  60

ctg aac cgc acc ccg atg ggt cgc cgt acc gaa gta gtc atc ggc gat   240
Leu Asn Arg Thr Pro Met Gly Arg Arg Thr Glu Val Val Ile Gly Asp
 65                  70                  75                  80

acc cct cca tcc cgc tac ctg tct cgt gtt caa tcc aag tcg ctc atg   288
Thr Pro Pro Ser Arg Tyr Leu Ser Arg Val Gln Ser Lys Ser Leu Met
                85                  90                  95

ggt gat gag gaa ttc gat cag atg ctg gat acc cac ctg ctc agc gcg   336
Gly Asp Glu Glu Phe Asp Gln Met Leu Asp Thr His Leu Leu Ser Ala
            100                 105                 110

gaa gac ctg cac agt tcc aac acc acg cac ttc ttt gct tct cga cgc   384
Glu Asp Leu His Ser Ser Asn Thr Thr His Phe Phe Ala Ser Arg Arg
        115                 120                 125

acc aac ttc atc gac atg gtc gag gat gcc atc ggt aaa gcg gtg atc   432
Thr Asn Phe Ile Asp Met Val Glu Asp Ala Ile Gly Lys Ala Val Ile
    130                 135                 140

agg gac gtc aac gag tca gat ctc acc                              459
Arg Asp Val Asn Glu Ser Asp Leu Thr
145                 150
```

<210> 506
<211> 153
<212> PRT
<213> Corynebacterium glutamicum

<400> 506

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Ser Ala Thr Gln Asp Thr Gly Val Trp Lys Gly Ile Phe Ala Leu Leu
  1               5                  10                  15

Met Gly Arg Gly Ala Arg Asp Trp Arg Thr Gly Gln Gln Phe Asp Arg
             20                  25                  30

Trp Thr Phe Asp Glu Leu Gly Cys Asn Phe His Gln Ile Phe Pro Thr
         35                  40                  45

Lys Trp Cys Lys Glu Arg Gly Ile Asp Pro Val Leu Thr Glu Ser Val
     50                  55                  60

Leu Asn Arg Thr Pro Met Gly Arg Arg Thr Glu Val Val Ile Gly Asp
 65                  70                  75                  80

Thr Pro Pro Ser Arg Tyr Leu Ser Arg Val Gln Ser Lys Ser Leu Met
                85                  90                  95

Gly Asp Glu Glu Phe Asp Gln Met Leu Asp Thr His Leu Leu Ser Ala
            100                 105                 110

Glu Asp Leu His Ser Ser Asn Thr Thr His Phe Phe Ala Ser Arg Arg
        115                 120                 125

Thr Asn Phe Ile Asp Met Val Glu Asp Ala Ile Gly Lys Ala Val Ile
    130                 135                 140
```

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Arg Asp Val Asn Glu Ser Asp Leu Thr
145                 150


<210> 507
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1033)
<223> RXN01140

<400> 507
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tataaccact gttcttcgtg gttttccagt aggtgtgctg atg gca cta gac acc   115
                                          Met Ala Leu Asp Thr
                                            1               5

cgc ggc gag gaa atg cgt ttc cgg cca cgc gcg ctg tcc ggc gcc cca   163
Arg Gly Glu Glu Met Arg Phe Arg Pro Arg Ala Leu Ser Gly Ala Pro
                 10                  15                  20

gat acg ggc aag gat cca ggt ctt ttg ctt ctc gac gga caa cag cgc   211
Asp Thr Gly Lys Asp Pro Gly Leu Leu Leu Leu Asp Gly Gln Gln Arg
            25                  30                  35

ctc acc acc ctt tat cat tgc ttc agt ggc gat ggc tat gta aat acg   259
Leu Thr Thr Leu Tyr His Cys Phe Ser Gly Asp Gly Tyr Val Asn Thr
        40                  45                  50

gtg gac ttc cga tca aag aaa gtg acc cgg aag ttt tat att gat gtt   307
Val Asp Phe Arg Ser Lys Lys Val Thr Arg Lys Phe Tyr Ile Asp Val
    55                  60                  65

gct aag gct gtt gaa tct ccg gtc atg tcc gat gag gct att ttt tca   355
Ala Lys Ala Val Glu Ser Pro Val Met Ser Asp Glu Ala Ile Phe Ser
70                  75                  80                  85

gtc gac gaa acc ggc aaa atc atc tcc cac ttc ggt cca gtg atc gac   403
Val Asp Glu Thr Gly Lys Ile Ile Ser His Phe Gly Pro Val Ile Asp
                90                  95                 100

ggc ggc atc acc gat tta gaa aca gca ctt gct cat ggt tgc ctt cca   451
Gly Gly Ile Thr Asp Leu Glu Thr Ala Leu Ala His Gly Cys Leu Pro
            105                 110                 115

gtt tct gtg ctg ctg gat gat aac ggc act gat ttc ctc ttt gac ctc   499
Val Ser Val Leu Leu Asp Asp Asn Gly Thr Asp Phe Leu Phe Asp Leu
        120                 125                 130

gcc gat atg gca gga gaa ggc gct cgc gaa cac gcg aag cgc ttc caa   547
Ala Asp Met Ala Gly Glu Gly Ala Arg Glu His Ala Lys Arg Phe Gln
    135                 140                 145

tca caa atc gtt aag acc tta gtt agt tac gac atc cca atg atc cga   595
Ser Gln Ile Val Lys Thr Leu Val Ser Tyr Asp Ile Pro Met Ile Arg
150                 155                 160                 165
```

```
ctg gat cgt gaa acc gcc aag ggt gga att ggt tcc atc ttt gct cag   643
Leu Asp Arg Glu Thr Ala Lys Gly Gly Ile Gly Ser Ile Phe Ala Gln
                170                 175                 180

gcc aat agc tct ggc ttg cag atg gat gtc ttt gat ttg ctc acc gcg   691
Ala Asn Ser Ser Gly Leu Gln Met Asp Val Phe Asp Leu Leu Thr Ala
            185                 190                 195

gtg ttc gca gcc gat gaa tcg gtg gag acc gaa ttc tca ctg cgt gat   739
Val Phe Ala Ala Asp Glu Ser Val Glu Thr Glu Phe Ser Leu Arg Asp
        200                 205                 210

gac tgg gtg cgg gtt gaa cga aac ctt cgc caa cac tcc gca ctt gat   787
Asp Trp Val Arg Val Glu Arg Asn Leu Arg Gln His Ser Ala Leu Asp
    215                 220                 225

ggc atc ggc agc acg gag ttc ctc acc gca gta gcc ctg ttg gtc agt   835
Gly Ile Gly Ser Thr Glu Phe Leu Thr Ala Val Ala Leu Leu Val Ser
230                 235                 240                 245

gcc cgc aag gga cat gcg tct ggt tac cgt gaa gat atc ttg aac ttg   883
Ala Arg Lys Gly His Ala Ser Gly Tyr Arg Glu Asp Ile Leu Asn Leu
                250                 255                 260

acg ctg gct gaa tac att cct gct gcc gat gaa atg atc aag ggc ttc   931
Thr Leu Ala Glu Tyr Ile Pro Ala Ala Asp Glu Met Ile Lys Gly Phe
            265                 270                 275

gac gag gcg gct gaa ttc ctg cgt cag cga tgc att ttt gag tct cga   979
Asp Glu Ala Ala Glu Phe Leu Arg Gln Arg Cys Ile Phe Glu Ser Arg
        280                 285                 290

cca ggt tcc ata cac cgc gca gat tgt tcc act ggc cgt gat cct cac   1027
Pro Gly Ser Ile His Arg Ala Asp Cys Ser Thr Gly Arg Asp Pro His
    295                 300                 305

cct gct tgatgcagaa gaaatggcca ccg                                1056
Pro Ala
310
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<210> 508
<211> 311
<212> PRT
<213> Corynebacterium glutamicum

<400> 508

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Met Ala Leu Asp Thr Arg Gly Glu Glu Met Arg Phe Arg Pro Arg Ala
  1               5                  10                  15

Leu Ser Gly Ala Pro Asp Thr Gly Lys Asp Pro Gly Leu Leu Leu Leu
            20                  25                  30

Asp Gly Gln Gln Arg Leu Thr Thr Leu Tyr His Cys Phe Ser Gly Asp
        35                  40                  45

Gly Tyr Val Asn Thr Val Asp Phe Arg Ser Lys Lys Val Thr Arg Lys
    50                  55                  60

Phe Tyr Ile Asp Val Ala Lys Ala Val Glu Ser Pro Val Met Ser Asp
```

```
 65                  70                  75                  80

Glu Ala Ile Phe Ser Val Asp Glu Thr Gly Lys Ile Ile Ser His Phe
                 85                  90                  95

Gly Pro Val Ile Asp Gly Gly Ile Thr Asp Leu Glu Thr Ala Leu Ala
            100                 105                 110

His Gly Cys Leu Pro Val Ser Val Leu Leu Asp Asp Asn Gly Thr Asp
        115                 120                 125

Phe Leu Phe Asp Leu Ala Asp Met Ala Gly Glu Gly Ala Arg Glu His
    130                 135                 140

Ala Lys Arg Phe Gln Ser Gln Ile Val Lys Thr Leu Val Ser Tyr Asp
145                 150                 155                 160

Ile Pro Met Ile Arg Leu Asp Arg Glu Thr Ala Lys Gly Gly Ile Gly
                165                 170                 175

Ser Ile Phe Ala Gln Ala Asn Ser Ser Gly Leu Gln Met Asp Val Phe
            180                 185                 190

Asp Leu Leu Thr Ala Val Phe Ala Ala Asp Glu Ser Val Glu Thr Glu
        195                 200                 205

Phe Ser Leu Arg Asp Asp Trp Val Arg Val Glu Arg Asn Leu Arg Gln
    210                 215                 220

His Ser Ala Leu Asp Gly Ile Gly Ser Thr Glu Phe Leu Thr Ala Val
225                 230                 235                 240

Ala Leu Leu Val Ser Ala Arg Lys Gly His Ala Ser Gly Tyr Arg Glu
                245                 250                 255

Asp Ile Leu Asn Leu Thr Leu Ala Glu Tyr Ile Pro Ala Ala Asp Glu
            260                 265                 270

Met Ile Lys Gly Phe Asp Glu Ala Ala Glu Phe Leu Arg Gln Arg Cys
        275                 280                 285

Ile Phe Glu Ser Arg Pro Gly Ser Ile His Arg Ala Asp Cys Ser Thr
    290                 295                 300

Gly Arg Asp Pro His Pro Ala
305                 310
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<210> 509
<211> 886
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(886)
<223> FRXA01140

<400> 509
tatccaactt cccgattttc aacgggatta cgcttgggat gttgatcgca tccgaagcct 60

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tataaccact gttcttcgtg gttttccagt aggtgtgctg atg gca cta gac acc   115
                                            Met Ala Leu Asp Thr
                                              1               5

cgc ggc gag gaa atg cgt ttc cgg cca cgc gcg ctg tcc ggc gcc cca   163
Arg Gly Glu Glu Met Arg Phe Arg Pro Arg Ala Leu Ser Gly Ala Pro
                10                  15                  20

gat acg ggc aag gat cca ggt ctt ttg ctt ctc gac gga caa cag cgc   211
Asp Thr Gly Lys Asp Pro Gly Leu Leu Leu Leu Asp Gly Gln Gln Arg
            25                  30                  35

ctc acc acc ctt tat cat tgc ttc agt ggc gat ggc tat gta aat acg   259
Leu Thr Thr Leu Tyr His Cys Phe Ser Gly Asp Gly Tyr Val Asn Thr
        40                  45                  50

gtg gac ttc cga tca aag aaa gtg acc cgg aag ttt tat att gat gtt   307
Val Asp Phe Arg Ser Lys Lys Val Thr Arg Lys Phe Tyr Ile Asp Val
    55                  60                  65

gct aag gct gtt gaa tct ccg gtc atg tcc gat gag gct att ttt tca   355
Ala Lys Ala Val Glu Ser Pro Val Met Ser Asp Glu Ala Ile Phe Ser
70                  75                  80                  85

gtc gac gaa acc ggc aaa atc atc tcc cac ttc ggt cca gtg atc gac   403
Val Asp Glu Thr Gly Lys Ile Ile Ser His Phe Gly Pro Val Ile Asp
                90                  95                  100

ggc ggc atc acc gat tta gaa aca gca ctt gct cat ggt tgc ctt cca   451
Gly Gly Ile Thr Asp Leu Glu Thr Ala Leu Ala His Gly Cys Leu Pro
            105                 110                 115

gtt tct gtg ctg ctg gat gat aac ggc act gat ttc ctc ttt gac ctc   499
Val Ser Val Leu Leu Asp Asp Asn Gly Thr Asp Phe Leu Phe Asp Leu
        120                 125                 130

gcc gat atg gca gga gaa ggc gct cgc gaa cac gcg aag cgc ttc caa   547
Ala Asp Met Ala Gly Glu Gly Ala Arg Glu His Ala Lys Arg Phe Gln
    135                 140                 145

tca caa atc gtt aag acc tta gtt agt tac gac atc cca atg atc cga   595
Ser Gln Ile Val Lys Thr Leu Val Ser Tyr Asp Ile Pro Met Ile Arg
150                 155                 160                 165

ctg gat cgt gaa acc gcc aag ggt gga att ggt tcc atc ttt gct cag   643
Leu Asp Arg Glu Thr Ala Lys Gly Gly Ile Gly Ser Ile Phe Ala Gln
                170                 175                 180

gcc aat agc tct ggc ttg cag atg gat gtc ttt gat ttg ctc acc gcg   691
Ala Asn Ser Ser Gly Leu Gln Met Asp Val Phe Asp Leu Leu Thr Ala
            185                 190                 195

gtg ttc gca gcc gat gaa tcg gtg gag acc gaa ttc tca ctg cgt gat   739
Val Phe Ala Ala Asp Glu Ser Val Glu Thr Glu Phe Ser Leu Arg Asp
        200                 205                 210

gac tgg gtg cgg gtt gaa cga aac ctt cgc caa cac tcc gca ctt gat   787
Asp Trp Val Arg Val Glu Arg Asn Leu Arg Gln His Ser Ala Leu Asp
    215                 220                 225

ggc atc ggc agc acg gag ttc ctc acc gca gta gcc ctg ttg gtc agt   835
```

```
Gly Ile Gly Ser Thr Glu Phe Leu Thr Ala Val Ala Leu Leu Val Ser
230                 235                 240                 245

gcc cgc aag gga cat gcg tct ggt tac cgt gaa gat atc ttg aac ttg   883
Ala Arg Lys Gly His Ala Ser Gly Tyr Arg Glu Asp Ile Leu Asn Leu
                250                 255                 260

acg                                                               886
Thr
```

<210> 510
<211> 262
<212> PRT
<213> Corynebacterium glutamicum

<400> 510

```
Met Ala Leu Asp Thr Arg Gly Glu Glu Met Arg Phe Arg Pro Arg Ala
  1               5                  10                  15

Leu Ser Gly Ala Pro Asp Thr Gly Lys Asp Pro Gly Leu Leu Leu Leu
             20                  25                  30

Asp Gly Gln Gln Arg Leu Thr Thr Leu Tyr His Cys Phe Ser Gly Asp
         35                  40                  45

Gly Tyr Val Asn Thr Val Asp Phe Arg Ser Lys Lys Val Thr Arg Lys
     50                  55                  60

Phe Tyr Ile Asp Val Ala Lys Ala Val Glu Ser Pro Val Met Ser Asp
 65                  70                  75                  80

Glu Ala Ile Phe Ser Val Asp Glu Thr Gly Lys Ile Ile Ser His Phe
                 85                  90                  95

Gly Pro Val Ile Asp Gly Gly Ile Thr Asp Leu Glu Thr Ala Leu Ala
            100                 105                 110

His Gly Cys Leu Pro Val Ser Val Leu Leu Asp Asp Asn Gly Thr Asp
        115                 120                 125

Phe Leu Phe Asp Leu Ala Asp Met Ala Gly Glu Gly Ala Arg Glu His
    130                 135                 140

Ala Lys Arg Phe Gln Ser Gln Ile Val Lys Thr Leu Val Ser Tyr Asp
145                 150                 155                 160

Ile Pro Met Ile Arg Leu Asp Arg Glu Thr Ala Lys Gly Gly Ile Gly
                165                 170                 175

Ser Ile Phe Ala Gln Ala Asn Ser Ser Gly Leu Gln Met Asp Val Phe
            180                 185                 190

Asp Leu Leu Thr Ala Val Phe Ala Ala Asp Glu Ser Val Glu Thr Glu
        195                 200                 205

Phe Ser Leu Arg Asp Asp Trp Val Arg Val Glu Arg Asn Leu Arg Gln
    210                 215                 220

His Ser Ala Leu Asp Gly Ile Gly Ser Thr Glu Phe Leu Thr Ala Val
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225 230 235 240

Ala Leu Leu Val Ser Ala Arg Lys Gly His Ala Ser Gly Tyr Arg Glu
245 250 255

Asp Ile Leu Asn Leu Thr
260

<210> 511
<211> 723
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(700)
<223> RXN01148

<400> 511
atagaacaag ggtagccaaa ttcttggaaa cagcgcgggc ccccgaatcc acaatgcgaa 60

tccacaatgt cacctgaagc cgttaaagta ggtgatcatt atg acc agc cca gtt 115
Met Thr Ser Pro Val
1 5

gaa aac gtt aag aaa aag cca cgc cca ttg gcg ctg tca ccg tcg cgc 163
Glu Asn Val Lys Lys Lys Pro Arg Pro Leu Ala Leu Ser Pro Ser Arg
10 15 20

gcc ggg gat tac cag cag tgt ccc ctg ttg tat cgc ttc cgc gcg att 211
Ala Gly Asp Tyr Gln Gln Cys Pro Leu Leu Tyr Arg Phe Arg Ala Ile
25 30 35

gat cgc ctg cca gag cct aag acc gtc gcc cag gtc aaa ggc acg ttg 259
Asp Arg Leu Pro Glu Pro Lys Thr Val Ala Gln Val Lys Gly Thr Leu
40 45 50

gtg cac gct gtg ttg gaa tat atg cac aag ttg ccg cgt gaa gaa cgc 307
Val His Ala Val Leu Glu Tyr Met His Lys Leu Pro Arg Glu Glu Arg
55 60 65

gaa tat cca gcc atg gtg aag caa ctc aag ccc acc tgg gcg cag atg 355
Glu Tyr Pro Ala Met Val Lys Gln Leu Lys Pro Thr Trp Ala Gln Met
70 75 80 85

tgt gaa gaa gac gca gag ctc aaa gag ctt gtt cca gaa gat gag ctt 403
Cys Glu Glu Asp Ala Glu Leu Lys Glu Leu Val Pro Glu Asp Glu Leu
90 95 100

tat gat ttc ctc gtg gat tcc cgc acc ctg ctg cgt ggc tac ttt gaa 451
Tyr Asp Phe Leu Val Asp Ser Arg Thr Leu Leu Arg Gly Tyr Phe Glu
105 110 115

atg gaa aat cct caa ggt ttc gac gcc acc gaa tgc gaa atg tac gtg 499
Met Glu Asn Pro Gln Gly Phe Asp Ala Thr Glu Cys Glu Met Tyr Val
120 125 130

gac act gtg ctg ccc aac ggc gtt cct gtt cgt ggt ttt atc gac cgt 547
Asp Thr Val Leu Pro Asn Gly Val Pro Val Arg Gly Phe Ile Asp Arg
135 140 145

```
gtg gat acc gcc cca ccg gcc aag tcc gag tta tcg act aca aga ctg   595
Val Asp Thr Ala Pro Pro Ala Lys Ser Glu Leu Ser Thr Thr Arg Leu
150                 155                 160                 165

gca aga aac caa agc cgc agt gga gcc agc aag cgc agt tcc aga tgc   643
Ala Arg Asn Gln Ser Arg Ser Gly Ala Ser Lys Arg Ser Ser Arg Cys
                170                 175                 180

tgt tct atg cac tgg tct act ggc gca tgt tca atg aaa tcc cag ctc   691
Cys Ser Met His Trp Ser Thr Gly Ala Cys Ser Met Lys Ser Gln Leu
            185                 190                 195

agc ttc gtt taatgtacct caaagtcaac gat                            723
Ser Phe Val
        200
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<210> 512
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 512

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Met Thr Ser Pro Val Glu Asn Val Lys Lys Lys Pro Arg Pro Leu Ala
  1               5                  10                  15

Leu Ser Pro Ser Arg Ala Gly Asp Tyr Gln Gln Cys Pro Leu Leu Tyr
             20                  25                  30

Arg Phe Arg Ala Ile Asp Arg Leu Pro Glu Pro Lys Thr Val Ala Gln
         35                  40                  45

Val Lys Gly Thr Leu Val His Ala Val Leu Glu Tyr Met His Lys Leu
     50                  55                  60

Pro Arg Glu Glu Arg Glu Tyr Pro Ala Met Val Lys Gln Leu Lys Pro
 65                  70                  75                  80

Thr Trp Ala Gln Met Cys Glu Glu Asp Ala Glu Leu Lys Glu Leu Val
                 85                  90                  95

Pro Glu Asp Glu Leu Tyr Asp Phe Leu Val Asp Ser Arg Thr Leu Leu
            100                 105                 110

Arg Gly Tyr Phe Glu Met Glu Asn Pro Gln Gly Phe Asp Ala Thr Glu
        115                 120                 125

Cys Glu Met Tyr Val Asp Thr Val Leu Pro Asn Gly Val Pro Val Arg
    130                 135                 140

Gly Phe Ile Asp Arg Val Asp Thr Ala Pro Pro Ala Lys Ser Glu Leu
145                 150                 155                 160

Ser Thr Thr Arg Leu Ala Arg Asn Gln Ser Arg Ser Gly Ala Ser Lys
                165                 170                 175

Arg Ser Ser Arg Cys Cys Ser Met His Trp Ser Thr Gly Ala Cys Ser
            180                 185                 190

Met Lys Ser Gln Leu Ser Phe Val
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195 200

<210> 513
<211> 723
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(700)
<223> FRXA01148

<400> 513
atagaacaag ggtagccaaa ttcttggaaa cagcgcgggc ccccgaatcc acaatgcgaa 60

tccacaatgt cacctgaagc cgttaaagta ggtgatcatt atg acc agc cca gtt 115
Met Thr Ser Pro Val
1 5

gaa aac gtt aag aaa aag cca cgc cca ttg gcg ctg tca ccg tcg cgc 163
Glu Asn Val Lys Lys Lys Pro Arg Pro Leu Ala Leu Ser Pro Ser Arg
10 15 20

gcc ggg gat tac cag cag tgt ccc ctg ttg tat cgc ttc cgc gcg att 211
Ala Gly Asp Tyr Gln Gln Cys Pro Leu Leu Tyr Arg Phe Arg Ala Ile
25 30 35

gat cgc ctg cca gag cct aag acc gtc gcc cag gtc aaa ggc acg ttg 259
Asp Arg Leu Pro Glu Pro Lys Thr Val Ala Gln Val Lys Gly Thr Leu
40 45 50

gtg cac gct gtg ttg gaa tat atg cac aag ttg ccg cgt gaa gaa cgc 307
Val His Ala Val Leu Glu Tyr Met His Lys Leu Pro Arg Glu Glu Arg
55 60 65

gaa tat cca gcc atg gtg aag caa ctc aag ccc acc tgg gcg cag atg 355
Glu Tyr Pro Ala Met Val Lys Gln Leu Lys Pro Thr Trp Ala Gln Met
70 75 80 85

tgt gaa gaa gac gca gag ctc aaa gag ctt gtt cca gaa gat gag ctt 403
Cys Glu Glu Asp Ala Glu Leu Lys Glu Leu Val Pro Glu Asp Glu Leu
90 95 100

tat gat ttc ctc gtg gat tcc cgc acc ctg ctg cgt ggc tac ttt gaa 451
Tyr Asp Phe Leu Val Asp Ser Arg Thr Leu Leu Arg Gly Tyr Phe Glu
105 110 115

atg gaa aat cct caa ggt ttc gac gcc acc gaa tgc gaa atg tac gtg 499
Met Glu Asn Pro Gln Gly Phe Asp Ala Thr Glu Cys Glu Met Tyr Val
120 125 130

gac act gtg ctg ccc aac ggc gtt cct gtt cgt ggt ttt atc gac cgt 547
Asp Thr Val Leu Pro Asn Gly Val Pro Val Arg Gly Phe Ile Asp Arg
135 140 145

gtg gat acc gcc cca ccg gcc aag tcc gag tta tcg act aca aga ctg 595
Val Asp Thr Ala Pro Pro Ala Lys Ser Glu Leu Ser Thr Thr Arg Leu
150 155 160 165

gca aga aac caa agc cgc agt gga gcc agc aag cgc agt tcc aga tgc 643

```
Ala Arg Asn Gln Ser Arg Ser Gly Ala Ser Lys Arg Ser Ser Arg Cys
                170                 175                 180

tgt tct atg cac tgg tct act ggc gca tgt tca atg aaa tcc cag ctc   691
Cys Ser Met His Trp Ser Thr Gly Ala Cys Ser Met Lys Ser Gln Leu
            185                 190                 195

agc ttc gtt taatgtacct caaagtcaac gat                             723
Ser Phe Val
        200


<210> 514
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 514
Met Thr Ser Pro Val Glu Asn Val Lys Lys Lys Pro Arg Pro Leu Ala
  1               5                  10                  15

Leu Ser Pro Ser Arg Ala Gly Asp Tyr Gln Gln Cys Pro Leu Leu Tyr
             20                  25                  30

Arg Phe Arg Ala Ile Asp Arg Leu Pro Glu Pro Lys Thr Val Ala Gln
         35                  40                  45

Val Lys Gly Thr Leu Val His Ala Val Leu Glu Tyr Met His Lys Leu
     50                  55                  60

Pro Arg Glu Glu Arg Glu Tyr Pro Ala Met Val Lys Gln Leu Lys Pro
 65                  70                  75                  80

Thr Trp Ala Gln Met Cys Glu Glu Asp Ala Glu Leu Lys Glu Leu Val
                 85                  90                  95

Pro Glu Asp Glu Leu Tyr Asp Phe Leu Val Asp Ser Arg Thr Leu Leu
            100                 105                 110

Arg Gly Tyr Phe Glu Met Glu Asn Pro Gln Gly Phe Asp Ala Thr Glu
        115                 120                 125

Cys Glu Met Tyr Val Asp Thr Val Leu Pro Asn Gly Val Pro Val Arg
    130                 135                 140

Gly Phe Ile Asp Arg Val Asp Thr Ala Pro Pro Ala Lys Ser Glu Leu
145                 150                 155                 160

Ser Thr Thr Arg Leu Ala Arg Asn Gln Ser Arg Ser Gly Ala Ser Lys
                165                 170                 175

Arg Ser Ser Arg Cys Cys Ser Met His Trp Ser Thr Gly Ala Cys Ser
            180                 185                 190

Met Lys Ser Gln Leu Ser Phe Val
        195                 200


<210> 515
<211> 543
<212> DNA
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<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(543)
<223> RXN01153

<400> 515

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ccg ttt tta agc ccg atc gtt act tcc acg cac gcg gtg gtg gcg tat   48
Pro Phe Leu Ser Pro Ile Val Thr Ser Thr His Ala Val Val Ala Tyr
  1               5                  10                  15

tcc acc gcg cgt gga ttt ggt gag cac cgg gtg cgt tgg gac tat gcg   96
Ser Thr Ala Arg Gly Phe Gly Glu His Arg Val Arg Trp Asp Tyr Ala
             20                  25                  30

caa gag tcc cca ctg cgc gat act cgt ggc ttt gat ctg cgc cga tac   144
Gln Glu Ser Pro Leu Arg Asp Thr Arg Gly Phe Asp Leu Arg Arg Tyr
         35                  40                  45

cac cag gcc cct gtg gtg gat ccg cac gcc att ggt gtg gcc aac gtg   192
His Gln Ala Pro Val Val Asp Pro His Ala Ile Gly Val Ala Asn Val
     50                  55                  60

ttt gtg ccc aat ggt gcc agg ttt tat gtc gat cac gcg cac ccg gaa   240
Phe Val Pro Asn Gly Ala Arg Phe Tyr Val Asp His Ala His Pro Glu
 65                  70                  75                  80

tac tcc tcc cca gag gtc acc aat gcg tgg gat gcc atg gtt tac gac   288
Tyr Ser Ser Pro Glu Val Thr Asn Ala Trp Asp Ala Met Val Tyr Asp
                 85                  90                  95

gcc gct ggt gac cac atc ctt atg cag gcc gtc tct gat gtt gcg agt   336
Ala Ala Gly Asp His Ile Leu Met Gln Ala Val Ser Asp Val Ala Ser
            100                 105                 110

ttc acc agc cag aat agg tct gtg ttg gac ggc cat gat ccg tgt cca   384
Phe Thr Ser Gln Asn Arg Ser Val Leu Asp Gly His Asp Pro Cys Pro
        115                 120                 125

gct ttg aaa atc tac aaa aac aat gtc gac ggt aag ggt gct agc tac   432
Ala Leu Lys Ile Tyr Lys Asn Asn Val Asp Gly Lys Gly Ala Ser Tyr
    130                 135                 140

ggg ttc cac gag aat tac ctc tac tca cgt gag acg gat ttt gat gtg   480
Gly Phe His Glu Asn Tyr Leu Tyr Ser Arg Glu Thr Asp Phe Asp Val
145                 150                 155                 160

ctg gct cag gca ttg atc cca ttt ttt gtg tgc cgg cag gtc atc atc   528
Leu Ala Gln Ala Leu Ile Pro Phe Phe Val Cys Arg Gln Val Ile Ile
                165                 170                 175

ggt gcc gga cgt gtg                                              543
Gly Ala Gly Arg Val
            180
```

<210> 516
<211> 181
<212> PRT
<213> Corynebacterium glutamicum

<400> 516
Pro Phe Leu Ser Pro Ile Val Thr Ser Thr His Ala Val Val Ala Tyr
1 5 10 15

Ser Thr Ala Arg Gly Phe Gly Glu His Arg Val Arg Trp Asp Tyr Ala
20 25 30

Gln Glu Ser Pro Leu Arg Asp Thr Arg Gly Phe Asp Leu Arg Arg Tyr
35 40 45

His Gln Ala Pro Val Val Asp Pro His Ala Ile Gly Val Ala Asn Val
50 55 60

Phe Val Pro Asn Gly Ala Arg Phe Tyr Val Asp His Ala His Pro Glu
65 70 75 80

Tyr Ser Ser Pro Glu Val Thr Asn Ala Trp Asp Ala Met Val Tyr Asp
85 90 95

Ala Ala Gly Asp His Ile Leu Met Gln Ala Val Ser Asp Val Ala Ser
100 105 110

Phe Thr Ser Gln Asn Arg Ser Val Leu Asp Gly His Asp Pro Cys Pro
115 120 125

Ala Leu Lys Ile Tyr Lys Asn Asn Val Asp Gly Lys Gly Ala Ser Tyr
130 135 140

Gly Phe His Glu Asn Tyr Leu Tyr Ser Arg Glu Thr Asp Phe Asp Val
145 150 155 160

Leu Ala Gln Ala Leu Ile Pro Phe Phe Val Cys Arg Gln Val Ile Ile
165 170 175

Gly Ala Gly Arg Val
180

<210> 517
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(543)
<223> FRXA01153

<400> 517
ccg ttt tta agc ccg atc gtt act tcc acg cac gcg gtg gtg gcg tat 48
Pro Phe Leu Ser Pro Ile Val Thr Ser Thr His Ala Val Val Ala Tyr
1 5 10 15

tcc acc gcg cgt gga ttt ggt gag cac cgg gtg cgt tgg gac tat gcg 96
Ser Thr Ala Arg Gly Phe Gly Glu His Arg Val Arg Trp Asp Tyr Ala
20 25 30

caa gag tcc cca ctg cgc gat act cgt ggc ttt gat ctg cgc cga tac 144
Gln Glu Ser Pro Leu Arg Asp Thr Arg Gly Phe Asp Leu Arg Arg Tyr
35 40 45

```
cac cag gcc cct gtg gtg gat ccg cac gcc att ggt gtg gcc aac gtg   192
His Gln Ala Pro Val Val Asp Pro His Ala Ile Gly Val Ala Asn Val
     50                  55                  60

ttt gtg ccc aat ggt gcc agg ttt tat gtc gat cac gcg cac ccg gaa   240
Phe Val Pro Asn Gly Ala Arg Phe Tyr Val Asp His Ala His Pro Glu
 65                  70                  75                  80

tac tcc tcc cca gag gtc acc aat gcg tgg gat gcc atg gtt tac gac   288
Tyr Ser Ser Pro Glu Val Thr Asn Ala Trp Asp Ala Met Val Tyr Asp
                85                  90                  95

gcc gct ggt gac cac atc ctt atg cag gcc gtc tct gat gtt gcg agt   336
Ala Ala Gly Asp His Ile Leu Met Gln Ala Val Ser Asp Val Ala Ser
            100                 105                 110

ttc acc agc cag aat agg tct gtg ttg gac ggc cat gat ccg tgt cca   384
Phe Thr Ser Gln Asn Arg Ser Val Leu Asp Gly His Asp Pro Cys Pro
        115                 120                 125

gct ttg aaa atc tac aaa aac aat gtc gac ggt aag ggt gct agc tac   432
Ala Leu Lys Ile Tyr Lys Asn Asn Val Asp Gly Lys Gly Ala Ser Tyr
    130                 135                 140

ggg ttc cac gag aat tac ctc tac tca cgt gag acg gat ttt gat gtg   480
Gly Phe His Glu Asn Tyr Leu Tyr Ser Arg Glu Thr Asp Phe Asp Val
145                 150                 155                 160

ctg gct cag gca ttg atc cca ttt ttt gtg tgc cgg cag gtc atc atc   528
Leu Ala Gln Ala Leu Ile Pro Phe Phe Val Cys Arg Gln Val Ile Ile
                165                 170                 175

ggt gcc gga cgt gtg                                              543
Gly Ala Gly Arg Val
            180
```

09605.0009.00000 # 09605.0009.00000

<210> 518
<211> 181
<212> PRT
<213> Corynebacterium glutamicum

<400> 518

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Pro Phe Leu Ser Pro Ile Val Thr Ser Thr His Ala Val Val Ala Tyr
  1               5                  10                  15

Ser Thr Ala Arg Gly Phe Gly Glu His Arg Val Arg Trp Asp Tyr Ala
             20                  25                  30

Gln Glu Ser Pro Leu Arg Asp Thr Arg Gly Phe Asp Leu Arg Arg Tyr
         35                  40                  45

His Gln Ala Pro Val Val Asp Pro His Ala Ile Gly Val Ala Asn Val
     50                  55                  60

Phe Val Pro Asn Gly Ala Arg Phe Tyr Val Asp His Ala His Pro Glu
 65                  70                  75                  80

Tyr Ser Ser Pro Glu Val Thr Asn Ala Trp Asp Ala Met Val Tyr Asp
                85                  90                  95
```

```
Ala Ala Gly Asp His Ile Leu Met Gln Ala Val Ser Asp Val Ala Ser
            100                 105                 110

Phe Thr Ser Gln Asn Arg Ser Val Leu Asp Gly His Asp Pro Cys Pro
        115                 120                 125

Ala Leu Lys Ile Tyr Lys Asn Asn Val Asp Gly Lys Gly Ala Ser Tyr
    130                 135                 140

Gly Phe His Glu Asn Tyr Leu Tyr Ser Arg Glu Thr Asp Phe Asp Val
145                 150                 155                 160

Leu Ala Gln Ala Leu Ile Pro Phe Phe Val Cys Arg Gln Val Ile Ile
                165                 170                 175

Gly Ala Gly Arg Val
            180
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<210> 519
<211> 677
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (39)..(677)
<223> RXN01154

<400> 519

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ccggggaatt ccaggtcagt cagcgagcct gactaccattg agc aag aaa att tca  56
                                              Leu Ser Lys Lys Ile Ser
                                                1               5

ctg gaa acc aca ctc aac cgc ggc att atc aac acc cgc gat gaa cca   104
Leu Glu Thr Thr Leu Asn Arg Gly Ile Ile Asn Thr Arg Asp Glu Pro
            10                  15                  20

cac acc gac gct gat cac tgg ggt cgc ctg cac gtg atc atc ggc gat   152
His Thr Asp Ala Asp His Trp Gly Arg Leu His Val Ile Ile Gly Asp
        25                  30                  35

gcc aac atg tcg cag act gcg aat ttc ctc aaa ttc ggc atg acc tcc   200
Ala Asn Met Ser Gln Thr Ala Asn Phe Leu Lys Phe Gly Met Thr Ser
    40                  45                  50

cta gtg ctg gat gcc att gag gct ggg gtg gat ttc tct gaa ctc aag   248
Leu Val Leu Asp Ala Ile Glu Ala Gly Val Asp Phe Ser Glu Leu Lys
55                  60                  65                  70

ctg aag aac gca gtg agt gaa gta gca aag gtc tcc cat gat ctt tcc   296
Leu Lys Asn Ala Val Ser Glu Val Ala Lys Val Ser His Asp Leu Ser
                75                  80                  85

ctt acc cac cag ctg cga ttg gcg gat ggt tca gag ctc acc gct att   344
Leu Thr His Gln Leu Arg Leu Ala Asp Gly Ser Glu Leu Thr Ala Ile
            90                  95                  100

gat att ctg cgc cgc tat ttg gac aag gtg cag ccg ttt gca gaa acc   392
Asp Ile Leu Arg Arg Tyr Leu Asp Lys Val Gln Pro Phe Ala Glu Thr
```

```
        105                 110                 115

cca gtg gaa cag cgt gtc act gcg ctg tgg ggt gaa gtg ctg ggg ctc   440
Pro Val Glu Gln Arg Val Thr Ala Leu Trp Gly Glu Val Leu Gly Leu
    120                 125                 130

ctg gag aat gat ctg ctc tcc acc agc cat ctc ctt gat tgg act gca   488
Leu Glu Asn Asp Leu Leu Ser Thr Ser His Leu Leu Asp Trp Thr Ala
135                 140                 145                 150

aaa ctt gcc ctg atc aag tct ttt gag gcg cgt ggg ctg tcc att aac   536
Lys Leu Ala Leu Ile Lys Ser Phe Glu Ala Arg Gly Leu Ser Ile Asn
                155                 160                 165

gat ccc aag atg tac ctc att gac ctg cag tac agc gat att gat cca   584
Asp Pro Lys Met Tyr Leu Ile Asp Leu Gln Tyr Ser Asp Ile Asp Pro
            170                 175                 180

cag aag agt ctg tat cac gca ctg gta tcc aag ggg cgg atg aaa aca   632
Gln Lys Ser Leu Tyr His Ala Leu Val Ser Lys Gly Arg Met Lys Thr
        185                 190                 195

ctg tgc agt gcg cag gac att gca gat gca gcg gcc act tca ccg       677
Leu Cys Ser Ala Gln Asp Ile Ala Asp Ala Ala Ala Thr Ser Pro
    200                 205                 210


<210> 520
<211> 213
<212> PRT
<213> Corynebacterium glutamicum

<400> 520
Leu Ser Lys Lys Ile Ser Leu Glu Thr Thr Leu Asn Arg Gly Ile Ile
  1               5                  10                  15

Asn Thr Arg Asp Glu Pro His Thr Asp Ala Asp His Trp Gly Arg Leu
             20                  25                  30

His Val Ile Ile Gly Asp Ala Asn Met Ser Gln Thr Ala Asn Phe Leu
         35                  40                  45

Lys Phe Gly Met Thr Ser Leu Val Leu Asp Ala Ile Glu Ala Gly Val
     50                  55                  60

Asp Phe Ser Glu Leu Lys Leu Lys Asn Ala Val Ser Glu Val Ala Lys
 65                  70                  75                  80

Val Ser His Asp Leu Ser Leu Thr His Gln Leu Arg Leu Ala Asp Gly
                 85                  90                  95

Ser Glu Leu Thr Ala Ile Asp Ile Leu Arg Arg Tyr Leu Asp Lys Val
            100                 105                 110

Gln Pro Phe Ala Glu Thr Pro Val Glu Gln Arg Val Thr Ala Leu Trp
        115                 120                 125

Gly Glu Val Leu Gly Leu Leu Glu Asn Asp Leu Leu Ser Thr Ser His
    130                 135                 140

Leu Leu Asp Trp Thr Ala Lys Leu Ala Leu Ile Lys Ser Phe Glu Ala
```

```
145                 150                 155                 160

Arg Gly Leu Ser Ile Asn Asp Pro Lys Met Tyr Leu Ile Asp Leu Gln
                165                 170                 175

Tyr Ser Asp Ile Asp Pro Gln Lys Ser Leu Tyr His Ala Leu Val Ser
            180                 185                 190

Lys Gly Arg Met Lys Thr Leu Cys Ser Ala Gln Asp Ile Ala Asp Ala
        195                 200                 205

Ala Ala Thr Ser Pro
    210
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<210> 521
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(603)
<223> FRXA01154

<400> 521

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gag ggc att atc aac acc cgc gat gaa cca cac acc gac gct gat cac   48
Glu Gly Ile Ile Asn Thr Arg Asp Glu Pro His Thr Asp Ala Asp His
  1               5                  10                  15

tgg ggt cgc ctg cac gtg atc atc ggc gat gcc aac atg tcg cag act   96
Trp Gly Arg Leu His Val Ile Ile Gly Asp Ala Asn Met Ser Gln Thr
             20                  25                  30

gcg aat ttc ctc aaa ttc ggc atg acc tcc cta gtg ctg gat gcc att  144
Ala Asn Phe Leu Lys Phe Gly Met Thr Ser Leu Val Leu Asp Ala Ile
         35                  40                  45

gag gct ggg gtg gat ttc tct gaa ctc aag ctg aag aac gca gtg agt  192
Glu Ala Gly Val Asp Phe Ser Glu Leu Lys Leu Lys Asn Ala Val Ser
     50                  55                  60

gaa gta gca aag gtc tcc cat gat ctt tcc ctt acc cac cag ctg cga  240
Glu Val Ala Lys Val Ser His Asp Leu Ser Leu Thr His Gln Leu Arg
 65                  70                  75                  80

ttg gcg gat ggt tca gag ctc acc gct att gat att ctg cgc cgc tat  288
Leu Ala Asp Gly Ser Glu Leu Thr Ala Ile Asp Ile Leu Arg Arg Tyr
                 85                  90                  95

ttg gac aag gtg cag ccg ttt gca gaa acc cca gtg gaa cag cgt gtc  336
Leu Asp Lys Val Gln Pro Phe Ala Glu Thr Pro Val Glu Gln Arg Val
            100                 105                 110

act gcg ctg tgg ggt gaa gtg ctg ggg ctc ctg gag aat gat ctg ctc  384
Thr Ala Leu Trp Gly Glu Val Leu Gly Leu Leu Glu Asn Asp Leu Leu
        115                 120                 125

tcc acc agc cat ctc ctt gat tgg act gca aaa ctt gcc ctg atc aag  432
Ser Thr Ser His Leu Leu Asp Trp Thr Ala Lys Leu Ala Leu Ile Lys
    130                 135                 140
```

```
tct ttt gag gcg cgt ggg ctg tcc att aac gat ccc aag atg tac ctc   480
Ser Phe Glu Ala Arg Gly Leu Ser Ile Asn Asp Pro Lys Met Tyr Leu
145                 150                 155                 160

att gac ctg cag tac agc gat att gat cca cag aag agt ctg tat cac   528
Ile Asp Leu Gln Tyr Ser Asp Ile Asp Pro Gln Lys Ser Leu Tyr His
                165                 170                 175

gca ctg gta tcc aag ggg cgg atg aaa aca ctg tgc agt gcg cag gac   576
Ala Leu Val Ser Lys Gly Arg Met Lys Thr Leu Cys Ser Ala Gln Asp
            180                 185                 190

att gca gat gca gcg gcc act tca ccg                               603
Ile Ala Asp Ala Ala Ala Thr Ser Pro
        195                 200
```

<210> 522
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 522

```
Glu Gly Ile Ile Asn Thr Arg Asp Glu Pro His Thr Asp Ala Asp His
  1               5                  10                  15

Trp Gly Arg Leu His Val Ile Ile Gly Asp Ala Asn Met Ser Gln Thr
             20                  25                  30

Ala Asn Phe Leu Lys Phe Gly Met Thr Ser Leu Val Leu Asp Ala Ile
         35                  40                  45

Glu Ala Gly Val Asp Phe Ser Glu Leu Lys Leu Lys Asn Ala Val Ser
     50                  55                  60

Glu Val Ala Lys Val Ser His Asp Leu Ser Leu Thr His Gln Leu Arg
 65                  70                  75                  80

Leu Ala Asp Gly Ser Glu Leu Thr Ala Ile Asp Ile Leu Arg Arg Tyr
                 85                  90                  95

Leu Asp Lys Val Gln Pro Phe Ala Glu Thr Pro Val Glu Gln Arg Val
            100                 105                 110

Thr Ala Leu Trp Gly Glu Val Leu Gly Leu Leu Glu Asn Asp Leu Leu
        115                 120                 125

Ser Thr Ser His Leu Leu Asp Trp Thr Ala Lys Leu Ala Leu Ile Lys
    130                 135                 140

Ser Phe Glu Ala Arg Gly Leu Ser Ile Asn Asp Pro Lys Met Tyr Leu
145                 150                 155                 160

Ile Asp Leu Gln Tyr Ser Asp Ile Asp Pro Gln Lys Ser Leu Tyr His
                165                 170                 175

Ala Leu Val Ser Lys Gly Arg Met Lys Thr Leu Cys Ser Ala Gln Asp
            180                 185                 190

Ile Ala Asp Ala Ala Ala Thr Ser Pro
```

195 200

<210> 523
<211> 1570
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1570)
<223> RXN01155

<400> 523
acagcttgct ggatgaaatc gacggactgt tggaaaacaa cgccgaggaa ttcgttcgtt 60

cctatgtaca aaagggtggc gaatagtcac tgtgagtacc gtg gaa tcc gca ttg 115
Val Glu Ser Ala Leu
1 5

acc cgc agg atc atg ggc att gaa acg gag tat ggc ctc acc ttt gtt 163
Thr Arg Arg Ile Met Gly Ile Glu Thr Glu Tyr Gly Leu Thr Phe Val
10 15 20

gat ggt gat tcc aaa aag ctt cgc cca gat gag ata gct cga agg atg 211
Asp Gly Asp Ser Lys Lys Leu Arg Pro Asp Glu Ile Ala Arg Arg Met
25 30 35

ttt cgt ccc atc gtg gag aaa tat tcc agc tct aat atc ttc ata ccc 259
Phe Arg Pro Ile Val Glu Lys Tyr Ser Ser Ser Asn Ile Phe Ile Pro
40 45 50

aat ggt tcc cgg ttg tat ctt gat gtg ggt tcc cac ccg gag tac gcc 307
Asn Gly Ser Arg Leu Tyr Leu Asp Val Gly Ser His Pro Glu Tyr Ala
55 60 65

acc gcc gag tgt gat aat ttg acc cag ctg atc aat ttt gaa aaa gct 355
Thr Ala Glu Cys Asp Asn Leu Thr Gln Leu Ile Asn Phe Glu Lys Ala
70 75 80 85

ggc gat gtt att gca gat cgc atg gct gta gat gcc gaa gag tcg ctg 403
Gly Asp Val Ile Ala Asp Arg Met Ala Val Asp Ala Glu Glu Ser Leu
90 95 100

gcg aaa gaa gac att gct ggg cag gtg tac ctg ttt aaa aac aat gtc 451
Ala Lys Glu Asp Ile Ala Gly Gln Val Tyr Leu Phe Lys Asn Asn Val
105 110 115

gat tcc gtg ggc aat tct tat ggc tgc cac gaa aac tac ctt gtg ggt 499
Asp Ser Val Gly Asn Ser Tyr Gly Cys His Glu Asn Tyr Leu Val Gly
120 125 130

cgc tcc atg ccg ttg aag gcg ttg ggt aaa agg ctg atg ccg ttt ctg 547
Arg Ser Met Pro Leu Lys Ala Leu Gly Lys Arg Leu Met Pro Phe Leu
135 140 145

att acc cgc cag ctc atc tgc ggc gcc ggc agg atc cat cac ccc aat 595
Ile Thr Arg Gln Leu Ile Cys Gly Ala Gly Arg Ile His His Pro Asn
150 155 160 165

cct ttg gat aaa ggc gaa tcc ttc ccc ttg ggc tac tgc ata tcc cag 643

```
Pro Leu Asp Lys Gly Glu Ser Phe Pro Leu Gly Tyr Cys Ile Ser Gln
                170                 175                 180

cgc tct gac cac gtg tgg gag ggc gta tca agt gcc acc act aga tca   691
Arg Ser Asp His Val Trp Glu Gly Val Ser Ser Ala Thr Thr Arg Ser
            185                 190                 195

cgc ccc att atc aac acc cgt gat gag cca cat gcg gat tcc cat tct   739
Arg Pro Ile Ile Asn Thr Arg Asp Glu Pro His Ala Asp Ser His Ser
        200                 205                 210

tac cgc agg ctg cac gtg att gtg ggt gat gcc aac atg gca gag ccc   787
Tyr Arg Arg Leu His Val Ile Val Gly Asp Ala Asn Met Ala Glu Pro
    215                 220                 225

agc atc gcg ttg aag gtc ggc tcc acg ttg ctg gtt ctg gaa atg att   835
Ser Ile Ala Leu Lys Val Gly Ser Thr Leu Leu Val Leu Glu Met Ile
230                 235                 240                 245

gag gca gat ttc ggt ttg ccc agc tta gag ctt gcc aat gat att gcc   883
Glu Ala Asp Phe Gly Leu Pro Ser Leu Glu Leu Ala Asn Asp Ile Ala
                250                 255                 260

tca att agg gaa atc tcc cgc gat gca aca gga tcc aca ctg ttg tcc   931
Ser Ile Arg Glu Ile Ser Arg Asp Ala Thr Gly Ser Thr Leu Leu Ser
            265                 270                 275

ctg aaa gat ggc acc acc atg act gcc ttg cag atc cag cag gtg gtc   979
Leu Lys Asp Gly Thr Thr Met Thr Ala Leu Gln Ile Gln Gln Val Val
        280                 285                 290

ttt gag cat gcc tcg aag tgg ttg gag cag cgc ccc gaa cca gaa ttt   1027
Phe Glu His Ala Ser Lys Trp Leu Glu Gln Arg Pro Glu Pro Glu Phe
    295                 300                 305

tct ggc acc tcc aac aca gag atg gcc cgc gtg ctg gat ctg tgg ggt   1075
Ser Gly Thr Ser Asn Thr Glu Met Ala Arg Val Leu Asp Leu Trp Gly
310                 315                 320                 325

cgc atg ttg aaa gcg att gag tcc ggt gat ttc agc gaa gtg gat aca   1123
Arg Met Leu Lys Ala Ile Glu Ser Gly Asp Phe Ser Glu Val Asp Thr
                330                 335                 340

gaa att gac tgg gtg atc aaa aag aag ctc att gat cgt ttc att cag   1171
Glu Ile Asp Trp Val Ile Lys Lys Lys Leu Ile Asp Arg Phe Ile Gln
            345                 350                 355

cgc ggc aac ctt ggg ttg gat gat cca aaa ctt gcc caa gtg gac ttg   1219
Arg Gly Asn Leu Gly Leu Asp Asp Pro Lys Leu Ala Gln Val Asp Leu
        360                 365                 370

act tat cac gat att agg cca ggt aga ggc cta ttt agc gtg ctg caa   1267
Thr Tyr His Asp Ile Arg Pro Gly Arg Gly Leu Phe Ser Val Leu Gln
    375                 380                 385

agc cgc ggc atg atc aaa cgg tgg act act gat gag gcg att tta gct   1315
Ser Arg Gly Met Ile Lys Arg Trp Thr Thr Asp Glu Ala Ile Leu Ala
390                 395                 400                 405

gcg gtg gat acc gct cct gat aca aca cgt gct cat ttg cgc ggg cga   1363
Ala Val Asp Thr Ala Pro Asp Thr Thr Arg Ala His Leu Arg Gly Arg
```

```
                410                 415                 420

atc ctt aaa gcg gcg gat act ctg gga gta cct gtg act gtc gat tgg   1411
Ile Leu Lys Ala Ala Asp Thr Leu Gly Val Pro Val Thr Val Asp Trp
            425                 430                 435

atg cgt cac aag gtc aac cga ccg gag cca caa tcg gtg gaa ttg ggg   1459
Met Arg His Lys Val Asn Arg Pro Glu Pro Gln Ser Val Glu Leu Gly
        440                 445                 450

gat cct ttt tcc ctt tta aat cct caa caa cca gcc caa gaa act gct   1507
Asp Pro Phe Ser Leu Leu Asn Pro Gln Gln Pro Ala Gln Glu Thr Ala
    455                 460                 465

ttg agc att ctt ctc cta ggc gga acc tct tac att gcc ggt gag att   1555
Leu Ser Ile Leu Leu Leu Gly Gly Thr Ser Tyr Ile Ala Gly Glu Ile
470                 475                 480                 485

gcc acg ttg acg ttt                                               1570
Ala Thr Leu Thr Phe
                490
```

<210> 524
<211> 490
<212> PRT
<213> Corynebacterium glutamicum

<400> 524

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Val Glu Ser Ala Leu Thr Arg Arg Ile Met Gly Ile Glu Thr Glu Tyr
  1               5                  10                  15

Gly Leu Thr Phe Val Asp Gly Asp Ser Lys Lys Leu Arg Pro Asp Glu
             20                  25                  30

Ile Ala Arg Arg Met Phe Arg Pro Ile Val Glu Lys Tyr Ser Ser Ser
         35                  40                  45

Asn Ile Phe Ile Pro Asn Gly Ser Arg Leu Tyr Leu Asp Val Gly Ser
     50                  55                  60

His Pro Glu Tyr Ala Thr Ala Glu Cys Asp Asn Leu Thr Gln Leu Ile
 65                  70                  75                  80

Asn Phe Glu Lys Ala Gly Asp Val Ile Ala Asp Arg Met Ala Val Asp
                 85                  90                  95

Ala Glu Glu Ser Leu Ala Lys Glu Asp Ile Ala Gly Gln Val Tyr Leu
            100                 105                 110

Phe Lys Asn Asn Val Asp Ser Val Gly Asn Ser Tyr Gly Cys His Glu
        115                 120                 125

Asn Tyr Leu Val Gly Arg Ser Met Pro Leu Lys Ala Leu Gly Lys Arg
    130                 135                 140

Leu Met Pro Phe Leu Ile Thr Arg Gln Leu Ile Cys Gly Ala Gly Arg
145                 150                 155                 160

Ile His His Pro Asn Pro Leu Asp Lys Gly Glu Ser Phe Pro Leu Gly
                165                 170                 175
```

```
Tyr Cys Ile Ser Gln Arg Ser Asp His Val Trp Glu Gly Val Ser Ser
            180                 185                 190

Ala Thr Thr Arg Ser Arg Pro Ile Ile Asn Thr Arg Asp Glu Pro His
        195                 200                 205

Ala Asp Ser His Ser Tyr Arg Arg Leu His Val Ile Val Gly Asp Ala
    210                 215                 220

Asn Met Ala Glu Pro Ser Ile Ala Leu Lys Val Gly Ser Thr Leu Leu
225                 230                 235                 240

Val Leu Glu Met Ile Glu Ala Asp Phe Gly Leu Pro Ser Leu Glu Leu
                245                 250                 255

Ala Asn Asp Ile Ala Ser Ile Arg Glu Ile Ser Arg Asp Ala Thr Gly
            260                 265                 270

Ser Thr Leu Leu Ser Leu Lys Asp Gly Thr Thr Met Thr Ala Leu Gln
        275                 280                 285

Ile Gln Gln Val Val Phe Glu His Ala Ser Lys Trp Leu Glu Gln Arg
    290                 295                 300

Pro Glu Pro Glu Phe Ser Gly Thr Ser Asn Thr Glu Met Ala Arg Val
305                 310                 315                 320

Leu Asp Leu Trp Gly Arg Met Leu Lys Ala Ile Glu Ser Gly Asp Phe
                325                 330                 335

Ser Glu Val Asp Thr Glu Ile Asp Trp Val Ile Lys Lys Lys Leu Ile
            340                 345                 350

Asp Arg Phe Ile Gln Arg Gly Asn Leu Gly Leu Asp Asp Pro Lys Leu
        355                 360                 365

Ala Gln Val Asp Leu Thr Tyr His Asp Ile Arg Pro Gly Arg Gly Leu
    370                 375                 380

Phe Ser Val Leu Gln Ser Arg Gly Met Ile Lys Arg Trp Thr Thr Asp
385                 390                 395                 400

Glu Ala Ile Leu Ala Ala Val Asp Thr Ala Pro Asp Thr Thr Arg Ala
                405                 410                 415

His Leu Arg Gly Arg Ile Leu Lys Ala Ala Asp Thr Leu Gly Val Pro
            420                 425                 430

Val Thr Val Asp Trp Met Arg His Lys Val Asn Arg Pro Glu Pro Gln
        435                 440                 445

Ser Val Glu Leu Gly Asp Pro Phe Ser Leu Leu Asn Pro Gln Gln Pro
    450                 455                 460

Ala Gln Glu Thr Ala Leu Ser Ile Leu Leu Leu Gly Gly Thr Ser Tyr
465                 470                 475                 480

Ile Ala Gly Glu Ile Ala Thr Leu Thr Phe
                485                 490
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<210> 525
<211> 1465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1465)
<223> FRXA01155

<400> 525
acagcttgct ggatgaaatc gacggactgt tggaaaacaa cgccgaggaa ttcgttcgtt 60

cctatgtaca aaagggtggc gaatagtcac tgtgagtacc gtg gaa tcc gca ttg 115
Val Glu Ser Ala Leu
1 5

acc cgc agg atc atg ggc att gaa acg gag tat ggc ctc acc ttt gtt 163
Thr Arg Arg Ile Met Gly Ile Glu Thr Glu Tyr Gly Leu Thr Phe Val
10 15 20

gat ggt gat tcc aaa aag ctt cgc cca gat gag ata gct cga agg atg 211
Asp Gly Asp Ser Lys Lys Leu Arg Pro Asp Glu Ile Ala Arg Arg Met
25 30 35

ttt cgt ccc atc gtg gag aaa tat tcc agc tct aat atc ttc ata ccc 259
Phe Arg Pro Ile Val Glu Lys Tyr Ser Ser Ser Asn Ile Phe Ile Pro
40 45 50

aat ggt tcc cgg ttg tat ctt gat gtg ggt tcc cac ccg gag tac gcc 307
Asn Gly Ser Arg Leu Tyr Leu Asp Val Gly Ser His Pro Glu Tyr Ala
55 60 65

acc gcc gag tgt gat aat ttg acc cag ctg atc aat ttt gaa aaa gct 355
Thr Ala Glu Cys Asp Asn Leu Thr Gln Leu Ile Asn Phe Glu Lys Ala
70 75 80 85

ggc gat gtt att gca gat cgc atg gct gta gat gcc gaa gag tcg ctg 403
Gly Asp Val Ile Ala Asp Arg Met Ala Val Asp Ala Glu Glu Ser Leu
90 95 100

gcg aaa gaa gac att gct ggg cag gtg tac ctg ttt aaa aac aat gtc 451
Ala Lys Glu Asp Ile Ala Gly Gln Val Tyr Leu Phe Lys Asn Asn Val
105 110 115

gat tcc gtg ggc aat tct tat ggc tgc cac gaa aac tac ctt gtg ggt 499
Asp Ser Val Gly Asn Ser Tyr Gly Cys His Glu Asn Tyr Leu Val Gly
120 125 130

cgc tcc atg ccg ttg aag gcg ttg ggt aaa agg ctg atg ccg ttt ctg 547
Arg Ser Met Pro Leu Lys Ala Leu Gly Lys Arg Leu Met Pro Phe Leu
135 140 145

att acc cgc cag ctc atc tgc ggc gcc ggc agg atc cat cac ccc aat 595
Ile Thr Arg Gln Leu Ile Cys Gly Ala Gly Arg Ile His His Pro Asn
150 155 160 165

cct ttg gat aaa ggc gaa tcc ttc ccc ttg ggc tac tgc ata tcc cag 643
Pro Leu Asp Lys Gly Glu Ser Phe Pro Leu Gly Tyr Cys Ile Ser Gln
170 175 180

```
cgc tct gac cac gtg tgg gag ggc gta tca agt gcc acc act aga tca   691
Arg Ser Asp His Val Trp Glu Gly Val Ser Ser Ala Thr Thr Arg Ser
            185                 190                 195

cgc ccc att atc aac acc cgt gat gag cca cat gcg gat tcc cat tct   739
Arg Pro Ile Ile Asn Thr Arg Asp Glu Pro His Ala Asp Ser His Ser
        200                 205                 210

tac cgc agg ctg cac gtg att gtg ggt gat gcc aac atg gca gag ccc   787
Tyr Arg Arg Leu His Val Ile Val Gly Asp Ala Asn Met Ala Glu Pro
    215                 220                 225

agc atc gcg ttg aag gtc ggc tcc acg ttg ctg gtt ctg gaa atg att   835
Ser Ile Ala Leu Lys Val Gly Ser Thr Leu Leu Val Leu Glu Met Ile
230                 235                 240                 245

gag gca gat ttc ggt ttg ccc agc tta gag ctt gcc aat gat att gcc   883
Glu Ala Asp Phe Gly Leu Pro Ser Leu Glu Leu Ala Asn Asp Ile Ala
                250                 255                 260

tca att agg gaa atc tcc cgc gat gca aca gga tcc aca ctg ttg tcc   931
Ser Ile Arg Glu Ile Ser Arg Asp Ala Thr Gly Ser Thr Leu Leu Ser
            265                 270                 275

ctg aaa gat ggc acc acc atg act gcc ttg cag atc cag cag gtg gtc   979
Leu Lys Asp Gly Thr Thr Met Thr Ala Leu Gln Ile Gln Gln Val Val
        280                 285                 290

ttt gag cat gcc tcg aag tgg ttg gag cag cgc ccc gaa cca gaa ttt   1027
Phe Glu His Ala Ser Lys Trp Leu Glu Gln Arg Pro Glu Pro Glu Phe
    295                 300                 305

tct ggc acc tcc aac aca gag atg gcc cgc gtg ctg gat ctg tgg ggt   1075
Ser Gly Thr Ser Asn Thr Glu Met Ala Arg Val Leu Asp Leu Trp Gly
310                 315                 320                 325

cgc atg ttg aaa gcg att gag tcc ggt gat ttc agc gaa gtg gat aca   1123
Arg Met Leu Lys Ala Ile Glu Ser Gly Asp Phe Ser Glu Val Asp Thr
                330                 335                 340

gaa att gac tgg gtg atc aaa aag aag ctc att gat cgt ttc att cag   1171
Glu Ile Asp Trp Val Ile Lys Lys Lys Leu Ile Asp Arg Phe Ile Gln
            345                 350                 355

cgc ggc aac ctt ggg ttg gat gat cca aaa ctt gcc caa gtg gac ttg   1219
Arg Gly Asn Leu Gly Leu Asp Asp Pro Lys Leu Ala Gln Val Asp Leu
        360                 365                 370

act tat cac gat att agg cca ggt aga ggc cta ttt agc gtg ctg caa   1267
Thr Tyr His Asp Ile Arg Pro Gly Arg Gly Leu Phe Ser Val Leu Gln
    375                 380                 385

agc cgc ggc atg atc aaa cgg tgg act act gat gag gcg att tta gct   1315
Ser Arg Gly Met Ile Lys Arg Trp Thr Thr Asp Glu Ala Ile Leu Ala
390                 395                 400                 405

gcg gtg gat acc gct cct gat aca aca cgt gct cat ttg cgc ggg cga   1363
Ala Val Asp Thr Ala Pro Asp Thr Thr Arg Ala His Leu Arg Gly Arg
                410                 415                 420
```

```
atc ctt aaa gcg gcg gat act ctg gga gta cct gtg act gtc gat tgg   1411
Ile Leu Lys Ala Ala Asp Thr Leu Gly Val Pro Val Thr Val Asp Trp
            425                 430                 435

atg cgt cac aag gtc aac cga ccg gag cca caa tcg gtg gaa ttg ggg   1459
Met Arg His Lys Val Asn Arg Pro Glu Pro Gln Ser Val Glu Leu Gly
        440                 445                 450

gat cct                                                          1465
Asp Pro
    455
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<210> 526
<211> 455
<212> PRT
<213> Corynebacterium glutamicum

<400> 526

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Val Glu Ser Ala Leu Thr Arg Arg Ile Met Gly Ile Glu Thr Glu Tyr
  1               5                  10                  15

Gly Leu Thr Phe Val Asp Gly Asp Ser Lys Lys Leu Arg Pro Asp Glu
             20                  25                  30

Ile Ala Arg Arg Met Phe Arg Pro Ile Val Glu Lys Tyr Ser Ser Ser
         35                  40                  45

Asn Ile Phe Ile Pro Asn Gly Ser Arg Leu Tyr Leu Asp Val Gly Ser
     50                  55                  60

His Pro Glu Tyr Ala Thr Ala Glu Cys Asp Asn Leu Thr Gln Leu Ile
 65                  70                  75                  80

Asn Phe Glu Lys Ala Gly Asp Val Ile Ala Asp Arg Met Ala Val Asp
                 85                  90                  95

Ala Glu Glu Ser Leu Ala Lys Glu Asp Ile Ala Gly Gln Val Tyr Leu
            100                 105                 110

Phe Lys Asn Asn Val Asp Ser Val Gly Asn Ser Tyr Gly Cys His Glu
        115                 120                 125

Asn Tyr Leu Val Gly Arg Ser Met Pro Leu Lys Ala Leu Gly Lys Arg
    130                 135                 140

Leu Met Pro Phe Leu Ile Thr Arg Gln Leu Ile Cys Gly Ala Gly Arg
145                 150                 155                 160

Ile His His Pro Asn Pro Leu Asp Lys Gly Glu Ser Phe Pro Leu Gly
                165                 170                 175

Tyr Cys Ile Ser Gln Arg Ser Asp His Val Trp Glu Gly Val Ser Ser
            180                 185                 190

Ala Thr Thr Arg Ser Arg Pro Ile Ile Asn Thr Arg Asp Glu Pro His
        195                 200                 205

Ala Asp Ser His Ser Tyr Arg Arg Leu His Val Ile Val Gly Asp Ala
    210                 215                 220
```

```
Asn Met Ala Glu Pro Ser Ile Ala Leu Lys Val Gly Ser Thr Leu Leu
225                 230                 235                 240

Val Leu Glu Met Ile Glu Ala Asp Phe Gly Leu Pro Ser Leu Glu Leu
                245                 250                 255

Ala Asn Asp Ile Ala Ser Ile Arg Glu Ile Ser Arg Asp Ala Thr Gly
            260                 265                 270

Ser Thr Leu Leu Ser Leu Lys Asp Gly Thr Thr Met Thr Ala Leu Gln
        275                 280                 285

Ile Gln Gln Val Val Phe Glu His Ala Ser Lys Trp Leu Glu Gln Arg
    290                 295                 300

Pro Glu Pro Glu Phe Ser Gly Thr Ser Asn Thr Glu Met Ala Arg Val
305                 310                 315                 320

Leu Asp Leu Trp Gly Arg Met Leu Lys Ala Ile Glu Ser Gly Asp Phe
                325                 330                 335

Ser Glu Val Asp Thr Glu Ile Asp Trp Val Ile Lys Lys Lys Leu Ile
            340                 345                 350

Asp Arg Phe Ile Gln Arg Gly Asn Leu Gly Leu Asp Asp Pro Lys Leu
        355                 360                 365

Ala Gln Val Asp Leu Thr Tyr His Asp Ile Arg Pro Gly Arg Gly Leu
    370                 375                 380

Phe Ser Val Leu Gln Ser Arg Gly Met Ile Lys Arg Trp Thr Thr Asp
385                 390                 395                 400

Glu Ala Ile Leu Ala Ala Val Asp Thr Ala Pro Asp Thr Thr Arg Ala
                405                 410                 415

His Leu Arg Gly Arg Ile Leu Lys Ala Ala Asp Thr Leu Gly Val Pro
            420                 425                 430

Val Thr Val Asp Trp Met Arg His Lys Val Asn Arg Pro Glu Pro Gln
        435                 440                 445

Ser Val Glu Leu Gly Asp Pro
    450                 455


<210> 527
<211> 519
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(496)
<223> RXN01167

<400> 527
gtgtcgtttt atttgcacac tagcaggtaa actgtgtgag acgaattctt ttgcggcaac 60

ttggaggccg cattctagta ggcaaaggac tgatacctag atg gca gat cgc gtt   115
                                                Met Ala Asp Arg Val
```

```
                                                        1               5

ctt cgt ggc agc cgc atg ggc gcc gtg agc tat gag acg gat agg gac   163
Leu Arg Gly Ser Arg Met Gly Ala Val Ser Tyr Glu Thr Asp Arg Asp
                10                  15                  20

cac gat ctg gct cct cgc cag ctc gtg aag tac aag acc gca gac ggg   211
His Asp Leu Ala Pro Arg Gln Leu Val Lys Tyr Lys Thr Ala Asp Gly
            25                  30                  35

gaa atc tat gag gtt ccc ttc gct gat gat gcg gaa atc ccc gag gag   259
Glu Ile Tyr Glu Val Pro Phe Ala Asp Asp Ala Glu Ile Pro Glu Glu
        40                  45                  50

tgg atg tgc aag aac ggt aag cta ggc atc ctc atg gaa ggt gag gga   307
Trp Met Cys Lys Asn Gly Lys Leu Gly Ile Leu Met Glu Gly Glu Gly
    55                  60                  65

gtc gag tcc aag ccg gtc aag cct cca cgt act cac tgg gat atg ttg   355
Val Glu Ser Lys Pro Val Lys Pro Pro Arg Thr His Trp Asp Met Leu
70                  75                  80                  85

cgt gag cgt cgc tca att gaa gag ctg gat gtg ctg ctg gaa gag cgc   403
Arg Glu Arg Arg Ser Ile Glu Glu Leu Asp Val Leu Leu Glu Glu Arg
                90                  95                  100

atc gag gca ctt cgt aag cgt cgt cgc aat gca gcg aaa ctg ctg aag   451
Ile Glu Ala Leu Arg Lys Arg Arg Arg Asn Ala Ala Lys Leu Leu Lys
            105                 110                 115

gct cag caa gag gct gaa gaa gca gaa aag gca gct gaa gag gtt       496
Ala Gln Gln Glu Ala Glu Glu Ala Glu Lys Ala Ala Glu Glu Val
        120                 125                 130

taatcttcct gcctaagtta gaa                                       519


<210> 528
<211> 132
<212> PRT
<213> Corynebacterium glutamicum

<400> 528
Met Ala Asp Arg Val Leu Arg Gly Ser Arg Met Gly Ala Val Ser Tyr
  1               5                  10                  15

Glu Thr Asp Arg Asp His Asp Leu Ala Pro Arg Gln Leu Val Lys Tyr
            20                  25                  30

Lys Thr Ala Asp Gly Glu Ile Tyr Glu Val Pro Phe Ala Asp Asp Ala
        35                  40                  45

Glu Ile Pro Glu Glu Trp Met Cys Lys Asn Gly Lys Leu Gly Ile Leu
    50                  55                  60

Met Glu Gly Glu Gly Val Glu Ser Lys Pro Val Lys Pro Pro Arg Thr
65                  70                  75                  80

His Trp Asp Met Leu Arg Glu Arg Arg Ser Ile Glu Glu Leu Asp Val
                85                  90                  95
```

```
Leu Leu Glu Glu Arg Ile Glu Ala Leu Arg Lys Arg Arg Arg Asn Ala
            100                 105                 110

Ala Lys Leu Leu Lys Ala Gln Gln Glu Ala Glu Glu Ala Glu Lys Ala
        115                 120                 125

Ala Glu Glu Val
    130
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<210> 529
<211> 344
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(321)
<223> FRXA01167

<400> 529

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cct cgc cag ctc gtg aag tac aag acc gca gac ggg gaa atc tat gag   48
Pro Arg Gln Leu Val Lys Tyr Lys Thr Ala Asp Gly Glu Ile Tyr Glu
  1               5                  10                  15

gtt ccc ttc gct gat gat gcg gaa atc ccc gag gag tgg atg tgc aag   96
Val Pro Phe Ala Asp Asp Ala Glu Ile Pro Glu Glu Trp Met Cys Lys
             20                  25                  30

aac ggt aag cta ggc atc ctc atg gaa ggt gag gga gtc gag tcc aag   144
Asn Gly Lys Leu Gly Ile Leu Met Glu Gly Glu Gly Val Glu Ser Lys
         35                  40                  45

ccg gtc aag cct cca cgt act cac tgg gat atg ttg cgt gag cgt cgc   192
Pro Val Lys Pro Pro Arg Thr His Trp Asp Met Leu Arg Glu Arg Arg
     50                  55                  60

tca att gaa gag ctg gat gtg ctg ctg gaa gag cgc atc gag gca ctt   240
Ser Ile Glu Glu Leu Asp Val Leu Leu Glu Glu Arg Ile Glu Ala Leu
 65                  70                  75                  80

cgt aag cgt cgt cgc aat gca gcg aaa ctg ctg aag gct cag caa gag   288
Arg Lys Arg Arg Arg Asn Ala Ala Lys Leu Leu Lys Ala Gln Gln Glu
                 85                  90                  95

gct gaa gaa gca gaa aag gca gct gaa gag gtt taatcttcct gcctaagtta 341
Ala Glu Glu Ala Glu Lys Ala Ala Glu Glu Val
            100                 105

gaa                                                               344
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<210> 530
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

<400> 530

```
Pro Arg Gln Leu Val Lys Tyr Lys Thr Ala Asp Gly Glu Ile Tyr Glu
  1               5                  10                  15
```

```
Val Pro Phe Ala Asp Asp Ala Glu Ile Pro Glu Glu Trp Met Cys Lys
            20                  25                  30

Asn Gly Lys Leu Gly Ile Leu Met Glu Gly Glu Gly Val Glu Ser Lys
        35                  40                  45

Pro Val Lys Pro Pro Arg Thr His Trp Asp Met Leu Arg Glu Arg Arg
    50                  55                  60

Ser Ile Glu Glu Leu Asp Val Leu Leu Glu Glu Arg Ile Glu Ala Leu
65                  70                  75                  80

Arg Lys Arg Arg Arg Asn Ala Ala Lys Leu Leu Lys Ala Gln Gln Glu
                85                  90                  95

Ala Glu Glu Ala Glu Lys Ala Ala Glu Glu Val
            100                 105


<210> 531
<211> 1119
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1096)
<223> RXN01169

<400> 531
tcttgatcgg aatcggcgca aacatcgtct acgaacacct cagcgcgtaa ccctcggcgc 60

attatcctca gacagctttt agcgcaaaca aggagcatca ttg aaa cgg gtc gtt   115
                                            Leu Lys Arg Val Val
                                              1               5

gaa gcg tgg gat aga ttt caa atc cca ctg tat atc acg gct ctt atc   163
Glu Ala Trp Asp Arg Phe Gln Ile Pro Leu Tyr Ile Thr Ala Leu Ile
                10                  15                  20

gcc gga gca ctg gtg ggt ttg cag tgg cca ggc tct aca ggg ggt ttc   211
Ala Gly Ala Leu Val Gly Leu Gln Trp Pro Gly Ser Thr Gly Gly Phe
            25                  30                  35

gaa agc gcc att aac cca gcg tta atg gcg ctg ctt tat gcc act ttt   259
Glu Ser Ala Ile Asn Pro Ala Leu Met Ala Leu Leu Tyr Ala Thr Phe
        40                  45                  50

ctc ggt att ccg atc act cgg att ggt gca gcg ctg aaa gat ctg aga   307
Leu Gly Ile Pro Ile Thr Arg Ile Gly Ala Ala Leu Lys Asp Leu Arg
    55                  60                  65

ttt ctc ata gtg ctc atg tcc gtc aat ttt gtt gca gtg cct ctg gtg   355
Phe Leu Ile Val Leu Met Ser Val Asn Phe Val Ala Val Pro Leu Val
70                  75                  80                  85

gct ttt gcg ttg agc aga ttc att gcg ggt gat gag gcg ctt cta atc   403
Ala Phe Ala Leu Ser Arg Phe Ile Ala Gly Asp Glu Ala Leu Leu Ile
                90                  95                  100

gga ttt tta ctg gtg att ctc gcg ccg tgc att gat tac gtc att gtc   451
```

```
Gly Phe Leu Leu Val Ile Leu Ala Pro Cys Ile Asp Tyr Val Ile Val
            105                 110                 115

ttt gct ggt ttg gcc agg gcc gcc caa gac aag ctc ctt gcc gcc acg   499
Phe Ala Gly Leu Ala Arg Ala Ala Gln Asp Lys Leu Leu Ala Ala Thr
        120                 125                 130

cca ata tta atg ctt gtc caa atc ctg ctg atc ccc gtc ttc ctg gct   547
Pro Ile Leu Met Leu Val Gln Ile Leu Leu Ile Pro Val Phe Leu Ala
    135                 140                 145

gtt ttt gtg ggt tca gat gcc ctt ggc tca atc tct ttc ggc cca ttt   595
Val Phe Val Gly Ser Asp Ala Leu Gly Ser Ile Ser Phe Gly Pro Phe
150                 155                 160                 165

gta gaa gca ttt ttc ctc ctg att ctc att cca ctt gtt gct gct gcg   643
Val Glu Ala Phe Phe Leu Leu Ile Leu Ile Pro Leu Val Ala Ala Ala
                170                 175                 180

gga act cag caa gtg gca aga aag tgg cag gta gga cgt aca att atg   691
Gly Thr Gln Gln Val Ala Arg Lys Trp Gln Val Gly Arg Thr Ile Met
            185                 190                 195

gct gct gca gaa gca atc atg gtg cct tta atg atg ctg acg ttg ttc   739
Ala Ala Ala Glu Ala Ile Met Val Pro Leu Met Met Leu Thr Leu Phe
        200                 205                 210

gct gtc atc gca tcg caa gtg gaa gct gtg agt ggt caa ttc acc gat   787
Ala Val Ile Ala Ser Gln Val Glu Ala Val Ser Gly Gln Phe Thr Asp
    215                 220                 225

atc gcc aca gta gtg cca cta tat gtc gcc ttt ttg atg gtg atg att   835
Ile Ala Thr Val Val Pro Leu Tyr Val Ala Phe Leu Met Val Met Ile
230                 235                 240                 245

cca att ggt ggc ggg ata tcc aaa ctc ggt ggc tta ggt ttc aaa gag   883
Pro Ile Gly Gly Gly Ile Ser Lys Leu Gly Gly Leu Gly Phe Lys Glu
                250                 255                 260

caa cga gcc atc gtt ttt agc gga gca acc cgt aac tct ttg gtc gtt   931
Gln Arg Ala Ile Val Phe Ser Gly Ala Thr Arg Asn Ser Leu Val Val
            265                 270                 275

tta cct tta gcg tta gca ctt ccc gca ggc ctg gaa ata gcg gcc gtc   979
Leu Pro Leu Ala Leu Ala Leu Pro Ala Gly Leu Glu Ile Ala Ala Val
        280                 285                 290

gta gtt gtc act caa acc ctc gtg gaa ctg att ggc atg gtt gtc tac  1027
Val Val Val Thr Gln Thr Leu Val Glu Leu Ile Gly Met Val Val Tyr
    295                 300                 305

gtg cgc atc atc cct tta att ttc cat gaa aag cag aca tac agg aaa  1075
Val Arg Ile Ile Pro Leu Ile Phe His Glu Lys Gln Thr Tyr Arg Lys
310                 315                 320                 325

ctt tca ggc ata ggg gag tca tgaaacagaa cggcaagcta agg            1119
Leu Ser Gly Ile Gly Glu Ser
                330
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<210> 532

<211> 332
<212> PRT
<213> Corynebacterium glutamicum

<400> 532
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Leu Lys Arg Val Val Glu Ala Trp Asp Arg Phe Gln Ile Pro Leu Tyr
  1               5                  10                  15

Ile Thr Ala Leu Ile Ala Gly Ala Leu Val Gly Leu Gln Trp Pro Gly
             20                  25                  30

Ser Thr Gly Gly Phe Glu Ser Ala Ile Asn Pro Ala Leu Met Ala Leu
         35                  40                  45

Leu Tyr Ala Thr Phe Leu Gly Ile Pro Ile Thr Arg Ile Gly Ala Ala
     50                  55                  60

Leu Lys Asp Leu Arg Phe Leu Ile Val Leu Met Ser Val Asn Phe Val
 65                  70                  75                  80

Ala Val Pro Leu Val Ala Phe Ala Leu Ser Arg Phe Ile Ala Gly Asp
                 85                  90                  95

Glu Ala Leu Leu Ile Gly Phe Leu Leu Val Ile Leu Ala Pro Cys Ile
            100                 105                 110

Asp Tyr Val Ile Val Phe Ala Gly Leu Ala Arg Ala Ala Gln Asp Lys
        115                 120                 125

Leu Leu Ala Ala Thr Pro Ile Leu Met Leu Val Gln Ile Leu Leu Ile
    130                 135                 140

Pro Val Phe Leu Ala Val Phe Val Gly Ser Asp Ala Leu Gly Ser Ile
145                 150                 155                 160

Ser Phe Gly Pro Phe Val Glu Ala Phe Phe Leu Leu Ile Leu Ile Pro
                165                 170                 175

Leu Val Ala Ala Ala Gly Thr Gln Gln Val Ala Arg Lys Trp Gln Val
            180                 185                 190

Gly Arg Thr Ile Met Ala Ala Ala Glu Ala Ile Met Val Pro Leu Met
        195                 200                 205

Met Leu Thr Leu Phe Ala Val Ile Ala Ser Gln Val Glu Ala Val Ser
    210                 215                 220

Gly Gln Phe Thr Asp Ile Ala Thr Val Val Pro Leu Tyr Val Ala Phe
225                 230                 235                 240

Leu Met Val Met Ile Pro Ile Gly Gly Gly Ile Ser Lys Leu Gly Gly
                245                 250                 255

Leu Gly Phe Lys Glu Gln Arg Ala Ile Val Phe Ser Gly Ala Thr Arg
            260                 265                 270

Asn Ser Leu Val Val Leu Pro Leu Ala Leu Ala Leu Pro Ala Gly Leu
        275                 280                 285

Glu Ile Ala Ala Val Val Val Val Thr Gln Thr Leu Val Glu Leu Ile
    290                 295                 300
```

```
Gly Met Val Val Tyr Val Arg Ile Ile Pro Leu Ile Phe His Glu Lys
305                 310                 315                 320

Gln Thr Tyr Arg Lys Leu Ser Gly Ile Gly Glu Ser
                325                 330
```

<210> 533
<211> 590
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(567)
<223> FRXA01169

<400> 533

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atc ccc gtc ttc ctg gct gtt ttt gtg ggt tca gat gcc ctt ggc tca   48
Ile Pro Val Phe Leu Ala Val Phe Val Gly Ser Asp Ala Leu Gly Ser
  1               5                  10                  15

atc tct ttc ggc cca ttt gta gaa gca ttt ttc ctc ctg att ctc att   96
Ile Ser Phe Gly Pro Phe Val Glu Ala Phe Phe Leu Leu Ile Leu Ile
             20                  25                  30

cca ctt gtt gct gct gcg gga act cag caa gtg gca aga aag tgg cag   144
Pro Leu Val Ala Ala Ala Gly Thr Gln Gln Val Ala Arg Lys Trp Gln
         35                  40                  45

gta gga cgt aca att atg gct gct gca gaa gca atc atg gtg cct tta   192
Val Gly Arg Thr Ile Met Ala Ala Ala Glu Ala Ile Met Val Pro Leu
     50                  55                  60

atg atg ctg acg ttg ttc gct gtc atc gca tcg caa gtg gaa gct gtg   240
Met Met Leu Thr Leu Phe Ala Val Ile Ala Ser Gln Val Glu Ala Val
 65                  70                  75                  80

agt ggt caa ttc acc gat atc gcc aca gta gtg cca cta tat gtc gcc   288
Ser Gly Gln Phe Thr Asp Ile Ala Thr Val Val Pro Leu Tyr Val Ala
                 85                  90                  95

ttt ttg atg gtg atg att cca att ggt ggc ggg ata tcc aaa ctc ggt   336
Phe Leu Met Val Met Ile Pro Ile Gly Gly Gly Ile Ser Lys Leu Gly
            100                 105                 110

ggc tta ggt ttc aaa gag caa cga gcc atc gtt ttt agc gga gca acc   384
Gly Leu Gly Phe Lys Glu Gln Arg Ala Ile Val Phe Ser Gly Ala Thr
        115                 120                 125

cgt aac tct ttg gtc gtt tta cct tta gcg tta gca ctt ccc gca ggc   432
Arg Asn Ser Leu Val Val Leu Pro Leu Ala Leu Ala Leu Pro Ala Gly
    130                 135                 140

ctg gaa ata gcg gcc gtc gta gtt gtc act caa acc ctc gtg gaa ctg   480
Leu Glu Ile Ala Ala Val Val Val Val Thr Gln Thr Leu Val Glu Leu
145                 150                 155                 160

att ggc atg gtt gtc tac gtg cgc atc atc cct tta att ttc cat gaa   528
Ile Gly Met Val Val Tyr Val Arg Ile Ile Pro Leu Ile Phe His Glu
```

```
                165                 170                 175

aag cag aca tac agg aaa ctt tca ggc ata ggg gag tca tgaaacagaa    577
Lys Gln Thr Tyr Arg Lys Leu Ser Gly Ile Gly Glu Ser
            180                 185

cggcaagcta agg                                                  590


<210> 534
<211> 189
<212> PRT
<213> Corynebacterium glutamicum

<400> 534
Ile Pro Val Phe Leu Ala Val Phe Val Gly Ser Asp Ala Leu Gly Ser
  1               5                  10                  15

Ile Ser Phe Gly Pro Phe Val Glu Ala Phe Phe Leu Leu Ile Leu Ile
             20                  25                  30

Pro Leu Val Ala Ala Ala Gly Thr Gln Gln Val Ala Arg Lys Trp Gln
         35                  40                  45

Val Gly Arg Thr Ile Met Ala Ala Ala Glu Ala Ile Met Val Pro Leu
     50                  55                  60

Met Met Leu Thr Leu Phe Ala Val Ile Ala Ser Gln Val Glu Ala Val
 65                  70                  75                  80

Ser Gly Gln Phe Thr Asp Ile Ala Thr Val Val Pro Leu Tyr Val Ala
                 85                  90                  95

Phe Leu Met Val Met Ile Pro Ile Gly Gly Gly Ile Ser Lys Leu Gly
            100                 105                 110

Gly Leu Gly Phe Lys Glu Gln Arg Ala Ile Val Phe Ser Gly Ala Thr
        115                 120                 125

Arg Asn Ser Leu Val Val Leu Pro Leu Ala Leu Ala Leu Pro Ala Gly
    130                 135                 140

Leu Glu Ile Ala Ala Val Val Val Val Thr Gln Thr Leu Val Glu Leu
145                 150                 155                 160

Ile Gly Met Val Val Tyr Val Arg Ile Ile Pro Leu Ile Phe His Glu
                165                 170                 175

Lys Gln Thr Tyr Arg Lys Leu Ser Gly Ile Gly Glu Ser
            180                 185


<210> 535
<211> 738
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(715)
<223> RXN01173
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<400> 535
agatctgttt ctatgtatta aagatcacac cgagtggtgg aatttcctca agtgatttac 60

ccacaatgga ctttgttgat acccaattcg agaaaggcca atg cac gtg agc act 115
Met His Val Ser Thr
1 5

ctt cca aac aag aaa ctg cgt act cgc att ttc gca ggc acc gct gcc 163
Leu Pro Asn Lys Lys Leu Arg Thr Arg Ile Phe Ala Gly Thr Ala Ala
10 15 20

gtc gca ctg tca ctt ggt gtt gcg tct tgc tca aac gca gaa gat gct 211
Val Ala Leu Ser Leu Gly Val Ala Ser Cys Ser Asn Ala Glu Asp Ala
25 30 35

gtg gat agc gca aca gat gct gcc aac tct gca acc tcc gcc gcg gga 259
Val Asp Ser Ala Thr Asp Ala Ala Asn Ser Ala Thr Ser Ala Ala Gly
40 45 50

tct gca att aac gat gcc acc ggc act tcc agc gca tcc acc aca gag 307
Ser Ala Ile Asn Asp Ala Thr Gly Thr Ser Ser Ala Ser Thr Thr Glu
55 60 65

cct tcc gga acc tct gga tcc gac tcc ggg tct gac tct gct gga gga 355
Pro Ser Gly Thr Ser Gly Ser Asp Ser Gly Ser Asp Ser Ala Gly Gly
70 75 80 85

gac acc act gaa gta gaa agc gcc gat ggg tcc acc atc agc atc cca 403
Asp Thr Thr Glu Val Glu Ser Ala Asp Gly Ser Thr Ile Ser Ile Pro
90 95 100

act gcc gtc gtc acc gct gca aat gct gca gga ttc agt acc ccg gaa 451
Thr Ala Val Val Thr Ala Ala Asn Ala Ala Gly Phe Ser Thr Pro Glu
105 110 115

tcc gtg gaa gaa ggc ccg aat ggt gag tca ttg gtg acg ttc cct gaa 499
Ser Val Glu Glu Gly Pro Asn Gly Glu Ser Leu Val Thr Phe Pro Glu
120 125 130

ggc tac att gtt aac tct gca gaa ggt ggt gca caa gca ctg gtc ggc 547
Gly Tyr Ile Val Asn Ser Ala Glu Gly Gly Ala Gln Ala Leu Val Gly
135 140 145

atg atc ggt gaa acc tgg atc ggc gaa ggc gga cta tcc gcg gca gtg 595
Met Ile Gly Glu Thr Trp Ile Gly Glu Gly Gly Leu Ser Ala Ala Val
150 155 160 165

ggt ctc cca act ggg cct gaa gaa gca aca aca aat ggt tgg act caa 643
Gly Leu Pro Thr Gly Pro Glu Glu Ala Thr Thr Asn Gly Trp Thr Gln
170 175 180

cag ttc aca tct gga gta att agc tgg ctt gat gat gga tca gga cag 691
Gln Phe Thr Ser Gly Val Ile Ser Trp Leu Asp Asp Gly Ser Gly Gln
185 190 195

ttc gca gct tct gtt gaa cct gct taagggaatc tcacctggcc tcc 738
Phe Ala Ala Ser Val Glu Pro Ala
200 205

<210> 536
<211> 205
<212> PRT
<213> Corynebacterium glutamicum

<400> 536
Met His Val Ser Thr Leu Pro Asn Lys Lys Leu Arg Thr Arg Ile Phe
1 5 10 15

Ala Gly Thr Ala Ala Val Ala Leu Ser Leu Gly Val Ala Ser Cys Ser
20 25 30

Asn Ala Glu Asp Ala Val Asp Ser Ala Thr Asp Ala Ala Asn Ser Ala
35 40 45

Thr Ser Ala Ala Gly Ser Ala Ile Asn Asp Ala Thr Gly Thr Ser Ser
50 55 60

Ala Ser Thr Thr Glu Pro Ser Gly Thr Ser Gly Ser Asp Ser Gly Ser
65 70 75 80

Asp Ser Ala Gly Gly Asp Thr Thr Glu Val Glu Ser Ala Asp Gly Ser
85 90 95

Thr Ile Ser Ile Pro Thr Ala Val Val Thr Ala Ala Asn Ala Ala Gly
100 105 110

Phe Ser Thr Pro Glu Ser Val Glu Glu Gly Pro Asn Gly Glu Ser Leu
115 120 125

Val Thr Phe Pro Glu Gly Tyr Ile Val Asn Ser Ala Glu Gly Gly Ala
130 135 140

Gln Ala Leu Val Gly Met Ile Gly Glu Thr Trp Ile Gly Glu Gly Gly
145 150 155 160

Leu Ser Ala Ala Val Gly Leu Pro Thr Gly Pro Glu Glu Ala Thr Thr
165 170 175

Asn Gly Trp Thr Gln Gln Phe Thr Ser Gly Val Ile Ser Trp Leu Asp
180 185 190

Asp Gly Ser Gly Gln Phe Ala Ala Ser Val Glu Pro Ala
195 200 205

<210> 537
<211> 738
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(715)
<223> FRXA01173

<400> 537
agatctgttt ctatgtatta aagatcacac cgagtggtgg aatttcctca agtgatttac 60

ccacaatgga ctttgttgat acccaattcg agaaaggcca atg cac gtg agc act 115
Met His Val Ser Thr

```
                                                    1               5

ctt cca aac aag aaa ctg cgt act cgc att ttc gca ggc acc gct gcc   163
Leu Pro Asn Lys Lys Leu Arg Thr Arg Ile Phe Ala Gly Thr Ala Ala
                10                  15                  20

gtc gca ctg tca ctt ggt gtt gcg tct tgc tca aac gca gaa gat gct   211
Val Ala Leu Ser Leu Gly Val Ala Ser Cys Ser Asn Ala Glu Asp Ala
            25                  30                  35

gtg gat agc gca aca gat gct gcc aac tct gca acc tcc gcc gcg gga   259
Val Asp Ser Ala Thr Asp Ala Ala Asn Ser Ala Thr Ser Ala Ala Gly
        40                  45                  50

tct gca att aac gat gcc acc ggc act tcc agc gca tcc acc aca gag   307
Ser Ala Ile Asn Asp Ala Thr Gly Thr Ser Ser Ala Ser Thr Thr Glu
    55                  60                  65

cct tcc gga acc tct gga tcc gac tcc ggg tct gac tct gct gga gga   355
Pro Ser Gly Thr Ser Gly Ser Asp Ser Gly Ser Asp Ser Ala Gly Gly
70                  75                  80                  85

gac acc act gaa gta gaa agc gcc gat ggg tcc acc atc agc atc cca   403
Asp Thr Thr Glu Val Glu Ser Ala Asp Gly Ser Thr Ile Ser Ile Pro
                90                  95                  100

act gcc gtc gtc acc gct gca aat gct gca gga ttc agt acc ccg gaa   451
Thr Ala Val Val Thr Ala Ala Asn Ala Ala Gly Phe Ser Thr Pro Glu
            105                 110                 115

tcc gtg gaa gaa ggc ccg aat ggt gag tca ttg gtg acg ttc cct gaa   499
Ser Val Glu Glu Gly Pro Asn Gly Glu Ser Leu Val Thr Phe Pro Glu
        120                 125                 130

ggc tac att gtt aac tct gca gaa ggt ggt gca caa gca ctg gtc ggc   547
Gly Tyr Ile Val Asn Ser Ala Glu Gly Gly Ala Gln Ala Leu Val Gly
    135                 140                 145

atg atc ggt gaa acc tgg atc ggc gaa ggc gga cta tcc gcg gca gtg   595
Met Ile Gly Glu Thr Trp Ile Gly Glu Gly Gly Leu Ser Ala Ala Val
150                 155                 160                 165

ggt ctc cca act ggg cct gaa gaa gca aca aca aat ggt tgg act caa   643
Gly Leu Pro Thr Gly Pro Glu Glu Ala Thr Thr Asn Gly Trp Thr Gln
                170                 175                 180

cag ttc aca tct gga gta att agc tgg ctt gat gat gga tca gga cag   691
Gln Phe Thr Ser Gly Val Ile Ser Trp Leu Asp Asp Gly Ser Gly Gln
            185                 190                 195

ttc gca gct tct gtt gaa cct gct taagggaatc tcacctggcc tcc         738
Phe Ala Ala Ser Val Glu Pro Ala
        200                 205
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<210> 538
<211> 205
<212> PRT
<213> Corynebacterium glutamicum

<400> 538

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Met His Val Ser Thr Leu Pro Asn Lys Lys Leu Arg Thr Arg Ile Phe
  1               5                  10                  15

Ala Gly Thr Ala Ala Val Ala Leu Ser Leu Gly Val Ala Ser Cys Ser
            20                  25                  30

Asn Ala Glu Asp Ala Val Asp Ser Ala Thr Asp Ala Ala Asn Ser Ala
         35                  40                  45

Thr Ser Ala Ala Gly Ser Ala Ile Asn Asp Ala Thr Gly Thr Ser Ser
     50                  55                  60

Ala Ser Thr Thr Glu Pro Ser Gly Thr Ser Gly Ser Asp Ser Gly Ser
 65                  70                  75                  80

Asp Ser Ala Gly Gly Asp Thr Thr Glu Val Glu Ser Ala Asp Gly Ser
                 85                  90                  95

Thr Ile Ser Ile Pro Thr Ala Val Val Thr Ala Ala Asn Ala Ala Gly
            100                 105                 110

Phe Ser Thr Pro Glu Ser Val Glu Glu Gly Pro Asn Gly Glu Ser Leu
        115                 120                 125

Val Thr Phe Pro Glu Gly Tyr Ile Val Asn Ser Ala Glu Gly Gly Ala
    130                 135                 140

Gln Ala Leu Val Gly Met Ile Gly Glu Thr Trp Ile Gly Glu Gly Gly
145                 150                 155                 160

Leu Ser Ala Ala Val Gly Leu Pro Thr Gly Pro Glu Glu Ala Thr Thr
                165                 170                 175

Asn Gly Trp Thr Gln Gln Phe Thr Ser Gly Val Ile Ser Trp Leu Asp
            180                 185                 190

Asp Gly Ser Gly Gln Phe Ala Ala Ser Val Glu Pro Ala
        195                 200                 205
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<210> 539
<211> 873
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(850)
<223> RXN01174

<400> 539
atatcgcaac cgctgttaat gaagaggaag aggctcgcga tatcgcgaag ctgtgccagg 60

agatggtgga attagctcgg aatattgaga agttgaggta atg agc aac atg cag 115
                                              Met Ser Asn Met Gln
                                                1   5

gga aac gat tcc aag aaa tct agc ggc gcg agt cgt gcg gag agc cca 163
Gly Asn Asp Ser Lys Lys Ser Ser Gly Ala Ser Arg Ala Glu Ser Pro
            10   15   20

```
ctg atc aag ttc cgg aca ttg att atc gtc atc ttt gtc atc ttg atc   211
Leu Ile Lys Phe Arg Thr Leu Ile Ile Val Ile Phe Val Ile Leu Ile
            25                  30                  35

gtt ggt ttg gca tct att gca gtg gga cct gtc gtg tac cag ctc atc   259
Val Gly Leu Ala Ser Ile Ala Val Gly Pro Val Val Tyr Gln Leu Ile
        40                  45                  50

atg gga cct ggt gtg aaa acc gaa gga atc cag gct gat ggc gca gca   307
Met Gly Pro Gly Val Lys Thr Glu Gly Ile Gln Ala Asp Gly Ala Ala
    55                  60                  65

cct gcg tcc acc gac atg aac ggc acc tgg gat gtt gcc cca ggg agt   355
Pro Ala Ser Thr Asp Met Asn Gly Thr Trp Asp Val Ala Pro Gly Ser
70                  75                  80                  85

att cca aac acc acc tca gct gga ttc acc ttc gct gag atc ctg cca   403
Ile Pro Asn Thr Thr Ser Ala Gly Phe Thr Phe Ala Glu Ile Leu Pro
                90                  95                  100

ggc gaa gaa aag atc acc tcc ggc tca acc act ggt gtc act ggc gaa   451
Gly Glu Glu Lys Ile Thr Ser Gly Ser Thr Thr Gly Val Thr Gly Glu
            105                 110                 115

gtg gtc atc gag gat aac tcc ctg atc tct ggt ctg att acc gtc aac   499
Val Val Ile Glu Asp Asn Ser Leu Ile Ser Gly Leu Ile Thr Val Asn
        120                 125                 130

atg act cac atc acc acc gat cag gaa aag cgc gac atc aac gtg cgc   547
Met Thr His Ile Thr Thr Asp Gln Glu Lys Arg Asp Ile Asn Val Arg
    135                 140                 145

act aag ctc ttc cac acc gat cag tac cca gaa gca acc ttt gag gtt   595
Thr Lys Leu Phe His Thr Asp Gln Tyr Pro Glu Ala Thr Phe Glu Val
150                 155                 160                 165

acc gat tcc gtt gat ctt tct gcg ctc cca gac acc gga tcc att gct   643
Thr Asp Ser Val Asp Leu Ser Ala Leu Pro Asp Thr Gly Ser Ile Ala
                170                 175                 180

cag gtt gtc atc cca ggc gag ttg acc atc cac ggt gaa acc aag gct   691
Gln Val Val Ile Pro Gly Glu Leu Thr Ile His Gly Glu Thr Lys Ala
            185                 190                 195

gtg gag cct acc ttt gat gta ctt cgt act ggt gac caa gtt atc gtg   739
Val Glu Pro Thr Phe Asp Val Leu Arg Thr Gly Asp Gln Val Ile Val
        200                 205                 210

gct tcc gat atc gaa atc aac cgc ctc gac ttc ggt gta gaa acc cca   787
Ala Ser Asp Ile Glu Ile Asn Arg Leu Asp Phe Gly Val Glu Thr Pro
    215                 220                 225

gag ttc atc gcc gca aag atc aat gag acc ggc gag atc aac gtc cga   835
Glu Phe Ile Ala Ala Lys Ile Asn Glu Thr Gly Glu Ile Asn Val Arg
230                 235                 240                 245

atc gta ttg gag aaa taaaccatga tggcatcacg gat                    873
Ile Val Leu Glu Lys
                250
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<210> 540
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 540
Met Ser Asn Met Gln Gly Asn Asp Ser Lys Lys Ser Ser Gly Ala Ser
1 5 10 15

Arg Ala Glu Ser Pro Leu Ile Lys Phe Arg Thr Leu Ile Ile Val Ile
20 25 30

Phe Val Ile Leu Ile Val Gly Leu Ala Ser Ile Ala Val Gly Pro Val
35 40 45

Val Tyr Gln Leu Ile Met Gly Pro Gly Val Lys Thr Glu Gly Ile Gln
50 55 60

Ala Asp Gly Ala Ala Pro Ala Ser Thr Asp Met Asn Gly Thr Trp Asp
65 70 75 80

Val Ala Pro Gly Ser Ile Pro Asn Thr Thr Ser Ala Gly Phe Thr Phe
85 90 95

Ala Glu Ile Leu Pro Gly Glu Glu Lys Ile Thr Ser Gly Ser Thr Thr
100 105 110

Gly Val Thr Gly Glu Val Val Ile Glu Asp Asn Ser Leu Ile Ser Gly
115 120 125

Leu Ile Thr Val Asn Met Thr His Ile Thr Thr Asp Gln Glu Lys Arg
130 135 140

Asp Ile Asn Val Arg Thr Lys Leu Phe His Thr Asp Gln Tyr Pro Glu
145 150 155 160

Ala Thr Phe Glu Val Thr Asp Ser Val Asp Leu Ser Ala Leu Pro Asp
165 170 175

Thr Gly Ser Ile Ala Gln Val Val Ile Pro Gly Glu Leu Thr Ile His
180 185 190

Gly Glu Thr Lys Ala Val Glu Pro Thr Phe Asp Val Leu Arg Thr Gly
195 200 205

Asp Gln Val Ile Val Ala Ser Asp Ile Glu Ile Asn Arg Leu Asp Phe
210 215 220

Gly Val Glu Thr Pro Glu Phe Ile Ala Ala Lys Ile Asn Glu Thr Gly
225 230 235 240

Glu Ile Asn Val Arg Ile Val Leu Glu Lys
245 250

<210> 541
<211> 873
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(850)
<223> FRXA01174

<400> 541
atatcgcaac cgctgttaat gaagaggaag aggctcgcga tatcgcgaag ctgtgccagg 60

agatggtgga attagctcgg aatattgaga agttgaggta atg agc aac atg cag 115
Met Ser Asn Met Gln
1 5

gga aac gat tcc aag aaa tct agc ggc gcg agt cgt gcg gag agc cca 163
Gly Asn Asp Ser Lys Lys Ser Ser Gly Ala Ser Arg Ala Glu Ser Pro
10 15 20

ctg atc aag ttc cgg aca ttg att atc gtc atc ttt gtc atc ttg atc 211
Leu Ile Lys Phe Arg Thr Leu Ile Ile Val Ile Phe Val Ile Leu Ile
25 30 35

gtt ggt ttg gca tct att gca gtg gga cct gtc gtg tac cag ctc atc 259
Val Gly Leu Ala Ser Ile Ala Val Gly Pro Val Val Tyr Gln Leu Ile
40 45 50

atg gga cct ggt gtg aaa acc gaa gga atc cag gct gat ggc gca gca 307
Met Gly Pro Gly Val Lys Thr Glu Gly Ile Gln Ala Asp Gly Ala Ala
55 60 65

cct gcg tcc acc gac atg aac ggc acc tgg gat gtt gcc cca ggg agt 355
Pro Ala Ser Thr Asp Met Asn Gly Thr Trp Asp Val Ala Pro Gly Ser
70 75 80 85

att cca aac acc acc tca gct gga ttc acc ttc gct gag atc ctg cca 403
Ile Pro Asn Thr Thr Ser Ala Gly Phe Thr Phe Ala Glu Ile Leu Pro
90 95 100

ggc gaa gaa aag atc acc tcc ggc tca acc act ggt gtc act ggc gaa 451
Gly Glu Glu Lys Ile Thr Ser Gly Ser Thr Thr Gly Val Thr Gly Glu
105 110 115

gtg gtc atc gag gat aac tcc ctg atc tct ggt ctg att acc gtc aac 499
Val Val Ile Glu Asp Asn Ser Leu Ile Ser Gly Leu Ile Thr Val Asn
120 125 130

atg act cac atc acc acc gat cag gaa aag cgc gac atc aac gtg cgc 547
Met Thr His Ile Thr Thr Asp Gln Glu Lys Arg Asp Ile Asn Val Arg
135 140 145

act aag ctc ttc cac acc gat cag tac cca gaa gca acc ttt gag gtt 595
Thr Lys Leu Phe His Thr Asp Gln Tyr Pro Glu Ala Thr Phe Glu Val
150 155 160 165

acc gat tcc gtt gat ctt tct gcg ctc cca gac acc gga tcc att gct 643
Thr Asp Ser Val Asp Leu Ser Ala Leu Pro Asp Thr Gly Ser Ile Ala
170 175 180

cag gtt gtc atc cca ggc gag ttg acc atc cac ggt gaa acc aag gct 691
Gln Val Val Ile Pro Gly Glu Leu Thr Ile His Gly Glu Thr Lys Ala
185 190 195

gtg gag cct acc ttt gat gta ctt cgt act ggt gac caa gtt atc gtg 739
Val Glu Pro Thr Phe Asp Val Leu Arg Thr Gly Asp Gln Val Ile Val

```
        200                 205                 210

gct tcc gat atc gaa atc aac cgc ctc gac ttc ggt gta gaa acc cca   787
Ala Ser Asp Ile Glu Ile Asn Arg Leu Asp Phe Gly Val Glu Thr Pro
    215                 220                 225

gag ttc atc gcc gca aag atc aat gag acc ggc gag atc aac gtc cga   835
Glu Phe Ile Ala Ala Lys Ile Asn Glu Thr Gly Glu Ile Asn Val Arg
230                 235                 240                 245

atc gta ttg gag aaa taaaccatga tggcatcacg gat                     873
Ile Val Leu Glu Lys
                250
```

<210> 542
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 542

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Met Ser Asn Met Gln Gly Asn Asp Ser Lys Lys Ser Ser Gly Ala Ser
  1               5                  10                  15

Arg Ala Glu Ser Pro Leu Ile Lys Phe Arg Thr Leu Ile Ile Val Ile
             20                  25                  30

Phe Val Ile Leu Ile Val Gly Leu Ala Ser Ile Ala Val Gly Pro Val
         35                  40                  45

Val Tyr Gln Leu Ile Met Gly Pro Gly Val Lys Thr Glu Gly Ile Gln
     50                  55                  60

Ala Asp Gly Ala Ala Pro Ala Ser Thr Asp Met Asn Gly Thr Trp Asp
 65                  70                  75                  80

Val Ala Pro Gly Ser Ile Pro Asn Thr Thr Ser Ala Gly Phe Thr Phe
                 85                  90                  95

Ala Glu Ile Leu Pro Gly Glu Glu Lys Ile Thr Ser Gly Ser Thr Thr
            100                 105                 110

Gly Val Thr Gly Glu Val Val Ile Glu Asp Asn Ser Leu Ile Ser Gly
        115                 120                 125

Leu Ile Thr Val Asn Met Thr His Ile Thr Thr Asp Gln Glu Lys Arg
    130                 135                 140

Asp Ile Asn Val Arg Thr Lys Leu Phe His Thr Asp Gln Tyr Pro Glu
145                 150                 155                 160

Ala Thr Phe Glu Val Thr Asp Ser Val Asp Leu Ser Ala Leu Pro Asp
                165                 170                 175

Thr Gly Ser Ile Ala Gln Val Val Ile Pro Gly Glu Leu Thr Ile His
            180                 185                 190

Gly Glu Thr Lys Ala Val Glu Pro Thr Phe Asp Val Leu Arg Thr Gly
        195                 200                 205

Asp Gln Val Ile Val Ala Ser Asp Ile Glu Ile Asn Arg Leu Asp Phe
```

```
    210                 215                 220

Gly Val Glu Thr Pro Glu Phe Ile Ala Ala Lys Ile Asn Glu Thr Gly
225                 230                 235                 240

Glu Ile Asn Val Arg Ile Val Leu Glu Lys
                245                 250


<210> 543
<211> 1401
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1378)
<223> RXN01229

<400> 543
tagccccgaa agacggcgag ggttggctct gcttcgttgt gggaaaacta ggcccttaat 60

aagctgtgct tatagggtct cctgcaccga taaaggactg atg atc atc tcc act   115
                                              Met Ile Ile Ser Thr
                                                1               5

aac acc gct cac ccc ctg cac gaa ccg cac gta ccc agc cac cac aat   163
Asn Thr Ala His Pro Leu His Glu Pro His Val Pro Ser His His Asn
                10                  15                  20

cgt atg aat act ctg cgt gcc ggt gtg ctg ggt gct aat gac ggt atc   211
Arg Met Asn Thr Leu Arg Ala Gly Val Leu Gly Ala Asn Asp Gly Ile
            25                  30                  35

gtc tcc att gct gcg cta ctg ctc ggt gtg atc gcc acc ggc gcc agt   259
Val Ser Ile Ala Ala Leu Leu Leu Gly Val Ile Ala Thr Gly Ala Ser
        40                  45                  50

gac acc gtc gtg ttc ggc gct ggt ttg gcc tca acg atc gcg ggg gcg   307
Asp Thr Val Val Phe Gly Ala Gly Leu Ala Ser Thr Ile Ala Gly Ala
    55                  60                  65

gta tct atg gct ctc ggt gag tac gtc tct gtc tcc tca cag cgt gat   355
Val Ser Met Ala Leu Gly Glu Tyr Val Ser Val Ser Ser Gln Arg Asp
70                  75                  80                  85

acc gaa cgg gtg ctc atc gca aaa gaa gcg aag gag ctg gcc gaa gac   403
Thr Glu Arg Val Leu Ile Ala Lys Glu Ala Lys Glu Leu Ala Glu Asp
                90                  95                  100

ccg acg gcc gag cac gtc gag ctg tcg gag atc cta cac tcc tac ggc   451
Pro Thr Ala Glu His Val Glu Leu Ser Glu Ile Leu His Ser Tyr Gly
            105                 110                 115

atc tmc mmt gwg amt smr ras sms gcs rmm ayc grg awm ggg mas ggc   499
Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly
        120                 125                 130

gac gcc ttg ggc gcc cac ctt cag ctc gag ctc ggt att gat aat gag   547
Asp Ala Leu Gly Ala His Leu Gln Leu Glu Leu Gly Ile Asp Asn Glu
    135                 140                 145
```

```
caa ctg acc agc ccc ttg gcc gcc gcc ttc tcc tcg gcc gtg gct ttc   595
Gln Leu Thr Ser Pro Leu Ala Ala Ala Phe Ser Ser Ala Val Ala Phe
150                 155                 160                 165

ctg ctc gga gca ctg ctg ccg atg gtg tyg gta ttc mty gcc ccy kca   643
Leu Leu Gly Ala Leu Leu Pro Met Val Xaa Val Phe Xaa Ala Xaa Xaa
                170                 175                 180

ggc tgg gac gcc ggc gtk gkc ttc gta gtc acg stg ctg gtc ctg gcg   691
Gly Trp Asp Ala Gly Xaa Xaa Phe Val Val Thr Xaa Leu Val Leu Ala
            185                 190                 195

gkk acc ggg ttc atc tca rcc cmg rtc ycg ggt acc tyc ccm atg cgc   739
Xaa Thr Gly Phe Ile Ser Xaa Xaa Xaa Xaa Gly Thr Xaa Xaa Met Arg
        200                 205                 210

gsg tgc sgg sgc ttk gkg rtc ggk ggt kcc ctc sgs cyg gcc ctg acc   787
Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Leu Xaa Xaa Ala Leu Thr
    215                 220                 225

mta ccg tct tgg aaw cwa tts kks gss gcm gyw ktm kgw gsy kcs ksr   835
Xaa Pro Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
230                 235                 240                 245

rra mar arr rgg rrk rmk gsk kkt ktk gtg gyk gsk sgk ykt tkt cgw   883
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa
                250                 255                 260

cgm cks sws ram gwr rts rkc gsc gmc swc cty syw gmm say cmk ssg   931
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            265                 270                 275

ssk scw kgr wss rcy gcy scm ssm ggs ksk csm swk wtr kks yss sks   979
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        280                 285                 290

wsw mtw cky ktt tyy cyy csg smr gkw amc mmm myk gkk syw wkr rrw   1027
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    295                 300                 305

tkt tty ykr rra rrm srm ywm csr rkw rgg cca cca ctg tca ggc gag   1075
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Pro Leu Ser Gly Glu
310                 315                 320                 325

att ctg ctt gct ggc ctc ggc ggt gag ata ggc atg ggg gaa ccg agg   1123
Ile Leu Leu Ala Gly Leu Gly Gly Glu Ile Gly Met Gly Glu Pro Arg
                330                 335                 340

atc cca gtg act act ggt gac ctg gaa acc cgc ggt ctc cag tgc ctg   1171
Ile Pro Val Thr Thr Gly Asp Leu Glu Thr Arg Gly Leu Gln Cys Leu
            345                 350                 355

ggc aag ctc ggg cag tgg cca ccg gta ggc ggt ggc cac ggg atg ata   1219
Gly Lys Leu Gly Gln Trp Pro Pro Val Gly Gly Gly His Gly Met Ile
        360                 365                 370

cat cgg ttc cag aga agg ccc gga gaa aaa gga cat cag cag gcc acc   1267
His Arg Phe Gln Arg Arg Pro Gly Glu Lys Gly His Gln Gln Ala Thr
    375                 380                 385
```

```
acc atc ctc cac cgc cat ccg cag tgc gac cag ggc gtc ggg cag ctc   1315
Thr Ile Leu His Arg His Pro Gln Cys Asp Gln Gly Val Gly Gln Leu
390                 395                 400                 405

gcc cgg gcc cat gtg gat cag gga gta cca ggc caa cag gcc tgc cca   1363
Ala Arg Ala His Val Asp Gln Gly Val Pro Gly Gln Gln Ala Cys Pro
                410                 415                 420

gcg ctt cgg cga gtc tgagaggtcg gtaatagtgc cgt                     1401
Ala Leu Arg Arg Val
            425


<210> 544
<211> 426
<212> PRT
<213> Corynebacterium glutamicum

<400> 544
Met Ile Ile Ser Thr Asn Thr Ala His Pro Leu His Glu Pro His Val
  1               5                  10                  15

Pro Ser His His Asn Arg Met Asn Thr Leu Arg Ala Gly Val Leu Gly
             20                  25                  30

Ala Asn Asp Gly Ile Val Ser Ile Ala Ala Leu Leu Leu Gly Val Ile
         35                  40                  45

Ala Thr Gly Ala Ser Asp Thr Val Val Phe Gly Ala Gly Leu Ala Ser
     50                  55                  60

Thr Ile Ala Gly Ala Val Ser Met Ala Leu Gly Glu Tyr Val Ser Val
 65                  70                  75                  80

Ser Ser Gln Arg Asp Thr Glu Arg Val Leu Ile Ala Lys Glu Ala Lys
                 85                  90                  95

Glu Leu Ala Glu Asp Pro Thr Ala Glu His Val Glu Leu Ser Glu Ile
            100                 105                 110

Leu His Ser Tyr Gly Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        115                 120                 125

Xaa Xaa Gly Xaa Gly Asp Ala Leu Gly Ala His Leu Gln Leu Glu Leu
    130                 135                 140

Gly Ile Asp Asn Glu Gln Leu Thr Ser Pro Leu Ala Ala Ala Phe Ser
145                 150                 155                 160

Ser Ala Val Ala Phe Leu Leu Gly Ala Leu Leu Pro Met Val Xaa Val
                165                 170                 175

Phe Xaa Ala Xaa Xaa Gly Trp Asp Ala Gly Xaa Xaa Phe Val Val Thr
            180                 185                 190

Xaa Leu Val Leu Ala Xaa Thr Gly Phe Ile Ser Xaa Xaa Xaa Xaa Gly
        195                 200                 205

Thr Xaa Xaa Met Arg Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Leu
    210                 215                 220
```

```
Xaa Xaa Ala Leu Thr Xaa Pro Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
225                 230                 235                 240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa
                245                 250                 255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            260                 265                 270

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        275                 280                 285

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    290                 295                 300

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro
305                 310                 315                 320

Pro Leu Ser Gly Glu Ile Leu Leu Ala Gly Leu Gly Gly Glu Ile Gly
                325                 330                 335

Met Gly Glu Pro Arg Ile Pro Val Thr Thr Gly Asp Leu Glu Thr Arg
            340                 345                 350

Gly Leu Gln Cys Leu Gly Lys Leu Gly Gln Trp Pro Pro Val Gly Gly
        355                 360                 365

Gly His Gly Met Ile His Arg Phe Gln Arg Arg Pro Gly Glu Lys Gly
    370                 375                 380

His Gln Gln Ala Thr Thr Ile Leu His Arg His Pro Gln Cys Asp Gln
385                 390                 395                 400

Gly Val Gly Gln Leu Ala Arg Ala His Val Asp Gln Gly Val Pro Gly
                405                 410                 415

Gln Gln Ala Cys Pro Ala Leu Arg Arg Val
            420                 425
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<210> 545
<211> 793
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> FRXA01229

<400> 545
tagccccgaa agacggcgag ggttggctct gcttcgttgt gggaaaacta ggcccttaat 60

aagctgtgct tatagggtct cctgcaccga taaaggactg atg atc atc tcc act 115
                                                Met Ile Ile Ser Thr
                                                  1   5

aac acc gct cac ccc ctg cac gaa ccg cac gta ccc agc cac cac aat 163
Asn Thr Ala His Pro Leu His Glu Pro His Val Pro Ser His His Asn
                 10   15   20

```
cgt atg aat act ctg cgt gcc ggt gtg ctg ggt gct aat gac ggt atc   211
Arg Met Asn Thr Leu Arg Ala Gly Val Leu Gly Ala Asn Asp Gly Ile
            25                  30                  35

gtc tcc att gct gcg cta ctg ctc ggt gtg atc gcc acc ggc gcc agt   259
Val Ser Ile Ala Ala Leu Leu Leu Gly Val Ile Ala Thr Gly Ala Ser
        40                  45                  50

gac acc gtc gtg ttc ggc gct ggt ttg gcc tca acg atc gcg ggg gcg   307
Asp Thr Val Val Phe Gly Ala Gly Leu Ala Ser Thr Ile Ala Gly Ala
    55                  60                  65

gta tct atg gct ctc ggt gag tac gtc tct gtc tcc tca cag cgt gat   355
Val Ser Met Ala Leu Gly Glu Tyr Val Ser Val Ser Ser Gln Arg Asp
70                  75                  80                  85

acc gaa cgg gtg ctc atc gca aaa gaa gcg aag gag ctg gcc gaa gac   403
Thr Glu Arg Val Leu Ile Ala Lys Glu Ala Lys Glu Leu Ala Glu Asp
                90                  95                  100

ccg acg gcc gag cac gtc gag ctg tcg gag atc cta cac tcc tac ggc   451
Pro Thr Ala Glu His Val Glu Leu Ser Glu Ile Leu His Ser Tyr Gly
            105                 110                 115

atc tcc cct gag act gcg aac cag gcg gcc acc gag atc ggg cag ggc   499
Ile Ser Pro Glu Thr Ala Asn Gln Ala Ala Thr Glu Ile Gly Gln Gly
        120                 125                 130

gac gcc ttg ggc gcc cac ctt cag ctc gag ctc ggt att gat aat gag   547
Asp Ala Leu Gly Ala His Leu Gln Leu Glu Leu Gly Ile Asp Asn Glu
    135                 140                 145

caa ctg acc agc ccc ttg gcc gcc gcc ttc tcc tcg gcc gtg gct ttc   595
Gln Leu Thr Ser Pro Leu Ala Ala Ala Phe Ser Ser Ala Val Ala Phe
150                 155                 160                 165

ctg ctc gga gca ctg ctg ccg atg gtg tcg gta ttc atc gcc cct gca   643
Leu Leu Gly Ala Leu Leu Pro Met Val Ser Val Phe Ile Ala Pro Ala
                170                 175                 180

ggc tgg gac gcc ggc gtg gtc ttc gta gtc acg ctg ctg gtc ctg gcg   691
Gly Trp Asp Ala Gly Val Val Phe Val Val Thr Leu Leu Val Leu Ala
            185                 190                 195

gtg acc ggg ttc atc tca gcc cag atc tcg ggt acc tcc cca atg cgc   739
Val Thr Gly Phe Ile Ser Ala Gln Ile Ser Gly Thr Ser Pro Met Arg
        200                 205                 210

gcg tgc ggg cgc ttg gtg atc ggt ggt gcc ctc ggc ctg gcc cta acc   787
Ala Cys Gly Arg Leu Val Ile Gly Gly Ala Leu Gly Leu Ala Leu Thr
    215                 220                 225

tac ggt                                                           793
Tyr Gly
230
```

<210> 546
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 546
Met Ile Ile Ser Thr Asn Thr Ala His Pro Leu His Glu Pro His Val
1 5 10 15

Pro Ser His His Asn Arg Met Asn Thr Leu Arg Ala Gly Val Leu Gly
20 25 30

Ala Asn Asp Gly Ile Val Ser Ile Ala Ala Leu Leu Leu Gly Val Ile
35 40 45

Ala Thr Gly Ala Ser Asp Thr Val Val Phe Gly Ala Gly Leu Ala Ser
50 55 60

Thr Ile Ala Gly Ala Val Ser Met Ala Leu Gly Glu Tyr Val Ser Val
65 70 75 80

Ser Ser Gln Arg Asp Thr Glu Arg Val Leu Ile Ala Lys Glu Ala Lys
85 90 95

Glu Leu Ala Glu Asp Pro Thr Ala Glu His Val Glu Leu Ser Glu Ile
100 105 110

Leu His Ser Tyr Gly Ile Ser Pro Glu Thr Ala Asn Gln Ala Ala Thr
115 120 125

Glu Ile Gly Gln Gly Asp Ala Leu Gly Ala His Leu Gln Leu Glu Leu
130 135 140

Gly Ile Asp Asn Glu Gln Leu Thr Ser Pro Leu Ala Ala Ala Phe Ser
145 150 155 160

Ser Ala Val Ala Phe Leu Leu Gly Ala Leu Leu Pro Met Val Ser Val
165 170 175

Phe Ile Ala Pro Ala Gly Trp Asp Ala Gly Val Val Phe Val Val Thr
180 185 190

Leu Leu Val Leu Ala Val Thr Gly Phe Ile Ser Ala Gln Ile Ser Gly
195 200 205

Thr Ser Pro Met Arg Ala Cys Gly Arg Leu Val Ile Gly Gly Ala Leu
210 215 220

Gly Leu Ala Leu Thr Tyr Gly
225 230

<210> 547
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(607)
<223> RXN01246

<400> 547
gggaaggagg agaaggctgc tgtgagctct gcagcccccg tccgctgact ttcaatgctt 60

```
catggactcc ccgatacaca acctccgaaa gggaaccccc atg aag cgc act atc   115
                                            Met Lys Arg Thr Ile
                                              1               5

acc atc gcc gct ctc gcc ttg acc tcc acc ctg gtt ttg tcc gcc tgc   163
Thr Ile Ala Ala Leu Ala Leu Thr Ser Thr Leu Val Leu Ser Ala Cys
                 10                  15                  20

gca gat aac act gag gga gaa aac acc gac acc acg acc atc gcc act   211
Ala Asp Asn Thr Glu Gly Glu Asn Thr Asp Thr Thr Thr Ile Ala Thr
             25                  30                  35

acg tcc gcc ccc gac acc acc gaa acg acc ggg gcc acc acg gat cct   259
Thr Ser Ala Pro Asp Thr Thr Glu Thr Thr Gly Ala Thr Thr Asp Pro
         40                  45                  50

gag aca gag acg ggg gcg gcc gga gag gtc tcc gcc gag cac aat gat   307
Glu Thr Glu Thr Gly Ala Ala Gly Glu Val Ser Ala Glu His Asn Asp
     55                  60                  65

gcg gac atc atg ttc gcg cag atg atg atc ccg cat cac caa cag gcc   355
Ala Asp Ile Met Phe Ala Gln Met Met Ile Pro His His Gln Gln Ala
 70                  75                  80                  85

gtg gag atg agt gaa atc ctc ctg gcc aag gac gat atc ccg gcc gag   403
Val Glu Met Ser Glu Ile Leu Leu Ala Lys Asp Asp Ile Pro Ala Glu
                 90                  95                 100

gtc atc gag ttc acc cag ggt gtt atc gat gcc cag ggc ccg gag atc   451
Val Ile Glu Phe Thr Gln Gly Val Ile Asp Ala Gln Gly Pro Glu Ile
             105                 110                 115

gac cgg atg aat acc atg ctc gag acc tgg gaa gaa gat ccg gtc acc   499
Asp Arg Met Asn Thr Met Leu Glu Thr Trp Glu Glu Asp Pro Val Thr
         120                 125                 130

ggt gat atg ggt gag atg gac cat ggc ggg atg agt gga atg atg agc   547
Gly Asp Met Gly Glu Met Asp His Gly Gly Met Ser Gly Met Met Ser
     135                 140                 145

gag gag gac atg aca gcc ctc gag gac gcc cag ggc acc cga ggc tgc   595
Glu Glu Asp Met Thr Ala Leu Glu Asp Ala Gln Gly Thr Arg Gly Cys
150                 155                 160                 165

ccg gct cta cct tgagcagatg accgcccacc atg                        630
Pro Ala Leu Pro
```

<210> 548
<211> 169
<212> PRT
<213> Corynebacterium glutamicum

<400> 548

```
Met Lys Arg Thr Ile Thr Ile Ala Ala Leu Ala Leu Thr Ser Thr Leu
  1               5                  10                  15

Val Leu Ser Ala Cys Ala Asp Asn Thr Glu Gly Glu Asn Thr Asp Thr
             20                  25                  30
```

```
Thr Thr Ile Ala Thr Thr Ser Ala Pro Asp Thr Thr Glu Thr Thr Gly
         35                  40                  45

Ala Thr Thr Asp Pro Glu Thr Glu Thr Gly Ala Ala Gly Glu Val Ser
     50                  55                  60

Ala Glu His Asn Asp Ala Asp Ile Met Phe Ala Gln Met Met Ile Pro
 65                  70                  75                  80

His His Gln Gln Ala Val Glu Met Ser Glu Ile Leu Leu Ala Lys Asp
                 85                  90                  95

Asp Ile Pro Ala Glu Val Ile Glu Phe Thr Gln Gly Val Ile Asp Ala
            100                 105                 110

Gln Gly Pro Glu Ile Asp Arg Met Asn Thr Met Leu Glu Thr Trp Glu
        115                 120                 125

Glu Asp Pro Val Thr Gly Asp Met Gly Glu Met Asp His Gly Gly Met
    130                 135                 140

Ser Gly Met Met Ser Glu Glu Asp Met Thr Ala Leu Glu Asp Ala Gln
145                 150                 155                 160

Gly Thr Arg Gly Cys Pro Ala Leu Pro
                165
```

<210> 549
<211> 739
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(739)
<223> FRXA01246

<400> 549

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gggaaggagg agaaggctgc tgtgagctct gcagcccccg tccgctgact ttcaatgctt 60

catggactcc ccgatacaca acctccgaaa gggaaccccc atg aag cgc act atc   115
                                            Met Lys Arg Thr Ile
                                              1               5

acc atc gcc gct ctc gcc ttg acc tcc acc ctg gtt ttg tcc gcc tgc   163
Thr Ile Ala Ala Leu Ala Leu Thr Ser Thr Leu Val Leu Ser Ala Cys
                 10                  15                  20

gca gat aac act gag gga gaa aac acc gac acc acg acc atc gcc act   211
Ala Asp Asn Thr Glu Gly Glu Asn Thr Asp Thr Thr Thr Ile Ala Thr
             25                  30                  35

acg tcc gcc ccc gac acc acc gaa acg acc ggg gcc acc acg gat cct   259
Thr Ser Ala Pro Asp Thr Thr Glu Thr Thr Gly Ala Thr Thr Asp Pro
         40                  45                  50

gag aca gag acg ggg gcg gcc gga gag gtc tcc gcc gag cac aat gat   307
Glu Thr Glu Thr Gly Ala Ala Gly Glu Val Ser Ala Glu His Asn Asp
     55                  60                  65
```

```
gcg gac atc atg ttc gcg cag atg atg atc ccg cat cac caa cag gcc   355
Ala Asp Ile Met Phe Ala Gln Met Met Ile Pro His His Gln Gln Ala
 70                  75                  80                  85

gtg gag atg agt gaa atc ctc ctg gcc aag gac gat atc ccg gcc gag   403
Val Glu Met Ser Glu Ile Leu Leu Ala Lys Asp Asp Ile Pro Ala Glu
                90                  95                 100

gtc atc gag ttc acc cag ggt gtt atc gat gcc cag ggc ccg gag atc   451
Val Ile Glu Phe Thr Gln Gly Val Ile Asp Ala Gln Gly Pro Glu Ile
            105                 110                 115

gac cgg atg aat acc atg ctc gag acc tgg gaa gaa gat ccg gtc acc   499
Asp Arg Met Asn Thr Met Leu Glu Thr Trp Glu Glu Asp Pro Val Thr
        120                 125                 130

ggt gat atg ggt gag atg gac cat ggc ggg atg agt gga atg atg agc   547
Gly Asp Met Gly Glu Met Asp His Gly Gly Met Ser Gly Met Met Ser
    135                 140                 145

gag gag gac atg aca gcc ctc gag gac gcc cag ggc acc gag gct gcc   595
Glu Glu Asp Met Thr Ala Leu Glu Asp Ala Gln Gly Thr Glu Ala Ala
150                 155                 160                 165

cgg ctc tac ctt gag cag atg acc gcc cac cat gag ggc gcg gtc gat   643
Arg Leu Tyr Leu Glu Gln Met Thr Ala His His Glu Gly Ala Val Asp
                170                 175                 180

atg gcc cgc gat gag gtc act gat ggc cag aac ccg cag gcc atc gct   691
Met Ala Arg Asp Glu Val Thr Asp Gly Gln Asn Pro Gln Ala Ile Ala
            185                 190                 195

ctg gct gag cag gtc att gaa gat cag gag gcc gag atc gcc gag att   739
Leu Ala Glu Gln Val Ile Glu Asp Gln Glu Ala Glu Ile Ala Glu Ile
        200                 205                 210
```

<210> 550
<211> 213
<212> PRT
<213> Corynebacterium glutamicum

<400> 550

```
Met Lys Arg Thr Ile Thr Ile Ala Ala Leu Ala Leu Thr Ser Thr Leu
  1               5                  10                  15

Val Leu Ser Ala Cys Ala Asp Asn Thr Glu Gly Glu Asn Thr Asp Thr
             20                  25                  30

Thr Thr Ile Ala Thr Thr Ser Ala Pro Asp Thr Thr Glu Thr Thr Gly
         35                  40                  45

Ala Thr Thr Asp Pro Glu Thr Glu Thr Gly Ala Ala Gly Glu Val Ser
     50                  55                  60

Ala Glu His Asn Asp Ala Asp Ile Met Phe Ala Gln Met Met Ile Pro
 65                  70                  75                  80

His His Gln Gln Ala Val Glu Met Ser Glu Ile Leu Leu Ala Lys Asp
                 85                  90                  95
```

```
Asp Ile Pro Ala Glu Val Ile Glu Phe Thr Gln Gly Val Ile Asp Ala
            100                 105                 110

Gln Gly Pro Glu Ile Asp Arg Met Asn Thr Met Leu Glu Thr Trp Glu
        115                 120                 125

Glu Asp Pro Val Thr Gly Asp Met Gly Glu Met Asp His Gly Gly Met
    130                 135                 140

Ser Gly Met Met Ser Glu Glu Asp Met Thr Ala Leu Glu Asp Ala Gln
145                 150                 155                 160

Gly Thr Glu Ala Ala Arg Leu Tyr Leu Glu Gln Met Thr Ala His His
                165                 170                 175

Glu Gly Ala Val Asp Met Ala Arg Asp Glu Val Thr Asp Gly Gln Asn
            180                 185                 190

Pro Gln Ala Ile Ala Leu Ala Glu Gln Val Ile Glu Asp Gln Glu Ala
        195                 200                 205

Glu Ile Ala Glu Ile
    210
```

<210> 551
<211> 471
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(471)
<223> RXN01249

<400> 551

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tct cag att gtg gcg gtg tct tct cac ggt ctt acc acg atc cag gag   48
Ser Gln Ile Val Ala Val Ser Ser His Gly Leu Thr Thr Ile Gln Glu
  1               5                  10                  15

att gac gtg aaa cga gca gcg atc gca gcc gcc gcc ctt acc ctc gcc   96
Ile Asp Val Lys Arg Ala Ala Ile Ala Ala Ala Ala Leu Thr Leu Ala
             20                  25                  30

ctc acg ggg tgt tcg gcc gcc gac ccg gaa ccc acc gcc gac ggg acg   144
Leu Thr Gly Cys Ser Ala Ala Asp Pro Glu Pro Thr Ala Asp Gly Thr
         35                  40                  45

gtg tcc cag gat aca ttc ctg act acc cat ggc ctg gcc gcc atg gac   192
Val Ser Gln Asp Thr Phe Leu Thr Thr His Gly Leu Ala Ala Met Asp
     50                  55                  60

gcg gtg gag atc att gat cac ctc gac cgg cag aag gtc act gag cgt   240
Ala Val Glu Ile Ile Asp His Leu Asp Arg Gln Lys Val Thr Glu Arg
 65                  70                  75                  80

ccc acg gat ctg atc gcc tca gtg cgt gcc gat gaa ctg ctg ctc tcg   288
Pro Thr Asp Leu Ile Ala Ser Val Arg Ala Asp Glu Leu Leu Leu Ser
                 85                  90                  95

agc gat gac cag gaa gtc gtg gtc gat ctt ccc gac aat cag acg tat   336
```

```
Ser Asp Asp Gln Glu Val Val Val Asp Leu Pro Asp Asn Gln Thr Tyr
            100                 105                 110

gtc tcg atc gca ccc tac ctc aac tcc acc cac gac tgc ttc tac cac   384
Val Ser Ile Ala Pro Tyr Leu Asn Ser Thr His Asp Cys Phe Tyr His
        115                 120                 125

agc ctc acg acc tgc ctg ggg gat ctc gac aat gag gat atc cat gtc   432
Ser Leu Thr Thr Cys Leu Gly Asp Leu Asp Asn Glu Asp Ile His Val
    130                 135                 140

atg atc acc gat gaa gcg acc ggc gag gtc ctg ttc gat               471
Met Ile Thr Asp Glu Ala Thr Gly Glu Val Leu Phe Asp
145                 150                 155


<210> 552
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 552
Ser Gln Ile Val Ala Val Ser Ser His Gly Leu Thr Thr Ile Gln Glu
  1               5                  10                  15

Ile Asp Val Lys Arg Ala Ala Ile Ala Ala Ala Ala Leu Thr Leu Ala
             20                  25                  30

Leu Thr Gly Cys Ser Ala Ala Asp Pro Glu Pro Thr Ala Asp Gly Thr
         35                  40                  45

Val Ser Gln Asp Thr Phe Leu Thr Thr His Gly Leu Ala Ala Met Asp
     50                  55                  60

Ala Val Glu Ile Ile Asp His Leu Asp Arg Gln Lys Val Thr Glu Arg
 65                  70                  75                  80

Pro Thr Asp Leu Ile Ala Ser Val Arg Ala Asp Glu Leu Leu Leu Ser
                 85                  90                  95

Ser Asp Asp Gln Glu Val Val Val Asp Leu Pro Asp Asn Gln Thr Tyr
            100                 105                 110

Val Ser Ile Ala Pro Tyr Leu Asn Ser Thr His Asp Cys Phe Tyr His
        115                 120                 125

Ser Leu Thr Thr Cys Leu Gly Asp Leu Asp Asn Glu Asp Ile His Val
    130                 135                 140

Met Ile Thr Asp Glu Ala Thr Gly Glu Val Leu Phe Asp
145                 150                 155


<210> 553
<211> 400
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(400)
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<223> FRXA01249

<400> 553
gaattgacgt ggaaccgagc agcgatcgca gcccgccgcc cttaccctcg ccctcacggg 60

gtgttcggcc gccgacccgg aacccaccgc cgacgggacg gtg tcc cag gat aca 115
Val Ser Gln Asp Thr
1 5

ttc ctg act acc cat ggc ctg gcc gcc atg gac gcg gtg gag atc att 163
Phe Leu Thr Thr His Gly Leu Ala Ala Met Asp Ala Val Glu Ile Ile
10 15 20

gat cac ctc gac cgg cag aag gtc act gag cgt ccc acg gat ctg atc 211
Asp His Leu Asp Arg Gln Lys Val Thr Glu Arg Pro Thr Asp Leu Ile
25 30 35

gcc tca gtg cgt gcc gat gaa ctg ctg ctc tcg agc gat gac cag gaa 259
Ala Ser Val Arg Ala Asp Glu Leu Leu Leu Ser Ser Asp Asp Gln Glu
40 45 50

gtc gtg gtc gat ctt ccc gac aat cag acg tat gtc tcg atc gca ccc 307
Val Val Val Asp Leu Pro Asp Asn Gln Thr Tyr Val Ser Ile Ala Pro
55 60 65

tac ctc aac tcc acc cac gac tgc ttc tac cac agc ctc acg acc tgc 355
Tyr Leu Asn Ser Thr His Asp Cys Phe Tyr His Ser Leu Thr Thr Cys
70 75 80 85

ctg ggg gat ctc gac aat gag gat atc cat gtc atg atc acc gat 400
Leu Gly Asp Leu Asp Asn Glu Asp Ile His Val Met Ile Thr Asp
90 95 100

<210> 554
<211> 100
<212> PRT
<213> Corynebacterium glutamicum

<400> 554
Val Ser Gln Asp Thr Phe Leu Thr Thr His Gly Leu Ala Ala Met Asp
1 5 10 15

Ala Val Glu Ile Ile Asp His Leu Asp Arg Gln Lys Val Thr Glu Arg
20 25 30

Pro Thr Asp Leu Ile Ala Ser Val Arg Ala Asp Glu Leu Leu Leu Ser
35 40 45

Ser Asp Asp Gln Glu Val Val Val Asp Leu Pro Asp Asn Gln Thr Tyr
50 55 60

Val Ser Ile Ala Pro Tyr Leu Asn Ser Thr His Asp Cys Phe Tyr His
65 70 75 80

Ser Leu Thr Thr Cys Leu Gly Asp Leu Asp Asn Glu Asp Ile His Val
85 90 95

Met Ile Thr Asp
100

<210> 555
<211> 432
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(409)
<223> RXN01251

<400> 555
tgtaagccga gagcgaacct gccaaaagta aggggcgggt tcgcggtgac gtcggtagga 60

tcgagcgaag aaaccaacaa acttcttagg agccattctc atg acc cag cca gat 115
Met Thr Gln Pro Asp
1 5

atg tcc cag atc ctc gcc caa gct cag cag atg cag gct caa cta cag 163
Met Ser Gln Ile Leu Ala Gln Ala Gln Gln Met Gln Ala Gln Leu Gln
10 15 20

gcc gct cag cag gaa atc ctg gca acc acc gtt gtc gga aat gca gga 211
Ala Ala Gln Gln Glu Ile Leu Ala Thr Thr Val Val Gly Asn Ala Gly
25 30 35

aac ggg ctg gtt acc gtc act atg gcc ggc aac ggc gag gtc tcc gca 259
Asn Gly Leu Val Thr Val Thr Met Ala Gly Asn Gly Glu Val Ser Ala
40 45 50

gtg acc gtt gac cca aag gtc gtt gac cct gaa gat gtc gaa acc cta 307
Val Thr Val Asp Pro Lys Val Val Asp Pro Glu Asp Val Glu Thr Leu
55 60 65

cag gac ctt ctg ctc ggt gca ttc aag gat gcc cat aac aag gtc gca 355
Gln Asp Leu Leu Leu Gly Ala Phe Lys Asp Ala His Asn Lys Val Ala
70 75 80 85

aac gtt gct gaa gag aag atg ggc cca cta tcc cag ggc atg ggt ggc 403
Asn Val Ala Glu Glu Lys Met Gly Pro Leu Ser Gln Gly Met Gly Gly
90 95 100

ctc ttc taattagttg ctaaacgcag ggc 432
Leu Phe

<210> 556
<211> 103
<212> PRT
<213> Corynebacterium glutamicum

<400> 556
Met Thr Gln Pro Asp Met Ser Gln Ile Leu Ala Gln Ala Gln Gln Met
1 5 10 15

Gln Ala Gln Leu Gln Ala Ala Gln Gln Glu Ile Leu Ala Thr Thr Val
20 25 30

Val Gly Asn Ala Gly Asn Gly Leu Val Thr Val Thr Met Ala Gly Asn
35 40 45

```
Gly Glu Val Ser Ala Val Thr Val Asp Pro Lys Val Val Asp Pro Glu
     50                  55                  60

Asp Val Glu Thr Leu Gln Asp Leu Leu Leu Gly Ala Phe Lys Asp Ala
 65                  70                  75                  80

His Asn Lys Val Ala Asn Val Ala Glu Glu Lys Met Gly Pro Leu Ser
                 85                  90                  95

Gln Gly Met Gly Gly Leu Phe
            100
```

<210> 557
<211> 432
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(409)
<223> FRXA01251

<400> 557

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tgtaagccga gagcgaacct gccaaaagta aggggcgggt tcgcggtgac gtcggtagga 60

tcgagcgaag aaaccaacaa acttcttagg agccattctc atg acc cag cca gat   115
                                              Met Thr Gln Pro Asp
                                                1               5

atg tcc cag atc ctc gcc caa gct cag cag atg cag gct caa cta cag   163
Met Ser Gln Ile Leu Ala Gln Ala Gln Gln Met Gln Ala Gln Leu Gln
                 10                  15                  20

gcc gct cag cag gaa atc ctg gca acc acc gtt gtc gga aat gca gga   211
Ala Ala Gln Gln Glu Ile Leu Ala Thr Thr Val Val Gly Asn Ala Gly
             25                  30                  35

aac ggg ctg gtt acc gtc act atg gcc ggc aac ggc gag gtc ttc gca   259
Asn Gly Leu Val Thr Val Thr Met Ala Gly Asn Gly Glu Val Phe Ala
         40                  45                  50

gtg acc gtt gac cca aag gtc gtt gac cct gaa gat gtc gaa acc cta   307
Val Thr Val Asp Pro Lys Val Val Asp Pro Glu Asp Val Glu Thr Leu
     55                  60                  65

cag gac ctt ctg ctc ggt gca ttc aag gat gcc cat aac aag gtc gca   355
Gln Asp Leu Leu Leu Gly Ala Phe Lys Asp Ala His Asn Lys Val Ala
 70                  75                  80                  85

aac gtt gct gaa gag aag atg ggc cca cta tcc cag ggc atg ggt ggc   403
Asn Val Ala Glu Glu Lys Met Gly Pro Leu Ser Gln Gly Met Gly Gly
                 90                  95                 100

ctc ttc taattagttg ctaaacgcag ggc                                432
Leu Phe
```

<210> 558

<211> 103
<212> PRT
<213> Corynebacterium glutamicum

<400> 558
Met Thr Gln Pro Asp Met Ser Gln Ile Leu Ala Gln Ala Gln Gln Met
1 5 10 15

Gln Ala Gln Leu Gln Ala Ala Gln Gln Glu Ile Leu Ala Thr Thr Val
20 25 30

Val Gly Asn Ala Gly Asn Gly Leu Val Thr Val Thr Met Ala Gly Asn
35 40 45

Gly Glu Val Phe Ala Val Thr Val Asp Pro Lys Val Val Asp Pro Glu
50 55 60

Asp Val Glu Thr Leu Gln Asp Leu Leu Leu Gly Ala Phe Lys Asp Ala
65 70 75 80

His Asn Lys Val Ala Asn Val Ala Glu Glu Lys Met Gly Pro Leu Ser
85 90 95

Gln Gly Met Gly Gly Leu Phe
100

<210> 559
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> RXN01263

<400> 559
agtggccttt ggagttattt tgatgacggt atcggcgact gctgggatcc tcctcttttt 60

atctccaaat agaagccaag ctgcgccacc ccaatttagt ttg acc ccg tat gat 115
Leu Thr Pro Tyr Asp
1 5

cca acc gct gta aat aag gag tcg gaa aaa gaa gca gca aag aat ctg 163
Pro Thr Ala Val Asn Lys Glu Ser Glu Lys Glu Ala Ala Lys Asn Leu
10 15 20

ttt ggc gct gag gcg ttg aca gtg gat ccg gat gcc ggt gag gtt gtt 211
Phe Gly Ala Glu Ala Leu Thr Val Asp Pro Asp Ala Gly Glu Val Val
25 30 35

gat cga gta gat aat ttt tat ccg acg act gct aag gca aaa cga gat 259
Asp Arg Val Asp Asn Phe Tyr Pro Thr Thr Ala Lys Ala Lys Arg Asp
40 45 50

tac cca agt aac tat gca gcg ggt tgt cac caa gaa gtc aat gag act 307
Tyr Pro Ser Asn Tyr Ala Ala Gly Cys His Gln Glu Val Asn Glu Thr
55 60 65

agt cct gag tca tgt gtt tat ggt gat aaa aat tct gat ttt tct gta 355

```
Ser Pro Glu Ser Cys Val Tyr Gly Asp Lys Asn Ser Asp Phe Ser Val
 70                  75                  80                  85

gca ctt gtc ggt gac tcc cac gct ggt cat tgg ctt cct gcc ttg gaa   403
Ala Leu Val Gly Asp Ser His Ala Gly His Trp Leu Pro Ala Leu Glu
                 90                  95                 100

cca att gct gaa gca cag ggg tgg aga ttg gaa gtt tat aca aag tca   451
Pro Ile Ala Glu Ala Gln Gly Trp Arg Leu Glu Val Tyr Thr Lys Ser
            105                 110                 115

cag tgt cca ctc ata agc act gcg atc aaa ctt ggt gaa act ttt tat   499
Gln Cys Pro Leu Ile Ser Thr Ala Ile Lys Leu Gly Glu Thr Phe Tyr
        120                 125                 130

gca gaa tgc tat gag tgg aat gaa aaa tta ctt gct aag cta act gga   547
Ala Glu Cys Tyr Glu Trp Asn Glu Lys Leu Leu Ala Lys Leu Thr Gly
    135                 140                 145

cct tct gca cca aat cat gtg att gta agt agc caa cgt tac gct tct   595
Pro Ser Ala Pro Asn His Val Ile Val Ser Ser Gln Arg Tyr Ala Ser
150                 155                 160                 165

gca aat ccg tta atc gat agt gtc gcg acg gga acc gtt tcc gaa gga   643
Ala Asn Pro Leu Ile Asp Ser Val Ala Thr Gly Thr Val Ser Glu Gly
                170                 175                 180

tat gaa atg gca tgg aat tca tta aaa gat gca ggt gtt tct att tct   691
Tyr Glu Met Ala Trp Asn Ser Leu Lys Asp Ala Gly Val Ser Ile Ser
            185                 190                 195

gta ctt ctt gat act cct cgg ccg caa att gat atc cca gaa tgt gta   739
Val Leu Leu Asp Thr Pro Arg Pro Gln Ile Asp Ile Pro Glu Cys Val
        200                 205                 210

gca tca aac cgc gat aat ctc tca gaa tgt tca gtt cac cgg agc gtt   787
Ala Ser Asn Arg Asp Asn Leu Ser Glu Cys Ser Val His Arg Ser Val
    215                 220                 225

gcg ctt ggg act gaa gct cat cct cag caa aaa act gca gct caa aat   835
Ala Leu Gly Thr Glu Ala His Pro Gln Gln Lys Thr Ala Ala Gln Asn
230                 235                 240                 245

ata gac gtg cct gta ttg gat ttg agt aat tgg att tgt ccg gaa gaa   883
Ile Asp Val Pro Val Leu Asp Leu Ser Asn Trp Ile Cys Pro Glu Glu
                250                 255                 260

tat tgc tcc gct gtt atc gga aat gtt ttg gta tac agg gat tca cat   931
Tyr Cys Ser Ala Val Ile Gly Asn Val Leu Val Tyr Arg Asp Ser His
            265                 270                 275

cat ttg acc gct acg tat gct cgt agt ctc tct agc gca tta tgg aat   979
His Leu Thr Ala Thr Tyr Ala Arg Ser Leu Ser Ser Ala Leu Trp Asn
        280                 285                 290

gag ttg gtt gcc tca aat ggt gag cct ttt aag taagaggtag ttgttcaagt 1032
Glu Leu Val Ala Ser Asn Gly Glu Pro Phe Lys
    295                 300

agc                                                               1035
```

<210> 560
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 560
Leu Thr Pro Tyr Asp Pro Thr Ala Val Asn Lys Glu Ser Glu Lys Glu
1 5 10 15

Ala Ala Lys Asn Leu Phe Gly Ala Glu Ala Leu Thr Val Asp Pro Asp
20 25 30

Ala Gly Glu Val Val Asp Arg Val Asp Asn Phe Tyr Pro Thr Thr Ala
35 40 45

Lys Ala Lys Arg Asp Tyr Pro Ser Asn Tyr Ala Ala Gly Cys His Gln
50 55 60

Glu Val Asn Glu Thr Ser Pro Glu Ser Cys Val Tyr Gly Asp Lys Asn
65 70 75 80

Ser Asp Phe Ser Val Ala Leu Val Gly Asp Ser His Ala Gly His Trp
85 90 95

Leu Pro Ala Leu Glu Pro Ile Ala Glu Ala Gln Gly Trp Arg Leu Glu
100 105 110

Val Tyr Thr Lys Ser Gln Cys Pro Leu Ile Ser Thr Ala Ile Lys Leu
115 120 125

Gly Glu Thr Phe Tyr Ala Glu Cys Tyr Glu Trp Asn Glu Lys Leu Leu
130 135 140

Ala Lys Leu Thr Gly Pro Ser Ala Pro Asn His Val Ile Val Ser Ser
145 150 155 160

Gln Arg Tyr Ala Ser Ala Asn Pro Leu Ile Asp Ser Val Ala Thr Gly
165 170 175

Thr Val Ser Glu Gly Tyr Glu Met Ala Trp Asn Ser Leu Lys Asp Ala
180 185 190

Gly Val Ser Ile Ser Val Leu Leu Asp Thr Pro Arg Pro Gln Ile Asp
195 200 205

Ile Pro Glu Cys Val Ala Ser Asn Arg Asp Asn Leu Ser Glu Cys Ser
210 215 220

Val His Arg Ser Val Ala Leu Gly Thr Glu Ala His Pro Gln Gln Lys
225 230 235 240

Thr Ala Ala Gln Asn Ile Asp Val Pro Val Leu Asp Leu Ser Asn Trp
245 250 255

Ile Cys Pro Glu Glu Tyr Cys Ser Ala Val Ile Gly Asn Val Leu Val
260 265 270

Tyr Arg Asp Ser His His Leu Thr Ala Thr Tyr Ala Arg Ser Leu Ser
275 280 285

```
Ser Ala Leu Trp Asn Glu Leu Val Ala Ser Asn Gly Glu Pro Phe Lys
    290                 295                 300
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<210> 561
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> FRXA01263

<400> 561

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agtggccttt ggagttattt tgatgacggt atcggcgact gctgggatcc tcctcttttt 60

atctccaaat agaagccaag ctgcgccacc ccaatttagt ttg acc ccg tat gat   115
                                              Leu Thr Pro Tyr Asp
                                                1               5

cca acc gct gta aat aag gag tcg gaa aaa gaa gca gca aag aat ctg   163
Pro Thr Ala Val Asn Lys Glu Ser Glu Lys Glu Ala Ala Lys Asn Leu
                10                  15                  20

ttt ggc gct gag gcg ttg aca gtg gat ccg gat gcc ggt gag gtt gtt   211
Phe Gly Ala Glu Ala Leu Thr Val Asp Pro Asp Ala Gly Glu Val Val
            25                  30                  35

gat cga gta gat aat ttt tat ccg acg act gct aag gca aaa cga gat   259
Asp Arg Val Asp Asn Phe Tyr Pro Thr Thr Ala Lys Ala Lys Arg Asp
        40                  45                  50

tac cca agt aac tat gca gcg ggt tgt cac caa gaa gtc aat gag act   307
Tyr Pro Ser Asn Tyr Ala Ala Gly Cys His Gln Glu Val Asn Glu Thr
    55                  60                  65

agt cct gag tca tgt gtt tat ggt gat aaa aat tct gat ttt tct gta   355
Ser Pro Glu Ser Cys Val Tyr Gly Asp Lys Asn Ser Asp Phe Ser Val
70                  75                  80                  85

gca ctt gtc ggt gac tcc cac gct ggt cat tgg ctt cct gcc ttg gaa   403
Ala Leu Val Gly Asp Ser His Ala Gly His Trp Leu Pro Ala Leu Glu
                90                  95                  100

cca att gct gaa gca cag ggg tgg aga ttg gaa gtt tat aca aag tca   451
Pro Ile Ala Glu Ala Gln Gly Trp Arg Leu Glu Val Tyr Thr Lys Ser
            105                 110                 115

cag tgt cca ctc ata agc act gcg atc aaa ctt ggt gaa act ttt tat   499
Gln Cys Pro Leu Ile Ser Thr Ala Ile Lys Leu Gly Glu Thr Phe Tyr
        120                 125                 130

gca gaa tgc tat gag tgg aat gaa aaa tta ctt gct aag cta act gga   547
Ala Glu Cys Tyr Glu Trp Asn Glu Lys Leu Leu Ala Lys Leu Thr Gly
    135                 140                 145

cct tct gca cca aat cat gtg att gta agt agc caa cgt tac gct tct   595
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Pro Ser Ala Pro Asn His Val Ile Val Ser Ser Gln Arg Tyr Ala Ser
150                 155                 160                 165

gca aat ccg tta atc gat agt gtc gcg acg gga acc gtt tcc gaa gga   643
Ala Asn Pro Leu Ile Asp Ser Val Ala Thr Gly Thr Val Ser Glu Gly
                170                 175                 180

tat gaa atg gca tgg aat tca tta aaa gat gca ggt gtt tct att tct   691
Tyr Glu Met Ala Trp Asn Ser Leu Lys Asp Ala Gly Val Ser Ile Ser
            185                 190                 195

gta ctt ctt gat act cct cgg ccg caa att gat atc cca gaa tgt gta   739
Val Leu Leu Asp Thr Pro Arg Pro Gln Ile Asp Ile Pro Glu Cys Val
        200                 205                 210

gca tca aac cgc gat aat ctc tca gaa tgt tca gtt cac cgg agc gtt   787
Ala Ser Asn Arg Asp Asn Leu Ser Glu Cys Ser Val His Arg Ser Val
    215                 220                 225

gcg ctt ggg act gaa gct cat cct cag caa aaa act gca gct caa aat   835
Ala Leu Gly Thr Glu Ala His Pro Gln Gln Lys Thr Ala Ala Gln Asn
230                 235                 240                 245

ata gac gtg cct gta ttg gat ttg agt aat tgg att tgt ccg gaa gaa   883
Ile Asp Val Pro Val Leu Asp Leu Ser Asn Trp Ile Cys Pro Glu Glu
                250                 255                 260

tat tgc tcc gct gtt atc gga aat gtt ttg gta tac agg gat tca cat   931
Tyr Cys Ser Ala Val Ile Gly Asn Val Leu Val Tyr Arg Asp Ser His
            265                 270                 275

cat ttg acc gct acg tat gct cgt agt ctc tct agc gca tta tgg aat   979
His Leu Thr Ala Thr Tyr Ala Arg Ser Leu Ser Ser Ala Leu Trp Asn
        280                 285                 290

gag ttg gtt gcc tca aat ggt gag cct ttt aag taagaggtag ttgttcaagt 1032
Glu Leu Val Ala Ser Asn Gly Glu Pro Phe Lys
    295                 300

agc                                                               1035


<210> 562
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 562
Leu Thr Pro Tyr Asp Pro Thr Ala Val Asn Lys Glu Ser Glu Lys Glu
  1               5                  10                  15

Ala Ala Lys Asn Leu Phe Gly Ala Glu Ala Leu Thr Val Asp Pro Asp
             20                  25                  30

Ala Gly Glu Val Val Asp Arg Val Asp Asn Phe Tyr Pro Thr Thr Ala
         35                  40                  45

Lys Ala Lys Arg Asp Tyr Pro Ser Asn Tyr Ala Ala Gly Cys His Gln
     50                  55                  60

Glu Val Asn Glu Thr Ser Pro Glu Ser Cys Val Tyr Gly Asp Lys Asn
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 65                  70                  75                  80

Ser Asp Phe Ser Val Ala Leu Val Gly Asp Ser His Ala Gly His Trp
                85                  90                  95

Leu Pro Ala Leu Glu Pro Ile Ala Glu Ala Gln Gly Trp Arg Leu Glu
            100                 105                 110

Val Tyr Thr Lys Ser Gln Cys Pro Leu Ile Ser Thr Ala Ile Lys Leu
        115                 120                 125

Gly Glu Thr Phe Tyr Ala Glu Cys Tyr Glu Trp Asn Glu Lys Leu Leu
    130                 135                 140

Ala Lys Leu Thr Gly Pro Ser Ala Pro Asn His Val Ile Val Ser Ser
145                 150                 155                 160

Gln Arg Tyr Ala Ser Ala Asn Pro Leu Ile Asp Ser Val Ala Thr Gly
                165                 170                 175

Thr Val Ser Glu Gly Tyr Glu Met Ala Trp Asn Ser Leu Lys Asp Ala
            180                 185                 190

Gly Val Ser Ile Ser Val Leu Leu Asp Thr Pro Arg Pro Gln Ile Asp
        195                 200                 205

Ile Pro Glu Cys Val Ala Ser Asn Arg Asp Asn Leu Ser Glu Cys Ser
    210                 215                 220

Val His Arg Ser Val Ala Leu Gly Thr Glu Ala His Pro Gln Gln Lys
225                 230                 235                 240

Thr Ala Ala Gln Asn Ile Asp Val Pro Val Leu Asp Leu Ser Asn Trp
                245                 250                 255

Ile Cys Pro Glu Glu Tyr Cys Ser Ala Val Ile Gly Asn Val Leu Val
            260                 265                 270

Tyr Arg Asp Ser His His Leu Thr Ala Thr Tyr Ala Arg Ser Leu Ser
        275                 280                 285

Ser Ala Leu Trp Asn Glu Leu Val Ala Ser Asn Gly Glu Pro Phe Lys
    290                 295                 300
```

<210> 563
<211> 1158
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1135)
<223> RXN01266

<400> 563
gattgtgaag ttttatatct gtcatattct ggtgattttc gccctgctca tgaagtggcg 60

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gacgagcaat ggcccgatat agatttagta aggaactaaa atg cca aaa gta agt   115
                                            Met Pro Lys Val Ser
                                              1               5

gtg gtt act ggt ttt tat aac cgc tgt gag cat tta gaa cga acc att   163
Val Val Thr Gly Phe Tyr Asn Arg Cys Glu His Leu Glu Arg Thr Ile
                 10                  15                  20

gag tct att ctt aac caa act tat agc gat ttt gaa tta att gtt ttt   211
Glu Ser Ile Leu Asn Gln Thr Tyr Ser Asp Phe Glu Leu Ile Val Phe
             25                  30                  35

gat gat gca tcg aca gat gga aca gct tca cga ttg tta gag tta aaa   259
Asp Asp Ala Ser Thr Asp Gly Thr Ala Ser Arg Leu Leu Glu Leu Lys
         40                  45                  50

gaa aaa tat gat gat ccg cgt ttc cga ttt atc att cat gaa gag aat   307
Glu Lys Tyr Asp Asp Pro Arg Phe Arg Phe Ile Ile His Glu Glu Asn
     55                  60                  65

aaa ggt ttc gta aaa ggg tta tca gaa gca att tct gga gct aaa ggg   355
Lys Gly Phe Val Lys Gly Leu Ser Glu Ala Ile Ser Gly Ala Lys Gly
 70                  75                  80                  85

cag tat att gca gtc cag gga tca ggc gat gta tct ctt cct cgc cgt   403
Gln Tyr Ile Ala Val Gln Gly Ser Gly Asp Val Ser Leu Pro Arg Arg
                 90                  95                 100

tta gag ctt cag gta gag ttt cta gac gcg aat cct tcg gta ggt gct   451
Leu Glu Leu Gln Val Glu Phe Leu Asp Ala Asn Pro Ser Val Gly Ala
             105                 110                 115

gtg ggt ggt gct atc tat aat att caa gaa gat acg gga aca cgc aac   499
Val Gly Gly Ala Ile Tyr Asn Ile Gln Glu Asp Thr Gly Thr Arg Asn
         120                 125                 130

cca cag aga ttt gaa aag cca att gct aca ttc gat gat tta ttg aca   547
Pro Gln Arg Phe Glu Lys Pro Ile Ala Thr Phe Asp Asp Leu Leu Thr
     135                 140                 145

tct aat ccg ttc act cac gga gaa gtg atg tat cgc tta gac ctt tat   595
Ser Asn Pro Phe Thr His Gly Glu Val Met Tyr Arg Leu Asp Leu Tyr
150                 155                 160                 165

aag agt ata ggt ggg tat cga agt ggc ttt act ttt gct caa gat cgt   643
Lys Ser Ile Gly Gly Tyr Arg Ser Gly Phe Thr Phe Ala Gln Asp Arg
                 170                 175                 180

gat tta tgg ttg agg atg gcg aaa aaa gca gat ctg ggt atc att cca   691
Asp Leu Trp Leu Arg Met Ala Lys Lys Ala Asp Leu Gly Ile Ile Pro
             185                 190                 195

gat ttt ctt tat cac cgt tac aca ctt tta gat ggt gtc tct ttc gtc   739
Asp Phe Leu Tyr His Arg Tyr Thr Leu Leu Asp Gly Val Ser Phe Val
         200                 205                 210

ccg gat aaa act ata cgt cag cga tgc ttt tca gaa gct gcg gtg cga   787
Pro Asp Lys Thr Ile Arg Gln Arg Cys Phe Ser Glu Ala Ala Val Arg
     215                 220                 225

ctg gca tta atg cca gaa gag gaa gga gct tta gcc tac tct agg ctg   835
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Leu Ala Leu Met Pro Glu Glu Glu Gly Ala Leu Ala Tyr Ser Arg Leu
230                 235                 240                 245

gaa gct gaa ggg cct act gcc gta gtt cct atc gct gat aga gct gtt   883
Glu Ala Glu Gly Pro Thr Ala Val Val Pro Ile Ala Asp Arg Ala Val
                250                 255                 260

cag aaa ttt gtc cct aaa gcg gct att cgc tta tgt cta tat ggt gct   931
Gln Lys Phe Val Pro Lys Ala Ala Ile Arg Leu Cys Leu Tyr Gly Ala
            265                 270                 275

ccg gaa act ggt tta cac atg gct cga gac tat atc cag aac cct ctg   979
Pro Glu Thr Gly Leu His Met Ala Arg Asp Tyr Ile Gln Asn Pro Leu
        280                 285                 290

cgc cgt acc ata gtt gta gtt ttg atc agc atc tat tcg tct aga tta   1027
Arg Arg Thr Ile Val Val Val Leu Ile Ser Ile Tyr Ser Ser Arg Leu
    295                 300                 305

att aag cct ctt caa gat att cta tat aag tct att ttt aag ggg gtc   1075
Ile Lys Pro Leu Gln Asp Ile Leu Tyr Lys Ser Ile Phe Lys Gly Val
310                 315                 320                 325

tcg att tct aaa cct att aag agt tca ctc gtg aag ttt aca aga aga   1123
Ser Ile Ser Lys Pro Ile Lys Ser Ser Leu Val Lys Phe Thr Arg Arg
                330                 335                 340

att caa ggg aag tagcgaaaaa ccgcatctac caa                        1158
Ile Gln Gly Lys
            345


<210> 564
<211> 345
<212> PRT
<213> Corynebacterium glutamicum

<400> 564
Met Pro Lys Val Ser Val Val Thr Gly Phe Tyr Asn Arg Cys Glu His
  1               5                  10                  15

Leu Glu Arg Thr Ile Glu Ser Ile Leu Asn Gln Thr Tyr Ser Asp Phe
             20                  25                  30

Glu Leu Ile Val Phe Asp Asp Ala Ser Thr Asp Gly Thr Ala Ser Arg
         35                  40                  45

Leu Leu Glu Leu Lys Glu Lys Tyr Asp Asp Pro Arg Phe Arg Phe Ile
     50                  55                  60

Ile His Glu Glu Asn Lys Gly Phe Val Lys Gly Leu Ser Glu Ala Ile
 65                  70                  75                  80

Ser Gly Ala Lys Gly Gln Tyr Ile Ala Val Gln Gly Ser Gly Asp Val
                 85                  90                  95

Ser Leu Pro Arg Arg Leu Glu Leu Gln Val Glu Phe Leu Asp Ala Asn
            100                 105                 110

Pro Ser Val Gly Ala Val Gly Gly Ala Ile Tyr Asn Ile Gln Glu Asp
        115                 120                 125
```

```
Thr Gly Thr Arg Asn Pro Gln Arg Phe Glu Lys Pro Ile Ala Thr Phe
    130                 135                 140

Asp Asp Leu Leu Thr Ser Asn Pro Phe Thr His Gly Glu Val Met Tyr
145                 150                 155                 160

Arg Leu Asp Leu Tyr Lys Ser Ile Gly Gly Tyr Arg Ser Gly Phe Thr
                165                 170                 175

Phe Ala Gln Asp Arg Asp Leu Trp Leu Arg Met Ala Lys Lys Ala Asp
            180                 185                 190

Leu Gly Ile Ile Pro Asp Phe Leu Tyr His Arg Tyr Thr Leu Leu Asp
        195                 200                 205

Gly Val Ser Phe Val Pro Asp Lys Thr Ile Arg Gln Arg Cys Phe Ser
    210                 215                 220

Glu Ala Ala Val Arg Leu Ala Leu Met Pro Glu Glu Glu Gly Ala Leu
225                 230                 235                 240

Ala Tyr Ser Arg Leu Glu Ala Glu Gly Pro Thr Ala Val Val Pro Ile
                245                 250                 255

Ala Asp Arg Ala Val Gln Lys Phe Val Pro Lys Ala Ala Ile Arg Leu
            260                 265                 270

Cys Leu Tyr Gly Ala Pro Glu Thr Gly Leu His Met Ala Arg Asp Tyr
        275                 280                 285

Ile Gln Asn Pro Leu Arg Arg Thr Ile Val Val Val Leu Ile Ser Ile
    290                 295                 300

Tyr Ser Ser Arg Leu Ile Lys Pro Leu Gln Asp Ile Leu Tyr Lys Ser
305                 310                 315                 320

Ile Phe Lys Gly Val Ser Ile Ser Lys Pro Ile Lys Ser Ser Leu Val
                325                 330                 335

Lys Phe Thr Arg Arg Ile Gln Gly Lys
            340                 345
```

<210> 565
<211> 1158
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1135)
<223> FRXA01266

<400> 565
gattgtgaag ttttatatct gtcatattct ggtgattttc gccctgctca tgaagtggcg 60

gacgagcaat ggcccgatat agatttagta aggaactaaa atg cca aaa gta agt 115
                                                Met Pro Lys Val Ser
                                                  1   5

```
gtg gtt act ggt ttt tat aac cgc tgt gag cat tta gaa cga acc att   163
Val Val Thr Gly Phe Tyr Asn Arg Cys Glu His Leu Glu Arg Thr Ile
                 10                  15                  20

gag tct att ctt aac caa act tat agc gat ttt gaa tta att gtt ttt   211
Glu Ser Ile Leu Asn Gln Thr Tyr Ser Asp Phe Glu Leu Ile Val Phe
             25                  30                  35

gat gat gca tcg aca gat gga aca gct tca cga ttg tta gag tta aaa   259
Asp Asp Ala Ser Thr Asp Gly Thr Ala Ser Arg Leu Leu Glu Leu Lys
         40                  45                  50

gaa aaa tat gat gat ccg cgt ttc cga ttt atc att cat gaa gag aat   307
Glu Lys Tyr Asp Asp Pro Arg Phe Arg Phe Ile Ile His Glu Glu Asn
     55                  60                  65

aaa ggt ttc gta aaa ggg tta tca gaa gca att tct gga gct aaa ggg   355
Lys Gly Phe Val Lys Gly Leu Ser Glu Ala Ile Ser Gly Ala Lys Gly
 70                  75                  80                  85

cag tat att gca gtc cag gga tca ggc gat gta tct ctt cct cgc cgt   403
Gln Tyr Ile Ala Val Gln Gly Ser Gly Asp Val Ser Leu Pro Arg Arg
                 90                  95                 100

tta gag ctt cag gta gag ttt cta gac gcg aat cct tcg gta ggt gct   451
Leu Glu Leu Gln Val Glu Phe Leu Asp Ala Asn Pro Ser Val Gly Ala
             105                 110                 115

gtg ggt ggt gct atc tat aat att caa gaa gat acg gga aca cgc aac   499
Val Gly Gly Ala Ile Tyr Asn Ile Gln Glu Asp Thr Gly Thr Arg Asn
         120                 125                 130

cca cag aga ttt gaa aag cca att gct aca ttc gat gat tta ttg aca   547
Pro Gln Arg Phe Glu Lys Pro Ile Ala Thr Phe Asp Asp Leu Leu Thr
     135                 140                 145

tct aat ccg ttc act cac gga gaa gtg atg tat cgc tta gac ctt tat   595
Ser Asn Pro Phe Thr His Gly Glu Val Met Tyr Arg Leu Asp Leu Tyr
150                 155                 160                 165

aag agt ata ggt ggg tat cga agt ggc ttt act ttt gct caa gat cgt   643
Lys Ser Ile Gly Gly Tyr Arg Ser Gly Phe Thr Phe Ala Gln Asp Arg
                 170                 175                 180

gat tta tgg ttg agg atg gcg aaa aaa gca gat ctg ggt atc att cca   691
Asp Leu Trp Leu Arg Met Ala Lys Lys Ala Asp Leu Gly Ile Ile Pro
             185                 190                 195

gat ttt ctt tat cac cgt tac aca ctt tta gat ggt gtc tct ttc gtc   739
Asp Phe Leu Tyr His Arg Tyr Thr Leu Leu Asp Gly Val Ser Phe Val
         200                 205                 210

ccg gat aaa act ata cgt cag cga tgc ttt tca gaa gct gcg gtg cga   787
Pro Asp Lys Thr Ile Arg Gln Arg Cys Phe Ser Glu Ala Ala Val Arg
     215                 220                 225

ctg gca tta atg cca gaa gag gaa gga gct tta gcc tac tct agg ctg   835
Leu Ala Leu Met Pro Glu Glu Glu Gly Ala Leu Ala Tyr Ser Arg Leu
230                 235                 240                 245

gaa gct gaa ggg cct act gcc gta gtt cct atc gct gat aga gct gtt   883
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```
Glu Ala Glu Gly Pro Thr Ala Val Val Pro Ile Ala Asp Arg Ala Val
                250                 255                 260

cag aaa ttt gtc cct aaa gcg gct att cgc tta tgt cta tat ggt gct   931
Gln Lys Phe Val Pro Lys Ala Ala Ile Arg Leu Cys Leu Tyr Gly Ala
            265                 270                 275

ccg gaa act ggt tta cac atg gct cga gac tat atc cag aac cct ctg   979
Pro Glu Thr Gly Leu His Met Ala Arg Asp Tyr Ile Gln Asn Pro Leu
        280                 285                 290

cgc cgt acc ata gtt gta gtt ttg atc agc atc tat tcg tct aga tta   1027
Arg Arg Thr Ile Val Val Val Leu Ile Ser Ile Tyr Ser Ser Arg Leu
    295                 300                 305

att aag cct ctt caa gat att cta tat aag tct att ttt aag ggg gtc   1075
Ile Lys Pro Leu Gln Asp Ile Leu Tyr Lys Ser Ile Phe Lys Gly Val
310                 315                 320                 325

tcg att tct aaa cct att aag agt tca ctc gtg aag ttt aca aga aga   1123
Ser Ile Ser Lys Pro Ile Lys Ser Ser Leu Val Lys Phe Thr Arg Arg
                330                 335                 340

att caa ggg aag tagcgaaaaa ccgcatctac caa                        1158
Ile Gln Gly Lys
            345


<210> 566
<211> 345
<212> PRT
<213> Corynebacterium glutamicum

<400> 566
Met Pro Lys Val Ser Val Val Thr Gly Phe Tyr Asn Arg Cys Glu His
  1               5                  10                  15

Leu Glu Arg Thr Ile Glu Ser Ile Leu Asn Gln Thr Tyr Ser Asp Phe
             20                  25                  30

Glu Leu Ile Val Phe Asp Asp Ala Ser Thr Asp Gly Thr Ala Ser Arg
         35                  40                  45

Leu Leu Glu Leu Lys Glu Lys Tyr Asp Asp Pro Arg Phe Arg Phe Ile
     50                  55                  60

Ile His Glu Glu Asn Lys Gly Phe Val Lys Gly Leu Ser Glu Ala Ile
 65                  70                  75                  80

Ser Gly Ala Lys Gly Gln Tyr Ile Ala Val Gln Gly Ser Gly Asp Val
                 85                  90                  95

Ser Leu Pro Arg Arg Leu Glu Leu Gln Val Glu Phe Leu Asp Ala Asn
            100                 105                 110

Pro Ser Val Gly Ala Val Gly Gly Ala Ile Tyr Asn Ile Gln Glu Asp
        115                 120                 125

Thr Gly Thr Arg Asn Pro Gln Arg Phe Glu Lys Pro Ile Ala Thr Phe
    130                 135                 140
```

```
Asp Asp Leu Leu Thr Ser Asn Pro Phe Thr His Gly Glu Val Met Tyr
145                 150                 155                 160

Arg Leu Asp Leu Tyr Lys Ser Ile Gly Gly Tyr Arg Ser Gly Phe Thr
                165                 170                 175

Phe Ala Gln Asp Arg Asp Leu Trp Leu Arg Met Ala Lys Lys Ala Asp
            180                 185                 190

Leu Gly Ile Ile Pro Asp Phe Leu Tyr His Arg Tyr Thr Leu Leu Asp
        195                 200                 205

Gly Val Ser Phe Val Pro Asp Lys Thr Ile Arg Gln Arg Cys Phe Ser
    210                 215                 220

Glu Ala Ala Val Arg Leu Ala Leu Met Pro Glu Glu Glu Gly Ala Leu
225                 230                 235                 240

Ala Tyr Ser Arg Leu Glu Ala Glu Gly Pro Thr Ala Val Val Pro Ile
                245                 250                 255

Ala Asp Arg Ala Val Gln Lys Phe Val Pro Lys Ala Ala Ile Arg Leu
            260                 265                 270

Cys Leu Tyr Gly Ala Pro Glu Thr Gly Leu His Met Ala Arg Asp Tyr
        275                 280                 285

Ile Gln Asn Pro Leu Arg Arg Thr Ile Val Val Val Leu Ile Ser Ile
    290                 295                 300

Tyr Ser Ser Arg Leu Ile Lys Pro Leu Gln Asp Ile Leu Tyr Lys Ser
305                 310                 315                 320

Ile Phe Lys Gly Val Ser Ile Ser Lys Pro Ile Lys Ser Ser Leu Val
                325                 330                 335

Lys Phe Thr Arg Arg Ile Gln Gly Lys
            340                 345
```

<210> 567
<211> 1041
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1018)
<223> RXN01275

<400> 567

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cgccatacta ggctcggcct tttcgacggg aactcggata ggcttctgta aaaccatccc 60

cgttgaagag agactcgtgg ctgaaataac caccccatta atg gaa aaa att cgc   115
                                            Met Glu Lys Ile Arg
                                              1               5

tca ccc gca gtc caa tca gat gca ctg cag gtt ttt aaa tca gca ctt   163
Ser Pro Ala Val Gln Ser Asp Ala Leu Gln Val Phe Lys Ser Ala Leu
                 10                  15                  20
```

```
gct gcg aca gtc acg tgg tgg att tcg gtt aac ctc ctt aac tcc caa   211
Ala Ala Thr Val Thr Trp Trp Ile Ser Val Asn Leu Leu Asn Ser Gln
            25                  30                  35

cta ccc ttt tta gct ccc tgg gta gcg tta atg acg atg caa ttc acc   259
Leu Pro Phe Leu Ala Pro Trp Val Ala Leu Met Thr Met Gln Phe Thr
        40                  45                  50

gtc tac cac acc ttt atc agt gga att cag act gca att gct tct gtc   307
Val Tyr His Thr Phe Ile Ser Gly Ile Gln Thr Ala Ile Ala Ser Val
    55                  60                  65

atc gga gtt gga ctt tcc ttt gtc ata ggc act tac tta gac gta agt   355
Ile Gly Val Gly Leu Ser Phe Val Ile Gly Thr Tyr Leu Asp Val Ser
70                  75                  80                  85

gtg tgg act ttt ggc ctt gca atg gtc ata gga tta ata ggt gca cga   403
Val Trp Thr Phe Gly Leu Ala Met Val Ile Gly Leu Ile Gly Ala Arg
                90                  95                  100

gta cca aag ctc cgc gcg gaa gga ata ggt att gct act aca tcc att   451
Val Pro Lys Leu Arg Ala Glu Gly Ile Gly Ile Ala Thr Thr Ser Ile
            105                 110                 115

ttt ctt ctt gcc tcc ggg ttt gat gat caa caa ccc ctt cta tac gac   499
Phe Leu Leu Ala Ser Gly Phe Asp Asp Gln Gln Pro Leu Leu Tyr Asp
        120                 125                 130

cgt att tta gag atc ctg ctc ggc gtg gct gtt gcc ata gcc atc aac   547
Arg Ile Leu Glu Ile Leu Leu Gly Val Ala Val Ala Ile Ala Ile Asn
    135                 140                 145

ctc atc atc ttt cct ccc tta cgc gac cag gag gca aac atg gtg gta   595
Leu Ile Ile Phe Pro Pro Leu Arg Asp Gln Glu Ala Asn Met Val Val
150                 155                 160                 165

gga aac tta gat cgg agg atg ggt gag gtt tta caa aaa atg gcc gat   643
Gly Asn Leu Asp Arg Arg Met Gly Glu Val Leu Gln Lys Met Ala Asp
                170                 175                 180

gag ctt gca gaa aag tgg aat atc gac aat gca gat gag tgg ctg gaa   691
Glu Leu Ala Glu Lys Trp Asn Ile Asp Asn Ala Asp Glu Trp Leu Glu
            185                 190                 195

gaa att aat tct att aac aat gac cta gaa aaa gcg tgg cac tcc gtg   739
Glu Ile Asn Ser Ile Asn Asn Asp Leu Glu Lys Ala Trp His Ser Val
        200                 205                 210

cgg ttc gtt cgc gaa agc cgt cga gtt aat cct cgt aaa atc cgc atc   787
Arg Phe Val Arg Glu Ser Arg Arg Val Asn Pro Arg Lys Ile Arg Ile
    215                 220                 225

caa gag ggc cgc ccc cag cct acg gaa aca agt tat gaa tca aac ctc   835
Gln Glu Gly Arg Pro Gln Pro Thr Glu Thr Ser Tyr Glu Ser Asn Leu
230                 235                 240                 245

acc agc att gat gaa ggg atc gct cat tta cgc cac ctt gcc cgt act   883
Thr Ser Ile Asp Glu Gly Ile Ala His Leu Arg His Leu Ala Arg Thr
                250                 255                 260

ctt cgt gat acc ccg att ata gat tcc gac tgg gga tcc agt att cca   931
```

```
Leu Arg Asp Thr Pro Ile Ile Asp Ser Asp Trp Gly Ser Ser Ile Pro
            265                 270                 275

gca aca gtg ggt atc cct tat gca cga tgc cgg agc ttt gct cgc aga   979
Ala Thr Val Gly Ile Pro Tyr Ala Arg Cys Arg Ser Phe Ala Arg Arg
        280                 285                 290

tcc gaa tca gga aat aga tcc tat ccg cga ccg gct ctc taaactttca   1028
Ser Glu Ser Gly Asn Arg Ser Tyr Pro Arg Pro Ala Leu
    295                 300                 305

agtgagatga gtg                                                  1041


<210> 568
<211> 306
<212> PRT
<213> Corynebacterium glutamicum

<400> 568
Met Glu Lys Ile Arg Ser Pro Ala Val Gln Ser Asp Ala Leu Gln Val
  1               5                  10                  15

Phe Lys Ser Ala Leu Ala Ala Thr Val Thr Trp Trp Ile Ser Val Asn
             20                  25                  30

Leu Leu Asn Ser Gln Leu Pro Phe Leu Ala Pro Trp Val Ala Leu Met
         35                  40                  45

Thr Met Gln Phe Thr Val Tyr His Thr Phe Ile Ser Gly Ile Gln Thr
     50                  55                  60

Ala Ile Ala Ser Val Ile Gly Val Gly Leu Ser Phe Val Ile Gly Thr
 65                  70                  75                  80

Tyr Leu Asp Val Ser Val Trp Thr Phe Gly Leu Ala Met Val Ile Gly
                 85                  90                  95

Leu Ile Gly Ala Arg Val Pro Lys Leu Arg Ala Glu Gly Ile Gly Ile
            100                 105                 110

Ala Thr Thr Ser Ile Phe Leu Leu Ala Ser Gly Phe Asp Asp Gln Gln
        115                 120                 125

Pro Leu Leu Tyr Asp Arg Ile Leu Glu Ile Leu Leu Gly Val Ala Val
    130                 135                 140

Ala Ile Ala Ile Asn Leu Ile Ile Phe Pro Pro Leu Arg Asp Gln Glu
145                 150                 155                 160

Ala Asn Met Val Val Gly Asn Leu Asp Arg Arg Met Gly Glu Val Leu
                165                 170                 175

Gln Lys Met Ala Asp Glu Leu Ala Glu Lys Trp Asn Ile Asp Asn Ala
            180                 185                 190

Asp Glu Trp Leu Glu Glu Ile Asn Ser Ile Asn Asn Asp Leu Glu Lys
        195                 200                 205

Ala Trp His Ser Val Arg Phe Val Arg Glu Ser Arg Arg Val Asn Pro
    210                 215                 220
```

```
Arg Lys Ile Arg Ile Gln Glu Gly Arg Pro Gln Pro Thr Glu Thr Ser
225                 230                 235                 240

Tyr Glu Ser Asn Leu Thr Ser Ile Asp Glu Gly Ile Ala His Leu Arg
                245                 250                 255

His Leu Ala Arg Thr Leu Arg Asp Thr Pro Ile Ile Asp Ser Asp Trp
            260                 265                 270

Gly Ser Ser Ile Pro Ala Thr Val Gly Ile Pro Tyr Ala Arg Cys Arg
        275                 280                 285

Ser Phe Ala Arg Arg Ser Glu Ser Gly Asn Arg Ser Tyr Pro Arg Pro
    290                 295                 300

Ala Leu
305
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<210> 569
<211> 1041
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1018)
<223> FRXA01275

<400> 569

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cgccatacta ggctcggcct tttcgacggg aactcggata ggcttctgta aaaccatccc 60

cgttgaagag agactcgtgg ctgaaataac caccccatta atg gaa aaa att cgc   115
                                            Met Glu Lys Ile Arg
                                              1               5

tca ccc gca gtc caa tca gat gca ctg cag gtt ttt aaa tca gca ctt   163
Ser Pro Ala Val Gln Ser Asp Ala Leu Gln Val Phe Lys Ser Ala Leu
                  10                  15                  20

gct gcg aca gtc acg tgg tgg att tcg gtt aac ctc ctt aac tcc caa   211
Ala Ala Thr Val Thr Trp Trp Ile Ser Val Asn Leu Leu Asn Ser Gln
              25                  30                  35

cta ccc ttt tta gct ccc tgg gta gcg tta atg acg atg caa ttc acc   259
Leu Pro Phe Leu Ala Pro Trp Val Ala Leu Met Thr Met Gln Phe Thr
          40                  45                  50

gtc tac cac acc ttt atc agt gga att cag act gca att gct tct gtc   307
Val Tyr His Thr Phe Ile Ser Gly Ile Gln Thr Ala Ile Ala Ser Val
      55                  60                  65

atc gga gtt gga ctt tcc ttt gtc ata ggc act tac tta gac gta agt   355
Ile Gly Val Gly Leu Ser Phe Val Ile Gly Thr Tyr Leu Asp Val Ser
  70                  75                  80                  85

gtg tgg act ttt ggc ctt gca atg gtc ata gga tta ata ggt gca cga   403
Val Trp Thr Phe Gly Leu Ala Met Val Ile Gly Leu Ile Gly Ala Arg
                  90                  95                 100
```

```
gta cca aag ctc cgc gcg gaa gga ata ggt att gct act aca tcc att   451
Val Pro Lys Leu Arg Ala Glu Gly Ile Gly Ile Ala Thr Thr Ser Ile
            105                 110                 115

ttt ctt ctt gcc tcc ggg ttt gat gat caa caa ccc ctt cta tac gac   499
Phe Leu Leu Ala Ser Gly Phe Asp Asp Gln Gln Pro Leu Leu Tyr Asp
        120                 125                 130

cgt att tta gag atc ctg ctc ggc gtg gct gtt gcc ata gcc atc aac   547
Arg Ile Leu Glu Ile Leu Leu Gly Val Ala Val Ala Ile Ala Ile Asn
    135                 140                 145

ctc atc atc ttt cct ccc tta cgc gac cag gag gca aac atg gtg gta   595
Leu Ile Ile Phe Pro Pro Leu Arg Asp Gln Glu Ala Asn Met Val Val
150                 155                 160                 165

gga aac tta gat cgg agg atg ggt gag gtt tta caa aaa atg gcc gat   643
Gly Asn Leu Asp Arg Arg Met Gly Glu Val Leu Gln Lys Met Ala Asp
                170                 175                 180

gag ctt gca gaa aag tgg aat atc gac aat gca gat gag tgg ctg gaa   691
Glu Leu Ala Glu Lys Trp Asn Ile Asp Asn Ala Asp Glu Trp Leu Glu
            185                 190                 195

gaa att aat tct att aac aat gac cta gaa aaa gcg tgg cac tcc gtg   739
Glu Ile Asn Ser Ile Asn Asn Asp Leu Glu Lys Ala Trp His Ser Val
        200                 205                 210

cgg ttc gtt cgc gaa agc cgt cga gtt aat cct cgt aaa atc cgc atc   787
Arg Phe Val Arg Glu Ser Arg Arg Val Asn Pro Arg Lys Ile Arg Ile
    215                 220                 225

caa gag ggc cgc ccc cag cct acg gaa aca agt tat gaa tca aac ctc   835
Gln Glu Gly Arg Pro Gln Pro Thr Glu Thr Ser Tyr Glu Ser Asn Leu
230                 235                 240                 245

acc agc att gat gaa ggg atc gct cat tta cgc cac ctt gcc cgt act   883
Thr Ser Ile Asp Glu Gly Ile Ala His Leu Arg His Leu Ala Arg Thr
                250                 255                 260

ctt cgt gat acc ccg att ata gat tcc gac tgg gga tcc agt att cca   931
Leu Arg Asp Thr Pro Ile Ile Asp Ser Asp Trp Gly Ser Ser Ile Pro
            265                 270                 275

gca aca gtg ggt atc cct tat gca cga tgc cgg agc ttt gct cgc aga   979
Ala Thr Val Gly Ile Pro Tyr Ala Arg Cys Arg Ser Phe Ala Arg Arg
        280                 285                 290

tcc gaa tca gga aat aga tcc tat ccg cga ccg gct ctc taaactttca   1028
Ser Glu Ser Gly Asn Arg Ser Tyr Pro Arg Pro Ala Leu
    295                 300                 305

agtgagatga gtg                                                  1041
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<210> 570
<211> 306
<212> PRT
<213> Corynebacterium glutamicum

<400> 570

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Met Glu Lys Ile Arg Ser Pro Ala Val Gln Ser Asp Ala Leu Gln Val
 1               5                  10                  15

Phe Lys Ser Ala Leu Ala Ala Thr Val Thr Trp Trp Ile Ser Val Asn
            20                  25                  30

Leu Leu Asn Ser Gln Leu Pro Phe Leu Ala Pro Trp Val Ala Leu Met
        35                  40                  45

Thr Met Gln Phe Thr Val Tyr His Thr Phe Ile Ser Gly Ile Gln Thr
    50                  55                  60

Ala Ile Ala Ser Val Ile Gly Val Gly Leu Ser Phe Val Ile Gly Thr
65                  70                  75                  80

Tyr Leu Asp Val Ser Val Trp Thr Phe Gly Leu Ala Met Val Ile Gly
                85                  90                  95

Leu Ile Gly Ala Arg Val Pro Lys Leu Arg Ala Glu Gly Ile Gly Ile
            100                 105                 110

Ala Thr Thr Ser Ile Phe Leu Leu Ala Ser Gly Phe Asp Asp Gln Gln
        115                 120                 125

Pro Leu Leu Tyr Asp Arg Ile Leu Glu Ile Leu Leu Gly Val Ala Val
    130                 135                 140

Ala Ile Ala Ile Asn Leu Ile Ile Phe Pro Pro Leu Arg Asp Gln Glu
145                 150                 155                 160

Ala Asn Met Val Val Gly Asn Leu Asp Arg Arg Met Gly Glu Val Leu
                165                 170                 175

Gln Lys Met Ala Asp Glu Leu Ala Glu Lys Trp Asn Ile Asp Asn Ala
            180                 185                 190

Asp Glu Trp Leu Glu Glu Ile Asn Ser Ile Asn Asn Asp Leu Glu Lys
        195                 200                 205

Ala Trp His Ser Val Arg Phe Val Arg Glu Ser Arg Arg Val Asn Pro
    210                 215                 220

Arg Lys Ile Arg Ile Gln Glu Gly Arg Pro Gln Pro Thr Glu Thr Ser
225                 230                 235                 240

Tyr Glu Ser Asn Leu Thr Ser Ile Asp Glu Gly Ile Ala His Leu Arg
                245                 250                 255

His Leu Ala Arg Thr Leu Arg Asp Thr Pro Ile Ile Asp Ser Asp Trp
            260                 265                 270

Gly Ser Ser Ile Pro Ala Thr Val Gly Ile Pro Tyr Ala Arg Cys Arg
        275                 280                 285

Ser Phe Ala Arg Arg Ser Glu Ser Gly Asn Arg Ser Tyr Pro Arg Pro
    290                 295                 300

Ala Leu
305
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<210> 571
<211> 885
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(862)
<223> RXN01281

<400> 571
ggacaacctc atcaaatgca aacatgcgcc accgcgtccc ggaaaaccag gggcgatacc 60

gcgcttgagt gcgaggtgcc gtcaattccc aactacaaga gtg gga ctc agc cgt 115
Val Gly Leu Ser Arg
1 5

tca cat tat cag cta gcc gca gaa aac acc aaa tcc ctt gtt aga atg 163
Ser His Tyr Gln Leu Ala Ala Glu Asn Thr Lys Ser Leu Val Arg Met
10 15 20

gtt ccc atg act gtt cct caa gga aac gaa cca gca aag aag ctc gcc 211
Val Pro Met Thr Val Pro Gln Gly Asn Glu Pro Ala Lys Lys Leu Ala
25 30 35

act gac ctt aac cga aac caa gtc gtg gat gaa ctt tct gca gct gtt 259
Thr Asp Leu Asn Arg Asn Gln Val Val Asp Glu Leu Ser Ala Ala Val
40 45 50

tcc cga ggt caa ctc act ttg gag gaa ttt gaa gat cgc tcc tcc aaa 307
Ser Arg Gly Gln Leu Thr Leu Glu Glu Phe Glu Asp Arg Ser Ser Lys
55 60 65

gca tgg aat gcc cgc cac tta gac act ctt gta gag ctg atc tct gat 355
Ala Trp Asn Ala Arg His Leu Asp Thr Leu Val Glu Leu Ile Ser Asp
70 75 80 85

gtg aac gac aat ccc tac act ctg ctt ggt cag caa ttt ccc ggc gcc 403
Val Asn Asp Asn Pro Tyr Thr Leu Leu Gly Gln Gln Phe Pro Gly Ala
90 95 100

tcc tat gcg ccg gcg gcc tac gag acc act ccc cca gcg atg ccc aat 451
Ser Tyr Ala Pro Ala Ala Tyr Glu Thr Thr Pro Pro Ala Met Pro Asn
105 110 115

gtg tca gat cct gta aat att gtc cgc aac agg att acc ggc aac ccg 499
Val Ser Asp Pro Val Asn Ile Val Arg Asn Arg Ile Thr Gly Asn Pro
120 125 130

aat ggc tcc aaa atg tcg gtc tcg ttt atg ggt ggc acc gtg cgc aaa 547
Asn Gly Ser Lys Met Ser Val Ser Phe Met Gly Gly Thr Val Arg Lys
135 140 145

ggt gga tgg cat gtg cct aat gtt cac aca tcc ttc gcc atg atg ggc 595
Gly Gly Trp His Val Pro Asn Val His Thr Ser Phe Ala Met Met Gly
150 155 160 165

ggc aat cag atc gat ttg cgc gac gcc ttc ctg gaa agc gac cgc att 643
Gly Asn Gln Ile Asp Leu Arg Asp Ala Phe Leu Glu Ser Asp Arg Ile
170 175 180

```
cag atc aac gcc tac aca ttc atg ggt ggc atc gag att att gtt ccc   691
Gln Ile Asn Ala Tyr Thr Phe Met Gly Gly Ile Glu Ile Ile Val Pro
            185                 190                 195

gag ggt gtt ttt gtc att tgt gat ggc atg ggc att ttc ggc ggc ttc   739
Glu Gly Val Phe Val Ile Cys Asp Gly Met Gly Ile Phe Gly Gly Phe
        200                 205                 210

gaa cag tct gtg gac aag gcc ggt gca ctc aat ccc gcg cgc ctg cca   787
Glu Gln Ser Val Asp Lys Ala Gly Ala Leu Asn Pro Ala Arg Leu Pro
    215                 220                 225

agc aac gcg ccc acg gtc cac atc aaa ggc ctg gcg ttc atg ggc gga   835
Ser Asn Ala Pro Thr Val His Ile Lys Gly Leu Ala Phe Met Gly Gly
230                 235                 240                 245

gtc agc gta gtc acc aag aaa aac att taaaaagctt gtcgacgcgc         882
Val Ser Val Val Thr Lys Lys Asn Ile
                250

ccc                                                              885
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09550456.0

<210> 572
<211> 254
<212> PRT
<213> Corynebacterium glutamicum

<400> 572

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Val Gly Leu Ser Arg Ser His Tyr Gln Leu Ala Ala Glu Asn Thr Lys
  1               5                  10                  15

Ser Leu Val Arg Met Val Pro Met Thr Val Pro Gln Gly Asn Glu Pro
             20                  25                  30

Ala Lys Lys Leu Ala Thr Asp Leu Asn Arg Asn Gln Val Val Asp Glu
         35                  40                  45

Leu Ser Ala Ala Val Ser Arg Gly Gln Leu Thr Leu Glu Glu Phe Glu
     50                  55                  60

Asp Arg Ser Ser Lys Ala Trp Asn Ala Arg His Leu Asp Thr Leu Val
 65                  70                  75                  80

Glu Leu Ile Ser Asp Val Asn Asp Asn Pro Tyr Thr Leu Leu Gly Gln
                 85                  90                  95

Gln Phe Pro Gly Ala Ser Tyr Ala Pro Ala Ala Tyr Glu Thr Thr Pro
            100                 105                 110

Pro Ala Met Pro Asn Val Ser Asp Pro Val Asn Ile Val Arg Asn Arg
        115                 120                 125

Ile Thr Gly Asn Pro Asn Gly Ser Lys Met Ser Val Ser Phe Met Gly
    130                 135                 140

Gly Thr Val Arg Lys Gly Gly Trp His Val Pro Asn Val His Thr Ser
145                 150                 155                 160

Phe Ala Met Met Gly Gly Asn Gln Ile Asp Leu Arg Asp Ala Phe Leu
                165                 170                 175
```

```
Glu Ser Asp Arg Ile Gln Ile Asn Ala Tyr Thr Phe Met Gly Gly Ile
            180                 185                 190

Glu Ile Ile Val Pro Glu Gly Val Phe Val Ile Cys Asp Gly Met Gly
        195                 200                 205

Ile Phe Gly Gly Phe Glu Gln Ser Val Asp Lys Ala Gly Ala Leu Asn
    210                 215                 220

Pro Ala Arg Leu Pro Ser Asn Ala Pro Thr Val His Ile Lys Gly Leu
225                 230                 235                 240

Ala Phe Met Gly Gly Val Ser Val Val Thr Lys Lys Asn Ile
                245                 250


<210> 573
<211> 885
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(862)
<223> FRXA01281

<400> 573
ggacaacctc atcaaatgca aacatgcgcc accgcgtccc ggaaaaccag gggcgatacc 60

gcgcttgagt gcgaggtgcc gtcaattccc aactacaaga gtg gga ctc agc cgt   115
                                              Val Gly Leu Ser Arg
                                                1               5

tca cat tat cag cta gcc gca gaa aac acc aaa tcc ctt gtt aga atg   163
Ser His Tyr Gln Leu Ala Ala Glu Asn Thr Lys Ser Leu Val Arg Met
                10                  15                  20

gtt ccc atg act gtt cct caa gga aac gaa cca gca aag aag ctc gcc   211
Val Pro Met Thr Val Pro Gln Gly Asn Glu Pro Ala Lys Lys Leu Ala
            25                  30                  35

act gac ctt aac cga aac caa gtc gtg gat gaa ctt tct gca gct gtt   259
Thr Asp Leu Asn Arg Asn Gln Val Val Asp Glu Leu Ser Ala Ala Val
        40                  45                  50

tcc cga ggt caa ctc act ttg gag gaa ttt gaa gat cgc tcc tcc aaa   307
Ser Arg Gly Gln Leu Thr Leu Glu Glu Phe Glu Asp Arg Ser Ser Lys
    55                  60                  65

gca tgg aat gcc cgc cac tta gac act ctt gta gag ctg atc tct gat   355
Ala Trp Asn Ala Arg His Leu Asp Thr Leu Val Glu Leu Ile Ser Asp
70                  75                  80                  85

gtg aac gac aat ccc tac act ctg ctt ggt cag caa ttt ccc ggc gcc   403
Val Asn Asp Asn Pro Tyr Thr Leu Leu Gly Gln Gln Phe Pro Gly Ala
                90                  95                  100

tcc tat gcg ccg gcg gcc tac gag acc act ccc cca gcg atg ccc aat   451
Ser Tyr Ala Pro Ala Ala Tyr Glu Thr Thr Pro Pro Ala Met Pro Asn
            105                 110                 115
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gtg tca gat cct gta aat att gtc cgc aac agg att acc ggc aac ccg   499
Val Ser Asp Pro Val Asn Ile Val Arg Asn Arg Ile Thr Gly Asn Pro
        120                 125                 130

aat ggc tcc aaa atg tcg gtc tcg ttt atg ggt ggc acc gtg cgc aaa   547
Asn Gly Ser Lys Met Ser Val Ser Phe Met Gly Gly Thr Val Arg Lys
    135                 140                 145

ggt gga tgg cat gtg cct aat gtt cac aca tcc ttc gcc atg atg ggc   595
Gly Gly Trp His Val Pro Asn Val His Thr Ser Phe Ala Met Met Gly
150                 155                 160                 165

ggc aat cag atc gat ttg cgc gac gcc ttc ctg gaa agc gac cgc att   643
Gly Asn Gln Ile Asp Leu Arg Asp Ala Phe Leu Glu Ser Asp Arg Ile
                170                 175                 180

cag atc aac gcc tac aca ttc atg ggt ggc atc gag att att gtt ccc   691
Gln Ile Asn Ala Tyr Thr Phe Met Gly Gly Ile Glu Ile Ile Val Pro
            185                 190                 195

gag ggt gtt ttt gtc att tgt gat ggc atg ggc att ttc ggc ggc ttc   739
Glu Gly Val Phe Val Ile Cys Asp Gly Met Gly Ile Phe Gly Gly Phe
        200                 205                 210

gaa cag tct gtg gac aag gcc ggt gca ctc aat ccc gcg cgc ctg cca   787
Glu Gln Ser Val Asp Lys Ala Gly Ala Leu Asn Pro Ala Arg Leu Pro
    215                 220                 225

agc aac gcg ccc acg gtc cac atc aaa ggc ctg gcg ttc atg ggc gga   835
Ser Asn Ala Pro Thr Val His Ile Lys Gly Leu Ala Phe Met Gly Gly
230                 235                 240                 245

gtc agc gta gtc acc aag aaa aac att taaaaagctt gtcgacgcgc         882
Val Ser Val Val Thr Lys Lys Asn Ile
                250

ccc                                                              885
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09/05/2005 09:55:50

<210> 574
<211> 254
<212> PRT
<213> Corynebacterium glutamicum

<400> 574

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Val Gly Leu Ser Arg Ser His Tyr Gln Leu Ala Ala Glu Asn Thr Lys
  1               5                  10                  15

Ser Leu Val Arg Met Val Pro Met Thr Val Pro Gln Gly Asn Glu Pro
             20                  25                  30

Ala Lys Lys Leu Ala Thr Asp Leu Asn Arg Asn Gln Val Val Asp Glu
         35                  40                  45

Leu Ser Ala Ala Val Ser Arg Gly Gln Leu Thr Leu Glu Glu Phe Glu
     50                  55                  60

Asp Arg Ser Ser Lys Ala Trp Asn Ala Arg His Leu Asp Thr Leu Val
 65                  70                  75                  80
```

```
Glu Leu Ile Ser Asp Val Asn Asp Asn Pro Tyr Thr Leu Leu Gly Gln
                 85                  90                  95

Gln Phe Pro Gly Ala Ser Tyr Ala Pro Ala Ala Tyr Glu Thr Thr Pro
            100                 105                 110

Pro Ala Met Pro Asn Val Ser Asp Pro Val Asn Ile Val Arg Asn Arg
        115                 120                 125

Ile Thr Gly Asn Pro Asn Gly Ser Lys Met Ser Val Ser Phe Met Gly
    130                 135                 140

Gly Thr Val Arg Lys Gly Gly Trp His Val Pro Asn Val His Thr Ser
145                 150                 155                 160

Phe Ala Met Met Gly Gly Asn Gln Ile Asp Leu Arg Asp Ala Phe Leu
                165                 170                 175

Glu Ser Asp Arg Ile Gln Ile Asn Ala Tyr Thr Phe Met Gly Gly Ile
            180                 185                 190

Glu Ile Ile Val Pro Glu Gly Val Phe Val Ile Cys Asp Gly Met Gly
        195                 200                 205

Ile Phe Gly Gly Phe Glu Gln Ser Val Asp Lys Ala Gly Ala Leu Asn
    210                 215                 220

Pro Ala Arg Leu Pro Ser Asn Ala Pro Thr Val His Ile Lys Gly Leu
225                 230                 235                 240

Ala Phe Met Gly Gly Val Ser Val Val Thr Lys Lys Asn Ile
                245                 250


<210> 575
<211> 1206
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1183)
<223> RXN01296

<400> 575
taaaactcct gttcgaaatt gcccagacag gtgtccacca acactgctac attgcattgg 60

agatccagaa tcgatcactc tacgaccagg aaaaactttc atg tcc atc gag caa   115
                                            Met Ser Ile Glu Gln
                                              1               5

gca atc act tca ctc tcc gca aga gtg cgg gaa cta aag ccc atc atc   163
Ala Ile Thr Ser Leu Ser Ala Arg Val Arg Glu Leu Lys Pro Ile Ile
                 10                  15                  20

gag act gaa gaa gcc acc aaa acc gca ctg atc atc ccc ttt atc agc   211
Glu Thr Glu Glu Ala Thr Lys Thr Ala Leu Ile Ile Pro Phe Ile Ser
             25                  30                  35

aac gtt ctc ggc tac gac gtc act gat cct cgt gaa gtc att ccg gaa   259
Asn Val Leu Gly Tyr Asp Val Thr Asp Pro Arg Glu Val Ile Pro Glu
```

```
         40                  45                  50

tac act gct gat gtt ggc gtc aaa aag ggt gag aag gtc gac ttc gct   307
Tyr Thr Ala Asp Val Gly Val Lys Lys Gly Glu Lys Val Asp Phe Ala
     55                  60                  65

atc aaa acc ggc gat gat ttc cac ttc ctc atc gaa tgc aaa aag gtc   355
Ile Lys Thr Gly Asp Asp Phe His Phe Leu Ile Glu Cys Lys Lys Val
 70                  75                  80                  85

ggc tcc cca ctc agc ctc gat cac gct aac cag ctc gtc cgc tat ttc   403
Gly Ser Pro Leu Ser Leu Asp His Ala Asn Gln Leu Val Arg Tyr Phe
                 90                  95                 100

aat gtc aca gac acc gaa ttt gcc att ctc acc aac ggc gaa atc tac   451
Asn Val Thr Asp Thr Glu Phe Ala Ile Leu Thr Asn Gly Glu Ile Tyr
            105                 110                 115

caa ttc tat gga caa ctc gat gca gcc aac cgc atg gat gca aaa cca   499
Gln Phe Tyr Gly Gln Leu Asp Ala Ala Asn Arg Met Asp Ala Lys Pro
        120                 125                 130

ttc atg acc ttg gat ttg aac aat att gat gcc cgt cag ttc cct cat   547
Phe Met Thr Leu Asp Leu Asn Asn Ile Asp Ala Arg Gln Phe Pro His
    135                 140                 145

ttg gaa atg tgt acc cgc aag cat ttc aac cca caa gcg cta gcc gcc   595
Leu Glu Met Cys Thr Arg Lys His Phe Asn Pro Gln Ala Leu Ala Ala
150                 155                 160                 165

aac gct gaa gaa ctg aag tac att gct gaa ttg aag aaa gtc atc gcg   643
Asn Ala Glu Glu Leu Lys Tyr Ile Ala Glu Leu Lys Lys Val Ile Ala
                170                 175                 180

aat caa ttc caa gaa cct gac gta gaa atc gtc aag atg ctt gcg gcg   691
Asn Gln Phe Gln Glu Pro Asp Val Glu Ile Val Lys Met Leu Ala Ala
            185                 190                 195

aca gtc acc aca aag cgt atg act gca caa aat ctg gaa ttc ttc acc   739
Thr Val Thr Thr Lys Arg Met Thr Ala Gln Asn Leu Glu Phe Phe Thr
        200                 205                 210

cgc ttg gtt aat act gcg tct tcc cag ttc ctc aaa gac gag gtc aat   787
Arg Leu Val Asn Thr Ala Ser Ser Gln Phe Leu Lys Asp Glu Val Asn
    215                 220                 225

cgt aga ttg cgc tcc gcc caa gtc ttt gag gat cct gtc caa aca caa   835
Arg Arg Leu Arg Ser Ala Gln Val Phe Glu Asp Pro Val Gln Thr Gln
230                 235                 240                 245

ggt gct gat gca gaa aca cca gca gag gac gaa gca gta atc gaa gaa   883
Gly Ala Asp Ala Glu Thr Pro Ala Glu Asp Glu Ala Val Ile Glu Glu
                250                 255                 260

gtg gtt tca gaa atc gtg acg aca gaa gag gaa atc cac ggt cat tca   931
Val Val Ser Glu Ile Val Thr Thr Glu Glu Glu Ile His Gly His Ser
            265                 270                 275

att gtc cgt gca att tgc tgc tca gag gta tcg gca caa gaa atc acc   979
Ile Val Arg Ala Ile Cys Cys Ser Glu Val Ser Ala Gln Glu Ile Thr
        280                 285                 290
```

```
atg cgt gac gca aaa tcc tac tgc gct att ctc ttc caa gac aac aac   1027
Met Arg Asp Ala Lys Ser Tyr Cys Ala Ile Leu Phe Gln Asp Asn Asn
    295                 300                 305

cga aag cca atc gcc cgt ttc tac ttt gat cgc aag att cca cgc atc   1075
Arg Lys Pro Ile Ala Arg Phe Tyr Phe Asp Arg Lys Ile Pro Arg Ile
310                 315                 320                 325

ggc atc ttc aat gct gaa ggc gag cag gaa cac ttt gat ttg gaa tcc   1123
Gly Ile Phe Asn Ala Glu Gly Glu Gln Glu His Phe Asp Leu Glu Ser
                330                 335                 340

atc gaa gat atc tac aac cac gct gat ctt ctg cat tcc cgc gtc gta   1171
Ile Glu Asp Ile Tyr Asn His Ala Asp Leu Leu His Ser Arg Val Val
            345                 350                 355

gca ttg aac gct taagttctgc ctttagttct gca                        1206
Ala Leu Asn Ala
        360
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<210> 576
<211> 361
<212> PRT
<213> Corynebacterium glutamicum

<400> 576

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Met Ser Ile Glu Gln Ala Ile Thr Ser Leu Ser Ala Arg Val Arg Glu
  1               5                  10                  15

Leu Lys Pro Ile Ile Glu Thr Glu Glu Ala Thr Lys Thr Ala Leu Ile
             20                  25                  30

Ile Pro Phe Ile Ser Asn Val Leu Gly Tyr Asp Val Thr Asp Pro Arg
         35                  40                  45

Glu Val Ile Pro Glu Tyr Thr Ala Asp Val Gly Val Lys Lys Gly Glu
     50                  55                  60

Lys Val Asp Phe Ala Ile Lys Thr Gly Asp Asp Phe His Phe Leu Ile
 65                  70                  75                  80

Glu Cys Lys Lys Val Gly Ser Pro Leu Ser Leu Asp His Ala Asn Gln
                85                  90                  95

Leu Val Arg Tyr Phe Asn Val Thr Asp Thr Glu Phe Ala Ile Leu Thr
            100                 105                 110

Asn Gly Glu Ile Tyr Gln Phe Tyr Gly Gln Leu Asp Ala Ala Asn Arg
        115                 120                 125

Met Asp Ala Lys Pro Phe Met Thr Leu Asp Leu Asn Asn Ile Asp Ala
    130                 135                 140

Arg Gln Phe Pro His Leu Glu Met Cys Thr Arg Lys His Phe Asn Pro
145                 150                 155                 160

Gln Ala Leu Ala Ala Asn Ala Glu Glu Leu Lys Tyr Ile Ala Glu Leu
                165                 170                 175
```

```
Lys Lys Val Ile Ala Asn Gln Phe Gln Glu Pro Asp Val Glu Ile Val
            180                 185                 190

Lys Met Leu Ala Ala Thr Val Thr Thr Lys Arg Met Thr Ala Gln Asn
        195                 200                 205

Leu Glu Phe Phe Thr Arg Leu Val Asn Thr Ala Ser Ser Gln Phe Leu
    210                 215                 220

Lys Asp Glu Val Asn Arg Arg Leu Arg Ser Ala Gln Val Phe Glu Asp
225                 230                 235                 240

Pro Val Gln Thr Gln Gly Ala Asp Ala Glu Thr Pro Ala Glu Asp Glu
                245                 250                 255

Ala Val Ile Glu Glu Val Val Ser Glu Ile Val Thr Thr Glu Glu Glu
            260                 265                 270

Ile His Gly His Ser Ile Val Arg Ala Ile Cys Cys Ser Glu Val Ser
        275                 280                 285

Ala Gln Glu Ile Thr Met Arg Asp Ala Lys Ser Tyr Cys Ala Ile Leu
    290                 295                 300

Phe Gln Asp Asn Asn Arg Lys Pro Ile Ala Arg Phe Tyr Phe Asp Arg
305                 310                 315                 320

Lys Ile Pro Arg Ile Gly Ile Phe Asn Ala Glu Gly Glu Gln Glu His
                325                 330                 335

Phe Asp Leu Glu Ser Ile Glu Asp Ile Tyr Asn His Ala Asp Leu Leu
            340                 345                 350

His Ser Arg Val Val Ala Leu Asn Ala
        355                 360


<210> 577
<211> 1206
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1183)
<223> FRXA01296

<400> 577
taaaactcct gttcgaaatt gcccagacag gtgtccacca acactgctac attgcattgg 60

agatccagaa tcgatcactc tacgaccagg aaaaactttc atg tcc atc gag caa  115
                                            Met Ser Ile Glu Gln
                                              1               5

gca atc act tca ctc tcc gca aga gtg cgg gaa cta aag ccc atc atc   163
Ala Ile Thr Ser Leu Ser Ala Arg Val Arg Glu Leu Lys Pro Ile Ile
                 10                  15                  20

gag act gaa gaa gcc acc aaa acc gca ctg atc atc ccc ttt atc agc   211
Glu Thr Glu Glu Ala Thr Lys Thr Ala Leu Ile Ile Pro Phe Ile Ser
             25                  30                  35
```

```
aac gtt ctc ggc tac gac gtc act gat cct cgt gaa gtc att ccg gaa   259
Asn Val Leu Gly Tyr Asp Val Thr Asp Pro Arg Glu Val Ile Pro Glu
         40                  45                  50

tac act gct gat gtt ggc gtc aaa aag ggt gag aag gtc gac ttc gct   307
Tyr Thr Ala Asp Val Gly Val Lys Lys Gly Glu Lys Val Asp Phe Ala
     55                  60                  65

atc aaa acc ggc gat gat ttc cac ttc ctc atc gaa tgc aaa aag gtc   355
Ile Lys Thr Gly Asp Asp Phe His Phe Leu Ile Glu Cys Lys Lys Val
 70                  75                  80                  85

ggc tcc cca ctc agc ctc gat cac gct aac cag ctc gtc cgc tat ttc   403
Gly Ser Pro Leu Ser Leu Asp His Ala Asn Gln Leu Val Arg Tyr Phe
                 90                  95                 100

aat gtc aca gac acc gaa ttt gcc att ctc acc aac ggc gaa atc tac   451
Asn Val Thr Asp Thr Glu Phe Ala Ile Leu Thr Asn Gly Glu Ile Tyr
            105                 110                 115

caa ttc tat gga caa ctc gat gca gcc aac cgc atg gat gca aaa cca   499
Gln Phe Tyr Gly Gln Leu Asp Ala Ala Asn Arg Met Asp Ala Lys Pro
        120                 125                 130

ttc atg acc ttg gat ttg aac aat att gat gcc cgt cag ttc cct cat   547
Phe Met Thr Leu Asp Leu Asn Asn Ile Asp Ala Arg Gln Phe Pro His
    135                 140                 145

ttg gaa atg tgt acc cgc aag cat ttc aac cca caa gcg cta gcc gcc   595
Leu Glu Met Cys Thr Arg Lys His Phe Asn Pro Gln Ala Leu Ala Ala
150                 155                 160                 165

aac gct gaa gaa ctg aag tac att gct gaa ttg aag aaa gtc atc gcg   643
Asn Ala Glu Glu Leu Lys Tyr Ile Ala Glu Leu Lys Lys Val Ile Ala
                170                 175                 180

aat caa ttc caa gaa cct gac gta gaa atc gtc aag atg ctt gcg gcg   691
Asn Gln Phe Gln Glu Pro Asp Val Glu Ile Val Lys Met Leu Ala Ala
            185                 190                 195

aca gtc acc aca aag cgt atg act gca caa aat ctg gaa ttc ttc acc   739
Thr Val Thr Thr Lys Arg Met Thr Ala Gln Asn Leu Glu Phe Phe Thr
        200                 205                 210

cgc ttg gtt aat act gcg tct tcc cag ttc ctc aaa gac gag gtc aat   787
Arg Leu Val Asn Thr Ala Ser Ser Gln Phe Leu Lys Asp Glu Val Asn
    215                 220                 225

cgt aga ttg cgc tcc gcc caa gtc ttt gag gat cct gtc caa aca caa   835
Arg Arg Leu Arg Ser Ala Gln Val Phe Glu Asp Pro Val Gln Thr Gln
230                 235                 240                 245

ggt gct gat gca gaa aca cca gca gag gac gaa gca gta atc gaa gaa   883
Gly Ala Asp Ala Glu Thr Pro Ala Glu Asp Glu Ala Val Ile Glu Glu
                250                 255                 260

gtg gtt tca gaa atc gtg acg aca gaa gag gaa atc cac ggt cat tca   931
Val Val Ser Glu Ile Val Thr Thr Glu Glu Glu Ile His Gly His Ser
            265                 270                 275
```

```
att gtc cgt gca att tgc tgc tca gag gta tcg gca caa gaa atc acc   979
Ile Val Arg Ala Ile Cys Cys Ser Glu Val Ser Ala Gln Glu Ile Thr
        280                 285                 290

atg cgt gac gca aaa tcc tac tgc gct att ctc ttc caa gac aac aac   1027
Met Arg Asp Ala Lys Ser Tyr Cys Ala Ile Leu Phe Gln Asp Asn Asn
    295                 300                 305

cga aag cca atc gcc cgt ttc tac ttt gat cgc aag att cca cgc atc   1075
Arg Lys Pro Ile Ala Arg Phe Tyr Phe Asp Arg Lys Ile Pro Arg Ile
310                 315                 320                 325

ggc atc ttc aat gct gaa ggc gag cag gaa cac ttt gat ttg gaa tcc   1123
Gly Ile Phe Asn Ala Glu Gly Glu Gln Glu His Phe Asp Leu Glu Ser
                330                 335                 340

atc gaa gat atc tac aac cac gct gat ctt ctg cat tcc cgc gtc gta   1171
Ile Glu Asp Ile Tyr Asn His Ala Asp Leu Leu His Ser Arg Val Val
            345                 350                 355

gca ttg aac gct taagttctgc ctttagttct gca                        1206
Ala Leu Asn Ala
        360
```

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<210> 578
<211> 361
<212> PRT
<213> Corynebacterium glutamicum

<400> 578

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Met Ser Ile Glu Gln Ala Ile Thr Ser Leu Ser Ala Arg Val Arg Glu
  1               5                  10                  15

Leu Lys Pro Ile Ile Glu Thr Glu Glu Ala Thr Lys Thr Ala Leu Ile
             20                  25                  30

Ile Pro Phe Ile Ser Asn Val Leu Gly Tyr Asp Val Thr Asp Pro Arg
         35                  40                  45

Glu Val Ile Pro Glu Tyr Thr Ala Asp Val Gly Val Lys Lys Gly Glu
     50                  55                  60

Lys Val Asp Phe Ala Ile Lys Thr Gly Asp Asp Phe His Phe Leu Ile
 65                  70                  75                  80

Glu Cys Lys Lys Val Gly Ser Pro Leu Ser Leu Asp His Ala Asn Gln
                 85                  90                  95

Leu Val Arg Tyr Phe Asn Val Thr Asp Thr Glu Phe Ala Ile Leu Thr
            100                 105                 110

Asn Gly Glu Ile Tyr Gln Phe Tyr Gly Gln Leu Asp Ala Ala Asn Arg
        115                 120                 125

Met Asp Ala Lys Pro Phe Met Thr Leu Asp Leu Asn Asn Ile Asp Ala
    130                 135                 140

Arg Gln Phe Pro His Leu Glu Met Cys Thr Arg Lys His Phe Asn Pro
145                 150                 155                 160
```

```
Gln Ala Leu Ala Ala Asn Ala Glu Glu Leu Lys Tyr Ile Ala Glu Leu
                165                 170                 175

Lys Lys Val Ile Ala Asn Gln Phe Gln Glu Pro Asp Val Glu Ile Val
            180                 185                 190

Lys Met Leu Ala Ala Thr Val Thr Thr Lys Arg Met Thr Ala Gln Asn
        195                 200                 205

Leu Glu Phe Phe Thr Arg Leu Val Asn Thr Ala Ser Ser Gln Phe Leu
    210                 215                 220

Lys Asp Glu Val Asn Arg Arg Leu Arg Ser Ala Gln Val Phe Glu Asp
225                 230                 235                 240

Pro Val Gln Thr Gln Gly Ala Asp Ala Glu Thr Pro Ala Glu Asp Glu
                245                 250                 255

Ala Val Ile Glu Glu Val Val Ser Glu Ile Val Thr Thr Glu Glu Glu
            260                 265                 270

Ile His Gly His Ser Ile Val Arg Ala Ile Cys Cys Ser Glu Val Ser
        275                 280                 285

Ala Gln Glu Ile Thr Met Arg Asp Ala Lys Ser Tyr Cys Ala Ile Leu
    290                 295                 300

Phe Gln Asp Asn Asn Arg Lys Pro Ile Ala Arg Phe Tyr Phe Asp Arg
305                 310                 315                 320

Lys Ile Pro Arg Ile Gly Ile Phe Asn Ala Glu Gly Glu Gln Glu His
                325                 330                 335

Phe Asp Leu Glu Ser Ile Glu Asp Ile Tyr Asn His Ala Asp Leu Leu
            340                 345                 350

His Ser Arg Val Val Ala Leu Asn Ala
        355                 360
```

<210> 579
<211> 1131
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1108)
<223> RXN01306

<400> 579
tgttttagag gtagagcgaa acgtgcctgt aaaactggcg ctcgctgtgc tcgaagacca 60

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cccagacaat caccccgctc cgaaggagaa tcgctaagcc atg act gaa tgg tat   115
                                              Met Thr Glu Trp Tyr
                                                1               5

gtc gtt tta ccc gcc act att cta ctc atc gcg ctg tct gcg ttt ttc   163
Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala Leu Ser Ala Phe Phe
                10                  15                  20
```

```
gtc atc att gag ttc gct ttg ctt gca gct agg cgg aac cgg tta gag   211
Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg Arg Asn Arg Leu Glu
            25                  30                  35

gag act gtg gaa acc tcg cgg tct tcc cgc gct gcg ttg cga agc ctc   259
Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala Ala Leu Arg Ser Leu
        40                  45                  50

aat gaa ctt act ctc atg ctc gcg ggc gcg cag ttg gga atc acc atg   307
Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln Leu Gly Ile Thr Met
    55                  60                  65

gtg act ttc gcg ttg ggt gct atc acg aag ccg tgg gtt cat tat gct   355
Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro Trp Val His Tyr Ala
70                  75                  80                  85

ttg atg ccg ctc ttc gaa tgg gcg cgt ata ccg ctg gtt atg gca gat   403
Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro Leu Val Met Ala Asp
                90                  95                  100

gtc att gcg ttt att ttg tcg ctg ttt atc gta acg ttt ctg cac ttg   451
Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val Thr Phe Leu His Leu
            105                 110                 115

gtc atc ggc gaa atg gct ccg aaa tcc tgg gca atc gcg cat ccg gag   499
Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala Ile Ala His Pro Glu
        120                 125                 130

acg gca ctt cga act atc gcg att ccc gca cgg ggc ttc att aac ctg   547
Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg Gly Phe Ile Asn Leu
    135                 140                 145

ttt cgt cca ttg ctg cag tgg atc aac aaa atg gcg aac gat ttg gtc   595
Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met Ala Asn Asp Leu Val
150                 155                 160                 165

cgc aaa gtt ggt gaa act ccc gtt gat cga gct gca gct ggt ggc tat   643
Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala Ala Ala Gly Gly Tyr
                170                 175                 180

gac acc gat acc ctc cat gcc ctc att gag cat tcc cga gaa act ggc   691
Asp Thr Asp Thr Leu His Ala Leu Ile Glu His Ser Arg Glu Thr Gly
            185                 190                 195

gct ctg gat cag caa tcc gcc gcc caa atc agc gga att atc aag ctg   739
Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser Gly Ile Ile Lys Leu
        200                 205                 210

gat aaa atc acg gtc ggt caa acc ctg acc gca tct cca ttt acg cac   787
Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala Ser Pro Phe Thr His
    215                 220                 225

agc gcc agc gcc acg gtt gct gag gtg caa gcc gca gct cag cgc agt   835
Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala Ala Ala Gln Arg Ser
230                 235                 240                 245

ggc agc ttg cgt gtg ctt atc gac gcc ccc tcc cac ctt ttc cca cac   883
Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser His Leu Phe Pro His
                250                 255                 260

gtc att cat gtg cga gac acc ctt ggt gcc tcg cca gac gag aag gct   931
```

```
Val Ile His Val Arg Asp Thr Leu Gly Ala Ser Pro Asp Glu Lys Ala
            265                 270                 275

tcg aag tgg tct cgc cca atc ctc acc gtt gct gag acc gac acg tta   979
Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala Glu Thr Asp Thr Leu
        280                 285                 290

cac caa gcg ctg gaa tac atg cgg gag cat aac gag cag atc agt gcg   1027
His Gln Ala Leu Glu Tyr Met Arg Glu His Asn Glu Gln Ile Ser Ala
    295                 300                 305

gtg ctt tcc gct gat ggg aaa acg gtg ctt ggt gta ata act tgg gat   1075
Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly Val Ile Thr Trp Asp
310                 315                 320                 325

cac atc ttg aaa tac ctg tgg cct gca tcg gtg tagctaattt gaggtgcgct 1128
His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val
                330                 335

gaa                                                               1131


<210> 580
<211> 336
<212> PRT
<213> Corynebacterium glutamicum

<400> 580
Met Thr Glu Trp Tyr Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala
  1               5                  10                  15

Leu Ser Ala Phe Phe Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg
             20                  25                  30

Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala
         35                  40                  45

Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln
     50                  55                  60

Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro
 65                  70                  75                  80

Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro
                 85                  90                  95

Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val
            100                 105                 110

Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala
        115                 120                 125

Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg
    130                 135                 140

Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met
145                 150                 155                 160

Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala
                165                 170                 175
```

```
Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His
            180                 185                 190

Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser
        195                 200                 205

Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala
    210                 215                 220

Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala
225                 230                 235                 240

Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser
                245                 250                 255

His Leu Phe Pro His Val Ile His Val Arg Asp Thr Leu Gly Ala Ser
            260                 265                 270

Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala
        275                 280                 285

Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met Arg Glu His Asn
    290                 295                 300

Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly
305                 310                 315                 320

Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val
                325                 330                 335
```

US20030148461A1

<210> 581
<211> 1107
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (77)..(1084)
<223> FRXA01306

<400> 581

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cgtgcctgta aaatgcgctc gctctgctga agaccaccca gacaatcacc ccgctccgaa 60

ggagaatcga taagccatg act gaa tgg tat gtc gtt tta ccc gcc act att  112
                 Met Thr Glu Trp Tyr Val Val Leu Pro Ala Thr Ile
                   1               5                  10

cta ctc atc gcg ctg tct gcg ttt ttc gtc atc att gag ttc gct ttg   160
Leu Leu Ile Ala Leu Ser Ala Phe Phe Val Ile Ile Glu Phe Ala Leu
         15                  20                  25

ctt gca gct agg cgg aac cgg tta gag gag act gtg gaa acc tcg cgg   208
Leu Ala Ala Arg Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg
     30                  35                  40

tct tcc cgc gct gcg ttg cga agc ctc aat gaa ctt act ctc atg ctc   256
Ser Ser Arg Ala Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu
```

```
 45                  50                  55                  60

gcg ggc gcg cag ttg gga atc acc atg gtg act ttc gcg ttg ggt gct   304
Ala Gly Ala Gln Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala
                65                  70                  75

atc acg aag ccg tgg gtt cat tat gct ttg atg ccg ctc ttc gaa tgg   352
Ile Thr Lys Pro Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp
            80                  85                  90

gcg cgt ata ccg ctg gtt atg gca gat gtc att gcg ttt att ttg tcg   400
Ala Arg Ile Pro Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser
        95                  100                 105

ctg ttt atc gta acg ttt ctg cac ttg gtc atc ggc gaa atg gct ccg   448
Leu Phe Ile Val Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro
    110                 115                 120

aaa tcc tgg gca atc gcg cat ccg gag acg gca ctt cga act atc gcg   496
Lys Ser Trp Ala Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala
125                 130                 135                 140

att ccc gca cgg ggc ttc att aac ctg ttt cgt cca ttg ctg cag tgg   544
Ile Pro Ala Arg Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp
                145                 150                 155

atc aac aaa atg gcg aac gat ttg gtc cgc aaa gtt ggt gaa act ccc   592
Ile Asn Lys Met Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro
            160                 165                 170

gtt gat cga gct gca gct ggt ggc tat gac acc gat acc ctc cat gcc   640
Val Asp Arg Ala Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala
        175                 180                 185

ctc att gag cat tcc cga gaa act ggc gct ctg gat cag caa tcc gcc   688
Leu Ile Glu His Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala
    190                 195                 200

gcc caa atc agc gga att atc aag ctg gat aaa atc acg gtc ggt caa   736
Ala Gln Ile Ser Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln
205                 210                 215                 220

acc ctg acc gca tct cca ttt acg cac agc gcc agc gcc acg gtt gct   784
Thr Leu Thr Ala Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala
                225                 230                 235

gag gtg caa gcc gca gct cag cgc agt ggc agc ttg cgt gtg ctt atc   832
Glu Val Gln Ala Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile
            240                 245                 250

gac gcc ccc tcc cac ctt ttc cca cac gtc att cat gtg cga gac acc   880
Asp Ala Pro Ser His Leu Phe Pro His Val Ile His Val Arg Asp Thr
        255                 260                 265

ctt ggt gcc tcg cca gac gag aag gct tcg aag tgg tct cgc cca atc   928
Leu Gly Ala Ser Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile
    270                 275                 280

ctc acc gtt gct gag acc gac acg tta cac caa gcg ctg gaa tac atg   976
Leu Thr Val Ala Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met
285                 290                 295                 300
```

```
cgg gag cat aac gag cag atc agt gcg gtg ctt tcc gct gat ggg aaa   1024
Arg Glu His Asn Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys
                305                 310                 315

acg gtg ctt ggt gta ata act tgg gat cac atc ttg aaa tac ctg tgg   1072
Thr Val Leu Gly Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp
            320                 325                 330

cct gca tcg gtg tagctaattt gaggtgcgct gaa                        1107
Pro Ala Ser Val
        335
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<210> 582
<211> 336
<212> PRT
<213> Corynebacterium glutamicum

<400> 582

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Met Thr Glu Trp Tyr Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala
  1               5                  10                  15

Leu Ser Ala Phe Phe Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg
             20                  25                  30

Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala
         35                  40                  45

Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln
     50                  55                  60

Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro
 65                  70                  75                  80

Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro
                 85                  90                  95

Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val
            100                 105                 110

Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala
        115                 120                 125

Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg
    130                 135                 140

Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met
145                 150                 155                 160

Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala
                165                 170                 175

Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His
            180                 185                 190

Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser
        195                 200                 205

Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala
    210                 215                 220
```

```
Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala
225                 230                 235                 240

Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser
                245                 250                 255

His Leu Phe Pro His Val Ile His Val Arg Asp Thr Leu Gly Ala Ser
            260                 265                 270

Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala
        275                 280                 285

Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met Arg Glu His Asn
    290                 295                 300

Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly
305                 310                 315                 320

Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val
                325                 330                 335
```

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<210> 583
<211> 423
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(400)
<223> RXN01324

<400> 583

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tcctcaaccc aatgcttgcc ggcattgcga tggccttcag ttcagttttc gtcgtctcca 60

attccttgcg tctgcgagga ttcaaagcaa ggagcaacta atg tcc aac agc gaa   115
                                            Met Ser Asn Ser Glu
                                              1               5

tgc cac acc cac ggt tac atc gaa gaa aag cag cgt tac ctc gca cgc   163
Cys His Thr His Gly Tyr Ile Glu Glu Lys Gln Arg Tyr Leu Ala Arg
                  10                  15                  20

ctc aaa aga atc gaa ggc caa acc cga ggc att cac cgc atg atc gac   211
Leu Lys Arg Ile Glu Gly Gln Thr Arg Gly Ile His Arg Met Ile Asp
             25                  30                  35

gag gaa caa tac tgc atc gac atc ctc acg cag atc tcc gca gtg aac   259
Glu Glu Gln Tyr Cys Ile Asp Ile Leu Thr Gln Ile Ser Ala Val Asn
         40                  45                  50

tcc gca ctc aaa aac gtg gcg ttc ggc ctc ctc gac gat cac ctc gct   307
Ser Ala Leu Lys Asn Val Ala Phe Gly Leu Leu Asp Asp His Leu Ala
     55                  60                  65

cac tgt gtc aaa gaa gca gct gac ctc ggc ggc gac gaa ctc gac gca   355
His Cys Val Lys Glu Ala Ala Asp Leu Gly Gly Asp Glu Leu Asp Ala
```

```
 70                  75                  80                  85

aaa ctc aaa gaa gtt tcc gac gcc atc gcc cgc ttc agt aag gcc       400
Lys Leu Lys Glu Val Ser Asp Ala Ile Ala Arg Phe Ser Lys Ala
                 90                  95                 100

taaacggatc cggtggcatt gga                                         423


<210> 584
<211> 100
<212> PRT
<213> Corynebacterium glutamicum

<400> 584
Met Ser Asn Ser Glu Cys His Thr His Gly Tyr Ile Glu Glu Lys Gln
  1               5                  10                  15

Arg Tyr Leu Ala Arg Leu Lys Arg Ile Glu Gly Gln Thr Arg Gly Ile
             20                  25                  30

His Arg Met Ile Asp Glu Glu Gln Tyr Cys Ile Asp Ile Leu Thr Gln
         35                  40                  45

Ile Ser Ala Val Asn Ser Ala Leu Lys Asn Val Ala Phe Gly Leu Leu
     50                  55                  60

Asp Asp His Leu Ala His Cys Val Lys Glu Ala Ala Asp Leu Gly Gly
 65                  70                  75                  80

Asp Glu Leu Asp Ala Lys Leu Lys Glu Val Ser Asp Ala Ile Ala Arg
                 85                  90                  95

Phe Ser Lys Ala
            100


<210> 585
<211> 2520
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2497)
<223> RXN01331

<400> 585
ctaaactcgt ctctcgtatc tttcagtcat ttatgtctga taagcaggcg cgtgcgccac 60

acaattggca caatcacaag aaagtgaagt gggaacctag atg ctg acg aca cta   115
                                              Met Leu Thr Thr Leu
                                                1               5

tgg att gcg gtg ttg gta ttt acc gtt cca gga ttg gtc gtc tcg tgg   163
Trp Ile Ala Val Leu Val Phe Thr Val Pro Gly Leu Val Val Ser Trp
                 10                  15                  20

gtt tct ggc ctt aaa gtg ccc tgg gct atc gca gcc tcc atc cca gcc   211
Val Ser Gly Leu Lys Val Pro Trp Ala Ile Ala Ala Ser Ile Pro Ala
             25                  30                  35
```

```
acc ttc ggt att tac ggc ctg tcc gcc tgg ttg ctg ggc ttg tgg gag   259
Thr Phe Gly Ile Tyr Gly Leu Ser Ala Trp Leu Leu Gly Leu Trp Glu
         40                  45                  50

atg cgt ttt gat ctc cat tct gta gtt att tcc aca ttg gtt ttc gct   307
Met Arg Phe Asp Leu His Ser Val Val Ile Ser Thr Leu Val Phe Ala
     55                  60                  65

gcg gtt gct ttg gta tgg cgc ttg ttt ttt gtc ggt ggt tgg ctt gta   355
Ala Val Ala Leu Val Trp Arg Leu Phe Phe Val Gly Gly Trp Leu Val
 70                  75                  80                  85

cgt cgg cgt aaa gca cgt atc cgc agg cag acg ctc gcg gat gaa gag   403
Arg Arg Arg Lys Ala Arg Ile Arg Arg Gln Thr Leu Ala Asp Glu Glu
                 90                  95                 100

cgg gca gaa aat gct gag gta tct gca ggg gag cct gcc gaa tcg agc   451
Arg Ala Glu Asn Ala Glu Val Ser Ala Gly Glu Pro Ala Glu Ser Ser
            105                 110                 115

aca aac gaa gca gcc gaa tct gaa tct gaa acc tcg gag cgt cgc gga   499
Thr Asn Glu Ala Ala Glu Ser Glu Ser Glu Thr Ser Glu Arg Arg Gly
        120                 125                 130

atc tgg cgc gtg atc ttt gat tac atg cgc gac ggt ggc atc ttg gat   547
Ile Trp Arg Val Ile Phe Asp Tyr Met Arg Asp Gly Gly Ile Leu Asp
    135                 140                 145

cac cgt tgg ctg ctg cct gcc gca ggt gct atc act ggt gcg tgg ctg   595
His Arg Trp Leu Leu Pro Ala Ala Gly Ala Ile Thr Gly Ala Trp Leu
150                 155                 160                 165

atc att gat cgt gcc gtt gat ctg ctc ttg agc acc gag cat ggt ttg   643
Ile Ile Asp Arg Ala Val Asp Leu Leu Leu Ser Thr Glu His Gly Leu
                170                 175                 180

ggc gat atc gtc caa ggc tgg gat gtc cat tgg cat gct tcg act gtc   691
Gly Asp Ile Val Gln Gly Trp Asp Val His Trp His Ala Ser Thr Val
            185                 190                 195

cgt ttt ata gat gag acc ggc att gcg tca tcc acg atg atg ggg cag   739
Arg Phe Ile Asp Glu Thr Gly Ile Ala Ser Ser Thr Met Met Gly Gln
        200                 205                 210

ctg cgc aat att gaa acg cag caa gat ctg ttc tac cca agc gca tgg   787
Leu Arg Asn Ile Glu Thr Gln Gln Asp Leu Phe Tyr Pro Ser Ala Trp
    215                 220                 225

cat gct ggt gca tgg gtg ctg tcg gat gtc gga aat ctg acg att gtt   835
His Ala Gly Ala Trp Val Leu Ser Asp Val Gly Asn Leu Thr Ile Val
230                 235                 240                 245

gaa gcc acc aac ctc act ggc att gtg ctg tcc gga ttg ttg ctg ccg   883
Glu Ala Thr Asn Leu Thr Gly Ile Val Leu Ser Gly Leu Leu Leu Pro
                250                 255                 260

tta gct gtt gca ctg att gca tgg cgg atg atc aac aat cgt gga ctg   931
Leu Ala Val Ala Leu Ile Ala Trp Arg Met Ile Asn Asn Arg Gly Leu
            265                 270                 275
```

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acc gcg cag att ggt gcg ggc ttt gct gga ctg atc acc att gcc tct   979
Thr Ala Gln Ile Gly Ala Gly Phe Ala Gly Leu Ile Thr Ile Ala Ser
        280                 285                 290

ccg gta ctg ttc tgg gtt ggt aac tac gtg ggt gcg tgg cct tat gtt   1027
Pro Val Leu Phe Trp Val Gly Asn Tyr Val Gly Ala Trp Pro Tyr Val
    295                 300                 305

gct gcg atc ggt gct tca ggt gtg gtg ctt gcg ctg ttt atg tcc act   1075
Ala Ala Ile Gly Ala Ser Gly Val Val Leu Ala Leu Phe Met Ser Thr
310                 315                 320                 325

ccg tct gtg ccg gta aga atc ttt gcc gca gca ttg gcg ttc atg ggt   1123
Pro Ser Val Pro Val Arg Ile Phe Ala Ala Ala Leu Ala Phe Met Gly
                330                 335                 340

atg ttc cag ctg cat cca gcc cca tcc acc atc gtg atc atg gtg ttg   1171
Met Phe Gln Leu His Pro Ala Pro Ser Thr Ile Val Ile Met Val Leu
            345                 350                 355

ctg ctg tgg tgg ctg ctc aaa ctc gtg gtg gtt cca agc cag aaa gtg   1219
Leu Leu Trp Trp Leu Leu Lys Leu Val Val Val Pro Ser Gln Lys Val
        360                 365                 370

aag ggc tgg aag gcg ggc atc ggt atc cgt ttg aag gat gtc ggc atc   1267
Lys Gly Trp Lys Ala Gly Ile Gly Ile Arg Leu Lys Asp Val Gly Ile
    375                 380                 385

ctg gcc atc acg ggc atc atc ggt gtg ctc ttc atg ctg cct cag gtg   1315
Leu Ala Ile Thr Gly Ile Ile Gly Val Leu Phe Met Leu Pro Gln Val
390                 395                 400                 405

att tca ggt tcc gaa caa acc gaa gat gtg ctg tca tat tct gct gag   1363
Ile Ser Gly Ser Glu Gln Thr Glu Asp Val Leu Ser Tyr Ser Ala Glu
                410                 415                 420

gaa caa gtc acc cgc agc gag tcc tgg ttg gtg tct att ttc atg gag   1411
Glu Gln Val Thr Arg Ser Glu Ser Trp Leu Val Ser Ile Phe Met Glu
            425                 430                 435

acc cgc cat gtt gat ttc ttc gga aat att gac atc gtc cca gtg ctg   1459
Thr Arg His Val Asp Phe Phe Gly Asn Ile Asp Ile Val Pro Val Leu
        440                 445                 450

gta ttc gca gca atc ggt ggc gtg gtt gct ttg gtg tgg cgc gga aac   1507
Val Phe Ala Ala Ile Gly Gly Val Val Ala Leu Val Trp Arg Gly Asn
    455                 460                 465

ttg tgg gcg ccg gtg ttt tac ttc gcc agc gtt gcg ttg acc gct aac   1555
Leu Trp Ala Pro Val Phe Tyr Phe Ala Ser Val Ala Leu Thr Ala Asn
470                 475                 480                 485

tcg ctg aag cct ttt gaa gag ccg tgg ggt gat tgg ctc aac atc gtg   1603
Ser Leu Lys Pro Phe Glu Glu Pro Trp Gly Asp Trp Leu Asn Ile Val
                490                 495                 500

ggc ggt ctg cat tac tcc aca gga cac cgt ttg atc atg cct gtc gcc   1651
Gly Gly Leu His Tyr Ser Thr Gly His Arg Leu Ile Met Pro Val Ala
            505                 510                 515

atg ttc act ttt gct gcc gca ggt atc ggc gct gcc gca gtg atc cgt   1699
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Met Phe Thr Phe Ala Ala Ala Gly Ile Gly Ala Ala Ala Val Ile Arg
        520                 525                 530

ttg atc tgc ttg gga cca ata aag aag ttc acc act gtt tcc ggt gtt   1747
Leu Ile Cys Leu Gly Pro Ile Lys Lys Phe Thr Thr Val Ser Gly Val
    535                 540                 545

gtt tct gtg gtg atg gct ctt gtt gtg gct gtg cca ttg cag act tgg   1795
Val Ser Val Val Met Ala Leu Val Val Ala Val Pro Leu Gln Thr Trp
550                 555                 560                 565

gcg aag gat ttt gta gag gaa gga tcc gaa acc aca atc ctt gcg cca   1843
Ala Lys Asp Phe Val Glu Glu Gly Ser Glu Thr Thr Ile Leu Ala Pro
                570                 575                 580

cac aat gat gaa cgt atg gtg agc aac aac gac ttg gct gcc tgg gac   1891
His Asn Asp Glu Arg Met Val Ser Asn Asn Asp Leu Ala Ala Trp Asp
            585                 590                 595

tgg tta atc caa cag cca ggt gga gct gac atg aac atc atg ggt gac   1939
Trp Leu Ile Gln Gln Pro Gly Gly Ala Asp Met Asn Ile Met Gly Asp
        600                 605                 610

ccc gca gat ggt aac ggc tgg atg tat gcc tac aac ggc ttg cac tcc   1987
Pro Ala Asp Gly Asn Gly Trp Met Tyr Ala Tyr Asn Gly Leu His Ser
    615                 620                 625

gtg gcc cgc cac tat gca tgg cca gca gca ggc gaa ggc tct gcc acc   2035
Val Ala Arg His Tyr Ala Trp Pro Ala Ala Gly Glu Gly Ser Ala Thr
630                 635                 640                 645

gcg atg ctg ttc tgg tgg cct caa ctt cta ggt gtg ggc acc gat gaa   2083
Ala Met Leu Phe Trp Trp Pro Gln Leu Leu Gly Val Gly Thr Asp Glu
                650                 655                 660

aac cca gat caa gtc aac gat gtg gat cag gct gct cgt gat ctc aac   2131
Asn Pro Asp Gln Val Asn Asp Val Asp Gln Ala Ala Arg Asp Leu Asn
            665                 670                 675

gtc ggc tac ttc atg atc agt ccg tgg acg ttc tgg gat ttc cag atc   2179
Val Gly Tyr Phe Met Ile Ser Pro Trp Thr Phe Trp Asp Phe Gln Ile
        680                 685                 690

ccc aac ttc cgc cag atc gat ctg ctg tgg caa acc cca ggc gtg aca   2227
Pro Asn Phe Arg Gln Ile Asp Leu Leu Trp Gln Thr Pro Gly Val Thr
    695                 700                 705

ccg gtg tgc aag aag ggc gac tcg gtg atc ttc gca gtc aac gat atg   2275
Pro Val Cys Lys Lys Gly Asp Ser Val Ile Phe Ala Val Asn Asp Met
710                 715                 720                 725

ttc act gac gcc gaa ctg gat cag atg cgt gca cct ggt aat tct cca   2323
Phe Thr Asp Ala Glu Leu Asp Gln Met Arg Ala Pro Gly Asn Ser Pro
                730                 735                 740

gaa cca ctg cca gag ctt cct acc ttg ggc gag ctt ggg ttg gct gaa   2371
Glu Pro Leu Pro Glu Leu Pro Thr Leu Gly Glu Leu Gly Leu Ala Glu
            745                 750                 755

act gaa gac gag gta gat cag act tat tac cat cgt cca acg gtt cct   2419
Thr Glu Asp Glu Val Asp Gln Thr Tyr Tyr His Arg Pro Thr Val Pro
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        760                 765                 770

gct ggt gtg aac tca gag atg cct tca gcc gaa act ctg tat gca ccg   2467
Ala Gly Val Asn Ser Glu Met Pro Ser Ala Glu Thr Leu Tyr Ala Pro
    775                 780                 785

gat cca acg aag ccg cat acg gtc cct aac taatcacaaa gagtattcag     2517
Asp Pro Thr Lys Pro His Thr Val Pro Asn
790                 795

taa                                                               2520


<210> 586
<211> 799
<212> PRT
<213> Corynebacterium glutamicum

<400> 586
Met Leu Thr Thr Leu Trp Ile Ala Val Leu Val Phe Thr Val Pro Gly
  1               5                  10                  15

Leu Val Val Ser Trp Val Ser Gly Leu Lys Val Pro Trp Ala Ile Ala
             20                  25                  30

Ala Ser Ile Pro Ala Thr Phe Gly Ile Tyr Gly Leu Ser Ala Trp Leu
         35                  40                  45

Leu Gly Leu Trp Glu Met Arg Phe Asp Leu His Ser Val Val Ile Ser
     50                  55                  60

Thr Leu Val Phe Ala Ala Val Ala Leu Val Trp Arg Leu Phe Phe Val
 65                  70                  75                  80

Gly Gly Trp Leu Val Arg Arg Arg Lys Ala Arg Ile Arg Arg Gln Thr
                 85                  90                  95

Leu Ala Asp Glu Glu Arg Ala Glu Asn Ala Glu Val Ser Ala Gly Glu
            100                 105                 110

Pro Ala Glu Ser Ser Thr Asn Glu Ala Ala Glu Ser Glu Ser Glu Thr
        115                 120                 125

Ser Glu Arg Arg Gly Ile Trp Arg Val Ile Phe Asp Tyr Met Arg Asp
    130                 135                 140

Gly Gly Ile Leu Asp His Arg Trp Leu Leu Pro Ala Ala Gly Ala Ile
145                 150                 155                 160

Thr Gly Ala Trp Leu Ile Ile Asp Arg Ala Val Asp Leu Leu Leu Ser
                165                 170                 175

Thr Glu His Gly Leu Gly Asp Ile Val Gln Gly Trp Asp Val His Trp
            180                 185                 190

His Ala Ser Thr Val Arg Phe Ile Asp Glu Thr Gly Ile Ala Ser Ser
        195                 200                 205

Thr Met Met Gly Gln Leu Arg Asn Ile Glu Thr Gln Gln Asp Leu Phe
    210                 215                 220
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Tyr Pro Ser Ala Trp His Ala Gly Ala Trp Val Leu Ser Asp Val Gly
225                 230                 235                 240

Asn Leu Thr Ile Val Glu Ala Thr Asn Leu Thr Gly Ile Val Leu Ser
                245                 250                 255

Gly Leu Leu Leu Pro Leu Ala Val Ala Leu Ile Ala Trp Arg Met Ile
            260                 265                 270

Asn Asn Arg Gly Leu Thr Ala Gln Ile Gly Ala Gly Phe Ala Gly Leu
        275                 280                 285

Ile Thr Ile Ala Ser Pro Val Leu Phe Trp Val Gly Asn Tyr Val Gly
    290                 295                 300

Ala Trp Pro Tyr Val Ala Ala Ile Gly Ala Ser Gly Val Val Leu Ala
305                 310                 315                 320

Leu Phe Met Ser Thr Pro Ser Val Pro Val Arg Ile Phe Ala Ala Ala
                325                 330                 335

Leu Ala Phe Met Gly Met Phe Gln Leu His Pro Ala Pro Ser Thr Ile
            340                 345                 350

Val Ile Met Val Leu Leu Leu Trp Trp Leu Leu Lys Leu Val Val Val
        355                 360                 365

Pro Ser Gln Lys Val Lys Gly Trp Lys Ala Gly Ile Gly Ile Arg Leu
    370                 375                 380

Lys Asp Val Gly Ile Leu Ala Ile Thr Gly Ile Ile Gly Val Leu Phe
385                 390                 395                 400

Met Leu Pro Gln Val Ile Ser Gly Ser Glu Gln Thr Glu Asp Val Leu
                405                 410                 415

Ser Tyr Ser Ala Glu Glu Gln Val Thr Arg Ser Glu Ser Trp Leu Val
            420                 425                 430

Ser Ile Phe Met Glu Thr Arg His Val Asp Phe Phe Gly Asn Ile Asp
        435                 440                 445

Ile Val Pro Val Leu Val Phe Ala Ala Ile Gly Gly Val Val Ala Leu
    450                 455                 460

Val Trp Arg Gly Asn Leu Trp Ala Pro Val Phe Tyr Phe Ala Ser Val
465                 470                 475                 480

Ala Leu Thr Ala Asn Ser Leu Lys Pro Phe Glu Glu Pro Trp Gly Asp
                485                 490                 495

Trp Leu Asn Ile Val Gly Gly Leu His Tyr Ser Thr Gly His Arg Leu
            500                 505                 510

Ile Met Pro Val Ala Met Phe Thr Phe Ala Ala Ala Gly Ile Gly Ala
        515                 520                 525

Ala Ala Val Ile Arg Leu Ile Cys Leu Gly Pro Ile Lys Lys Phe Thr
    530                 535                 540

Thr Val Ser Gly Val Val Ser Val Val Met Ala Leu Val Val Ala Val
```

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545                 550                 555                 560

Pro Leu Gln Thr Trp Ala Lys Asp Phe Val Glu Glu Gly Ser Glu Thr
                565                 570                 575

Thr Ile Leu Ala Pro His Asn Asp Glu Arg Met Val Ser Asn Asn Asp
            580                 585                 590

Leu Ala Ala Trp Asp Trp Leu Ile Gln Gln Pro Gly Gly Ala Asp Met
        595                 600                 605

Asn Ile Met Gly Asp Pro Ala Asp Gly Asn Gly Trp Met Tyr Ala Tyr
    610                 615                 620

Asn Gly Leu His Ser Val Ala Arg His Tyr Ala Trp Pro Ala Ala Gly
625                 630                 635                 640

Glu Gly Ser Ala Thr Ala Met Leu Phe Trp Trp Pro Gln Leu Leu Gly
                645                 650                 655

Val Gly Thr Asp Glu Asn Pro Asp Gln Val Asn Asp Val Asp Gln Ala
            660                 665                 670

Ala Arg Asp Leu Asn Val Gly Tyr Phe Met Ile Ser Pro Trp Thr Phe
        675                 680                 685

Trp Asp Phe Gln Ile Pro Asn Phe Arg Gln Ile Asp Leu Leu Trp Gln
    690                 695                 700

Thr Pro Gly Val Thr Pro Val Cys Lys Lys Gly Asp Ser Val Ile Phe
705                 710                 715                 720

Ala Val Asn Asp Met Phe Thr Asp Ala Glu Leu Asp Gln Met Arg Ala
                725                 730                 735

Pro Gly Asn Ser Pro Glu Pro Leu Pro Glu Leu Pro Thr Leu Gly Glu
            740                 745                 750

Leu Gly Leu Ala Glu Thr Glu Asp Glu Val Asp Gln Thr Tyr Tyr His
        755                 760                 765

Arg Pro Thr Val Pro Ala Gly Val Asn Ser Glu Met Pro Ser Ala Glu
    770                 775                 780

Thr Leu Tyr Ala Pro Asp Pro Thr Lys Pro His Thr Val Pro Asn
785                 790                 795


<210> 587
<211> 638
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (40)..(615)
<223> FRXA01331

<400> 587
gcctcggact ggttaatcca acagccaggt ggagctgacatg aac atc atg ggt gac 57
                                                Met Asn Ile Met Gly Asp
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                                                  1               5

ccc gca gat ggt aac ggc tgg atg tat gcc tac aac ggc ttg cac tcc   105
Pro Ala Asp Gly Asn Gly Trp Met Tyr Ala Tyr Asn Gly Leu His Ser
            10                  15                  20

gtg gcc cgc cac tat gca tgg cca gca gca ggc gaa ggc tct gcc acc   153
Val Ala Arg His Tyr Ala Trp Pro Ala Ala Gly Glu Gly Ser Ala Thr
        25                  30                  35

gcg atg ctg ttc tgg tgg cct caa ctt cta ggt gtg ggc acc gat gaa   201
Ala Met Leu Phe Trp Trp Pro Gln Leu Leu Gly Val Gly Thr Asp Glu
    40                  45                  50

aac cca gat caa gtc aac gat gtg gat cag gct gct cgt gat ctc aac   249
Asn Pro Asp Gln Val Asn Asp Val Asp Gln Ala Ala Arg Asp Leu Asn
55                  60                  65                  70

gtc ggc tac ttc atg atc agt ccg tgg acg ttc tgg gat ttc cag atc   297
Val Gly Tyr Phe Met Ile Ser Pro Trp Thr Phe Trp Asp Phe Gln Ile
                75                  80                  85

ccc aac ttc cgc cag atc gat ctg ctg tgg caa acc cca ggc gtg aca   345
Pro Asn Phe Arg Gln Ile Asp Leu Leu Trp Gln Thr Pro Gly Val Thr
            90                  95                  100

ccg gtg tgc aag aag ggc gac tcg gtg atc ttc gca gtc aac gat atg   393
Pro Val Cys Lys Lys Gly Asp Ser Val Ile Phe Ala Val Asn Asp Met
        105                 110                 115

ttc act gac gcc gaa ctg gat cag atg cgt gca cct ggt aat tct cca   441
Phe Thr Asp Ala Glu Leu Asp Gln Met Arg Ala Pro Gly Asn Ser Pro
    120                 125                 130

gaa cca ctg cca gag ctt cct acc ttg ggc gag ctt ggg ttg gct gaa   489
Glu Pro Leu Pro Glu Leu Pro Thr Leu Gly Glu Leu Gly Leu Ala Glu
135                 140                 145                 150

act gaa gac gag gta gat cag act tat tac cat cgt cca acg gtt cct   537
Thr Glu Asp Glu Val Asp Gln Thr Tyr Tyr His Arg Pro Thr Val Pro
                155                 160                 165

gct ggt gtg aac tca gag atg cct tca gcc gaa act ctg tat gca ccg   585
Ala Gly Val Asn Ser Glu Met Pro Ser Ala Glu Thr Leu Tyr Ala Pro
            170                 175                 180

gat cca acg aag ccg cat acg gtc cct aac taatcacaaa gagtattcag     635
Asp Pro Thr Lys Pro His Thr Val Pro Asn
        185                 190

taa                                                               638


<210> 588
<211> 192
<212> PRT
<213> Corynebacterium glutamicum

<400> 588
Met Asn Ile Met Gly Asp Pro Ala Asp Gly Asn Gly Trp Met Tyr Ala
  1               5                  10                  15
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Tyr Asn Gly Leu His Ser Val Ala Arg His Tyr Ala Trp Pro Ala Ala
            20                  25                  30

Gly Glu Gly Ser Ala Thr Ala Met Leu Phe Trp Trp Pro Gln Leu Leu
        35                  40                  45

Gly Val Gly Thr Asp Glu Asn Pro Asp Gln Val Asn Asp Val Asp Gln
    50                  55                  60

Ala Ala Arg Asp Leu Asn Val Gly Tyr Phe Met Ile Ser Pro Trp Thr
65                  70                  75                  80

Phe Trp Asp Phe Gln Ile Pro Asn Phe Arg Gln Ile Asp Leu Leu Trp
                85                  90                  95

Gln Thr Pro Gly Val Thr Pro Val Cys Lys Lys Gly Asp Ser Val Ile
            100                 105                 110

Phe Ala Val Asn Asp Met Phe Thr Asp Ala Glu Leu Asp Gln Met Arg
        115                 120                 125

Ala Pro Gly Asn Ser Pro Glu Pro Leu Pro Glu Leu Pro Thr Leu Gly
    130                 135                 140

Glu Leu Gly Leu Ala Glu Thr Glu Asp Glu Val Asp Gln Thr Tyr Tyr
145                 150                 155                 160

His Arg Pro Thr Val Pro Ala Gly Val Asn Ser Glu Met Pro Ser Ala
                165                 170                 175

Glu Thr Leu Tyr Ala Pro Asp Pro Thr Lys Pro His Thr Val Pro Asn
            180                 185                 190
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US20050176109A1

<210> 589
<211> 892
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(892)
<223> FRXA00668

<400> 589
ctaaactcgt ctctcgtatc tttcagtcat ttatgtctga taagcaggcg cgtgcgccac 60

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acaattggca caatcacaag aaagtgaagt gggaacctag atg ctg acg aca cta   115
                                              Met Leu Thr Thr Leu
                                                1               5

tgg att gcg gtg ttg gta ttt acc gtt cca gga ttg gtc gtc tcg tgg   163
Trp Ile Ala Val Leu Val Phe Thr Val Pro Gly Leu Val Val Ser Trp
                10                  15                  20

gtt tct ggc ctt aaa gtg ccc tgg gct atc gca gcc tcc atc cca gcc   211
Val Ser Gly Leu Lys Val Pro Trp Ala Ile Ala Ala Ser Ile Pro Ala
```

```
                25                  30                  35

acc ttc ggt att tac ggc ctg tcc gcc tgg ttg ctg ggc ttg tgg gag   259
Thr Phe Gly Ile Tyr Gly Leu Ser Ala Trp Leu Leu Gly Leu Trp Glu
         40                  45                  50

atg cgt ttt gat ctc cat tct gta gtt att tcc aca ttg gtt ttc gct   307
Met Arg Phe Asp Leu His Ser Val Val Ile Ser Thr Leu Val Phe Ala
     55                  60                  65

gcg gtt gct ttg gta tgg cgc ttg ttt ttt gtc ggt ggt tgg ctt gta   355
Ala Val Ala Leu Val Trp Arg Leu Phe Phe Val Gly Gly Trp Leu Val
 70                  75                  80                  85

cgt cgg cgt aaa gca cgt atc cgc agg cag acg ctc gcg gat gaa gag   403
Arg Arg Arg Lys Ala Arg Ile Arg Arg Gln Thr Leu Ala Asp Glu Glu
                 90                  95                 100

cgg gca gaa aat gct gag gta tct gca ggg gag cct gcc gaa tcg agc   451
Arg Ala Glu Asn Ala Glu Val Ser Ala Gly Glu Pro Ala Glu Ser Ser
            105                 110                 115

aca aac gaa gca gcc gaa tct gaa tct gaa acc tcg gag cgt cgc gga   499
Thr Asn Glu Ala Ala Glu Ser Glu Ser Glu Thr Ser Glu Arg Arg Gly
        120                 125                 130

atc tgg cgc gtg atc ttt gat tac atg cgc gac ggt ggc atc ttg gat   547
Ile Trp Arg Val Ile Phe Asp Tyr Met Arg Asp Gly Gly Ile Leu Asp
    135                 140                 145

cac cgt tgg ctg ctg cct gcc gca ggt gct atc act ggt gcg tgg ctg   595
His Arg Trp Leu Leu Pro Ala Ala Gly Ala Ile Thr Gly Ala Trp Leu
150                 155                 160                 165

atc att gat cgt gcc gtt gat ctg ctc ttg agc acc gag cat ggt ttg   643
Ile Ile Asp Arg Ala Val Asp Leu Leu Leu Ser Thr Glu His Gly Leu
                170                 175                 180

ggc gat atc gtc caa ggc tgg gat gtc cat tgg cat gct tcg act gtc   691
Gly Asp Ile Val Gln Gly Trp Asp Val His Trp His Ala Ser Thr Val
            185                 190                 195

cgt ttt ata gat gag acc ggc att gcg tca tcc acg atg atg ggg cag   739
Arg Phe Ile Asp Glu Thr Gly Ile Ala Ser Ser Thr Met Met Gly Gln
        200                 205                 210

ctg cgc aat att gaa acg cag caa gat ctg ttc tac cca agc gca tgg   787
Leu Arg Asn Ile Glu Thr Gln Gln Asp Leu Phe Tyr Pro Ser Ala Trp
    215                 220                 225

cat gct ggt gca tgg gtg ctg tcg gat gtc gga aat ctg acg att gtt   835
His Ala Gly Ala Trp Val Leu Ser Asp Val Gly Asn Leu Thr Ile Val
230                 235                 240                 245

gaa gcc acc aac ctc act ggc att gtg ctg tcc gga ttg ttg ctg ccg   883
Glu Ala Thr Asn Leu Thr Gly Ile Val Leu Ser Gly Leu Leu Leu Pro
                250                 255                 260

tta gct gtt                                                      892
Leu Ala Val
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<210> 590
<211> 264
<212> PRT
<213> Corynebacterium glutamicum

<400> 590
Met Leu Thr Thr Leu Trp Ile Ala Val Leu Val Phe Thr Val Pro Gly
1 5 10 15

Leu Val Val Ser Trp Val Ser Gly Leu Lys Val Pro Trp Ala Ile Ala
20 25 30

Ala Ser Ile Pro Ala Thr Phe Gly Ile Tyr Gly Leu Ser Ala Trp Leu
35 40 45

Leu Gly Leu Trp Glu Met Arg Phe Asp Leu His Ser Val Val Ile Ser
50 55 60

Thr Leu Val Phe Ala Ala Val Ala Leu Val Trp Arg Leu Phe Phe Val
65 70 75 80

Gly Gly Trp Leu Val Arg Arg Arg Lys Ala Arg Ile Arg Arg Gln Thr
85 90 95

Leu Ala Asp Glu Glu Arg Ala Glu Asn Ala Glu Val Ser Ala Gly Glu
100 105 110

Pro Ala Glu Ser Ser Thr Asn Glu Ala Ala Glu Ser Glu Ser Glu Thr
115 120 125

Ser Glu Arg Arg Gly Ile Trp Arg Val Ile Phe Asp Tyr Met Arg Asp
130 135 140

Gly Gly Ile Leu Asp His Arg Trp Leu Leu Pro Ala Ala Gly Ala Ile
145 150 155 160

Thr Gly Ala Trp Leu Ile Ile Asp Arg Ala Val Asp Leu Leu Leu Ser
165 170 175

Thr Glu His Gly Leu Gly Asp Ile Val Gln Gly Trp Asp Val His Trp
180 185 190

His Ala Ser Thr Val Arg Phe Ile Asp Glu Thr Gly Ile Ala Ser Ser
195 200 205

Thr Met Met Gly Gln Leu Arg Asn Ile Glu Thr Gln Gln Asp Leu Phe
210 215 220

Tyr Pro Ser Ala Trp His Ala Gly Ala Trp Val Leu Ser Asp Val Gly
225 230 235 240

Asn Leu Thr Ile Val Glu Ala Thr Asn Leu Thr Gly Ile Val Leu Ser
245 250 255

Gly Leu Leu Leu Pro Leu Ala Val
260

<210> 591

<211> 750
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(750)
<223> FRXA00674

<400> 591

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atc ttt gcc gca gca ttg gcg ttc atg ggt atg ttc cag ctg cat cca   48
Ile Phe Ala Ala Ala Leu Ala Phe Met Gly Met Phe Gln Leu His Pro
  1               5                  10                  15

gcc cca tcc acc atc gtg atc atg gtg ttg ctg ctg tgg tgg ctg ctc   96
Ala Pro Ser Thr Ile Val Ile Met Val Leu Leu Leu Trp Trp Leu Leu
             20                  25                  30

aaa ctc gtg gtg gtt cca agc cag aaa gtg aag ggc tgg aag gcg ggc   144
Lys Leu Val Val Val Pro Ser Gln Lys Val Lys Gly Trp Lys Ala Gly
         35                  40                  45

atc ggt atc cgt ttg aag gat gtc ggc atc ctg gcc atc acg ggc atc   192
Ile Gly Ile Arg Leu Lys Asp Val Gly Ile Leu Ala Ile Thr Gly Ile
     50                  55                  60

atc ggt gtg ctc ttc atg ctg cct cag gtg att tca ggt tcc gaa caa   240
Ile Gly Val Leu Phe Met Leu Pro Gln Val Ile Ser Gly Ser Glu Gln
 65                  70                  75                  80

acc gaa gat gtg ctg tca tat tct gct gag gaa caa gtc acc cgc agc   288
Thr Glu Asp Val Leu Ser Tyr Ser Ala Glu Glu Gln Val Thr Arg Ser
                 85                  90                  95

gag tcc tgg ttg gtg tct att ttc atg gag acc cgc cat gtt gat ttc   336
Glu Ser Trp Leu Val Ser Ile Phe Met Glu Thr Arg His Val Asp Phe
            100                 105                 110

ttc gga aat att gac atc gtc cca gtg ctg gta ttc gca gca atc ggt   384
Phe Gly Asn Ile Asp Ile Val Pro Val Leu Val Phe Ala Ala Ile Gly
        115                 120                 125

ggc gtg gtt gct ttg gtg tgg cgc gga aac ttg tgg gcg ccg gtg ttt   432
Gly Val Val Ala Leu Val Trp Arg Gly Asn Leu Trp Ala Pro Val Phe
    130                 135                 140

tac ttc gcc agc gtt gcg ttg acc gct aac tcg ctg aag cct ttt gaa   480
Tyr Phe Ala Ser Val Ala Leu Thr Ala Asn Ser Leu Lys Pro Phe Glu
145                 150                 155                 160

gag ccg tgg ggt gat tgg ctc aac atc gtg ggc ggt ctg cat tac tcc   528
Glu Pro Trp Gly Asp Trp Leu Asn Ile Val Gly Gly Leu His Tyr Ser
                165                 170                 175

aca gga cac cgt ttg atc atg cct gtc gcc atg ttc act ttt gct gcc   576
Thr Gly His Arg Leu Ile Met Pro Val Ala Met Phe Thr Phe Ala Ala
            180                 185                 190

gca ggt atc ggc gct gcc gca gtg atc cgt ttg atc tgc ttg gga cca   624
Ala Gly Ile Gly Ala Ala Ala Val Ile Arg Leu Ile Cys Leu Gly Pro
        195                 200                 205
```

```
ata aag aag ttc acc act gtt tcc ggt gtt gtt tct gtg gtg atg gct   672
Ile Lys Lys Phe Thr Thr Val Ser Gly Val Val Ser Val Val Met Ala
    210                 215                 220

ctt gtt gtg gct gtg cca ttg cag act tgg gcg aag gat ttt gta gag   720
Leu Val Val Ala Val Pro Leu Gln Thr Trp Ala Lys Asp Phe Val Glu
225                 230                 235                 240

gaa gga tcc gaa acc aca atc ctt gcg cca                          750
Glu Gly Ser Glu Thr Thr Ile Leu Ala Pro
                245                 250
```

<210> 592
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 592

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Ile Phe Ala Ala Ala Leu Ala Phe Met Gly Met Phe Gln Leu His Pro
  1               5                  10                  15

Ala Pro Ser Thr Ile Val Ile Met Val Leu Leu Leu Trp Trp Leu Leu
             20                  25                  30

Lys Leu Val Val Val Pro Ser Gln Lys Val Lys Gly Trp Lys Ala Gly
         35                  40                  45

Ile Gly Ile Arg Leu Lys Asp Val Gly Ile Leu Ala Ile Thr Gly Ile
     50                  55                  60

Ile Gly Val Leu Phe Met Leu Pro Gln Val Ile Ser Gly Ser Glu Gln
 65                  70                  75                  80

Thr Glu Asp Val Leu Ser Tyr Ser Ala Glu Glu Gln Val Thr Arg Ser
                 85                  90                  95

Glu Ser Trp Leu Val Ser Ile Phe Met Glu Thr Arg His Val Asp Phe
            100                 105                 110

Phe Gly Asn Ile Asp Ile Val Pro Val Leu Val Phe Ala Ala Ile Gly
        115                 120                 125

Gly Val Val Ala Leu Val Trp Arg Gly Asn Leu Trp Ala Pro Val Phe
    130                 135                 140

Tyr Phe Ala Ser Val Ala Leu Thr Ala Asn Ser Leu Lys Pro Phe Glu
145                 150                 155                 160

Glu Pro Trp Gly Asp Trp Leu Asn Ile Val Gly Gly Leu His Tyr Ser
                165                 170                 175

Thr Gly His Arg Leu Ile Met Pro Val Ala Met Phe Thr Phe Ala Ala
            180                 185                 190

Ala Gly Ile Gly Ala Ala Ala Val Ile Arg Leu Ile Cys Leu Gly Pro
        195                 200                 205

Ile Lys Lys Phe Thr Thr Val Ser Gly Val Val Ser Val Val Met Ala
    210                 215                 220
```

```
Leu Val Val Ala Val Pro Leu Gln Thr Trp Ala Lys Asp Phe Val Glu
225                 230                 235                 240

Glu Gly Ser Glu Thr Thr Ile Leu Ala Pro
                245                 250


<210> 593
<211> 1536
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1513)
<223> RXN01337

<400> 593
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tacgcaagaa aaagtttctt agcagggtaa cctaaatgtc gtg aca ttt cga ggc   115
                                            Val Thr Phe Arg Gly
                                              1               5

gga aac act ggc gca aag cac gcg gtc gtt gtt ggt tct ggc ccc aat   163
Gly Asn Thr Gly Ala Lys His Ala Val Val Val Gly Ser Gly Pro Asn
                  10                  15                  20

ggg ttg acc acg gcg gcg gtg ctg gcc aaa gca ggt tgg caa gta gat   211
Gly Leu Thr Thr Ala Ala Val Leu Ala Lys Ala Gly Trp Gln Val Asp
              25                  30                  35

gtg tat gag gcg gcg cca acc cct gga ggg gcg gcg cgc tca gaa agc   259
Val Tyr Glu Ala Ala Pro Thr Pro Gly Gly Ala Ala Arg Ser Glu Ser
          40                  45                  50

gtt ctg ggg gag ggg act atc agc gat ttg ggt gcc gca ggg cat cct   307
Val Leu Gly Glu Gly Thr Ile Ser Asp Leu Gly Ala Ala Gly His Pro
      55                  60                  65

ttc ggg gtg gca agc cca gct ttt cac tat ttg ggt ctg gaa gat cac   355
Phe Gly Val Ala Ser Pro Ala Phe His Tyr Leu Gly Leu Glu Asp His
  70                  75                  80                  85

ggc ctg gaa tgg gcg tat tct ccc ttt gcg atg gcc cac ccg tta gat   403
Gly Leu Glu Trp Ala Tyr Ser Pro Phe Ala Met Ala His Pro Leu Asp
                  90                  95                 100

tat ggc agg gcc gga ctg ctg gaa acg tca ctc cca gag acc gcc aaa   451
Tyr Gly Arg Ala Gly Leu Leu Glu Thr Ser Leu Pro Glu Thr Ala Lys
              105                 110                 115

aag ctt gga cct gat gca cgt cgt tgg aag aat ttg cac cag ggc tta   499
Lys Leu Gly Pro Asp Ala Arg Arg Trp Lys Asn Leu His Gln Gly Leu
          120                 125                 130

acc aaa aac att gat aaa cac ttg gcc aat cta tta ggg ccg gtg ctg   547
Thr Lys Asn Ile Asp Lys His Leu Ala Asn Leu Leu Gly Pro Val Leu
      135                 140                 145
```

```
aaa tgg cca gca cat ccg att cgg atg gca aag ttt ggc cca ttt gcg   595
Lys Trp Pro Ala His Pro Ile Arg Met Ala Lys Phe Gly Pro Phe Ala
150                 155                 160                 165

ttg ctg ccc gcg aaa cgt cta gcc agt gcc gct ttt gaa aca gaa gaa   643
Leu Leu Pro Ala Lys Arg Leu Ala Ser Ala Ala Phe Glu Thr Glu Glu
                170                 175                 180

gcc cga tcc ctg ttt atc ggt tcg gcg atg cac tcg gtg act cca cca   691
Ala Arg Ser Leu Phe Ile Gly Ser Ala Met His Ser Val Thr Pro Pro
            185                 190                 195

cac aag ccg atg acc gca tca ctt gga ttg ctt ttt ggc gct ctg ggg   739
His Lys Pro Met Thr Ala Ser Leu Gly Leu Leu Phe Gly Ala Leu Gly
        200                 205                 210

atg tcg cga gga tgg ccg gtt gca gtt ggg gga agc gga cgg atc gtc   787
Met Ser Arg Gly Trp Pro Val Ala Val Gly Gly Ser Gly Arg Ile Val
    215                 220                 225

gat gct ctg gtc aat gtc ata aac cat cac ggt ggc acc att cac tgc   835
Asp Ala Leu Val Asn Val Ile Asn His His Gly Gly Thr Ile His Cys
230                 235                 240                 245

gat tca cag att gat tcc ctc tca caa ttc cgc gac acc gat gcc att   883
Asp Ser Gln Ile Asp Ser Leu Ser Gln Phe Arg Asp Thr Asp Ala Ile
                250                 255                 260

att ctg aac caa acc ccc tca cag gtg ctg aaa ctc aaa gga act gac   931
Ile Leu Asn Gln Thr Pro Ser Gln Val Leu Lys Leu Lys Gly Thr Asp
            265                 270                 275

ctt aat gca ggg ctt ccg caa cgc atg agc acc tgg aaa cac gga cca   979
Leu Asn Ala Gly Leu Pro Gln Arg Met Ser Thr Trp Lys His Gly Pro
        280                 285                 290

agt tcc tac aaa gtg gac tac ctc ctt gac gaa cca att ccc tgg agc   1027
Ser Ser Tyr Lys Val Asp Tyr Leu Leu Asp Glu Pro Ile Pro Trp Ser
    295                 300                 305

aat ccc cag gta ggc cag gcc aca acc gtc cat gtg ggc gga agc tct   1075
Asn Pro Gln Val Gly Gln Ala Thr Thr Val His Val Gly Gly Ser Ser
310                 315                 320                 325

gag gaa atc gct ttc gca gaa gca gaa gtc gca gcg ggg cgg atg ccc   1123
Glu Glu Ile Ala Phe Ala Glu Ala Glu Val Ala Ala Gly Arg Met Pro
                330                 335                 340

gaa cgc ccg ttt atc att ttg tgc caa caa caa gtg gcg gat cct tca   1171
Glu Arg Pro Phe Ile Ile Leu Cys Gln Gln Gln Val Ala Asp Pro Ser
            345                 350                 355

cgc gcc cgg gag ggg cgc cac gtc gtg tgg gcc tac gcg cat gtg ccg   1219
Arg Ala Arg Glu Gly Arg His Val Val Trp Ala Tyr Ala His Val Pro
        360                 365                 370

cgg ggt ttc gtc gat aag cga gct gct tta tta atc act gcg cag att   1267
Arg Gly Phe Val Asp Lys Arg Ala Ala Leu Leu Ile Thr Ala Gln Ile
    375                 380                 385

gaa cgc ttc gcc ccc ggt ttc cgt gat cgc atc gtg cat tca gtg gat   1315
```

```
Glu Arg Phe Ala Pro Gly Phe Arg Asp Arg Ile Val His Ser Val Asp
390                 395                 400                 405

acc aac gcg gag gat tta gag gcg tgg aac ccc aat ctt gtt ggc gga   1363
Thr Asn Ala Glu Asp Leu Glu Ala Trp Asn Pro Asn Leu Val Gly Gly
                410                 415                 420

gac atc acc gca ggg tcc gcg ctg ctt cgg cga atg ccg acc aaa atc   1411
Asp Ile Thr Ala Gly Ser Ala Leu Leu Arg Arg Met Pro Thr Lys Ile
            425                 430                 435

ggc gag aaa acg tac atg gca tcc gcc tcc aac gcg ccg ggc ggg gga   1459
Gly Glu Lys Thr Tyr Met Ala Ser Ala Ser Asn Ala Pro Gly Gly Gly
        440                 445                 450

gtc cac gga atg ccc ggc tgg tgg gca gcg caa gcc gtt tta gca gat   1507
Val His Gly Met Pro Gly Trp Trp Ala Ala Gln Ala Val Leu Ala Asp
    455                 460                 465

cac agg tagaattgcg acatggagcc cac                                1536
His Arg
470
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EP 1 108 790 A2

<210> 594
<211> 471
<212> PRT
<213> Corynebacterium glutamicum

<400> 594

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Val Thr Phe Arg Gly Gly Asn Thr Gly Ala Lys His Ala Val Val Val
  1               5                  10                  15

Gly Ser Gly Pro Asn Gly Leu Thr Thr Ala Ala Val Leu Ala Lys Ala
             20                  25                  30

Gly Trp Gln Val Asp Val Tyr Glu Ala Ala Pro Thr Pro Gly Gly Ala
         35                  40                  45

Ala Arg Ser Glu Ser Val Leu Gly Glu Gly Thr Ile Ser Asp Leu Gly
     50                  55                  60

Ala Ala Gly His Pro Phe Gly Val Ala Ser Pro Ala Phe His Tyr Leu
 65                  70                  75                  80

Gly Leu Glu Asp His Gly Leu Glu Trp Ala Tyr Ser Pro Phe Ala Met
                 85                  90                  95

Ala His Pro Leu Asp Tyr Gly Arg Ala Gly Leu Leu Glu Thr Ser Leu
            100                 105                 110

Pro Glu Thr Ala Lys Lys Leu Gly Pro Asp Ala Arg Arg Trp Lys Asn
        115                 120                 125

Leu His Gln Gly Leu Thr Lys Asn Ile Asp Lys His Leu Ala Asn Leu
    130                 135                 140

Leu Gly Pro Val Leu Lys Trp Pro Ala His Pro Ile Arg Met Ala Lys
145                 150                 155                 160

Phe Gly Pro Phe Ala Leu Leu Pro Ala Lys Arg Leu Ala Ser Ala Ala
```

```
                 165                 170                 175

Phe Glu Thr Glu Glu Ala Arg Ser Leu Phe Ile Gly Ser Ala Met His
            180                 185                 190

Ser Val Thr Pro Pro His Lys Pro Met Thr Ala Ser Leu Gly Leu Leu
        195                 200                 205

Phe Gly Ala Leu Gly Met Ser Arg Gly Trp Pro Val Ala Val Gly Gly
    210                 215                 220

Ser Gly Arg Ile Val Asp Ala Leu Val Asn Val Ile Asn His His Gly
225                 230                 235                 240

Gly Thr Ile His Cys Asp Ser Gln Ile Asp Ser Leu Ser Gln Phe Arg
                245                 250                 255

Asp Thr Asp Ala Ile Ile Leu Asn Gln Thr Pro Ser Gln Val Leu Lys
            260                 265                 270

Leu Lys Gly Thr Asp Leu Asn Ala Gly Leu Pro Gln Arg Met Ser Thr
        275                 280                 285

Trp Lys His Gly Pro Ser Ser Tyr Lys Val Asp Tyr Leu Leu Asp Glu
    290                 295                 300

Pro Ile Pro Trp Ser Asn Pro Gln Val Gly Gln Ala Thr Thr Val His
305                 310                 315                 320

Val Gly Gly Ser Ser Glu Glu Ile Ala Phe Ala Glu Ala Glu Val Ala
                325                 330                 335

Ala Gly Arg Met Pro Glu Arg Pro Phe Ile Ile Leu Cys Gln Gln Gln
            340                 345                 350

Val Ala Asp Pro Ser Arg Ala Arg Glu Gly Arg His Val Val Trp Ala
        355                 360                 365

Tyr Ala His Val Pro Arg Gly Phe Val Asp Lys Arg Ala Ala Leu Leu
    370                 375                 380

Ile Thr Ala Gln Ile Glu Arg Phe Ala Pro Gly Phe Arg Asp Arg Ile
385                 390                 395                 400

Val His Ser Val Asp Thr Asn Ala Glu Asp Leu Glu Ala Trp Asn Pro
                405                 410                 415

Asn Leu Val Gly Gly Asp Ile Thr Ala Gly Ser Ala Leu Leu Arg Arg
            420                 425                 430

Met Pro Thr Lys Ile Gly Glu Lys Thr Tyr Met Ala Ser Ala Ser Asn
        435                 440                 445

Ala Pro Gly Gly Gly Val His Gly Met Pro Gly Trp Trp Ala Ala Gln
    450                 455                 460

Ala Val Leu Ala Asp His Arg
465                 470
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<210> 595

<211> 1536
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1513)
<223> FRXA01337

<400> 595
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tacgcaagaa aaagtttctt agcagggtaa cctaaatgtc gtg aca ttt cga ggc 115
Val Thr Phe Arg Gly
1 5

gga aac act ggc gca aag cac gcg gtc gtt gtt ggt tct ggc ccc aat 163
Gly Asn Thr Gly Ala Lys His Ala Val Val Val Gly Ser Gly Pro Asn
10 15 20

ggg ttg acc acg gcg gcg gtg ctg gcc aaa gca ggt tgg caa gta gat 211
Gly Leu Thr Thr Ala Ala Val Leu Ala Lys Ala Gly Trp Gln Val Asp
25 30 35

gtg tat gag gcg gcg cca acc cct gga ggg gcg gcg cgc tca gaa agc 259
Val Tyr Glu Ala Ala Pro Thr Pro Gly Gly Ala Ala Arg Ser Glu Ser
40 45 50

gtt ctg ggg gag ggg act atc agc gat ttg ggt gcc gca ggg cat cct 307
Val Leu Gly Glu Gly Thr Ile Ser Asp Leu Gly Ala Ala Gly His Pro
55 60 65

ttc ggg gtg gca agc cca gct ttt cac tat ttg ggt ctg gaa gat cac 355
Phe Gly Val Ala Ser Pro Ala Phe His Tyr Leu Gly Leu Glu Asp His
70 75 80 85

ggc ctg gaa tgg gcg tat tct ccc ttt gcg atg gcc cac ccg tta gat 403
Gly Leu Glu Trp Ala Tyr Ser Pro Phe Ala Met Ala His Pro Leu Asp
90 95 100

tat ggc agg gcc gga ctg ctg gaa acg tca ctc cca gag acc gcc aaa 451
Tyr Gly Arg Ala Gly Leu Leu Glu Thr Ser Leu Pro Glu Thr Ala Lys
105 110 115

aag ctt gga cct gat gca cgt cgt tgg aag aat ttg cac cag ggc tta 499
Lys Leu Gly Pro Asp Ala Arg Arg Trp Lys Asn Leu His Gln Gly Leu
120 125 130

acc aaa aac att gat aaa cac ttg gcc aat cta tta ggg ccg gtg ctg 547
Thr Lys Asn Ile Asp Lys His Leu Ala Asn Leu Leu Gly Pro Val Leu
135 140 145

aaa tgg cca gca cat ccg att cgg atg gca aag ttt ggc cca ttt gcg 595
Lys Trp Pro Ala His Pro Ile Arg Met Ala Lys Phe Gly Pro Phe Ala
150 155 160 165

ttg ctg ccc gcg aaa cgt cta gcc agt gcc gct ttt gaa aca gaa gaa 643
Leu Leu Pro Ala Lys Arg Leu Ala Ser Ala Ala Phe Glu Thr Glu Glu
170 175 180

gcc cga tcc ctg ttt atc ggt tcg gcg atg cac tcg gtg act cca cca 691

```
Ala Arg Ser Leu Phe Ile Gly Ser Ala Met His Ser Val Thr Pro Pro
           185                 190                 195

cac aag ccg atg acc gca tca ctt gga ttg ctt ttt ggc gct ctg ggg   739
His Lys Pro Met Thr Ala Ser Leu Gly Leu Leu Phe Gly Ala Leu Gly
        200                 205                 210

atg tcg cga gga tgg ccg gtt gca gtt ggg gga agc gga cgg atc gtc   787
Met Ser Arg Gly Trp Pro Val Ala Val Gly Gly Ser Gly Arg Ile Val
    215                 220                 225

gat gct ctg gtc aat gtc ata aac cat cac ggt ggc acc att cac tgc   835
Asp Ala Leu Val Asn Val Ile Asn His His Gly Gly Thr Ile His Cys
230                 235                 240                 245

gat tca cag att gat tcc ctc tca caa ttc cgc gac acc gat gcc att   883
Asp Ser Gln Ile Asp Ser Leu Ser Gln Phe Arg Asp Thr Asp Ala Ile
                250                 255                 260

att ctg aac caa acc ccc tca cag gtg ctg aaa ctc aaa gga act gac   931
Ile Leu Asn Gln Thr Pro Ser Gln Val Leu Lys Leu Lys Gly Thr Asp
           265                 270                 275

ctt aat gca ggg ctt ccg caa cgc atg agc acc tgg aaa cac gga cca   979
Leu Asn Ala Gly Leu Pro Gln Arg Met Ser Thr Trp Lys His Gly Pro
        280                 285                 290

agt tcc tac aaa gtg gac tac ctc ctt gac gaa cca att ccc tgg agc   1027
Ser Ser Tyr Lys Val Asp Tyr Leu Leu Asp Glu Pro Ile Pro Trp Ser
    295                 300                 305

aat ccc cag gta ggc cag gcc aca acc gtc cat gtg ggc gga agc tct   1075
Asn Pro Gln Val Gly Gln Ala Thr Thr Val His Val Gly Gly Ser Ser
310                 315                 320                 325

gag gaa atc gct ttc gca gaa gca gaa gtc gca gcg ggg cgg atg ccc   1123
Glu Glu Ile Ala Phe Ala Glu Ala Glu Val Ala Ala Gly Arg Met Pro
                330                 335                 340

gaa cgc ccg ttt atc att ttg tgc caa caa caa gtg gcg gat cct tca   1171
Glu Arg Pro Phe Ile Ile Leu Cys Gln Gln Gln Val Ala Asp Pro Ser
           345                 350                 355

cgc gcc cgg gag ggg cgc cac gtc gtg tgg gcc tac gcg cat gtg ccg   1219
Arg Ala Arg Glu Gly Arg His Val Val Trp Ala Tyr Ala His Val Pro
        360                 365                 370

cgg ggt ttc gtc gat aag cga gct gct tta tta atc act gcg cag att   1267
Arg Gly Phe Val Asp Lys Arg Ala Ala Leu Leu Ile Thr Ala Gln Ile
    375                 380                 385

gaa cgc ttc gcc ccc ggt ttc cgt gat cgc atc gtg cat tca gtg gat   1315
Glu Arg Phe Ala Pro Gly Phe Arg Asp Arg Ile Val His Ser Val Asp
390                 395                 400                 405

acc aac gcg gag gat tta gag gcg tgg aac ccc aat ctt gtt ggc gga   1363
Thr Asn Ala Glu Asp Leu Glu Ala Trp Asn Pro Asn Leu Val Gly Gly
                410                 415                 420

gac atc acc gca ggg tcc gcg ctg ctt cgg cga atg ccg acc aaa atc   1411
Asp Ile Thr Ala Gly Ser Ala Leu Leu Arg Arg Met Pro Thr Lys Ile
```

```
            425                 430                 435

ggc gag aaa acg tac atg gca tcc gcc tcc aac gcg ccg ggc ggg gga   1459
Gly Glu Lys Thr Tyr Met Ala Ser Ala Ser Asn Ala Pro Gly Gly Gly
        440                 445                 450

gtc cac gga atg ccc ggc tgg tgg gca gcg caa gcc gtt tta gca gat   1507
Val His Gly Met Pro Gly Trp Trp Ala Ala Gln Ala Val Leu Ala Asp
    455                 460                 465

cac agg tagaattgcg acatggagcc cac                                 1536
His Arg
470
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<210> 596
<211> 471
<212> PRT
<213> Corynebacterium glutamicum

<400> 596

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Val Thr Phe Arg Gly Gly Asn Thr Gly Ala Lys His Ala Val Val Val
  1               5                  10                  15

Gly Ser Gly Pro Asn Gly Leu Thr Thr Ala Ala Val Leu Ala Lys Ala
             20                  25                  30

Gly Trp Gln Val Asp Val Tyr Glu Ala Ala Pro Thr Pro Gly Gly Ala
         35                  40                  45

Ala Arg Ser Glu Ser Val Leu Gly Glu Gly Thr Ile Ser Asp Leu Gly
     50                  55                  60

Ala Ala Gly His Pro Phe Gly Val Ala Ser Pro Ala Phe His Tyr Leu
 65                  70                  75                  80

Gly Leu Glu Asp His Gly Leu Glu Trp Ala Tyr Ser Pro Phe Ala Met
                 85                  90                  95

Ala His Pro Leu Asp Tyr Gly Arg Ala Gly Leu Leu Glu Thr Ser Leu
            100                 105                 110

Pro Glu Thr Ala Lys Lys Leu Gly Pro Asp Ala Arg Arg Trp Lys Asn
        115                 120                 125

Leu His Gln Gly Leu Thr Lys Asn Ile Asp Lys His Leu Ala Asn Leu
    130                 135                 140

Leu Gly Pro Val Leu Lys Trp Pro Ala His Pro Ile Arg Met Ala Lys
145                 150                 155                 160

Phe Gly Pro Phe Ala Leu Leu Pro Ala Lys Arg Leu Ala Ser Ala Ala
                165                 170                 175

Phe Glu Thr Glu Glu Ala Arg Ser Leu Phe Ile Gly Ser Ala Met His
            180                 185                 190

Ser Val Thr Pro Pro His Lys Pro Met Thr Ala Ser Leu Gly Leu Leu
        195                 200                 205

Phe Gly Ala Leu Gly Met Ser Arg Gly Trp Pro Val Ala Val Gly Gly
```

```
    210                 215                 220

Ser Gly Arg Ile Val Asp Ala Leu Val Asn Val Ile Asn His His Gly
225                 230                 235                 240

Gly Thr Ile His Cys Asp Ser Gln Ile Asp Ser Leu Ser Gln Phe Arg
                245                 250                 255

Asp Thr Asp Ala Ile Ile Leu Asn Gln Thr Pro Ser Gln Val Leu Lys
            260                 265                 270

Leu Lys Gly Thr Asp Leu Asn Ala Gly Leu Pro Gln Arg Met Ser Thr
        275                 280                 285

Trp Lys His Gly Pro Ser Ser Tyr Lys Val Asp Tyr Leu Leu Asp Glu
    290                 295                 300

Pro Ile Pro Trp Ser Asn Pro Gln Val Gly Gln Ala Thr Thr Val His
305                 310                 315                 320

Val Gly Gly Ser Ser Glu Glu Ile Ala Phe Ala Glu Ala Glu Val Ala
                325                 330                 335

Ala Gly Arg Met Pro Glu Arg Pro Phe Ile Ile Leu Cys Gln Gln Gln
            340                 345                 350

Val Ala Asp Pro Ser Arg Ala Arg Glu Gly Arg His Val Val Trp Ala
        355                 360                 365

Tyr Ala His Val Pro Arg Gly Phe Val Asp Lys Arg Ala Ala Leu Leu
    370                 375                 380

Ile Thr Ala Gln Ile Glu Arg Phe Ala Pro Gly Phe Arg Asp Arg Ile
385                 390                 395                 400

Val His Ser Val Asp Thr Asn Ala Glu Asp Leu Glu Ala Trp Asn Pro
                405                 410                 415

Asn Leu Val Gly Gly Asp Ile Thr Ala Gly Ser Ala Leu Leu Arg Arg
            420                 425                 430

Met Pro Thr Lys Ile Gly Glu Lys Thr Tyr Met Ala Ser Ala Ser Asn
        435                 440                 445

Ala Pro Gly Gly Gly Val His Gly Met Pro Gly Trp Trp Ala Ala Gln
    450                 455                 460

Ala Val Leu Ala Asp His Arg
465                 470


<210> 597
<211> 708
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(685)
<223> RXN01351
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<400> 597
ctggagattt ccgatttcca gcgcgcccgc atcgacgcga atgctcagga attgcaggcc 60

gagcgcgagg cagtgcgcga cttgctctaa tctttaacgc atg act tcg ctt ttc 115
Met Thr Ser Leu Phe
1 5

gac gcc cca acc ctc caa cgc gtc acc gtt ttc acg ggc tcg gcg ctc 163
Asp Ala Pro Thr Leu Gln Arg Val Thr Val Phe Thr Gly Ser Ala Leu
10 15 20

ggc agt tcc tcg ctg tac acg caa gcg gct caa acc ttg gcg aaa acc 211
Gly Ser Ser Ser Leu Tyr Thr Gln Ala Ala Gln Thr Leu Ala Lys Thr
25 30 35

gcg gta gac cgc ggc atc gac ttg gtt tac ggt ggc gga aaa gtg ggg 259
Ala Val Asp Arg Gly Ile Asp Leu Val Tyr Gly Gly Gly Lys Val Gly
40 45 50

ctc atg ggt atc gtc gcg gat gcg ttc ctg gaa tca ggt ggc gaa gcc 307
Leu Met Gly Ile Val Ala Asp Ala Phe Leu Glu Ser Gly Gly Glu Ala
55 60 65

ttt ggc gtc atc acg gaa tca ctt atg aag ggt gag ctt ggg cat gaa 355
Phe Gly Val Ile Thr Glu Ser Leu Met Lys Gly Glu Leu Gly His Glu
70 75 80 85

aag ctc acc gaa ctt gaa atc gtt cct gat atg cac atc cgc aag cgt 403
Lys Leu Thr Glu Leu Glu Ile Val Pro Asp Met His Ile Arg Lys Arg
90 95 100

cgc atg gca gaa ctt ggc gat ggt ttt atc gcc atg ccc ggt ggc gcc 451
Arg Met Ala Glu Leu Gly Asp Gly Phe Ile Ala Met Pro Gly Gly Ala
105 110 115

ggc acc ttg gaa gaa ctt ttc gag gtc tgg acc tgg caa cag ctg ggc 499
Gly Thr Leu Glu Glu Leu Phe Glu Val Trp Thr Trp Gln Gln Leu Gly
120 125 130

att cat caa aag ccc gtc gca ctt tat gat gtc gat ggt ttt tgg cag 547
Ile His Gln Lys Pro Val Ala Leu Tyr Asp Val Asp Gly Phe Trp Gln
135 140 145

ccc ctg ctg gaa atg ctt gag cag atg acc cag cgt gga ttt atc aag 595
Pro Leu Leu Glu Met Leu Glu Gln Met Thr Gln Arg Gly Phe Ile Lys
150 155 160 165

cga gac ttc ttt gag tgc ctc atc gtg gaa tcc gac ccg cat gcc ctg 643
Arg Asp Phe Phe Glu Cys Leu Ile Val Glu Ser Asp Pro His Ala Leu
170 175 180

cta aag gca atg cag acc tgg act cca cca gca cca aaa tgg 685
Leu Lys Ala Met Gln Thr Trp Thr Pro Pro Ala Pro Lys Trp
185 190 195

taactaaatt gtgtgctcga cgg 708

<210> 598
<211> 195
<212> PRT

<213> Corynebacterium glutamicum

<400> 598

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Met Thr Ser Leu Phe Asp Ala Pro Thr Leu Gln Arg Val Thr Val Phe
  1               5                  10                  15

Thr Gly Ser Ala Leu Gly Ser Ser Ser Leu Tyr Thr Gln Ala Ala Gln
             20                  25                  30

Thr Leu Ala Lys Thr Ala Val Asp Arg Gly Ile Asp Leu Val Tyr Gly
         35                  40                  45

Gly Gly Lys Val Gly Leu Met Gly Ile Val Ala Asp Ala Phe Leu Glu
     50                  55                  60

Ser Gly Gly Glu Ala Phe Gly Val Ile Thr Glu Ser Leu Met Lys Gly
 65                  70                  75                  80

Glu Leu Gly His Glu Lys Leu Thr Glu Leu Glu Ile Val Pro Asp Met
                 85                  90                  95

His Ile Arg Lys Arg Arg Met Ala Glu Leu Gly Asp Gly Phe Ile Ala
            100                 105                 110

Met Pro Gly Gly Ala Gly Thr Leu Glu Glu Leu Phe Glu Val Trp Thr
        115                 120                 125

Trp Gln Gln Leu Gly Ile His Gln Lys Pro Val Ala Leu Tyr Asp Val
    130                 135                 140

Asp Gly Phe Trp Gln Pro Leu Leu Glu Met Leu Glu Gln Met Thr Gln
145                 150                 155                 160

Arg Gly Phe Ile Lys Arg Asp Phe Phe Glu Cys Leu Ile Val Glu Ser
                165                 170                 175

Asp Pro His Ala Leu Leu Lys Ala Met Gln Thr Trp Thr Pro Pro Ala
            180                 185                 190

Pro Lys Trp
        195
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<210> 599
<211> 3677
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<213> Corynebacterium glutamicum

<220>
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<222> (1)..(3654)
<223> RXN01362

<400> 599

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aaa tgg ctt ggc acg cct gcg cag agc tta ttc tta atc ccc cca gtt   48
Lys Trp Leu Gly Thr Pro Ala Gln Ser Leu Phe Leu Ile Pro Pro Val
  1               5                  10                  15

acc cag cat gct cgc acg ggc acc cac ctt tat gat tcc ctg cag ctg   96
Thr Gln His Ala Arg Thr Gly Thr His Leu Tyr Asp Ser Leu Gln Leu
             20                  25                  30
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ctg ttc act ctg gtg gat aaa ggc cac cac cca aca gat gct aag gct   144
Leu Phe Thr Leu Val Asp Lys Gly His His Pro Thr Asp Ala Lys Ala
        35                  40                  45

gta gct ttt gat gcc gag gct gga gaa gaa ggc ctg cac ttc cgc aac   192
Val Ala Phe Asp Ala Glu Ala Gly Glu Glu Gly Leu His Phe Arg Asn
    50                  55                  60

ctt tca gcg gat ctc ttc ctc cct gca gcc aca gaa ctt att gat cga   240
Leu Ser Ala Asp Leu Phe Leu Pro Ala Ala Thr Glu Leu Ile Asp Arg
65                  70                  75                  80

gtt ggt ctt tcc aat gaa gcc cta aac aag gtc ttg gaa aac ctc ctg   288
Val Gly Leu Ser Asn Glu Ala Leu Asn Lys Val Leu Glu Asn Leu Leu
                85                  90                  95

ctc tcc cgg gtg caa tcc ggt aaa gac cgc ggc ttt atc tcc tat gcc   336
Leu Ser Arg Val Gln Ser Gly Lys Asp Arg Gly Phe Ile Ser Tyr Ala
            100                 105                 110

acc ttg ggt gtt acc gag ctt ggc caa gtt tat gag ggt ctg atg tcc   384
Thr Leu Gly Val Thr Glu Leu Gly Gln Val Tyr Glu Gly Leu Met Ser
        115                 120                 125

tat acc ggc ttt atc gcc cag gaa gat ctt ttt gag gtt gca cca cat   432
Tyr Thr Gly Phe Ile Ala Gln Glu Asp Leu Phe Glu Val Ala Pro His
    130                 135                 140

ggc aaa gcc gat aaa ggt tcc tgg atg ctc ccg gtc tca aag gct gat   480
Gly Lys Ala Asp Lys Gly Ser Trp Met Leu Pro Val Ser Lys Ala Asp
145                 150                 155                 160

gaa gtc cct gcc gat agc ttt atc gaa gtt gat caa gaa gcc cct ggt   528
Glu Val Pro Ala Asp Ser Phe Ile Glu Val Asp Gln Glu Ala Pro Gly
                165                 170                 175

ggc ggc gta atc aag gtg cgt aaa cgc cac ccg cgc gga tca ttt gtg   576
Gly Gly Val Ile Lys Val Arg Lys Arg His Pro Arg Gly Ser Phe Val
            180                 185                 190

ttc cgt cag tcc tct cgt gac cgc gaa cgc tca gcg tcc ttc tac acc   624
Phe Arg Gln Ser Ser Arg Asp Arg Glu Arg Ser Ala Ser Phe Tyr Thr
        195                 200                 205

cca caa gta ctc acc agc ttt act gtc acc cag gct att gaa gaa ctc   672
Pro Gln Val Leu Thr Ser Phe Thr Val Thr Gln Ala Ile Glu Glu Leu
    210                 215                 220

cag gca tca aag cgc atc acc aca gcc aat gat gtt ctc agc ctc acc   720
Gln Ala Ser Lys Arg Ile Thr Thr Ala Asn Asp Val Leu Ser Leu Thr
225                 230                 235                 240

atc tgt gaa cct gcc atg ggt tcc ggc gcc ttc gct gtg gaa gca gta   768
Ile Cys Glu Pro Ala Met Gly Ser Gly Ala Phe Ala Val Glu Ala Val
                245                 250                 255

cgc caa tta gca gag ctt tat ttg gaa ttg cgc caa gaa gaa cta gag   816
Arg Gln Leu Ala Glu Leu Tyr Leu Glu Leu Arg Gln Glu Glu Leu Glu
            260                 265                 270
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cag cag att cca gcg gaa gac cgt gcc aag gaa ctc caa aag gtc aaa   864
Gln Gln Ile Pro Ala Glu Asp Arg Ala Lys Glu Leu Gln Lys Val Lys
        275                 280                 285

gcg cac att gcg ctg cac cag gtt tat ggt gtg gac ctt aac agc act   912
Ala His Ile Ala Leu His Gln Val Tyr Gly Val Asp Leu Asn Ser Thr
    290                 295                 300

gct gtg gag ttg gcg gaa atc tcg ctg tgg cta gac acc atg aat gca   960
Ala Val Glu Leu Ala Glu Ile Ser Leu Trp Leu Asp Thr Met Asn Ala
305                 310                 315                 320

gaa atg gac gca cct tgg tat ggc ctg cac ctg cgt aat ggt aac tcc  1008
Glu Met Asp Ala Pro Trp Tyr Gly Leu His Leu Arg Asn Gly Asn Ser
                325                 330                 335

ctc gtt ggt gcc acc cgt tcg ctg tat gca cct agt ctg ctt aat aaa  1056
Leu Val Gly Ala Thr Arg Ser Leu Tyr Ala Pro Ser Leu Leu Asn Lys
            340                 345                 350

aaa gcc tgg tta act gct act cca acc cgc tat cgg ctt gat gat atc  1104
Lys Ala Trp Leu Thr Ala Thr Pro Thr Arg Tyr Arg Leu Asp Asp Ile
        355                 360                 365

gcg cag gct att gat gaa aac aaa gca gaa ccc ctc ttc aac cac ggc  1152
Ala Gln Ala Ile Asp Glu Asn Lys Ala Glu Pro Leu Phe Asn His Gly
    370                 375                 380

atc cac cac ttc ctc ttg ccc tct act ggc tgg gga gcc act gca gat  1200
Ile His His Phe Leu Leu Pro Ser Thr Gly Trp Gly Ala Thr Ala Asp
385                 390                 395                 400

gcc aaa gat ctt aaa gat ctt atg gct act gaa atc aag gag ctt aaa  1248
Ala Lys Asp Leu Lys Asp Leu Met Ala Thr Glu Ile Lys Glu Leu Lys
                405                 410                 415

tct tgg cgt act tcc atc cgt gcg tct ttg agt aaa act cag att aag  1296
Ser Trp Arg Thr Ser Ile Arg Ala Ser Leu Ser Lys Thr Gln Ile Lys
            420                 425                 430

cag ctc aat aac ctt gcc cta cgc gtg gaa aca cta tgg cga ttt gtg  1344
Gln Leu Asn Asn Leu Ala Leu Arg Val Glu Thr Leu Trp Arg Phe Val
        435                 440                 445

ctg atg cgt att cgc att gca gaa tcc cag atc tca cgt agc act act  1392
Leu Met Arg Ile Arg Ile Ala Glu Ser Gln Ile Ser Arg Ser Thr Thr
    450                 455                 460

ctc tgg ggt caa gag cca gct gag gtt tcg gag gtt gtc aca cgt gag  1440
Leu Trp Gly Gln Glu Pro Ala Glu Val Ser Glu Val Val Thr Arg Glu
465                 470                 475                 480

caa att gaa caa gac ctc ttt ggc aat att gat ggt gca tat aac cgt  1488
Gln Ile Glu Gln Asp Leu Phe Gly Asn Ile Asp Gly Ala Tyr Asn Arg
                485                 490                 495

cta cgc ttg gtg atg gat gct tgg tgt gcg ctg tgg ttc tgg cct ttg  1536
Leu Arg Leu Val Met Asp Ala Trp Cys Ala Leu Trp Phe Trp Pro Leu
            500                 505                 510

gat gct gtt gct acc gct gag cat ccg gag cgt cca gcc ctt cca gat  1584
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Asp Ala Val Ala Thr Ala Glu His Pro Glu Arg Pro Ala Leu Pro Asp
        515                 520                 525

ctt gat gag tgg cta gcc acc ctg acg gag att ctg ggt att gat ctc   1632
Leu Asp Glu Trp Leu Ala Thr Leu Thr Glu Ile Leu Gly Ile Asp Leu
    530                 535                 540

cct ctg aag tcc aaa aac gaa aat cag att gtc tta ggt cca gat acc   1680
Pro Leu Lys Ser Lys Asn Glu Asn Gln Ile Val Leu Gly Pro Asp Thr
545                 550                 555                 560

aat tgg cta gcc att aat gat gcc gag gct act gat ctt ggt ttt tct   1728
Asn Trp Leu Ala Ile Asn Asp Ala Glu Ala Thr Asp Leu Gly Phe Ser
                565                 570                 575

ggg gca ttg agc ttt gag cgt gtt agc gcg aat cac ccg tgg atc aat   1776
Gly Ala Leu Ser Phe Glu Arg Val Ser Ala Asn His Pro Trp Ile Asn
            580                 585                 590

gtt gcc cgc caa gtg gct aaa caa cag agc ttc ttc cac tgg gat cta   1824
Val Ala Arg Gln Val Ala Lys Gln Gln Ser Phe Phe His Trp Asp Leu
        595                 600                 605

gac ttc gcc cac gtt ttt gcc aag ggt gga ttt gat ctg cag gtt ggt   1872
Asp Phe Ala His Val Phe Ala Lys Gly Gly Phe Asp Leu Gln Val Gly
    610                 615                 620

aat cca cca tgg gtg cga cca gat gtg aac ttt gag gat ctg ctt gct   1920
Asn Pro Pro Trp Val Arg Pro Asp Val Asn Phe Glu Asp Leu Leu Ala
625                 630                 635                 640

gaa cat gat ccg tgg tgg gct gta atg agt aaa cca acc cag gca tcc   1968
Glu His Asp Pro Trp Trp Ala Val Met Ser Lys Pro Thr Gln Ala Ser
                645                 650                 655

aaa aaa gaa cgc cag aag aat ttt cac aac aat cct aag agc ctc gaa   2016
Lys Lys Glu Arg Gln Lys Asn Phe His Asn Asn Pro Lys Ser Leu Glu
            660                 665                 670

cat gtg gtc agt ggt gca ggt gaa ccc gtg gct act tct gcg atc ctc   2064
His Val Val Ser Gly Ala Gly Glu Pro Val Ala Thr Ser Ala Ile Leu
        675                 680                 685

ggt tcg gtt act ctc tat ccg cat ctt aaa gat caa cgc ccg gac ctc   2112
Gly Ser Val Thr Leu Tyr Pro His Leu Lys Asp Gln Arg Pro Asp Leu
    690                 695                 700

tac cgg ggc ttt atg gaa aag act tgg tct aat gcc tcc ccg gca ggt   2160
Tyr Arg Gly Phe Met Glu Lys Thr Trp Ser Asn Ala Ser Pro Ala Gly
705                 710                 715                 720

gcg atc tca ctg atc cac ccc gaa tcc cac ttc act gag aaa aaa gct   2208
Ala Ile Ser Leu Ile His Pro Glu Ser His Phe Thr Glu Lys Lys Ala
                725                 730                 735

gcc ccg cta cgt cgg gga gca tat gag cgt ctg cgc cgc cac tgg cag   2256
Ala Pro Leu Arg Arg Gly Ala Tyr Glu Arg Leu Arg Arg His Trp Gln
            740                 745                 750

ttc att aat gag ttg att ctt ttt gac gtc cac gac ttg gtt aaa tat   2304
Phe Ile Asn Glu Leu Ile Leu Phe Asp Val His Asp Leu Val Lys Tyr
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        755                 760                 765

ggc gta cat gtc tat ggc gct ccg cag gaa tct att aac ttt tta agt   2352
Gly Val His Val Tyr Gly Ala Pro Gln Glu Ser Ile Asn Phe Leu Ser
    770                 775                 780

gct gcg tcg ctt tat cac cca caa aca gtg ctt gat tca ttt gat cat   2400
Ala Ala Ser Leu Tyr His Pro Gln Thr Val Leu Asp Ser Phe Asp His
785                 790                 795                 800

gac ggt tca ggt aat ctc cct ggt ctt aaa gac gac aat ggc aac tgg   2448
Asp Gly Ser Gly Asn Leu Pro Gly Leu Lys Asp Asp Asn Gly Asn Trp
                805                 810                 815

gac cgt cgc cca cac aag gac cgt atc caa ctg gtc aat gcc gat act   2496
Asp Arg Arg Pro His Lys Asp Arg Ile Gln Leu Val Asn Ala Asp Thr
            820                 825                 830

ttg acg gtg tgg aag tcc atc ctg gag gat gaa caa acg cca tac ttg   2544
Leu Thr Val Trp Lys Ser Ile Leu Glu Asp Glu Gln Thr Pro Tyr Leu
        835                 840                 845

gat acc cgc atg gtt tat acc gtc aac acg gaa gca gca gca gcg ttg   2592
Asp Thr Arg Met Val Tyr Thr Val Asn Thr Glu Ala Ala Ala Ala Leu
    850                 855                 860

gaa aag ttg gct tct gca cct cgt atc aaa gaa ctc ggg ctg cag ttc   2640
Glu Lys Leu Ala Ser Ala Pro Arg Ile Lys Glu Leu Gly Leu Gln Phe
865                 870                 875                 880

tcc agt ggc tgg aat gaa acc acc gat aag aaa aag gga tac ttt gac   2688
Ser Ser Gly Trp Asn Glu Thr Thr Asp Lys Lys Lys Gly Tyr Phe Asp
                885                 890                 895

gtt ggt tgg ggc tac cca gct tcc tgg tct gat gcc att ttg cag ggg   2736
Val Gly Trp Gly Tyr Pro Ala Ser Trp Ser Asp Ala Ile Leu Gln Gly
            900                 905                 910

ccg cac ctg ggt gtt gct aca cca atg atc aag cag ccc aat ccg aca   2784
Pro His Leu Gly Val Ala Thr Pro Met Ile Lys Gln Pro Asn Pro Thr
        915                 920                 925

atg aag cat aat caa gat tgg tct gaa att gat ttc gag gcc att cct   2832
Met Lys His Asn Gln Asp Trp Ser Glu Ile Asp Phe Glu Ala Ile Pro
    930                 935                 940

gca aac ttc ata cct gca acg gcg tac cag ccc gat cgc caa aca aag   2880
Ala Asn Phe Ile Pro Ala Thr Ala Tyr Gln Pro Asp Arg Gln Thr Lys
945                 950                 955                 960

ccc act tat gat gct gac tac ggc acc tgg act ttc ggg gac aag cag   2928
Pro Thr Tyr Asp Ala Asp Tyr Gly Thr Trp Thr Phe Gly Asp Lys Gln
                965                 970                 975

gta cca gtt gca gac act ttc cga att gca tgg agg gag atg gct gcc   2976
Val Pro Val Ala Asp Thr Phe Arg Ile Ala Trp Arg Glu Met Ala Ala
            980                 985                 990

acc acg gga ttt agg act gtc tac cca tca gta att cca ccg gga gcc   3024
Thr Thr Gly Phe Arg Thr Val Tyr Pro Ser Val Ile Pro Pro Gly Ala
        995                 1000                1005
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aac cat gtg cac aca gtt aat agc gct gca tca cgt tca aac tta aaa   3072
Asn His Val His Thr Val Asn Ser Ala Ala Ser Arg Ser Asn Leu Lys
    1010                1015                1020

acc att ctc gtt gga gca cag ctt ggt gca att cta agt gac tat ttt   3120
Thr Ile Leu Val Gly Ala Gln Leu Gly Ala Ile Leu Ser Asp Tyr Phe
1025                1030                1035                1040

gct cgg tcc tcg ggt tca agc cac ata ttt aac gac att gtt cgc aag   3168
Ala Arg Ser Ser Gly Ser Ser His Ile Phe Asn Asp Ile Val Arg Lys
                1045                1050                1055

att cca ctt cca aat ttc aca tcc ttg gaa aag cag ttc gcc cgc aca   3216
Ile Pro Leu Pro Asn Phe Thr Ser Leu Glu Lys Gln Phe Ala Arg Thr
            1060                1065                1070

tac ctc cgc ctc aac tgc ctg acc tca gct tat gcc cca ttg tgg gaa   3264
Tyr Leu Arg Leu Asn Cys Leu Thr Ser Ala Tyr Ala Pro Leu Trp Glu
        1075                1080                1085

gag atc acc ggt gag ccg tgg gat gtt cag gtg cct ttg cgc aat gcc   3312
Glu Ile Thr Gly Glu Pro Trp Asp Val Gln Val Pro Leu Arg Asn Ala
    1090                1095                1100

gag caa cgt cga gca gcg caa aac gat att gat gcc atg gtg gca ttg   3360
Glu Gln Arg Arg Ala Ala Gln Asn Asp Ile Asp Ala Met Val Ala Leu
1105                1110                1115                1120

tct ttg ggt att agt gct gat gag ctg tgc atg att tat cgc act caa   3408
Ser Leu Gly Ile Ser Ala Asp Glu Leu Cys Met Ile Tyr Arg Thr Gln
                1125                1130                1135

ttc cca gtg atg cgt aga tat gat caa gaa gat cat ttt gat gcc aat   3456
Phe Pro Val Met Arg Arg Tyr Asp Gln Glu Asp His Phe Asp Ala Asn
            1140                1145                1150

ggc cgt aaa gtt cct aaa gag atc atc aag ctg cag cag aaa ctt aaa   3504
Gly Arg Lys Val Pro Lys Glu Ile Ile Lys Leu Gln Gln Lys Leu Lys
        1155                1160                1165

gat ggc caa gag ctc agc gtg gaa aag cgc acc tgg gtg cat ccc caa   3552
Asp Gly Gln Glu Leu Ser Val Glu Lys Arg Thr Trp Val His Pro Gln
    1170                1175                1180

tca gaa gtg tcc tat acc ttt gaa tat cct ttc cgg gtg ttg gat cgt   3600
Ser Glu Val Ser Tyr Thr Phe Glu Tyr Pro Phe Arg Val Leu Asp Arg
1185                1190                1195                1200

gaa gct gat ctg cgt gct gca tat gca aaa ttt gaa aac cag ctt aag   3648
Glu Ala Asp Leu Arg Ala Ala Tyr Ala Lys Phe Glu Asn Gln Leu Lys
                1205                1210                1215

gag cca tagagcgctt atgtcctcac tca                                3677
Glu Pro
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<210> 600
<211> 1218
<212> PRT

<213> Corynebacterium glutamicum

<400> 600

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Lys Trp Leu Gly Thr Pro Ala Gln Ser Leu Phe Leu Ile Pro Pro Val
  1               5                  10                  15

Thr Gln His Ala Arg Thr Gly Thr His Leu Tyr Asp Ser Leu Gln Leu
             20                  25                  30

Leu Phe Thr Leu Val Asp Lys Gly His His Pro Thr Asp Ala Lys Ala
         35                  40                  45

Val Ala Phe Asp Ala Glu Ala Gly Glu Glu Gly Leu His Phe Arg Asn
     50                  55                  60

Leu Ser Ala Asp Leu Phe Leu Pro Ala Ala Thr Glu Leu Ile Asp Arg
 65                  70                  75                  80

Val Gly Leu Ser Asn Glu Ala Leu Asn Lys Val Leu Glu Asn Leu Leu
                 85                  90                  95

Leu Ser Arg Val Gln Ser Gly Lys Asp Arg Gly Phe Ile Ser Tyr Ala
            100                 105                 110

Thr Leu Gly Val Thr Glu Leu Gly Gln Val Tyr Glu Gly Leu Met Ser
        115                 120                 125

Tyr Thr Gly Phe Ile Ala Gln Glu Asp Leu Phe Glu Val Ala Pro His
    130                 135                 140

Gly Lys Ala Asp Lys Gly Ser Trp Met Leu Pro Val Ser Lys Ala Asp
145                 150                 155                 160

Glu Val Pro Ala Asp Ser Phe Ile Glu Val Asp Gln Glu Ala Pro Gly
                165                 170                 175

Gly Gly Val Ile Lys Val Arg Lys Arg His Pro Arg Gly Ser Phe Val
            180                 185                 190

Phe Arg Gln Ser Ser Arg Asp Arg Glu Arg Ser Ala Ser Phe Tyr Thr
        195                 200                 205

Pro Gln Val Leu Thr Ser Phe Thr Val Thr Gln Ala Ile Glu Glu Leu
    210                 215                 220

Gln Ala Ser Lys Arg Ile Thr Thr Ala Asn Asp Val Leu Ser Leu Thr
225                 230                 235                 240

Ile Cys Glu Pro Ala Met Gly Ser Gly Ala Phe Ala Val Glu Ala Val
                245                 250                 255

Arg Gln Leu Ala Glu Leu Tyr Leu Glu Leu Arg Gln Glu Glu Leu Glu
            260                 265                 270

Gln Gln Ile Pro Ala Glu Asp Arg Ala Lys Glu Leu Gln Lys Val Lys
        275                 280                 285

Ala His Ile Ala Leu His Gln Val Tyr Gly Val Asp Leu Asn Ser Thr
    290                 295                 300

Ala Val Glu Leu Ala Glu Ile Ser Leu Trp Leu Asp Thr Met Asn Ala
```

```
305                 310                 315                 320

Glu Met Asp Ala Pro Trp Tyr Gly Leu His Leu Arg Asn Gly Asn Ser
                325                 330                 335

Leu Val Gly Ala Thr Arg Ser Leu Tyr Ala Pro Ser Leu Leu Asn Lys
            340                 345                 350

Lys Ala Trp Leu Thr Ala Thr Pro Thr Arg Tyr Arg Leu Asp Asp Ile
        355                 360                 365

Ala Gln Ala Ile Asp Glu Asn Lys Ala Glu Pro Leu Phe Asn His Gly
    370                 375                 380

Ile His His Phe Leu Leu Pro Ser Thr Gly Trp Gly Ala Thr Ala Asp
385                 390                 395                 400

Ala Lys Asp Leu Lys Asp Leu Met Ala Thr Glu Ile Lys Glu Leu Lys
                405                 410                 415

Ser Trp Arg Thr Ser Ile Arg Ala Ser Leu Ser Lys Thr Gln Ile Lys
            420                 425                 430

Gln Leu Asn Asn Leu Ala Leu Arg Val Glu Thr Leu Trp Arg Phe Val
        435                 440                 445

Leu Met Arg Ile Arg Ile Ala Glu Ser Gln Ile Ser Arg Ser Thr Thr
    450                 455                 460

Leu Trp Gly Gln Glu Pro Ala Glu Val Ser Glu Val Val Thr Arg Glu
465                 470                 475                 480

Gln Ile Glu Gln Asp Leu Phe Gly Asn Ile Asp Gly Ala Tyr Asn Arg
                485                 490                 495

Leu Arg Leu Val Met Asp Ala Trp Cys Ala Leu Trp Phe Trp Pro Leu
            500                 505                 510

Asp Ala Val Ala Thr Ala Glu His Pro Glu Arg Pro Ala Leu Pro Asp
        515                 520                 525

Leu Asp Glu Trp Leu Ala Thr Leu Thr Glu Ile Leu Gly Ile Asp Leu
    530                 535                 540

Pro Leu Lys Ser Lys Asn Glu Asn Gln Ile Val Leu Gly Pro Asp Thr
545                 550                 555                 560

Asn Trp Leu Ala Ile Asn Asp Ala Glu Ala Thr Asp Leu Gly Phe Ser
                565                 570                 575

Gly Ala Leu Ser Phe Glu Arg Val Ser Ala Asn His Pro Trp Ile Asn
            580                 585                 590

Val Ala Arg Gln Val Ala Lys Gln Gln Ser Phe Phe His Trp Asp Leu
        595                 600                 605

Asp Phe Ala His Val Phe Ala Lys Gly Gly Phe Asp Leu Gln Val Gly
    610                 615                 620

Asn Pro Pro Trp Val Arg Pro Asp Val Asn Phe Glu Asp Leu Leu Ala
625                 630                 635                 640
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Glu His Asp Pro Trp Trp Ala Val Met Ser Lys Pro Thr Gln Ala Ser
645 650 655

Lys Lys Glu Arg Gln Lys Asn Phe His Asn Asn Pro Lys Ser Leu Glu
660 665 670

His Val Val Ser Gly Ala Gly Glu Pro Val Ala Thr Ser Ala Ile Leu
675 680 685

Gly Ser Val Thr Leu Tyr Pro His Leu Lys Asp Gln Arg Pro Asp Leu
690 695 700

Tyr Arg Gly Phe Met Glu Lys Thr Trp Ser Asn Ala Ser Pro Ala Gly
705 710 715 720

Ala Ile Ser Leu Ile His Pro Glu Ser His Phe Thr Glu Lys Lys Ala
725 730 735

Ala Pro Leu Arg Arg Gly Ala Tyr Glu Arg Leu Arg Arg His Trp Gln
740 745 750

Phe Ile Asn Glu Leu Ile Leu Phe Asp Val His Asp Leu Val Lys Tyr
755 760 765

Gly Val His Val Tyr Gly Ala Pro Gln Glu Ser Ile Asn Phe Leu Ser
770 775 780

Ala Ala Ser Leu Tyr His Pro Gln Thr Val Leu Asp Ser Phe Asp His
785 790 795 800

Asp Gly Ser Gly Asn Leu Pro Gly Leu Lys Asp Asp Asn Gly Asn Trp
805 810 815

Asp Arg Arg Pro His Lys Asp Arg Ile Gln Leu Val Asn Ala Asp Thr
820 825 830

Leu Thr Val Trp Lys Ser Ile Leu Glu Asp Glu Gln Thr Pro Tyr Leu
835 840 845

Asp Thr Arg Met Val Tyr Thr Val Asn Thr Glu Ala Ala Ala Ala Leu
850 855 860

Glu Lys Leu Ala Ser Ala Pro Arg Ile Lys Glu Leu Gly Leu Gln Phe
865 870 875 880

Ser Ser Gly Trp Asn Glu Thr Thr Asp Lys Lys Lys Gly Tyr Phe Asp
885 890 895

Val Gly Trp Gly Tyr Pro Ala Ser Trp Ser Asp Ala Ile Leu Gln Gly
900 905 910

Pro His Leu Gly Val Ala Thr Pro Met Ile Lys Gln Pro Asn Pro Thr
915 920 925

Met Lys His Asn Gln Asp Trp Ser Glu Ile Asp Phe Glu Ala Ile Pro
930 935 940

Ala Asn Phe Ile Pro Ala Thr Ala Tyr Gln Pro Asp Arg Gln Thr Lys
945 950 955 960

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Pro Thr Tyr Asp Ala Asp Tyr Gly Thr Trp Thr Phe Gly Asp Lys Gln
                965                 970                 975

Val Pro Val Ala Asp Thr Phe Arg Ile Ala Trp Arg Glu Met Ala Ala
            980                 985                 990

Thr Thr Gly Phe Arg Thr Val Tyr Pro Ser Val Ile Pro Pro Gly Ala
        995                1000                1005

Asn His Val His Thr Val Asn Ser Ala Ala Ser Arg Ser Asn Leu Lys
    1010                1015                1020

Thr Ile Leu Val Gly Ala Gln Leu Gly Ala Ile Leu Ser Asp Tyr Phe
1025                1030                1035                1040

Ala Arg Ser Ser Gly Ser Ser His Ile Phe Asn Asp Ile Val Arg Lys
                1045                1050                1055

Ile Pro Leu Pro Asn Phe Thr Ser Leu Glu Lys Gln Phe Ala Arg Thr
            1060                1065                1070

Tyr Leu Arg Leu Asn Cys Leu Thr Ser Ala Tyr Ala Pro Leu Trp Glu
        1075                1080                1085

Glu Ile Thr Gly Glu Pro Trp Asp Val Gln Val Pro Leu Arg Asn Ala
    1090                1095                1100

Glu Gln Arg Arg Ala Ala Gln Asn Asp Ile Asp Ala Met Val Ala Leu
1105                1110                1115                1120

Ser Leu Gly Ile Ser Ala Asp Glu Leu Cys Met Ile Tyr Arg Thr Gln
                1125                1130                1135

Phe Pro Val Met Arg Arg Tyr Asp Gln Glu Asp His Phe Asp Ala Asn
            1140                1145                1150

Gly Arg Lys Val Pro Lys Glu Ile Ile Lys Leu Gln Gln Lys Leu Lys
        1155                1160                1165

Asp Gly Gln Glu Leu Ser Val Glu Lys Arg Thr Trp Val His Pro Gln
    1170                1175                1180

Ser Glu Val Ser Tyr Thr Phe Glu Tyr Pro Phe Arg Val Leu Asp Arg
1185                1190                1195                1200

Glu Ala Asp Leu Arg Ala Ala Tyr Ala Lys Phe Glu Asn Gln Leu Lys
                1205                1210                1215

Glu Pro
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<210> 601
<211> 1418
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1395)
<223> FRXA01362

<400> 601

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att aat gag ttg att ctt ttt gac gta cac gac ttg gtt aaa tat ggc   48
Ile Asn Glu Leu Ile Leu Phe Asp Val His Asp Leu Val Lys Tyr Gly
  1               5                  10                  15

gta cat gtc tat ggc gct ccg cag gaa tct att aac ttt tta agt gct   96
Val His Val Tyr Gly Ala Pro Gln Glu Ser Ile Asn Phe Leu Ser Ala
             20                  25                  30

gcg tcg ctt tat cac cca caa aca gtg ctt gat tca ttt gat cat gac   144
Ala Ser Leu Tyr His Pro Gln Thr Val Leu Asp Ser Phe Asp His Asp
         35                  40                  45

ggt tca ggt aat ctc cct ggt ctt aaa gac gac aat ggc aac tgg gac   192
Gly Ser Gly Asn Leu Pro Gly Leu Lys Asp Asp Asn Gly Asn Trp Asp
     50                  55                  60

cgt cgc cca cac aag gac cgt atc caa ctg gtc aat gcc gat act ttg   240
Arg Arg Pro His Lys Asp Arg Ile Gln Leu Val Asn Ala Asp Thr Leu
 65                  70                  75                  80

acg gtg tgg aag tcc atc ctg gag gat gaa caa acg cca tac ttg gat   288
Thr Val Trp Lys Ser Ile Leu Glu Asp Glu Gln Thr Pro Tyr Leu Asp
                 85                  90                  95

acc cgc atg gtt tat acc gtc aac acg gaa gca gca gca gcg ttg gaa   336
Thr Arg Met Val Tyr Thr Val Asn Thr Glu Ala Ala Ala Ala Leu Glu
            100                 105                 110

aag ttg gct tct gca cct cgt atc aaa gaa ctc ggg ctg cag ttc tcc   384
Lys Leu Ala Ser Ala Pro Arg Ile Lys Glu Leu Gly Leu Gln Phe Ser
        115                 120                 125

agt ggc tgg aat gaa acc acc gat aag aaa aag gga tac ttt gac gtt   432
Ser Gly Trp Asn Glu Thr Thr Asp Lys Lys Lys Gly Tyr Phe Asp Val
    130                 135                 140

ggt tgg ggc tac cca gct tcc tgg tct gat gcc att ttg cag ggg ccg   480
Gly Trp Gly Tyr Pro Ala Ser Trp Ser Asp Ala Ile Leu Gln Gly Pro
145                 150                 155                 160

cac ctg ggt gtt gct aca cca atg atc aag cag ccc aat ccg aca atg   528
His Leu Gly Val Ala Thr Pro Met Ile Lys Gln Pro Asn Pro Thr Met
                165                 170                 175

aag cat aat caa gat tgg tct gaa att gat ttc gag gcc att cct gca   576
Lys His Asn Gln Asp Trp Ser Glu Ile Asp Phe Glu Ala Ile Pro Ala
            180                 185                 190

aac ttc ata cct gca acg gcg tac cag ccc gat cgc caa aca aag ccc   624
Asn Phe Ile Pro Ala Thr Ala Tyr Gln Pro Asp Arg Gln Thr Lys Pro
        195                 200                 205

act tat gat gct gac tac ggc acc tgg act ttc ggg gac aag cag gta   672
Thr Tyr Asp Ala Asp Tyr Gly Thr Trp Thr Phe Gly Asp Lys Gln Val
    210                 215                 220

cca gtt gca gac act ttc cga att gca tgg agg gag atg gct gcc acc   720
Pro Val Ala Asp Thr Phe Arg Ile Ala Trp Arg Glu Met Ala Ala Thr
225                 230                 235                 240
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acg gga ttt agg act gtc tac cca tca gta att cca ccg gga gcc aac   768
Thr Gly Phe Arg Thr Val Tyr Pro Ser Val Ile Pro Pro Gly Ala Asn
                245                 250                 255

cat gtg cac aca gtt aat agc gct gca tca cgt tca aac tta aaa acc   816
His Val His Thr Val Asn Ser Ala Ala Ser Arg Ser Asn Leu Lys Thr
            260                 265                 270

att ctc gtt gga gca cag ctt ggt gca att cta agt gac tat ttt gct   864
Ile Leu Val Gly Ala Gln Leu Gly Ala Ile Leu Ser Asp Tyr Phe Ala
        275                 280                 285

cgg tcc tcg ggt tca agc cac ata ttt aac gac att gtt cgc aag att   912
Arg Ser Ser Gly Ser Ser His Ile Phe Asn Asp Ile Val Arg Lys Ile
    290                 295                 300

cca ctt cca aat ttc aca tcc ttg gaa aag cag ttc gcc cgc aca tac   960
Pro Leu Pro Asn Phe Thr Ser Leu Glu Lys Gln Phe Ala Arg Thr Tyr
305                 310                 315                 320

ctc cgc ctc aac tgc ctg acc tca gct tat gcc cca ttg tgg gaa gag   1008
Leu Arg Leu Asn Cys Leu Thr Ser Ala Tyr Ala Pro Leu Trp Glu Glu
                325                 330                 335

atc acc ggt gag ccg tgg gat gtt cag gtg cct ttg cgc aat gcc gag   1056
Ile Thr Gly Glu Pro Trp Asp Val Gln Val Pro Leu Arg Asn Ala Glu
            340                 345                 350

caa cgt cga gca gcg caa aac gat att gat gcc atg gtg gca ttg tct   1104
Gln Arg Arg Ala Ala Gln Asn Asp Ile Asp Ala Met Val Ala Leu Ser
        355                 360                 365

ttg ggt att agt gct gat gag ctg tgc atg att tat cgc act caa ttc   1152
Leu Gly Ile Ser Ala Asp Glu Leu Cys Met Ile Tyr Arg Thr Gln Phe
    370                 375                 380

cca gtg atg cgt aga tat gat caa gaa gat cat ttt gat gcc aat ggc   1200
Pro Val Met Arg Arg Tyr Asp Gln Glu Asp His Phe Asp Ala Asn Gly
385                 390                 395                 400

cgt aaa gtt cct aaa gag atc atc aag ctg cag cag aaa ctt aaa gat   1248
Arg Lys Val Pro Lys Glu Ile Ile Lys Leu Gln Gln Lys Leu Lys Asp
                405                 410                 415

ggc caa gag ctc agc gtg gaa aag cgc acc tgg gtg cat ccc caa tca   1296
Gly Gln Glu Leu Ser Val Glu Lys Arg Thr Trp Val His Pro Gln Ser
            420                 425                 430

gaa gtg tcc tat acc ttt gaa tat cct ttc cgg gtg ttg gat cgt gaa   1344
Glu Val Ser Tyr Thr Phe Glu Tyr Pro Phe Arg Val Leu Asp Arg Glu
        435                 440                 445

gct gat ctg cgt gct gca tat gca aaa ttt gaa aac cag ctt aag gag   1392
Ala Asp Leu Arg Ala Ala Tyr Ala Lys Phe Glu Asn Gln Leu Lys Glu
    450                 455                 460

cca tagagcgctt atgtcctcac tca                                    1418
Pro
465
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<210> 602
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<213> Corynebacterium glutamicum

<400> 602

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Val His Val Tyr Gly Ala Pro Gln Glu Ser Ile Asn Phe Leu Ser Ala
             20                  25                  30

Ala Ser Leu Tyr His Pro Gln Thr Val Leu Asp Ser Phe Asp His Asp
         35                  40                  45

Gly Ser Gly Asn Leu Pro Gly Leu Lys Asp Asp Asn Gly Asn Trp Asp
     50                  55                  60

Arg Arg Pro His Lys Asp Arg Ile Gln Leu Val Asn Ala Asp Thr Leu
 65                  70                  75                  80

Thr Val Trp Lys Ser Ile Leu Glu Asp Glu Gln Thr Pro Tyr Leu Asp
                 85                  90                  95

Thr Arg Met Val Tyr Thr Val Asn Thr Glu Ala Ala Ala Ala Leu Glu
            100                 105                 110

Lys Leu Ala Ser Ala Pro Arg Ile Lys Glu Leu Gly Leu Gln Phe Ser
        115                 120                 125

Ser Gly Trp Asn Glu Thr Thr Asp Lys Lys Lys Gly Tyr Phe Asp Val
    130                 135                 140

Gly Trp Gly Tyr Pro Ala Ser Trp Ser Asp Ala Ile Leu Gln Gly Pro
145                 150                 155                 160

His Leu Gly Val Ala Thr Pro Met Ile Lys Gln Pro Asn Pro Thr Met
                165                 170                 175

Lys His Asn Gln Asp Trp Ser Glu Ile Asp Phe Glu Ala Ile Pro Ala
            180                 185                 190

Asn Phe Ile Pro Ala Thr Ala Tyr Gln Pro Asp Arg Gln Thr Lys Pro
        195                 200                 205

Thr Tyr Asp Ala Asp Tyr Gly Thr Trp Thr Phe Gly Asp Lys Gln Val
    210                 215                 220

Pro Val Ala Asp Thr Phe Arg Ile Ala Trp Arg Glu Met Ala Ala Thr
225                 230                 235                 240

Thr Gly Phe Arg Thr Val Tyr Pro Ser Val Ile Pro Pro Gly Ala Asn
                245                 250                 255

His Val His Thr Val Asn Ser Ala Ala Ser Arg Ser Asn Leu Lys Thr
            260                 265                 270

Ile Leu Val Gly Ala Gln Leu Gly Ala Ile Leu Ser Asp Tyr Phe Ala
        275                 280                 285
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Arg Ser Ser Gly Ser Ser His Ile Phe Asn Asp Ile Val Arg Lys Ile
    290                 295                 300

Pro Leu Pro Asn Phe Thr Ser Leu Glu Lys Gln Phe Ala Arg Thr Tyr
305                 310                 315                 320

Leu Arg Leu Asn Cys Leu Thr Ser Ala Tyr Ala Pro Leu Trp Glu Glu
                325                 330                 335

Ile Thr Gly Glu Pro Trp Asp Val Gln Val Pro Leu Arg Asn Ala Glu
            340                 345                 350

Gln Arg Arg Ala Ala Gln Asn Asp Ile Asp Ala Met Val Ala Leu Ser
        355                 360                 365

Leu Gly Ile Ser Ala Asp Glu Leu Cys Met Ile Tyr Arg Thr Gln Phe
    370                 375                 380

Pro Val Met Arg Arg Tyr Asp Gln Glu Asp His Phe Asp Ala Asn Gly
385                 390                 395                 400

Arg Lys Val Pro Lys Glu Ile Ile Lys Leu Gln Gln Lys Leu Lys Asp
                405                 410                 415

Gly Gln Glu Leu Ser Val Glu Lys Arg Thr Trp Val His Pro Gln Ser
            420                 425                 430

Glu Val Ser Tyr Thr Phe Glu Tyr Pro Phe Arg Val Leu Asp Arg Glu
        435                 440                 445

Ala Asp Leu Arg Ala Ala Tyr Ala Lys Phe Glu Asn Gln Leu Lys Glu
    450                 455                 460

Pro
465
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SEQUENCE LISTING

<210> 603
<211> 1866
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<213> Corynebacterium glutamicum

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<222> (1)..(1866)
<223> FRXA01364

<400> 603

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Thr Gly Thr His Leu Tyr Asp Ser Leu Gln Leu Leu Phe Thr Leu Val
  1               5                  10                  15

gat aaa ggc cac cac cca aca gat gct aag gct gta gct ttt gat gcc   96
Asp Lys Gly His His Pro Thr Asp Ala Lys Ala Val Ala Phe Asp Ala
             20                  25                  30

gag gct gga gaa gaa ggc ctg cac ttc cgc aac ctt tca gcg gat ctc   144
Glu Ala Gly Glu Glu Gly Leu His Phe Arg Asn Leu Ser Ala Asp Leu
         35                  40                  45

ttc ctc cct gca gcc aca gaa ctt att gat cga gtt ggt ctt tcc aat   192
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Phe Leu Pro Ala Ala Thr Glu Leu Ile Asp Arg Val Gly Leu Ser Asn
     50                  55                  60

gaa gcc cta aac aag gtc ttg gaa aac ctc ctg ctc tcc cgg gtg caa   240
Glu Ala Leu Asn Lys Val Leu Glu Asn Leu Leu Leu Ser Arg Val Gln
 65                  70                  75                  80

tcc ggt aaa gac cgc ggc ttt atc tcc tat gcc acc ttg ggt gtt acc   288
Ser Gly Lys Asp Arg Gly Phe Ile Ser Tyr Ala Thr Leu Gly Val Thr
            85                  90                  95

gag ctt ggc caa gtt tat gag ggt ctg atg tcc tat acc ggc ttt atc   336
Glu Leu Gly Gln Val Tyr Glu Gly Leu Met Ser Tyr Thr Gly Phe Ile
        100                 105                 110

gcc cag gaa gat ctt ttt gag gtt gca cca cat ggc aaa gcc gat aaa   384
Ala Gln Glu Asp Leu Phe Glu Val Ala Pro His Gly Lys Ala Asp Lys
    115                 120                 125

ggt tcc tgg atg ctc ccg gtc tca aag gct gat gaa gtc cct gcc gat   432
Gly Ser Trp Met Leu Pro Val Ser Lys Ala Asp Glu Val Pro Ala Asp
130                 135                 140

agc ttt atc gaa gtt gat caa gaa gcc cct ggt ggc ggc gta atc aag   480
Ser Phe Ile Glu Val Asp Gln Glu Ala Pro Gly Gly Gly Val Ile Lys
145                 150                 155                 160

gtg cgt aaa cgc cac ccg cgc gga tca ttt gtg ttc cgt cag tcc tct   528
Val Arg Lys Arg His Pro Arg Gly Ser Phe Val Phe Arg Gln Ser Ser
                165                 170                 175

cgt gac cgc gaa cgc tca gcg tcc ttc tac acc cca caa gta ctc acc   576
Arg Asp Arg Glu Arg Ser Ala Ser Phe Tyr Thr Pro Gln Val Leu Thr
            180                 185                 190

agc ttt act gtc acc cag gct att gaa gaa ctc cag gca tca aag cgc   624
Ser Phe Thr Val Thr Gln Ala Ile Glu Glu Leu Gln Ala Ser Lys Arg
        195                 200                 205

atc acc aca gcc aat gat gtt ctc agc ctc acc atc tgt gaa cct gcc   672
Ile Thr Thr Ala Asn Asp Val Leu Ser Leu Thr Ile Cys Glu Pro Ala
    210                 215                 220

atg ggt tcc ggc gcc ttc gct gtg gaa gca gta cgc caa tta gca gag   720
Met Gly Ser Gly Ala Phe Ala Val Glu Ala Val Arg Gln Leu Ala Glu
225                 230                 235                 240

ctt tat ttg gaa ttg cgc caa gaa gaa cta gag cag cag att cca gcg   768
Leu Tyr Leu Glu Leu Arg Gln Glu Glu Leu Glu Gln Gln Ile Pro Ala
                245                 250                 255

gaa gac cgt gcc aag gaa ctc caa aag gtc aaa gcg cac att gcg ctg   816
Glu Asp Arg Ala Lys Glu Leu Gln Lys Val Lys Ala His Ile Ala Leu
            260                 265                 270

cac cag gtt tat ggt gtg gac ctt aac agc act gct gtg gag ttg gcg   864
His Gln Val Tyr Gly Val Asp Leu Asn Ser Thr Ala Val Glu Leu Ala
        275                 280                 285

gaa atc tcg ctg tgg cta gac acc atg aat gca gaa atg gac gca cct   912
Glu Ile Ser Leu Trp Leu Asp Thr Met Asn Ala Glu Met Asp Ala Pro
```

```
    290                 295                 300

tgg tat ggc ctg cac ctg cgt aat ggt aac tcc ctc gtt ggt gcc acc   960
Trp Tyr Gly Leu His Leu Arg Asn Gly Asn Ser Leu Val Gly Ala Thr
305                 310                 315                 320

cgt tcg ctg tat gca cct agt ctg ctt aat aaa aaa gcc tgg tta act   1008
Arg Ser Leu Tyr Ala Pro Ser Leu Leu Asn Lys Lys Ala Trp Leu Thr
                325                 330                 335

gct act cca acc cgc tat cgg ctt gat gat atc gcg cag gct att gat   1056
Ala Thr Pro Thr Arg Tyr Arg Leu Asp Asp Ile Ala Gln Ala Ile Asp
            340                 345                 350

gaa aac aaa gca gaa ccc ctc ttc aac cac ggc atc cac cac ttc ctc   1104
Glu Asn Lys Ala Glu Pro Leu Phe Asn His Gly Ile His His Phe Leu
        355                 360                 365

ttg ccc tct act ggc tgg gga gcc act gca gat gcc aaa gat ctt aaa   1152
Leu Pro Ser Thr Gly Trp Gly Ala Thr Ala Asp Ala Lys Asp Leu Lys
    370                 375                 380

gat ctt atg gct act gaa atc aag gag ctt aaa tct tgg cgt act tcc   1200
Asp Leu Met Ala Thr Glu Ile Lys Glu Leu Lys Ser Trp Arg Thr Ser
385                 390                 395                 400

atc cgt gcg tct ttg agt aaa act cag att aag cag ctc aat aac ctt   1248
Ile Arg Ala Ser Leu Ser Lys Thr Gln Ile Lys Gln Leu Asn Asn Leu
                405                 410                 415

gcc cta cgc gtg gaa aca cta tgg cga ttt gtg ctg atg cgt att cgc   1296
Ala Leu Arg Val Glu Thr Leu Trp Arg Phe Val Leu Met Arg Ile Arg
            420                 425                 430

att gca gaa tcc cag atc tca cgt agc act act ctc tgg ggt caa gag   1344
Ile Ala Glu Ser Gln Ile Ser Arg Ser Thr Thr Leu Trp Gly Gln Glu
        435                 440                 445

cca gct gag gtt tcg gag gtt gtc aca cgt gag caa att gaa caa gac   1392
Pro Ala Glu Val Ser Glu Val Val Thr Arg Glu Gln Ile Glu Gln Asp
    450                 455                 460

ctc ttt ggc aat att gat ggt gca tat aac cgt cta cgc ttg gtg atg   1440
Leu Phe Gly Asn Ile Asp Gly Ala Tyr Asn Arg Leu Arg Leu Val Met
465                 470                 475                 480

gat gct tgg tgt gcg ctg tgg ttc tgg cct ttg gat gct gtt gct acc   1488
Asp Ala Trp Cys Ala Leu Trp Phe Trp Pro Leu Asp Ala Val Ala Thr
                485                 490                 495

gct gag cat ccg gag cgt cca gcc ctt cca gat ctt gat gag tgg cta   1536
Ala Glu His Pro Glu Arg Pro Ala Leu Pro Asp Leu Asp Glu Trp Leu
            500                 505                 510

gcc acc ctg acg gag att ctg ggt att gat ctc cct ctg aag tcc aaa   1584
Ala Thr Leu Thr Glu Ile Leu Gly Ile Asp Leu Pro Leu Lys Ser Lys
        515                 520                 525

aac gaa aat cag att gtc tta ggt cca gat acc aat tgg cta gcc att   1632
Asn Glu Asn Gln Ile Val Leu Gly Pro Asp Thr Asn Trp Leu Ala Ile
    530                 535                 540
```

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aat gat gcc gag gct act gat ctt ggt ttt tct ggg gca ttg agc ttt   1680
Asn Asp Ala Glu Ala Thr Asp Leu Gly Phe Ser Gly Ala Leu Ser Phe
545                 550                 555                 560

gag cgt gtt agc gcg aat cac ccg tgg atc aat gtt gcc cgc caa gtg   1728
Glu Arg Val Ser Ala Asn His Pro Trp Ile Asn Val Ala Arg Gln Val
                565                 570                 575

gct aaa caa cag agc ttc ttc cac tgg gat cta gac ttc gcc cac gtt   1776
Ala Lys Gln Gln Ser Phe Phe His Trp Asp Leu Asp Phe Ala His Val
            580                 585                 590

ttt gcc aag ggt gga ttt gat ctg cag gtt ggt aat cca cca tgg gtg   1824
Phe Ala Lys Gly Gly Phe Asp Leu Gln Val Gly Asn Pro Pro Trp Val
        595                 600                 605

cga cca gat gtg aac ttt gag gat ctg ctt gct gaa cat gat           1866
Arg Pro Asp Val Asn Phe Glu Asp Leu Leu Ala Glu His Asp
    610                 615                 620
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<210> 604
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<212> PRT
<213> Corynebacterium glutamicum

<400> 604

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Thr Gly Thr His Leu Tyr Asp Ser Leu Gln Leu Leu Phe Thr Leu Val
  1               5                  10                  15

Asp Lys Gly His His Pro Thr Asp Ala Lys Ala Val Ala Phe Asp Ala
             20                  25                  30

Glu Ala Gly Glu Glu Gly Leu His Phe Arg Asn Leu Ser Ala Asp Leu
         35                  40                  45

Phe Leu Pro Ala Ala Thr Glu Leu Ile Asp Arg Val Gly Leu Ser Asn
     50                  55                  60

Glu Ala Leu Asn Lys Val Leu Glu Asn Leu Leu Leu Ser Arg Val Gln
 65                  70                  75                  80

Ser Gly Lys Asp Arg Gly Phe Ile Ser Tyr Ala Thr Leu Gly Val Thr
                 85                  90                  95

Glu Leu Gly Gln Val Tyr Glu Gly Leu Met Ser Tyr Thr Gly Phe Ile
            100                 105                 110

Ala Gln Glu Asp Leu Phe Glu Val Ala Pro His Gly Lys Ala Asp Lys
        115                 120                 125

Gly Ser Trp Met Leu Pro Val Ser Lys Ala Asp Glu Val Pro Ala Asp
    130                 135                 140

Ser Phe Ile Glu Val Asp Gln Glu Ala Pro Gly Gly Gly Val Ile Lys
145                 150                 155                 160

Val Arg Lys Arg His Pro Arg Gly Ser Phe Val Phe Arg Gln Ser Ser
                165                 170                 175
```

```
Arg Asp Arg Glu Arg Ser Ala Ser Phe Tyr Thr Pro Gln Val Leu Thr
            180                 185                 190

Ser Phe Thr Val Thr Gln Ala Ile Glu Glu Leu Gln Ala Ser Lys Arg
        195                 200                 205

Ile Thr Thr Ala Asn Asp Val Leu Ser Leu Thr Ile Cys Glu Pro Ala
    210                 215                 220

Met Gly Ser Gly Ala Phe Ala Val Glu Ala Val Arg Gln Leu Ala Glu
225                 230                 235                 240

Leu Tyr Leu Glu Leu Arg Gln Glu Glu Leu Glu Gln Gln Ile Pro Ala
                245                 250                 255

Glu Asp Arg Ala Lys Glu Leu Gln Lys Val Lys Ala His Ile Ala Leu
            260                 265                 270

His Gln Val Tyr Gly Val Asp Leu Asn Ser Thr Ala Val Glu Leu Ala
        275                 280                 285

Glu Ile Ser Leu Trp Leu Asp Thr Met Asn Ala Glu Met Asp Ala Pro
    290                 295                 300

Trp Tyr Gly Leu His Leu Arg Asn Gly Asn Ser Leu Val Gly Ala Thr
305                 310                 315                 320

Arg Ser Leu Tyr Ala Pro Ser Leu Leu Asn Lys Lys Ala Trp Leu Thr
                325                 330                 335

Ala Thr Pro Thr Arg Tyr Arg Leu Asp Asp Ile Ala Gln Ala Ile Asp
            340                 345                 350

Glu Asn Lys Ala Glu Pro Leu Phe Asn His Gly Ile His His Phe Leu
        355                 360                 365

Leu Pro Ser Thr Gly Trp Gly Ala Thr Ala Asp Ala Lys Asp Leu Lys
    370                 375                 380

Asp Leu Met Ala Thr Glu Ile Lys Glu Leu Lys Ser Trp Arg Thr Ser
385                 390                 395                 400

Ile Arg Ala Ser Leu Ser Lys Thr Gln Ile Lys Gln Leu Asn Asn Leu
                405                 410                 415

Ala Leu Arg Val Glu Thr Leu Trp Arg Phe Val Leu Met Arg Ile Arg
            420                 425                 430

Ile Ala Glu Ser Gln Ile Ser Arg Ser Thr Thr Leu Trp Gly Gln Glu
        435                 440                 445

Pro Ala Glu Val Ser Glu Val Val Thr Arg Glu Gln Ile Glu Gln Asp
    450                 455                 460

Leu Phe Gly Asn Ile Asp Gly Ala Tyr Asn Arg Leu Arg Leu Val Met
465                 470                 475                 480

Asp Ala Trp Cys Ala Leu Trp Phe Trp Pro Leu Asp Ala Val Ala Thr
                485                 490                 495

Ala Glu His Pro Glu Arg Pro Ala Leu Pro Asp Leu Asp Glu Trp Leu
```

```
            500                 505                 510

Ala Thr Leu Thr Glu Ile Leu Gly Ile Asp Leu Pro Leu Lys Ser Lys
        515                 520                 525

Asn Glu Asn Gln Ile Val Leu Gly Pro Asp Thr Asn Trp Leu Ala Ile
    530                 535                 540

Asn Asp Ala Glu Ala Thr Asp Leu Gly Phe Ser Gly Ala Leu Ser Phe
545                 550                 555                 560

Glu Arg Val Ser Ala Asn His Pro Trp Ile Asn Val Ala Arg Gln Val
                565                 570                 575

Ala Lys Gln Gln Ser Phe Phe His Trp Asp Leu Asp Phe Ala His Val
            580                 585                 590

Phe Ala Lys Gly Gly Phe Asp Leu Gln Val Gly Asn Pro Pro Trp Val
        595                 600                 605

Arg Pro Asp Val Asn Phe Glu Asp Leu Leu Ala Glu His Asp
    610                 615                 620
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CN 1670170 A 20050921

<210> 605
<211> 1042
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1042)
<223> RXN01379

<400> 605

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cttccgcagc ccgcaacttt gaacaccgag gtttaacaca atg agt gca ttt gat   115
                                              Met Ser Ala Phe Asp
                                                1               5

tcg atc cta aat gtt gaa gag tgg atc agt gac cac tac ctc acc aat   163
Ser Ile Leu Asn Val Glu Glu Trp Ile Ser Asp His Tyr Leu Thr Asn
                10                  15                  20

gac gat gcc aaa ggt gcc tca ttt tcc aag cgg gtg cgc gag cgc att   211
Asp Asp Ala Lys Gly Ala Ser Phe Ser Lys Arg Val Arg Glu Arg Ile
            25                  30                  35

aaa gaa tgg aaa acc acc gag gac gca acc cag cag agt ggc cct tta   259
Lys Glu Trp Lys Thr Thr Glu Asp Ala Thr Gln Gln Ser Gly Pro Leu
        40                  45                  50

act cgt ttt tcc agc aac cgc ctg cag ttg cag cat gct ctt tct gag   307
Thr Arg Phe Ser Ser Asn Arg Leu Gln Leu Gln His Ala Leu Ser Glu
    55                  60                  65

ctt gac gac gcc acc acc gcc gcc agt tta gtg gcc tct gca ctg ggg   355
Leu Asp Asp Ala Thr Thr Ala Ala Ser Leu Val Ala Ser Ala Leu Gly
70                  75                  80                  85
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tat ggt gtc ccc agc gcg cgc cac gcg cag cgc ggc tcc gac aca ata   403
Tyr Gly Val Pro Ser Ala Arg His Ala Gln Arg Gly Ser Asp Thr Ile
                 90                  95                 100

tcc tat tcc tct tgg gtg gga aat gcc ggc agt gtg gaa ttt ctt gca   451
Ser Tyr Ser Ser Trp Val Gly Asn Ala Gly Ser Val Glu Phe Leu Ala
            105                 110                 115

gcg act ccc gct gaa agc ttt gaa gag aac ttc cga tcc ctt ccc ctt   499
Ala Thr Pro Ala Glu Ser Phe Glu Glu Asn Phe Arg Ser Leu Pro Leu
        120                 125                 130

gag cca gta gcg gtc aat gac aag ccc cag gat atc acc gca gcc aaa   547
Glu Pro Val Ala Val Asn Asp Lys Pro Gln Asp Ile Thr Ala Ala Lys
    135                 140                 145

ttg gtg ggc cag att ttc ctt agt gat act ccc cct gct ttt gtt gtt   595
Leu Val Gly Gln Ile Phe Leu Ser Asp Thr Pro Pro Ala Phe Val Val
150                 155                 160                 165

atc acc gct ggt aaa tgg gtg gtt tta gcc gag cgt gaa acc tgg cct   643
Ile Thr Ala Gly Lys Trp Val Val Leu Ala Glu Arg Glu Thr Trp Pro
                170                 175                 180

cta ggc cgc cac cta gct att gat att tcc ctg gtg gtg gaa cgt aat   691
Leu Gly Arg His Leu Ala Ile Asp Ile Ser Leu Val Val Glu Arg Asn
            185                 190                 195

gac acc aaa gcc cag ggt gag atg cag cag acg gtc gta gca cta gcc   739
Asp Thr Lys Ala Gln Gly Glu Met Gln Gln Thr Val Val Ala Leu Ala
        200                 205                 210

cgc gaa aat acc gag cgt gcc gcc gat ggc acc acc tgg tgg gaa gaa   787
Arg Glu Asn Thr Glu Arg Ala Ala Asp Gly Thr Thr Trp Trp Glu Glu
    215                 220                 225

acc att gag caa tcc cgc gaa cat gct gtc aag gtt tct ggc gag cta   835
Thr Ile Glu Gln Ser Arg Glu His Ala Val Lys Val Ser Gly Glu Leu
230                 235                 240                 245

cgc agt gcg gtg cgt gaa tcc att gaa atc ctg ggc aat gac gtg ctc   883
Arg Ser Ala Val Arg Glu Ser Ile Glu Ile Leu Gly Asn Asp Val Leu
                250                 255                 260

aca cgc tat gaa gct aaa gag ctc tcc acc gct gag atc gac ggt ggc   931
Thr Arg Tyr Glu Ala Lys Glu Leu Ser Thr Ala Glu Ile Asp Gly Gly
            265                 270                 275

gag cta gct aag caa tct ttg cgc tat ctc tac cgc att ttg ttc ctg   979
Glu Leu Ala Lys Gln Ser Leu Arg Tyr Leu Tyr Arg Ile Leu Phe Leu
        280                 285                 290

ctt ttt gcc gag gct tca cca gag ctt gaa atc ctg cca acc ggc acc   1027
Leu Phe Ala Glu Ala Ser Pro Glu Leu Glu Ile Leu Pro Thr Gly Thr
    295                 300                 305

ccg gaa tat gac gag                                               1042
Pro Glu Tyr Asp Glu
310
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<210> 606
<211> 314
<212> PRT
<213> Corynebacterium glutamicum

<400> 606
Met Ser Ala Phe Asp Ser Ile Leu Asn Val Glu Glu Trp Ile Ser Asp
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His Tyr Leu Thr Asn Asp Asp Ala Lys Gly Ala Ser Phe Ser Lys Arg
20 25 30

Val Arg Glu Arg Ile Lys Glu Trp Lys Thr Thr Glu Asp Ala Thr Gln
35 40 45

Gln Ser Gly Pro Leu Thr Arg Phe Ser Ser Asn Arg Leu Gln Leu Gln
50 55 60

His Ala Leu Ser Glu Leu Asp Asp Ala Thr Thr Ala Ala Ser Leu Val
65 70 75 80

Ala Ser Ala Leu Gly Tyr Gly Val Pro Ser Ala Arg His Ala Gln Arg
85 90 95

Gly Ser Asp Thr Ile Ser Tyr Ser Ser Trp Val Gly Asn Ala Gly Ser
100 105 110

Val Glu Phe Leu Ala Ala Thr Pro Ala Glu Ser Phe Glu Glu Asn Phe
115 120 125

Arg Ser Leu Pro Leu Glu Pro Val Ala Val Asn Asp Lys Pro Gln Asp
130 135 140

Ile Thr Ala Ala Lys Leu Val Gly Gln Ile Phe Leu Ser Asp Thr Pro
145 150 155 160

Pro Ala Phe Val Val Ile Thr Ala Gly Lys Trp Val Val Leu Ala Glu
165 170 175

Arg Glu Thr Trp Pro Leu Gly Arg His Leu Ala Ile Asp Ile Ser Leu
180 185 190

Val Val Glu Arg Asn Asp Thr Lys Ala Gln Gly Glu Met Gln Gln Thr
195 200 205

Val Val Ala Leu Ala Arg Glu Asn Thr Glu Arg Ala Ala Asp Gly Thr
210 215 220

Thr Trp Trp Glu Glu Thr Ile Glu Gln Ser Arg Glu His Ala Val Lys
225 230 235 240

Val Ser Gly Glu Leu Arg Ser Ala Val Arg Glu Ser Ile Glu Ile Leu
245 250 255

Gly Asn Asp Val Leu Thr Arg Tyr Glu Ala Lys Glu Leu Ser Thr Ala
260 265 270

Glu Ile Asp Gly Gly Glu Leu Ala Lys Gln Ser Leu Arg Tyr Leu Tyr
275 280 285

Arg Ile Leu Phe Leu Leu Phe Ala Glu Ala Ser Pro Glu Leu Glu Ile

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Leu Pro Thr Gly Thr Pro Glu Tyr Asp Glu
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<220>
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<222> (1)..(921)
<223> FRXA01379

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Leu Asn Val Glu Glu Trp Ile Ser Asp His Tyr Leu Thr Asn Asp Asp
  1               5                  10                  15

gcc aaa ggt gcc tca ttt tcc aag cgg gtg cgc gag cgc att aaa gaa   96
Ala Lys Gly Ala Ser Phe Ser Lys Arg Val Arg Glu Arg Ile Lys Glu
             20                  25                  30

tgg aaa acc acc gag gac gca acc cag cag agt ggc cct tta act cgt   144
Trp Lys Thr Thr Glu Asp Ala Thr Gln Gln Ser Gly Pro Leu Thr Arg
         35                  40                  45

ttt tcc agc aac cgc ctg cag ttg cag cat gct ctt tct gag ctt gac   192
Phe Ser Ser Asn Arg Leu Gln Leu Gln His Ala Leu Ser Glu Leu Asp
     50                  55                  60

gac gcc acc acc gcc gcc agt tta gtg gcc tct gca ctg ggg tat ggt   240
Asp Ala Thr Thr Ala Ala Ser Leu Val Ala Ser Ala Leu Gly Tyr Gly
 65                  70                  75                  80

gtc ccc agc gcg cgc cac gcg cag cgc ggc tcc gac aca ata tcc tat   288
Val Pro Ser Ala Arg His Ala Gln Arg Gly Ser Asp Thr Ile Ser Tyr
                 85                  90                  95

tcc tct tgg gtg gga aat gcc ggc agt gtg gaa ttt ctt gca gcg act   336
Ser Ser Trp Val Gly Asn Ala Gly Ser Val Glu Phe Leu Ala Ala Thr
            100                 105                 110

ccc gct gaa agc ttt gaa gag aac ttc cga tcc ctt ccc ctt gag cca   384
Pro Ala Glu Ser Phe Glu Glu Asn Phe Arg Ser Leu Pro Leu Glu Pro
        115                 120                 125

gta gcg gtc aat gac aag ccc cag gat atc acc gca gcc aaa ttg gtg   432
Val Ala Val Asn Asp Lys Pro Gln Asp Ile Thr Ala Ala Lys Leu Val
    130                 135                 140

ggc cag att ttc ctt agt gat act ccc cct gct ttt gtt gtt atc acc   480
Gly Gln Ile Phe Leu Ser Asp Thr Pro Pro Ala Phe Val Val Ile Thr
145                 150                 155                 160

gct ggt aaa tgg gtg gtt tta gcc gag cgt gaa acc tgg cct cta ggc   528
Ala Gly Lys Trp Val Val Leu Ala Glu Arg Glu Thr Trp Pro Leu Gly
                165                 170                 175
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cgc cac cta gct att gat att tcc ctg gtg gtg gaa cgt aat gac acc   576
Arg His Leu Ala Ile Asp Ile Ser Leu Val Val Glu Arg Asn Asp Thr
            180                 185                 190

aaa gcc cag ggt gag atg cag cag acg gtc gta gca cta gcc cgc gaa   624
Lys Ala Gln Gly Glu Met Gln Gln Thr Val Val Ala Leu Ala Arg Glu
        195                 200                 205

aat acc gag cgt gcc gcc gat ggc acc acc tgg tgg gaa gaa acc att   672
Asn Thr Glu Arg Ala Ala Asp Gly Thr Thr Trp Trp Glu Glu Thr Ile
    210                 215                 220

gag caa tcc cgc gaa cat gct gtc aag gtt tct ggc gag cta cgc agt   720
Glu Gln Ser Arg Glu His Ala Val Lys Val Ser Gly Glu Leu Arg Ser
225                 230                 235                 240

gcg gtg cgt gaa tcc att gaa atc ctg ggc aat gac gtg ctc aca cgc   768
Ala Val Arg Glu Ser Ile Glu Ile Leu Gly Asn Asp Val Leu Thr Arg
                245                 250                 255

tat gaa gct aaa gag ctc tcc acc gct gag atc gac ggt ggc gag cta   816
Tyr Glu Ala Lys Glu Leu Ser Thr Ala Glu Ile Asp Gly Gly Glu Leu
            260                 265                 270

gct aag caa tct ttg cgc tat ctc tac cgc att ttg ttc ctg ctt ttt   864
Ala Lys Gln Ser Leu Arg Tyr Leu Tyr Arg Ile Leu Phe Leu Leu Phe
        275                 280                 285

gcc gag gct tca cca gag ctt gaa atc ctg cca acc ggc acc ccg gaa   912
Ala Glu Ala Ser Pro Glu Leu Glu Ile Leu Pro Thr Gly Thr Pro Glu
    290                 295                 300

tat gac gag                                                      921
Tyr Asp Glu
305
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09605-0005 Doc 09605-0005 Doc 09605-0005 Doc 09605-0005 Doc 09605-0005 Doc

<210> 608
<211> 307
<212> PRT
<213> Corynebacterium glutamicum

<400> 608

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Leu Asn Val Glu Glu Trp Ile Ser Asp His Tyr Leu Thr Asn Asp Asp
  1               5                  10                  15

Ala Lys Gly Ala Ser Phe Ser Lys Arg Val Arg Glu Arg Ile Lys Glu
            20                  25                  30

Trp Lys Thr Thr Glu Asp Ala Thr Gln Gln Ser Gly Pro Leu Thr Arg
        35                  40                  45

Phe Ser Ser Asn Arg Leu Gln Leu Gln His Ala Leu Ser Glu Leu Asp
    50                  55                  60

Asp Ala Thr Thr Ala Ala Ser Leu Val Ala Ser Ala Leu Gly Tyr Gly
65                  70                  75                  80

Val Pro Ser Ala Arg His Ala Gln Arg Gly Ser Asp Thr Ile Ser Tyr
                85                  90                  95
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Ser Ser Trp Val Gly Asn Ala Gly Ser Val Glu Phe Leu Ala Ala Thr
            100                 105                 110

Pro Ala Glu Ser Phe Glu Glu Asn Phe Arg Ser Leu Pro Leu Glu Pro
        115                 120                 125

Val Ala Val Asn Asp Lys Pro Gln Asp Ile Thr Ala Ala Lys Leu Val
    130                 135                 140

Gly Gln Ile Phe Leu Ser Asp Thr Pro Pro Ala Phe Val Val Ile Thr
145                 150                 155                 160

Ala Gly Lys Trp Val Val Leu Ala Glu Arg Glu Thr Trp Pro Leu Gly
                165                 170                 175

Arg His Leu Ala Ile Asp Ile Ser Leu Val Val Glu Arg Asn Asp Thr
            180                 185                 190

Lys Ala Gln Gly Glu Met Gln Gln Thr Val Val Ala Leu Ala Arg Glu
        195                 200                 205

Asn Thr Glu Arg Ala Ala Asp Gly Thr Thr Trp Trp Glu Glu Thr Ile
    210                 215                 220

Glu Gln Ser Arg Glu His Ala Val Lys Val Ser Gly Glu Leu Arg Ser
225                 230                 235                 240

Ala Val Arg Glu Ser Ile Glu Ile Leu Gly Asn Asp Val Leu Thr Arg
                245                 250                 255

Tyr Glu Ala Lys Glu Leu Ser Thr Ala Glu Ile Asp Gly Gly Glu Leu
            260                 265                 270

Ala Lys Gln Ser Leu Arg Tyr Leu Tyr Arg Ile Leu Phe Leu Leu Phe
        275                 280                 285

Ala Glu Ala Ser Pro Glu Leu Glu Ile Leu Pro Thr Gly Thr Pro Glu
    290                 295                 300

Tyr Asp Glu
305
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<210> 609
<211> 780
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(757)
<223> RXN01390

<400> 609
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gcaagctctg gtgcattagc atccgatgct ccgacgtctt atg ttc agg cgc agc 115
                                                Met Phe Arg Arg Ser
                                                  1   5

ctt ccc agc aac aag aca tcc tca gca agt tcc gcc agc tcc gcc gac 163

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Leu Pro Ser Asn Lys Thr Ser Ser Ala Ser Ser Ala Ser Ser Ala Asp
                10                  15                  20

aca agt tac tca gtc aga tta ggc cgt cct gaa gag cct ggt tac cag   211
Thr Ser Tyr Ser Val Arg Leu Gly Arg Pro Glu Glu Pro Gly Tyr Gln
            25                  30                  35

cca gaa ccg tct tat tcg gag cct tac act gac tct gat ttc gcg cca   259
Pro Glu Pro Ser Tyr Ser Glu Pro Tyr Thr Asp Ser Asp Phe Ala Pro
        40                  45                  50

gca ggt gcg gcc gct gcg gca gct gca gta gct cca cca atg att gcg   307
Ala Gly Ala Ala Ala Ala Ala Ala Ala Val Ala Pro Pro Met Ile Ala
    55                  60                  65

gaa cag cca caa att gtt gaa gat gcc cgc cga ggt acc ctc gat ttc   355
Glu Gln Pro Gln Ile Val Glu Asp Ala Arg Arg Gly Thr Leu Asp Phe
70                  75                  80                  85

ggc ctg ttg att atc cgc gca gtc att ggt gtc tat ttg atc gtc cgt   403
Gly Leu Leu Ile Ile Arg Ala Val Ile Gly Val Tyr Leu Ile Val Arg
                90                  95                  100

gga gtc ttt aca ttc ttc acc ctt gga gga tct gcc ggt ctt gct ggc   451
Gly Val Phe Thr Phe Phe Thr Leu Gly Gly Ser Ala Gly Leu Ala Gly
            105                 110                 115

ctc gag gca gag ttc gct ggt tac cag tgg cct gaa atc ctc gcg atc   499
Leu Glu Ala Glu Phe Ala Gly Tyr Gln Trp Pro Glu Ile Leu Ala Ile
        120                 125                 130

ctg ctt cca tct att gaa ctt gcg gct ggt gtc ttc ctg ctc ctt ggt   547
Leu Leu Pro Ser Ile Glu Leu Ala Ala Gly Val Phe Leu Leu Leu Gly
    135                 140                 145

ctg atg acc cca gtg gca gca gcg gta gcc acg gtg gcg aca tcc ttt   595
Leu Met Thr Pro Val Ala Ala Ala Val Ala Thr Val Ala Thr Ser Phe
150                 155                 160                 165

acc acc ctt cac caa gtc aac act cat gaa ggt ggt tgg ggt gaa ctt   643
Thr Thr Leu His Gln Val Asn Thr His Glu Gly Gly Trp Gly Glu Leu
                170                 175                 180

agt gag cca ttg atg ctg gca ctg atc ctc act atc gtg gtt gtc gga   691
Ser Glu Pro Leu Met Leu Ala Leu Ile Leu Thr Ile Val Val Val Gly
            185                 190                 195

ctt cag ttc acc ggc ccc ggc aag att tcc ctt gac tct ggc cga ggt   739
Leu Gln Phe Thr Gly Pro Gly Lys Ile Ser Leu Asp Ser Gly Arg Gly
        200                 205                 210

tgg caa agc gtc cac tgg tgagctcgtg gatcttcgtg gtc                 780
Trp Gln Ser Val His Trp
    215
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<210> 610
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

<400> 610
Met Phe Arg Arg Ser Leu Pro Ser Asn Lys Thr Ser Ser Ala Ser Ser
1 5 10 15

Ala Ser Ser Ala Asp Thr Ser Tyr Ser Val Arg Leu Gly Arg Pro Glu
20 25 30

Glu Pro Gly Tyr Gln Pro Glu Pro Ser Tyr Ser Glu Pro Tyr Thr Asp
35 40 45

Ser Asp Phe Ala Pro Ala Gly Ala Ala Ala Ala Ala Ala Ala Val Ala
50 55 60

Pro Pro Met Ile Ala Glu Gln Pro Gln Ile Val Glu Asp Ala Arg Arg
65 70 75 80

Gly Thr Leu Asp Phe Gly Leu Leu Ile Ile Arg Ala Val Ile Gly Val
85 90 95

Tyr Leu Ile Val Arg Gly Val Phe Thr Phe Phe Thr Leu Gly Gly Ser
100 105 110

Ala Gly Leu Ala Gly Leu Glu Ala Glu Phe Ala Gly Tyr Gln Trp Pro
115 120 125

Glu Ile Leu Ala Ile Leu Leu Pro Ser Ile Glu Leu Ala Ala Gly Val
130 135 140

Phe Leu Leu Leu Gly Leu Met Thr Pro Val Ala Ala Ala Val Ala Thr
145 150 155 160

Val Ala Thr Ser Phe Thr Thr Leu His Gln Val Asn Thr His Glu Gly
165 170 175

Gly Trp Gly Glu Leu Ser Glu Pro Leu Met Leu Ala Leu Ile Leu Thr
180 185 190

Ile Val Val Val Gly Leu Gln Phe Thr Gly Pro Gly Lys Ile Ser Leu
195 200 205

Asp Ser Gly Arg Gly Trp Gln Ser Val His Trp
210 215

<210> 611
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<213> Corynebacterium glutamicum

<220>
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<222> (101)..(757)
<223> FRXA01390

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gcaagctctg gtgcattagc atccgatgct ccgacgtctt atg ttc agg cgc agc 115
Met Phe Arg Arg Ser
1 5

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ctt ccc agc aac aag aca tcc tca gca agt tcc gcc agc tcc gcc gac   163
Leu Pro Ser Asn Lys Thr Ser Ser Ala Ser Ser Ala Ser Ser Ala Asp
                10                  15                  20

aca agt tac tca gtc aga tta ggc cgt cct gaa gag cct ggt tac cag   211
Thr Ser Tyr Ser Val Arg Leu Gly Arg Pro Glu Glu Pro Gly Tyr Gln
            25                  30                  35

cca gaa ccg tct tat tcg gag cct tac act gac tct gat ttc gcg cca   259
Pro Glu Pro Ser Tyr Ser Glu Pro Tyr Thr Asp Ser Asp Phe Ala Pro
        40                  45                  50

gca ggt gcg gcc gct gcg gca gct gca gta gct cca cca atg att gcg   307
Ala Gly Ala Ala Ala Ala Ala Ala Ala Val Ala Pro Pro Met Ile Ala
    55                  60                  65

gaa cag cca caa att gtt gaa gat gcc cgc cga ggt acc ctc gat ttc   355
Glu Gln Pro Gln Ile Val Glu Asp Ala Arg Arg Gly Thr Leu Asp Phe
70                  75                  80                  85

ggc ctg ttg att atc cgc gca gtc att ggt gtc tat ttg atc gtc cgt   403
Gly Leu Leu Ile Ile Arg Ala Val Ile Gly Val Tyr Leu Ile Val Arg
                90                  95                  100

gga gtc ttt aca ttc ttc acc ctt gga gga tct gcc ggt ctt gct ggc   451
Gly Val Phe Thr Phe Phe Thr Leu Gly Gly Ser Ala Gly Leu Ala Gly
            105                 110                 115

ctc gag gca gag ttc gct ggt tac cag tgg cct gaa atc ctc gcg atc   499
Leu Glu Ala Glu Phe Ala Gly Tyr Gln Trp Pro Glu Ile Leu Ala Ile
        120                 125                 130

ctg ctt cca tct att gaa ctt gcg gct ggt gtc ttc ctg ctc ctt ggt   547
Leu Leu Pro Ser Ile Glu Leu Ala Ala Gly Val Phe Leu Leu Leu Gly
    135                 140                 145

ctg atg acc cca gtg gca gca gcg gta gcc acg gtg gcg aca tcc ttt   595
Leu Met Thr Pro Val Ala Ala Ala Val Ala Thr Val Ala Thr Ser Phe
150                 155                 160                 165

acc acc ctt cac caa gtc aac act cat gaa ggt ggt tgg ggt gaa ctt   643
Thr Thr Leu His Gln Val Asn Thr His Glu Gly Gly Trp Gly Glu Leu
                170                 175                 180

agt gag cca ttg atg ctg gca ctg atc ctc act atc gtg gtt gtc gga   691
Ser Glu Pro Leu Met Leu Ala Leu Ile Leu Thr Ile Val Val Val Gly
            185                 190                 195

ctt cag ttc acc ggc ccc ggc aag att tcc ctt gac tct ggc cga ggt   739
Leu Gln Phe Thr Gly Pro Gly Lys Ile Ser Leu Asp Ser Gly Arg Gly
        200                 205                 210

tgg caa agc gtc cac tgg tgagctcgtg gatcttcgtg gtc                 780
Trp Gln Ser Val His Trp
    215
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<210> 612
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<212> PRT
<213> Corynebacterium glutamicum

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Met Phe Arg Arg Ser Leu Pro Ser Asn Lys Thr Ser Ser Ala Ser Ser
1 5 10 15

Ala Ser Ser Ala Asp Thr Ser Tyr Ser Val Arg Leu Gly Arg Pro Glu
20 25 30

Glu Pro Gly Tyr Gln Pro Glu Pro Ser Tyr Ser Glu Pro Tyr Thr Asp
35 40 45

Ser Asp Phe Ala Pro Ala Gly Ala Ala Ala Ala Ala Ala Ala Val Ala
50 55 60

Pro Pro Met Ile Ala Glu Gln Pro Gln Ile Val Glu Asp Ala Arg Arg
65 70 75 80

Gly Thr Leu Asp Phe Gly Leu Leu Ile Ile Arg Ala Val Ile Gly Val
85 90 95

Tyr Leu Ile Val Arg Gly Val Phe Thr Phe Phe Thr Leu Gly Gly Ser
100 105 110

Ala Gly Leu Ala Gly Leu Glu Ala Glu Phe Ala Gly Tyr Gln Trp Pro
115 120 125

Glu Ile Leu Ala Ile Leu Leu Pro Ser Ile Glu Leu Ala Ala Gly Val
130 135 140

Phe Leu Leu Leu Gly Leu Met Thr Pro Val Ala Ala Ala Val Ala Thr
145 150 155 160

Val Ala Thr Ser Phe Thr Thr Leu His Gln Val Asn Thr His Glu Gly
165 170 175

Gly Trp Gly Glu Leu Ser Glu Pro Leu Met Leu Ala Leu Ile Leu Thr
180 185 190

Ile Val Val Val Gly Leu Gln Phe Thr Gly Pro Gly Lys Ile Ser Leu
195 200 205

Asp Ser Gly Arg Gly Trp Gln Ser Val His Trp
210 215

<210> 613
<211> 813
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(790)
<223> RXN01391

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atggtgtgaa accatcatgg ctcgatcaca aaaaagaaca cctgctatca ggtcaaccaa 60

aaaagttaaa agtgtaatat ccagcatcat cacgattgcc gtg gct gca gtc gct 115
Val Ala Ala Val Ala
1 5

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ttt gca gct tac gtt ata gat ggt ggg gta gaa gag gcg tct gga aca   163
Phe Ala Ala Tyr Val Ile Asp Gly Gly Val Glu Glu Ala Ser Gly Thr
                 10                  15                  20

ccg acg tct tcg gaa agc tcg gta gcg gca act gct cca gcg gca tct   211
Pro Thr Ser Ser Glu Ser Ser Val Ala Ala Thr Ala Pro Ala Ala Ser
             25                  30                  35

agc gag act gcg gct gaa tac cgt gcg atg ctc gct tcc ctt gac gtt   259
Ser Glu Thr Ala Ala Glu Tyr Arg Ala Met Leu Ala Ser Leu Asp Val
         40                  45                  50

aaa ggt cgt gcg cca gga aca gga tat gac cgc gaa tta ttc gga cca   307
Lys Gly Arg Ala Pro Gly Thr Gly Tyr Asp Arg Glu Leu Phe Gly Pro
     55                  60                  65

gca tgg acc gac act gtt tcc gtg gaa tat gga cac aat ggc tgc gat   355
Ala Trp Thr Asp Thr Val Ser Val Glu Tyr Gly His Asn Gly Cys Asp
 70                  75                  80                  85

acc cgc aac gac atc ctg caa cgc gac ctg gat gac atc caa ctt cgc   403
Thr Arg Asn Asp Ile Leu Gln Arg Asp Leu Asp Asp Ile Gln Leu Arg
                 90                  95                 100

gaa ggc acc aag gat tgt atc gtc acg agc ggc ctg ctc agc gat cca   451
Glu Gly Thr Lys Asp Cys Ile Val Thr Ser Gly Leu Leu Ser Asp Pro
            105                 110                 115

ttt tct ggc gaa ctt att gat ttc gtt cgc ggt gaa cgt tcc ggc gac   499
Phe Ser Gly Glu Leu Ile Asp Phe Val Arg Gly Glu Arg Ser Gly Asp
        120                 125                 130

gtg cag atc gat cac ctg gtc cca tta cat gac gca tgg gtc aag gga   547
Val Gln Ile Asp His Leu Val Pro Leu His Asp Ala Trp Val Lys Gly
    135                 140                 145

gca cag cag tgg gat gag caa act cga aag aac ttt gcc aac gat ccc   595
Ala Gln Gln Trp Asp Glu Gln Thr Arg Lys Asn Phe Ala Asn Asp Pro
150                 155                 160                 165

gac aac ctt ctc gcc gtt aaa ggt acg ctt aac cag caa aaa ggt gca   643
Asp Asn Leu Leu Ala Val Lys Gly Thr Leu Asn Gln Gln Lys Gly Ala
                170                 175                 180

ggc gat gca gca acc tgg ctt cca cca aac aca gct ttt agg tgc gat   691
Gly Asp Ala Ala Thr Trp Leu Pro Pro Asn Thr Ala Phe Arg Cys Asp
            185                 190                 195

tac gca aag aaa atc atc acc gtt aaa gat cgc tac aac gtg tgg gtg   739
Tyr Ala Lys Lys Ile Ile Thr Val Lys Asp Arg Tyr Asn Val Trp Val
        200                 205                 210

act gag gct gaa gca agc gcc ctg gaa cgc caa tta gat acg tgt gct   787
Thr Glu Ala Glu Ala Ser Ala Leu Glu Arg Gln Leu Asp Thr Cys Ala
    215                 220                 225

gca taacagtcac ataagcattt ggg                                    813
Ala
230
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<210> 614
<211> 230
<212> PRT
<213> Corynebacterium glutamicum

<400> 614
Val Ala Ala Val Ala Phe Ala Ala Tyr Val Ile Asp Gly Gly Val Glu
1 5 10 15

Glu Ala Ser Gly Thr Pro Thr Ser Ser Glu Ser Ser Val Ala Ala Thr
20 25 30

Ala Pro Ala Ala Ser Ser Glu Thr Ala Ala Glu Tyr Arg Ala Met Leu
35 40 45

Ala Ser Leu Asp Val Lys Gly Arg Ala Pro Gly Thr Gly Tyr Asp Arg
50 55 60

Glu Leu Phe Gly Pro Ala Trp Thr Asp Thr Val Ser Val Glu Tyr Gly
65 70 75 80

His Asn Gly Cys Asp Thr Arg Asn Asp Ile Leu Gln Arg Asp Leu Asp
85 90 95

Asp Ile Gln Leu Arg Glu Gly Thr Lys Asp Cys Ile Val Thr Ser Gly
100 105 110

Leu Leu Ser Asp Pro Phe Ser Gly Glu Leu Ile Asp Phe Val Arg Gly
115 120 125

Glu Arg Ser Gly Asp Val Gln Ile Asp His Leu Val Pro Leu His Asp
130 135 140

Ala Trp Val Lys Gly Ala Gln Gln Trp Asp Glu Gln Thr Arg Lys Asn
145 150 155 160

Phe Ala Asn Asp Pro Asp Asn Leu Leu Ala Val Lys Gly Thr Leu Asn
165 170 175

Gln Gln Lys Gly Ala Gly Asp Ala Ala Thr Trp Leu Pro Pro Asn Thr
180 185 190

Ala Phe Arg Cys Asp Tyr Ala Lys Lys Ile Ile Thr Val Lys Asp Arg
195 200 205

Tyr Asn Val Trp Val Thr Glu Ala Glu Ala Ser Ala Leu Glu Arg Gln
210 215 220

Leu Asp Thr Cys Ala Ala
225 230

<210> 615
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(790)

<223> FRXA01391

<400> 615

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atggtgtgaa accatcatgg ctcgatcaca aaaaagaaca cctgctatca ggtcaaccaa 60

aaaagttaaa agtgtaatat ccagcatcat cacgattgcc gtg gct gca gtc gct   115
                                          Val Ala Ala Val Ala
                                            1               5

ttt gca gct tac gtt ata gat ggt ggg gta gaa gag gcg tct gga aca   163
Phe Ala Ala Tyr Val Ile Asp Gly Gly Val Glu Glu Ala Ser Gly Thr
                10                  15                  20

ccg acg tct tcg gaa agc tcg gta gcg gca act gct cca gcg gca tct   211
Pro Thr Ser Ser Glu Ser Ser Val Ala Ala Thr Ala Pro Ala Ala Ser
            25                  30                  35

agc gag act gcg gct gaa tac cgt gcg atg ctc gct tcc ctt gac gtt   259
Ser Glu Thr Ala Ala Glu Tyr Arg Ala Met Leu Ala Ser Leu Asp Val
        40                  45                  50

aaa ggt cgt gcg cca gga aca gga tat gac cgc gaa tta ttc gga cca   307
Lys Gly Arg Ala Pro Gly Thr Gly Tyr Asp Arg Glu Leu Phe Gly Pro
    55                  60                  65

gca tgg acc gac act gtt tcc gtg gaa tat gga cac aat ggc tgc gat   355
Ala Trp Thr Asp Thr Val Ser Val Glu Tyr Gly His Asn Gly Cys Asp
70                  75                  80                  85

acc cgc aac gac atc ctg caa cgc gac ctg gat gac atc caa ctt cgc   403
Thr Arg Asn Asp Ile Leu Gln Arg Asp Leu Asp Asp Ile Gln Leu Arg
                90                  95                  100

gaa ggc acc aag gat tgt atc gtc acg agc ggc ctg ctc agc gat cca   451
Glu Gly Thr Lys Asp Cys Ile Val Thr Ser Gly Leu Leu Ser Asp Pro
            105                 110                 115

ttt tct ggc gaa ctt att gat ttc gtt cgc ggt gaa cgt tcc ggc gac   499
Phe Ser Gly Glu Leu Ile Asp Phe Val Arg Gly Glu Arg Ser Gly Asp
        120                 125                 130

gtg cag atc gat cac ctg gtc cca tta cat gac gca tgg gtc aag gga   547
Val Gln Ile Asp His Leu Val Pro Leu His Asp Ala Trp Val Lys Gly
    135                 140                 145

gca cag cag tgg gat gag caa act cga aag aac ttt gcc aac gat ccc   595
Ala Gln Gln Trp Asp Glu Gln Thr Arg Lys Asn Phe Ala Asn Asp Pro
150                 155                 160                 165

gac aac ctt ctc gcc gtt aaa ggt acg ctt aac cag caa aaa ggt gca   643
Asp Asn Leu Leu Ala Val Lys Gly Thr Leu Asn Gln Gln Lys Gly Ala
                170                 175                 180

ggc gat gca gca acc tgg ctt cca cca aac aca gct ttt agg tgc gat   691
Gly Asp Ala Ala Thr Trp Leu Pro Pro Asn Thr Ala Phe Arg Cys Asp
            185                 190                 195

tac gca aag aaa atc atc acc gtt aaa gat cgc tac aac gtg tgg gtg   739
Tyr Ala Lys Lys Ile Ile Thr Val Lys Asp Arg Tyr Asn Val Trp Val
        200                 205                 210
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act gag gct gaa gca agc gcc ctg gaa cgc caa tta gat acg tgt gct 787
Thr Glu Ala Glu Ala Ser Ala Leu Glu Arg Gln Leu Asp Thr Cys Ala
215 220 225

gca taacagtcac ataagcattt ggg 813
Ala
230

<210> 616
<211> 230
<212> PRT
<213> Corynebacterium glutamicum

<400> 616
Val Ala Ala Val Ala Phe Ala Ala Tyr Val Ile Asp Gly Gly Val Glu
1 5 10 15

Glu Ala Ser Gly Thr Pro Thr Ser Ser Glu Ser Ser Val Ala Ala Thr
20 25 30

Ala Pro Ala Ala Ser Ser Glu Thr Ala Ala Glu Tyr Arg Ala Met Leu
35 40 45

Ala Ser Leu Asp Val Lys Gly Arg Ala Pro Gly Thr Gly Tyr Asp Arg
50 55 60

Glu Leu Phe Gly Pro Ala Trp Thr Asp Thr Val Ser Val Glu Tyr Gly
65 70 75 80

His Asn Gly Cys Asp Thr Arg Asn Asp Ile Leu Gln Arg Asp Leu Asp
85 90 95

Asp Ile Gln Leu Arg Glu Gly Thr Lys Asp Cys Ile Val Thr Ser Gly
100 105 110

Leu Leu Ser Asp Pro Phe Ser Gly Glu Leu Ile Asp Phe Val Arg Gly
115 120 125

Glu Arg Ser Gly Asp Val Gln Ile Asp His Leu Val Pro Leu His Asp
130 135 140

Ala Trp Val Lys Gly Ala Gln Gln Trp Asp Glu Gln Thr Arg Lys Asn
145 150 155 160

Phe Ala Asn Asp Pro Asp Asn Leu Leu Ala Val Lys Gly Thr Leu Asn
165 170 175

Gln Gln Lys Gly Ala Gly Asp Ala Ala Thr Trp Leu Pro Pro Asn Thr
180 185 190

Ala Phe Arg Cys Asp Tyr Ala Lys Lys Ile Ile Thr Val Lys Asp Arg
195 200 205

Tyr Asn Val Trp Val Thr Glu Ala Glu Ala Ser Ala Leu Glu Arg Gln
210 215 220

Leu Asp Thr Cys Ala Ala
225 230

<210> 617
<211> 1623
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1600)
<223> RXN01400

<400> 617
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gcaacgacat gtgggtgccg gcgagcgacc gggtagttgg atg gcg att agt gtt 115
Met Ala Ile Ser Val
1 5

tct atg cct aag gcg atc agc cgt gag gaa ttg gag cgc gcg tgg ctt 163
Ser Met Pro Lys Ala Ile Ser Arg Glu Glu Leu Glu Arg Ala Trp Leu
10 15 20

gaa gtg att gaa cgg cac ggc acc ttg cgc aca gta ttt agc acg gga 211
Glu Val Ile Glu Arg His Gly Thr Leu Arg Thr Val Phe Ser Thr Gly
25 30 35

atg ggt ggg gaa gtg cag caa cac cgc att gat gtg ggc ccg gga aaa 259
Met Gly Gly Glu Val Gln Gln His Arg Ile Asp Val Gly Pro Gly Lys
40 45 50

tgg att gac cac gcc gtt gcg cct ggt gag agc att aat gag gcg ttg 307
Trp Ile Asp His Ala Val Ala Pro Gly Glu Ser Ile Asn Glu Ala Leu
55 60 65

cgg gcg gtg ttg aat cgg cag tgt tcg ccg tac tcg agg cca tcg cat 355
Arg Ala Val Leu Asn Arg Gln Cys Ser Pro Tyr Ser Arg Pro Ser His
70 75 80 85

agt ttg tgc att att gat gcg cat ccg cgt ccc acg gtg att att ggt 403
Ser Leu Cys Ile Ile Asp Ala His Pro Arg Pro Thr Val Ile Ile Gly
90 95 100

agt gat cat tcg cat gtg gat atg tgg tcc atg ctg gtg att gtg cgc 451
Ser Asp His Ser His Val Asp Met Trp Ser Met Leu Val Ile Val Arg
105 110 115

gat ttg ttg gct gcg ctc gat atg gaa ctt ccc gtt gag ccg ccg ttg 499
Asp Leu Leu Ala Ala Leu Asp Met Glu Leu Pro Val Glu Pro Pro Leu
120 125 130

gcg ttt gaa tcg cac acc gcg gaa ctc ctc gcg gct cca cct gca ccg 547
Ala Phe Glu Ser His Thr Ala Glu Leu Leu Ala Ala Pro Pro Ala Pro
135 140 145

gag cgg att cac cag cgg tgg cgt gaa att ttg gaa gct ggt ggt gga 595
Glu Arg Ile His Gln Arg Trp Arg Glu Ile Leu Glu Ala Gly Gly Gly
150 155 160 165

aaa atg cct cag ttc ccg ctt ccg ctt ggc gat gcc atc tcc atg cct 643
Lys Met Pro Gln Phe Pro Leu Pro Leu Gly Asp Ala Ile Ser Met Pro
170 175 180

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gaa cgc gtt gaa gtc cgc gac att ttc ggg gtc aat ggc ttg gcg att   691
Glu Arg Val Glu Val Arg Asp Ile Phe Gly Val Asn Gly Leu Ala Ile
            185                 190                 195

tac tcg gca cgc gcc cgc gca caa cag gta agc tcc ctg gcc ttg act   739
Tyr Ser Ala Arg Ala Arg Ala Gln Gln Val Ser Ser Leu Ala Leu Thr
        200                 205                 210

att tca gtg atg gct gat gtt acg gcg gcg ctg gcg gac ctt ccg ttg   787
Ile Ser Val Met Ala Asp Val Thr Ala Ala Leu Ala Asp Leu Pro Leu
    215                 220                 225

cgt gct gta ttc cca gtc cat agc cgt ttc gat cag cgc tgg cac gat   835
Arg Ala Val Phe Pro Val His Ser Arg Phe Asp Gln Arg Trp His Asp
230                 235                 240                 245

agt gtc ggg tgg ttt atc tcc aat tcg gtc att gag gtg cca gat tcc   883
Ser Val Gly Trp Phe Ile Ser Asn Ser Val Ile Glu Val Pro Asp Ser
                250                 255                 260

gat cct cac act gca gcc caa gct gtt cgc gag gct gtt tct ttg gga   931
Asp Pro His Thr Ala Ala Gln Ala Val Arg Glu Ala Val Ser Leu Gly
            265                 270                 275

agc tac ccg ctg gct gag ctg ctt gaa ccg tgg ggt ggc atg ccg gaa   979
Ser Tyr Pro Leu Ala Glu Leu Leu Glu Pro Trp Gly Gly Met Pro Glu
        280                 285                 290

acg cca gga atg ttt gct att tct tgg ctt gac ctg cgc cga ctc cca   1027
Thr Pro Gly Met Phe Ala Ile Ser Trp Leu Asp Leu Arg Arg Leu Pro
    295                 300                 305

gtg agc att gac gat att ggc ctc caa gcc cag tat gtc agc gct tca   1075
Val Ser Ile Asp Asp Ile Gly Leu Gln Ala Gln Tyr Val Ser Ala Ser
310                 315                 320                 325

ctg cgc acc gat ggt gtg atg ctg tgg ttt att ttg gat cgc tcc ggc   1123
Leu Arg Thr Asp Gly Val Met Leu Trp Phe Ile Leu Asp Arg Ser Gly
                330                 335                 340

gcg cac ctt cgc tgt cgt tat cct gac tct ttg gtg gcg cgg gaa aat   1171
Ala His Leu Arg Cys Arg Tyr Pro Asp Ser Leu Val Ala Arg Glu Asn
            345                 350                 355

gta ggc cgc tgg att gat gcg att gtt gct cag atg cgc gcc gaa gct   1219
Val Gly Arg Trp Ile Asp Ala Ile Val Ala Gln Met Arg Ala Glu Ala
        360                 365                 370

ggg acg gtg aat ctg cag gcc ggc ggg gaa cag ctg aca ctt cgg cat   1267
Gly Thr Val Asn Leu Gln Ala Gly Gly Glu Gln Leu Thr Leu Arg His
    375                 380                 385

gga act cgc gcc gat att tcc gag atc gcc ccg cta ctt gcc cga aac   1315
Gly Thr Arg Ala Asp Ile Ser Glu Ile Ala Pro Leu Leu Ala Arg Asn
390                 395                 400                 405

gca gct gac cct tgt gag ctg gtg gat ctt gaa cat gcc ctt gac ctg   1363
Ala Ala Asp Pro Cys Glu Leu Val Asp Leu Glu His Ala Leu Asp Leu
                410                 415                 420

ctg aca cac gag tct tcg cat ttc ctg gcg gtg gtt cga aac gct cgt   1411
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Leu Thr His Glu Ser Ser His Phe Leu Ala Val Val Arg Asn Ala Arg
            425                 430                 435

ggc aag ata atc gca gcg atg cag ttg act att gtt ccg gag ttt tcc   1459
Gly Lys Ile Ile Ala Ala Met Gln Leu Thr Ile Val Pro Glu Phe Ser
        440                 445                 450

cgc ggt ggt gcg ctt cat ctt cac atc gag ggg ccg ttc att att ccg   1507
Arg Gly Gly Ala Leu His Leu His Ile Glu Gly Pro Phe Ile Ile Pro
    455                 460                 465

gaa tat cgc acc acc gat ttg gat aaa aag ctg cgc gcc tgg gct gtg   1555
Glu Tyr Arg Thr Thr Asp Leu Asp Lys Lys Leu Arg Ala Trp Ala Val
470                 475                 480                 485

gag cat ggg cgt gcg cga ggg gtg aag gtt gag gag gtg gtg gga       1600
Glu His Gly Arg Ala Arg Gly Val Lys Val Glu Glu Val Val Gly
                490                 495                 500

tagttggttt attggcgcct cgt                                        1623


<210> 618
<211> 500
<212> PRT
<213> Corynebacterium glutamicum

<400> 618
Met Ala Ile Ser Val Ser Met Pro Lys Ala Ile Ser Arg Glu Glu Leu
  1               5                  10                  15

Glu Arg Ala Trp Leu Glu Val Ile Glu Arg His Gly Thr Leu Arg Thr
            20                  25                  30

Val Phe Ser Thr Gly Met Gly Gly Glu Val Gln Gln His Arg Ile Asp
        35                  40                  45

Val Gly Pro Gly Lys Trp Ile Asp His Ala Val Ala Pro Gly Glu Ser
    50                  55                  60

Ile Asn Glu Ala Leu Arg Ala Val Leu Asn Arg Gln Cys Ser Pro Tyr
65                  70                  75                  80

Ser Arg Pro Ser His Ser Leu Cys Ile Ile Asp Ala His Pro Arg Pro
                85                  90                  95

Thr Val Ile Ile Gly Ser Asp His Ser His Val Asp Met Trp Ser Met
            100                 105                 110

Leu Val Ile Val Arg Asp Leu Leu Ala Ala Leu Asp Met Glu Leu Pro
        115                 120                 125

Val Glu Pro Pro Leu Ala Phe Glu Ser His Thr Ala Glu Leu Leu Ala
    130                 135                 140

Ala Pro Pro Ala Pro Glu Arg Ile His Gln Arg Trp Arg Glu Ile Leu
145                 150                 155                 160

Glu Ala Gly Gly Gly Lys Met Pro Gln Phe Pro Leu Pro Leu Gly Asp
                165                 170                 175
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```
Ala Ile Ser Met Pro Glu Arg Val Glu Val Arg Asp Ile Phe Gly Val
            180                 185                 190

Asn Gly Leu Ala Ile Tyr Ser Ala Arg Ala Arg Ala Gln Gln Val Ser
        195                 200                 205

Ser Leu Ala Leu Thr Ile Ser Val Met Ala Asp Val Thr Ala Ala Leu
    210                 215                 220

Ala Asp Leu Pro Leu Arg Ala Val Phe Pro Val His Ser Arg Phe Asp
225                 230                 235                 240

Gln Arg Trp His Asp Ser Val Gly Trp Phe Ile Ser Asn Ser Val Ile
                245                 250                 255

Glu Val Pro Asp Ser Asp Pro His Thr Ala Ala Gln Ala Val Arg Glu
            260                 265                 270

Ala Val Ser Leu Gly Ser Tyr Pro Leu Ala Glu Leu Leu Glu Pro Trp
        275                 280                 285

Gly Gly Met Pro Glu Thr Pro Gly Met Phe Ala Ile Ser Trp Leu Asp
    290                 295                 300

Leu Arg Arg Leu Pro Val Ser Ile Asp Asp Ile Gly Leu Gln Ala Gln
305                 310                 315                 320

Tyr Val Ser Ala Ser Leu Arg Thr Asp Gly Val Met Leu Trp Phe Ile
                325                 330                 335

Leu Asp Arg Ser Gly Ala His Leu Arg Cys Arg Tyr Pro Asp Ser Leu
            340                 345                 350

Val Ala Arg Glu Asn Val Gly Arg Trp Ile Asp Ala Ile Val Ala Gln
        355                 360                 365

Met Arg Ala Glu Ala Gly Thr Val Asn Leu Gln Ala Gly Gly Glu Gln
    370                 375                 380

Leu Thr Leu Arg His Gly Thr Arg Ala Asp Ile Ser Glu Ile Ala Pro
385                 390                 395                 400

Leu Leu Ala Arg Asn Ala Ala Asp Pro Cys Glu Leu Val Asp Leu Glu
                405                 410                 415

His Ala Leu Asp Leu Leu Thr His Glu Ser Ser His Phe Leu Ala Val
            420                 425                 430

Val Arg Asn Ala Arg Gly Lys Ile Ile Ala Ala Met Gln Leu Thr Ile
        435                 440                 445

Val Pro Glu Phe Ser Arg Gly Gly Ala Leu His Leu His Ile Glu Gly
    450                 455                 460

Pro Phe Ile Ile Pro Glu Tyr Arg Thr Thr Asp Leu Asp Lys Lys Leu
465                 470                 475                 480

Arg Ala Trp Ala Val Glu His Gly Arg Ala Arg Gly Val Lys Val Glu
                485                 490                 495

Glu Val Val Gly
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500

<210> 619
<211> 1623
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1600)
<223> FRXA01400

<400> 619
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gcaacgacat gtgggtgccg gcgagcgacc gggtagttgg atg gcg att agt gtt 115
Met Ala Ile Ser Val
1 5

tct atg cct aag gcg atc agc cgt gag gaa ttg gag cgc gcg tgg ctt 163
Ser Met Pro Lys Ala Ile Ser Arg Glu Glu Leu Glu Arg Ala Trp Leu
10 15 20

gaa gtg att gaa cgg cac ggc acc ttg cgc aca gta ttt agc acg gga 211
Glu Val Ile Glu Arg His Gly Thr Leu Arg Thr Val Phe Ser Thr Gly
25 30 35

atg ggt ggg gaa gtg cag caa cac cgc att gat gtg ggc ccg gga aaa 259
Met Gly Gly Glu Val Gln Gln His Arg Ile Asp Val Gly Pro Gly Lys
40 45 50

tgg att gac cac gcc gtt gcg cct ggt gag agc att aat gag gcg ttg 307
Trp Ile Asp His Ala Val Ala Pro Gly Glu Ser Ile Asn Glu Ala Leu
55 60 65

cgg gcg gtg ttg aat cgg cag tgt tcg ccg tac tcg agg cca tcg cat 355
Arg Ala Val Leu Asn Arg Gln Cys Ser Pro Tyr Ser Arg Pro Ser His
70 75 80 85

agt ttg tgc att att gat gcg cat ccg cgt ccc acg gtg att att ggt 403
Ser Leu Cys Ile Ile Asp Ala His Pro Arg Pro Thr Val Ile Ile Gly
90 95 100

agt gat cat tcg cat gtg gat atg tgg tcc atg ctg gtg att gtg cgc 451
Ser Asp His Ser His Val Asp Met Trp Ser Met Leu Val Ile Val Arg
105 110 115

gat ttg ttg gct gcg ctc gat atg gaa ctt ccc gtt gag ccg ccg ttg 499
Asp Leu Leu Ala Ala Leu Asp Met Glu Leu Pro Val Glu Pro Pro Leu
120 125 130

gcg ttt gaa tcg cac acc gcg gaa ctc ctc gcg gct cca cct gca ccg 547
Ala Phe Glu Ser His Thr Ala Glu Leu Leu Ala Ala Pro Pro Ala Pro
135 140 145

gag cgg att cac cag cgg tgg cgt gaa att ttg gaa gct ggt ggt gga 595
Glu Arg Ile His Gln Arg Trp Arg Glu Ile Leu Glu Ala Gly Gly Gly
150 155 160 165

aaa atg cct cag ttc ccg ctt ccg ctt ggc gat gcc atc tcc atg cct 643

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Lys Met Pro Gln Phe Pro Leu Pro Leu Gly Asp Ala Ile Ser Met Pro
                170                 175                 180

gaa cgc gtt gaa gtc cgc gac att ttc ggg gtc aat ggc ttg gcg att   691
Glu Arg Val Glu Val Arg Asp Ile Phe Gly Val Asn Gly Leu Ala Ile
            185                 190                 195

tac tcg gca cgc gcc cgc gca caa cag gta agc tcc ctg gcc ttg act   739
Tyr Ser Ala Arg Ala Arg Ala Gln Gln Val Ser Ser Leu Ala Leu Thr
        200                 205                 210

att tca gtg atg gct gat gtt acg gcg gcg ctg gcg gac ctt ccg ttg   787
Ile Ser Val Met Ala Asp Val Thr Ala Ala Leu Ala Asp Leu Pro Leu
    215                 220                 225

cgt gct gta ttc cca gtc cat agc cgt ttc gat cag cgc tgg cac gat   835
Arg Ala Val Phe Pro Val His Ser Arg Phe Asp Gln Arg Trp His Asp
230                 235                 240                 245

agt gtc ggg tgg ttt atc tcc aat tcg gtc att gag gtg cca gat tcc   883
Ser Val Gly Trp Phe Ile Ser Asn Ser Val Ile Glu Val Pro Asp Ser
                250                 255                 260

gat cct cac act gca gcc caa gct gtt cgc gag gct gtt tct ttg gga   931
Asp Pro His Thr Ala Ala Gln Ala Val Arg Glu Ala Val Ser Leu Gly
            265                 270                 275

agc tac ccg ctg gct gag ctg ctt gaa ccg tgg ggt ggc atg ccg gaa   979
Ser Tyr Pro Leu Ala Glu Leu Leu Glu Pro Trp Gly Gly Met Pro Glu
        280                 285                 290

acg cca gga atg ttt gct att tct tgg ctt gac ctg cgc cga ctc cca   1027
Thr Pro Gly Met Phe Ala Ile Ser Trp Leu Asp Leu Arg Arg Leu Pro
    295                 300                 305

gtg agc att gac gat att ggc ctc caa gcc cag tat gtc agc gct tca   1075
Val Ser Ile Asp Asp Ile Gly Leu Gln Ala Gln Tyr Val Ser Ala Ser
310                 315                 320                 325

ctg cgc acc gat ggt gtg atg ctg tgg ttt att ttg gat cgc tcc ggc   1123
Leu Arg Thr Asp Gly Val Met Leu Trp Phe Ile Leu Asp Arg Ser Gly
                330                 335                 340

gcg cac ctt cgc tgt cgt tat cct gac tct ttg gtg gcg cgg gaa aat   1171
Ala His Leu Arg Cys Arg Tyr Pro Asp Ser Leu Val Ala Arg Glu Asn
            345                 350                 355

gta ggc cgc tgg att gat gcg att gtt gct cag atg cgc gcc gaa gct   1219
Val Gly Arg Trp Ile Asp Ala Ile Val Ala Gln Met Arg Ala Glu Ala
        360                 365                 370

ggg acg gtg aat ctg cag gcc ggc ggg gaa cag ctg aca ctt cgg cat   1267
Gly Thr Val Asn Leu Gln Ala Gly Gly Glu Gln Leu Thr Leu Arg His
    375                 380                 385

gga act cgc gcc gat att tcc gag atc gcc ccg cta ctt gcc cga aac   1315
Gly Thr Arg Ala Asp Ile Ser Glu Ile Ala Pro Leu Leu Ala Arg Asn
390                 395                 400                 405

gca gct gac cct tgt gag ctg gtg gat ctt gaa cat gcc ctt gac ctg   1363
Ala Ala Asp Pro Cys Glu Leu Val Asp Leu Glu His Ala Leu Asp Leu
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                410                 415                 420

ctg aca cac gag tct tcg cat ttc ctg gcg gtg gtt cga aac gct cgt   1411
Leu Thr His Glu Ser Ser His Phe Leu Ala Val Val Arg Asn Ala Arg
            425                 430                 435

ggc aag ata atc gca gcg atg cag ttg act att gtt ccg gag ttt tcc   1459
Gly Lys Ile Ile Ala Ala Met Gln Leu Thr Ile Val Pro Glu Phe Ser
        440                 445                 450

cgc ggt ggt gcg ctt cat ctt cac atc gag ggg ccg ttc att att ccg   1507
Arg Gly Gly Ala Leu His Leu His Ile Glu Gly Pro Phe Ile Ile Pro
    455                 460                 465

gaa tat cgc acc acc gat ttg gat aaa aag ctg cgc gcc tgg gct gtg   1555
Glu Tyr Arg Thr Thr Asp Leu Asp Lys Lys Leu Arg Ala Trp Ala Val
470                 475                 480                 485

gag cat ggg cgt gcg cga ggg gtg aag gtt gag gag gtg gtg gga       1600
Glu His Gly Arg Ala Arg Gly Val Lys Val Glu Glu Val Val Gly
                490                 495                 500

tagttggttt attggcgcct cgt                                        1623


<210> 620
<211> 500
<212> PRT
<213> Corynebacterium glutamicum

<400> 620
Met Ala Ile Ser Val Ser Met Pro Lys Ala Ile Ser Arg Glu Glu Leu
  1               5                  10                  15

Glu Arg Ala Trp Leu Glu Val Ile Glu Arg His Gly Thr Leu Arg Thr
             20                  25                  30

Val Phe Ser Thr Gly Met Gly Gly Glu Val Gln Gln His Arg Ile Asp
         35                  40                  45

Val Gly Pro Gly Lys Trp Ile Asp His Ala Val Ala Pro Gly Glu Ser
     50                  55                  60

Ile Asn Glu Ala Leu Arg Ala Val Leu Asn Arg Gln Cys Ser Pro Tyr
 65                  70                  75                  80

Ser Arg Pro Ser His Ser Leu Cys Ile Ile Asp Ala His Pro Arg Pro
                 85                  90                  95

Thr Val Ile Ile Gly Ser Asp His Ser His Val Asp Met Trp Ser Met
            100                 105                 110

Leu Val Ile Val Arg Asp Leu Leu Ala Ala Leu Asp Met Glu Leu Pro
        115                 120                 125

Val Glu Pro Pro Leu Ala Phe Glu Ser His Thr Ala Glu Leu Leu Ala
    130                 135                 140

Ala Pro Pro Ala Pro Glu Arg Ile His Gln Arg Trp Arg Glu Ile Leu
145                 150                 155                 160
```

```
Glu Ala Gly Gly Gly Lys Met Pro Gln Phe Pro Leu Pro Leu Gly Asp
                165                 170                 175

Ala Ile Ser Met Pro Glu Arg Val Glu Val Arg Asp Ile Phe Gly Val
            180                 185                 190

Asn Gly Leu Ala Ile Tyr Ser Ala Arg Ala Arg Ala Gln Gln Val Ser
        195                 200                 205

Ser Leu Ala Leu Thr Ile Ser Val Met Ala Asp Val Thr Ala Ala Leu
    210                 215                 220

Ala Asp Leu Pro Leu Arg Ala Val Phe Pro Val His Ser Arg Phe Asp
225                 230                 235                 240

Gln Arg Trp His Asp Ser Val Gly Trp Phe Ile Ser Asn Ser Val Ile
                245                 250                 255

Glu Val Pro Asp Ser Asp Pro His Thr Ala Ala Gln Ala Val Arg Glu
            260                 265                 270

Ala Val Ser Leu Gly Ser Tyr Pro Leu Ala Glu Leu Leu Glu Pro Trp
        275                 280                 285

Gly Gly Met Pro Glu Thr Pro Gly Met Phe Ala Ile Ser Trp Leu Asp
    290                 295                 300

Leu Arg Arg Leu Pro Val Ser Ile Asp Asp Ile Gly Leu Gln Ala Gln
305                 310                 315                 320

Tyr Val Ser Ala Ser Leu Arg Thr Asp Gly Val Met Leu Trp Phe Ile
                325                 330                 335

Leu Asp Arg Ser Gly Ala His Leu Arg Cys Arg Tyr Pro Asp Ser Leu
            340                 345                 350

Val Ala Arg Glu Asn Val Gly Arg Trp Ile Asp Ala Ile Val Ala Gln
        355                 360                 365

Met Arg Ala Glu Ala Gly Thr Val Asn Leu Gln Ala Gly Gly Glu Gln
    370                 375                 380

Leu Thr Leu Arg His Gly Thr Arg Ala Asp Ile Ser Glu Ile Ala Pro
385                 390                 395                 400

Leu Leu Ala Arg Asn Ala Ala Asp Pro Cys Glu Leu Val Asp Leu Glu
                405                 410                 415

His Ala Leu Asp Leu Leu Thr His Glu Ser Ser His Phe Leu Ala Val
            420                 425                 430

Val Arg Asn Ala Arg Gly Lys Ile Ile Ala Ala Met Gln Leu Thr Ile
        435                 440                 445

Val Pro Glu Phe Ser Arg Gly Gly Ala Leu His Leu His Ile Glu Gly
    450                 455                 460

Pro Phe Ile Ile Pro Glu Tyr Arg Thr Thr Asp Leu Asp Lys Lys Leu
465                 470                 475                 480

Arg Ala Trp Ala Val Glu His Gly Arg Ala Arg Gly Val Lys Val Glu
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                485                 490                 495

Glu Val Val Gly
            500


<210> 621
<211> 845
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(822)
<223> RXN01409

<400> 621
tgg gtg gat ttc ccc gac gtc acc gca cgt ttg ggg tat gaa tac atg   48
Trp Val Asp Phe Pro Asp Val Thr Ala Arg Leu Gly Tyr Glu Tyr Met
  1               5                  10                  15

cag ctg acc cct cat gta gat ttc ggt cct ttc ttc cgc cac ccc aag   96
Gln Leu Thr Pro His Val Asp Phe Gly Pro Phe Phe Arg His Pro Lys
             20                  25                  30

gca gac gat gat ctc gtg gca gcc ctg aaa aag cgt gcc aag gat gcc   144
Ala Asp Asp Asp Leu Val Ala Ala Leu Lys Lys Arg Ala Lys Asp Ala
         35                  40                  45

gga gtc acc att cct gca ctg ttg cca gtg cag cgt att tcc tgg ccg   192
Gly Val Thr Ile Pro Ala Leu Leu Pro Val Gln Arg Ile Ser Trp Pro
     50                  55                  60

gag gaa acc cag cgt gtt gca gca gta cgc aac atc aag cgc atc atc   240
Glu Glu Thr Gln Arg Val Ala Ala Val Arg Asn Ile Lys Arg Ile Ile
 65                  70                  75                  80

cag ttg gcc gtt gat ctg gaa gta gac acc ctc aac acg gag ttt tct   288
Gln Leu Ala Val Asp Leu Glu Val Asp Thr Leu Asn Thr Glu Phe Ser
                 85                  90                  95

gga cgc cca gaa cgc tcc gag gat tcc gaa gat gcc ttc tac cgc tcc   336
Gly Arg Pro Glu Arg Ser Glu Asp Ser Glu Asp Ala Phe Tyr Arg Ser
            100                 105                 110

atg gaa gaa ctc ctg cca atc ctg gaa aaa gag ggc atc aag ttc aac   384
Met Glu Glu Leu Leu Pro Ile Leu Glu Lys Glu Gly Ile Lys Phe Asn
        115                 120                 125

atc gac cca cac cct gat gat ttc gtg gaa aac ggt att gaa gca tgg   432
Ile Asp Pro His Pro Asp Asp Phe Val Glu Asn Gly Ile Glu Ala Trp
    130                 135                 140

cga gtc atc cgc ggt ctg aac tcc aag cag gtg ggc ttt gtt tac gtg   480
Arg Val Ile Arg Gly Leu Asn Ser Lys Gln Val Gly Phe Val Tyr Val
145                 150                 155                 160

gca cct cac tca ttc cac atg ggt gat cag gct gag gca atc ctg cca   528
Ala Pro His Ser Phe His Met Gly Asp Gln Ala Glu Ala Ile Leu Pro
                165                 170                 175
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gca gta ggc gat cgc ctt ggg gct gtg tac ctg tca gat acc ttc gac   576
Ala Val Gly Asp Arg Leu Gly Ala Val Tyr Leu Ser Asp Thr Phe Asp
            180                 185                 190

cac cac aaa tcc cac ggc ctg cgc tac atc act aac cct cca ggc aac   624
His His Lys Ser His Gly Leu Arg Tyr Ile Thr Asn Pro Pro Gly Asn
        195                 200                 205

gca gtg cgc gtg cac cag cac cta aaa atc ggt gat ggc gat gtg aac   672
Ala Val Arg Val His Gln His Leu Lys Ile Gly Asp Gly Asp Val Asn
    210                 215                 220

ttt gaa gag atc ttc tca ctg ctg cgc tct acc ggt tac ctt gac cgt   720
Phe Glu Glu Ile Phe Ser Leu Leu Arg Ser Thr Gly Tyr Leu Asp Arg
225                 230                 235                 240

gaa gat gca ctg ttg gtc tcc aac gtg ttt gca gaa gat gaa gca gca   768
Glu Asp Ala Leu Leu Val Ser Asn Val Phe Ala Glu Asp Glu Ala Ala
                245                 250                 255

gat gaa gta tcc cgc tac cag ctg gag aaa atc cgc tca ctc atc gaa   816
Asp Glu Val Ser Arg Tyr Gln Leu Glu Lys Ile Arg Ser Leu Ile Glu
            260                 265                 270

aac gca tagagttatc tcgaaactac caa                                845
Asn Ala
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<210> 622
<211> 274
<212> PRT
<213> Corynebacterium glutamicum

<400> 622

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Trp Val Asp Phe Pro Asp Val Thr Ala Arg Leu Gly Tyr Glu Tyr Met
  1               5                  10                  15

Gln Leu Thr Pro His Val Asp Phe Gly Pro Phe Phe Arg His Pro Lys
             20                  25                  30

Ala Asp Asp Asp Leu Val Ala Ala Leu Lys Lys Arg Ala Lys Asp Ala
         35                  40                  45

Gly Val Thr Ile Pro Ala Leu Leu Pro Val Gln Arg Ile Ser Trp Pro
     50                  55                  60

Glu Glu Thr Gln Arg Val Ala Ala Val Arg Asn Ile Lys Arg Ile Ile
 65                  70                  75                  80

Gln Leu Ala Val Asp Leu Glu Val Asp Thr Leu Asn Thr Glu Phe Ser
                 85                  90                  95

Gly Arg Pro Glu Arg Ser Glu Asp Ser Glu Asp Ala Phe Tyr Arg Ser
            100                 105                 110

Met Glu Glu Leu Leu Pro Ile Leu Glu Lys Glu Gly Ile Lys Phe Asn
        115                 120                 125

Ile Asp Pro His Pro Asp Asp Phe Val Glu Asn Gly Ile Glu Ala Trp
    130                 135                 140
```

```
Arg Val Ile Arg Gly Leu Asn Ser Lys Gln Val Gly Phe Val Tyr Val
145                 150                 155                 160

Ala Pro His Ser Phe His Met Gly Asp Gln Ala Glu Ala Ile Leu Pro
                165                 170                 175

Ala Val Gly Asp Arg Leu Gly Ala Val Tyr Leu Ser Asp Thr Phe Asp
            180                 185                 190

His His Lys Ser His Gly Leu Arg Tyr Ile Thr Asn Pro Pro Gly Asn
        195                 200                 205

Ala Val Arg Val His Gln His Leu Lys Ile Gly Asp Gly Asp Val Asn
    210                 215                 220

Phe Glu Glu Ile Phe Ser Leu Leu Arg Ser Thr Gly Tyr Leu Asp Arg
225                 230                 235                 240

Glu Asp Ala Leu Leu Val Ser Asn Val Phe Ala Glu Asp Glu Ala Ala
                245                 250                 255

Asp Glu Val Ser Arg Tyr Gln Leu Glu Lys Ile Arg Ser Leu Ile Glu
            260                 265                 270

Asn Ala
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CONFIDENTIAL

<210> 623
<211> 839
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<220>
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<222> (1)..(816)
<223> FRXA01409

<400> 623

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Asp Phe Pro Asp Val Thr Ala Arg Leu Gly Tyr Glu Tyr Met Gln Leu
  1               5                  10                  15

acc cct cat gta gat ttc ggt cct ttc ttc cgc cac ccc aag gca gac   96
Thr Pro His Val Asp Phe Gly Pro Phe Phe Arg His Pro Lys Ala Asp
             20                  25                  30

gat gat ctc gtg gca gcc ctg aaa aag cgt gcc aag gat gcc gga gtc   144
Asp Asp Leu Val Ala Ala Leu Lys Lys Arg Ala Lys Asp Ala Gly Val
         35                  40                  45

acc att cct gca ctg ttg cca gtg cag cgt att tcc tgg ccg gag gaa   192
Thr Ile Pro Ala Leu Leu Pro Val Gln Arg Ile Ser Trp Pro Glu Glu
     50                  55                  60

acc cag cgt gtt gca gca gta cgc aac atc aag cgc atc atc cag ttg   240
Thr Gln Arg Val Ala Ala Val Arg Asn Ile Lys Arg Ile Ile Gln Leu
 65                  70                  75                  80

gcc gtt gat ctg gaa gta gac acc ctc aac acg gag ttt tct gga cgc   288
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Ala Val Asp Leu Glu Val Asp Thr Leu Asn Thr Glu Phe Ser Gly Arg
                 85                  90                  95

cca gaa cgc tcc gag gat tcc gaa gat gcc ttc tac cgc tcc atg gaa   336
Pro Glu Arg Ser Glu Asp Ser Glu Asp Ala Phe Tyr Arg Ser Met Glu
            100                 105                 110

gaa ctc ctg cca atc ctg gaa aaa gag ggc atc aag ttc aac atc gac   384
Glu Leu Leu Pro Ile Leu Glu Lys Glu Gly Ile Lys Phe Asn Ile Asp
        115                 120                 125

cca cac cct gat gat ttc gtg gaa aac ggt att gaa gca tgg cga gtc   432
Pro His Pro Asp Asp Phe Val Glu Asn Gly Ile Glu Ala Trp Arg Val
    130                 135                 140

atc cgc ggt ctg aac tcc aag cag gtg ggc ttt gtt tac gtg gca cct   480
Ile Arg Gly Leu Asn Ser Lys Gln Val Gly Phe Val Tyr Val Ala Pro
145                 150                 155                 160

cac tca ttc cac atg ggt gat cag gct gag gca atc ctg cca gca gta   528
His Ser Phe His Met Gly Asp Gln Ala Glu Ala Ile Leu Pro Ala Val
                165                 170                 175

ggc gat cgc ctt ggg gct gtg tac ctg tca gat acc ttc gac cac cac   576
Gly Asp Arg Leu Gly Ala Val Tyr Leu Ser Asp Thr Phe Asp His His
            180                 185                 190

aaa tcc cac ggc ctg cgc tac atc act aac cct cca ggc aac gca gtg   624
Lys Ser His Gly Leu Arg Tyr Ile Thr Asn Pro Pro Gly Asn Ala Val
        195                 200                 205

cgc gtg cac cag cac cta aaa atc ggt gat ggc gat gtg aac ttt gaa   672
Arg Val His Gln His Leu Lys Ile Gly Asp Gly Asp Val Asn Phe Glu
    210                 215                 220

gag atc ttc tca ctg ctg cgc tct acc ggt tac ctt gac cgt gaa gat   720
Glu Ile Phe Ser Leu Leu Arg Ser Thr Gly Tyr Leu Asp Arg Glu Asp
225                 230                 235                 240

gca ctg ttg gtc tcc aac gtg ttt gca gaa gat gaa gca gca gat gaa   768
Ala Leu Leu Val Ser Asn Val Phe Ala Glu Asp Glu Ala Ala Asp Glu
                245                 250                 255

gta tcc cgc tac cag ctg gag aaa atc cgc tca ctc atc gaa aac gca   816
Val Ser Arg Tyr Gln Leu Glu Lys Ile Arg Ser Leu Ile Glu Asn Ala
            260                 265                 270

tagagttatc tcgaaactac caa                                        839


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<212> PRT
<213> Corynebacterium glutamicum

<400> 624
Asp Phe Pro Asp Val Thr Ala Arg Leu Gly Tyr Glu Tyr Met Gln Leu
  1               5                  10                  15

Thr Pro His Val Asp Phe Gly Pro Phe Phe Arg His Pro Lys Ala Asp
             20                  25                  30
```

```
Asp Asp Leu Val Ala Ala Leu Lys Lys Arg Ala Lys Asp Ala Gly Val
         35                  40                  45

Thr Ile Pro Ala Leu Leu Pro Val Gln Arg Ile Ser Trp Pro Glu Glu
     50                  55                  60

Thr Gln Arg Val Ala Ala Val Arg Asn Ile Lys Arg Ile Ile Gln Leu
 65                  70                  75                  80

Ala Val Asp Leu Glu Val Asp Thr Leu Asn Thr Glu Phe Ser Gly Arg
                 85                  90                  95

Pro Glu Arg Ser Glu Asp Ser Glu Asp Ala Phe Tyr Arg Ser Met Glu
            100                 105                 110

Glu Leu Leu Pro Ile Leu Glu Lys Glu Gly Ile Lys Phe Asn Ile Asp
        115                 120                 125

Pro His Pro Asp Asp Phe Val Glu Asn Gly Ile Glu Ala Trp Arg Val
    130                 135                 140

Ile Arg Gly Leu Asn Ser Lys Gln Val Gly Phe Val Tyr Val Ala Pro
145                 150                 155                 160

His Ser Phe His Met Gly Asp Gln Ala Glu Ala Ile Leu Pro Ala Val
                165                 170                 175

Gly Asp Arg Leu Gly Ala Val Tyr Leu Ser Asp Thr Phe Asp His His
            180                 185                 190

Lys Ser His Gly Leu Arg Tyr Ile Thr Asn Pro Pro Gly Asn Ala Val
        195                 200                 205

Arg Val His Gln His Leu Lys Ile Gly Asp Gly Asp Val Asn Phe Glu
    210                 215                 220

Glu Ile Phe Ser Leu Leu Arg Ser Thr Gly Tyr Leu Asp Arg Glu Asp
225                 230                 235                 240

Ala Leu Leu Val Ser Asn Val Phe Ala Glu Asp Glu Ala Ala Asp Glu
                245                 250                 255

Val Ser Arg Tyr Gln Leu Glu Lys Ile Arg Ser Leu Ile Glu Asn Ala
            260                 265                 270
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<223> RXN01434

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aacactgcca acacgctgcc caacctgatc actggaaatc gtg ttg ggt gcg gtg   115
                                            Val Leu Gly Ala Val
                                              1               5

ctg aca tcg ctg gtt att ccg gtc ctt acc cgc gcg gaa aaa gaa gac   163
Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp
                 10                  15                  20

gcc gac ggc ggt tcc ggg ttc ttc agg cgg ctg ctc acc ctg tcg gtg   211
Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu Leu Thr Leu Ser Val
             25                  30                  35

acg ctg ctg ggt ggt gtc acc atc ctg tcg att atc ggc gcg ccg ctg   259
Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu
         40                  45                  50

ctg aca cgg atg atg ctg tcc tct gag gga caa gtc aac gtg gtc atg   307
Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln Val Asn Val Val Met
     55                  60                  65

tcc acg gcc ttt gcg tat tgg ctg ctg cca cag att ttc ttc tac ggc   355
Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly
 70                  75                  80                  85

ctg ttt gcc ctg ttc atg gct gtg ttg aac acc cgt gaa gtg ttc aaa   403
Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr Arg Glu Val Phe Lys
                 90                  95                 100

ccc ggc gcg tgg gca cct gtt gtc aac aat gtg atc acc ttg acc gtg   451
Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val Ile Thr Leu Thr Val
            105                 110                 115

ctg ggc gtg tac atg gtg ctg cct gcg cgt ttg cac ccg cat gag cag   499
Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln
        120                 125                 130

gtg ggc att ttt gat ccg cag atc att ttc ctc ggc gtg ggc acc acc   547
Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr
    135                 140                 145

ctt ggt gtg gtt gca cag tgt cta atc atg att ccg tac ctg cgt cgc   595
Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg
150                 155                 160                 165

gcg ggc att gat atg cgc cct ctg tgg ggt atc gat gcg cgt ttg aag   643
Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile Asp Ala Arg Leu Lys
                170                 175                 180

caa ttc ggt ggc atg gcg atg gcg atc atc gtg tac gtg gca atc tcc   691
Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser
            185                 190                 195

cag ttc ggt tac atc atc acc act cgc att gcg tcg att gca gac gat   739
Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp
        200                 205                 210

gct gcg ccg ttt att tat cag cag cac tgg atg ttg ctg caa gtt cct   787
Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro
    215                 220                 225
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tat ggc atc atc ggc gtc acc ttg ctc acc gcg att atg ccg cga ctg   835
Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu
230                 235                 240                 245

tcc cgc aac gcg gca gac ggc gat gat agg gca gta gtc tct gac ctt   883
Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu
                250                 255                 260

cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg   931
Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val
            265                 270                 275

ttc ttc acc gcc ttc ggt gtc cct att gcc aat ggc ctt ttt gcc tac   979
Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr
        280                 285                 290

ggc caa ttc gat gcc aac gcc gcc aac atc ctt ggt tgg act ctg agc   1027
Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser
    295                 300                 305

ttc tct gct ttc acg ctg att cct tac gct ttg gtg ctg cta cat ctg   1075
Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu
310                 315                 320                 325

cgt gtg ttt tat gcg cgt gaa gag gtc tgg acc cca acc ttc atc atc   1123
Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr Pro Thr Phe Ile Ile
                330                 335                 340

gcc ggc atc acc gcc acc aag gtc gtg ctt tcc ctg ttg gca ccg ctg   1171
Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu
            345                 350                 355

ctg tcg agc tcc ccg gag cgt gtg gtg gtg ctt ctt ggt gcg gcc aac   1219
Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn
        360                 365                 370

ggt ttc agt ttc atc acc ggc gcg gtc atc ggc gcg tat ctg ttg cgc   1267
Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg
    375                 380                 385

aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg   1315
Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu
390                 395                 400                 405

tgg gcg ttg ggc tct gcg gcg gtt ggt gca gca gca gca tgg gcg ttg   1363
Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu
                410                 415                 420

ggg tgg ctg att caa gcc gtc gtg ggc gat ttc ttg ctg ggc act cta   1411
Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu
            425                 430                 435

agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc   1459
Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe
        440                 445                 450

atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc   1507
Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val
    455                 460                 465
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caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt   1555
Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe
470                 475                 480                 485

att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag   1603
Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu
                490                 495                 500

cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc   1651
Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr
            505                 510                 515

cct gtg ccg cca ccg atg tcc gcc ggt att gtc cgc gga cct cgc ctg   1699
Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu
        520                 525                 530

gtt ccc ggc gcc cca gtc ggc gac ggt cgt ttc cgt ctg ctc gcc gat   1747
Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp
    535                 540                 545

cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc   1795
His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala
550                 555                 560                 565

acc ggc aag gaa gtc gcg ctg atc ttt gtg gat act tcc ggc aac gcc   1843
Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala
                570                 575                 580

cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag   1891
Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu
            585                 590                 595

gtg cag cgc cgc acc aag aag ctg gcc agc ttg ggc agc ttg gcg gta   1939
Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val
        600                 605                 610

gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg   1987
Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val
    615                 620                 625

gcc gat tgg gtg cct ggc tcc agc ttg agc gcc gtc gcg gaa tcc ggt   2035
Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly
630                 635                 640                 645

gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc   2083
Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr
                650                 655                 660

atc ggc gag gcc cac gag atg ggt atc ccg gcc ggc ttg gac aac aag   2131
Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys
            665                 670                 675

tgc cga att cgt atc aac acc gac ggc cat gcc gtc ctc gcc ttg ccg   2179
Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro
        680                 685                 690

gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc   2227
Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala
    695                 700                 705

tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc   2275
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Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val
710                 715                 720                 725

aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc   2323
Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro
                730                 735                 740

gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc   2371
Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr
            745                 750                 755

gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct   2419
Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro
        760                 765                 770

gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg   2467
Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met
    775                 780                 785

gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc   2515
Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala
790                 795                 800                 805

ggt acc gcg ttc ctc acc agc ttc ttc ggc agc agc acc aac gaa caa   2563
Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln
                810                 815                 820

tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct   2611
Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro
            825                 830                 835

gtg ggg cca ccg gtc tac ctg gat ctg gat caa gcc cgc acg tgg gat   2659
Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp
        840                 845                 850

gac ggt gca gga aca gat gtc acc gac gtc acc gac ggc aac acc tcc   2707
Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser
    855                 860                 865

acc gca tgg acc tcc acc ggc ggc gac ggc ctc cta gtt gac ctg tcc   2755
Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser
870                 875                 880                 885

acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc   2803
Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser
                890                 895                 900

gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc   2851
Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala
            905                 910                 915

tca cca cac tcc ctg tcg gaa ggc atc gag atc ggc acc gtg gat tat   2899
Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr
        920                 925                 930

tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg   2947
Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro
    935                 940                 945

ggt cag gtg gaa tcc gtg gtg att ctg gtc gat gag gtt cgt tcc tca   2995
Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser
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950 955 960 965

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt 3043
Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu
970 975 980

gtt ggt tgg taaattacgc gtttgtgatt gac 3075
Val Gly Trp

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<213> Corynebacterium glutamicum

<400> 626
Val Leu Gly Ala Val Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg
1 5 10 15

Ala Glu Lys Glu Asp Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu
20 25 30

Leu Thr Leu Ser Val Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile
35 40 45

Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln
50 55 60

Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln
65 70 75 80

Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr
85 90 95

Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val
100 105 110

Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu
115 120 125

His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu
130 135 140

Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile
145 150 155 160

Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile
165 170 175

Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val
180 185 190

Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala
195 200 205

Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met
210 215 220

Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala
225 230 235 240

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Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala
                245                 250                 255

Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu
            260                 265                 270

Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn
        275                 280                 285

Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu
    290                 295                 300

Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu
305                 310                 315                 320

Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr
                325                 330                 335

Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser
            340                 345                 350

Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu
        355                 360                 365

Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly
    370                 375                 380

Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu
385                 390                 395                 400

Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala
                405                 410                 415

Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe
            420                 425                 430

Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val
        435                 440                 445

Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser
    450                 455                 460

Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro
465                 470                 475                 480

Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val
                485                 490                 495

Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser
            500                 505                 510

Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val
        515                 520                 525

Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe
    530                 535                 540

Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln
545                 550                 555                 560
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Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp
                565                 570                 575

Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala
            580                 585                 590

Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu
        595                 600                 605

Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn
    610                 615                 620

Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala
625                 630                 635                 640

Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala
                645                 650                 655

Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala
            660                 665                 670

Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala
        675                 680                 685

Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp
    690                 695                 700

Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu
705                 710                 715                 720

Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala
                725                 730                 735

Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr
            740                 745                 750

Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu
        755                 760                 765

Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr
    770                 775                 780

Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val
785                 790                 795                 800

Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser
                805                 810                 815

Ser Thr Asn Glu Gln Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser
            820                 825                 830

Ala Thr Pro Glu Pro Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln
        835                 840                 845

Ala Arg Thr Trp Asp Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr
    850                 855                 860

Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu
865                 870                 875                 880

Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr
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                885                 890                 895

Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr
            900                 905                 910

Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile
        915                 920                 925

Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp
    930                 935                 940

Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu Val Asp
945                 950                 955                 960

Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile
                965                 970                 975

Ala Glu Val Gln Leu Val Gly Trp
            980
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EP 1 505 148 A2

<210> 627
<211> 389
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<220>
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<223> FRXA01434

<400> 627

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Val Thr Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp
  1               5                  10                  15

ggc ctc cta gtt gac ctg tcc acg cct gcc cgc ctc gac cgc gtc atc   96
Gly Leu Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile
             20                  25                  30

ttg acc acc ggc acc ggc tcc gac agc aac gtg acc tcg acc gtg aag  144
Leu Thr Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys
         35                  40                  45

atc tac gca ttc aac gac gcc tca cca cac tcc ctg tcg gaa ggc atc  192
Ile Tyr Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile
     50                  55                  60

gag atc ggc acc gtg gat tat tcc ggc cgc agt ctc agc cac agc atc  240
Glu Ile Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile
 65                  70                  75                  80

cgc gat tcc tcc aag ctt ccg ggt cag gtg gaa tcc gtg gtg att ctg  288
Arg Asp Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu
                 85                  90                  95

gtc gat gag gtt cgt tcc tca caa acc tca gac acc aat cca cag atg  336
Val Asp Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met
            100                 105                 110

cag atc gct gaa gta caa ctt gtt ggt tgg taaattacgc gtttgtgatt    386
```

```
Gln Ile Ala Glu Val Gln Leu Val Gly Trp
        115                 120

gac                                                                    389


<210> 628
<211> 122
<212> PRT
<213> Corynebacterium glutamicum

<400> 628
Val Thr Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp
  1               5                  10                  15

Gly Leu Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile
             20                  25                  30

Leu Thr Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys
         35                  40                  45

Ile Tyr Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile
     50                  55                  60

Glu Ile Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile
 65                  70                  75                  80

Arg Asp Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu
                 85                  90                  95

Val Asp Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met
            100                 105                 110

Gln Ile Ala Glu Val Gln Leu Val Gly Trp
        115                 120


<210> 629
<211> 1290
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1267)
<223> RXN01448

<400> 629
gtaatctcag cagttaaaaa gggcagttcc gcatcagggg gactgccctt tttcgtgtct 60

tctcatgctc ttgtgaatat gcatagctaa tcttgaggcc atg gca aag aag aaa   115
                                              Met Ala Lys Lys Lys
                                                1               5

ctg ggg act gtc gcc aga ctg tct gaa ctg gat aag tcc ctg cgc aat   163
Leu Gly Thr Val Ala Arg Leu Ser Glu Leu Asp Lys Ser Leu Arg Asn
                10                  15                  20

aga ttg ctg cgg gtt cgt tcc cga ctg ctg ttt att gtt cat tcc gca   211
Arg Leu Leu Arg Val Arg Ser Arg Leu Leu Phe Ile Val His Ser Ala
            25                  30                  35
```

```
att ggt gcg ggt gtg gcg tat tgg atc gcc gtg gaa gtg atc aaa cac   259
Ile Gly Ala Gly Val Ala Tyr Trp Ile Ala Val Glu Val Ile Lys His
         40                  45                  50

gga caa ccg ttt ttc gca ccg atg tcc gcg gtg att att ttg ggt ctc   307
Gly Gln Pro Phe Phe Ala Pro Met Ser Ala Val Ile Ile Leu Gly Leu
     55                  60                  65

tcc gga gga gac cgc atc aaa aga gcc acg gaa ctc acc ctg ggc tgt   355
Ser Gly Gly Asp Arg Ile Lys Arg Ala Thr Glu Leu Thr Leu Gly Cys
 70                  75                  80                  85

gct tta ggc gtt ggt ttg ggt gat tta ctg atc atg caa atc ggc acg   403
Ala Leu Gly Val Gly Leu Gly Asp Leu Leu Ile Met Gln Ile Gly Thr
             90                  95                 100

ggc tat tgg cag ata ttt gtg gta gtt gga tta gcg ctg ctg gtg gcc   451
Gly Tyr Trp Gln Ile Phe Val Val Val Gly Leu Ala Leu Leu Val Ala
        105                 110                 115

tcg ttt gtt tca ccg gca ccg ttg gtg agt aat cag atg gcc att ggt   499
Ser Phe Val Ser Pro Ala Pro Leu Val Ser Asn Gln Met Ala Ile Gly
    120                 125                 130

ggc att ttg att gcc acg atg ttc ccg cca ggt gat ggt gga agc att   547
Gly Ile Leu Ile Ala Thr Met Phe Pro Pro Gly Asp Gly Gly Ser Ile
135                 140                 145

gac cgt atg atc gac gcc ttc att ggt ggt ggc gtg gga att ttg gtc   595
Asp Arg Met Ile Asp Ala Phe Ile Gly Gly Gly Val Gly Ile Leu Val
150                 155                 160                 165

atc gca ctt ctt ccc tca tct cct ctt gac gca ggc cgg cat caa gtg   643
Ile Ala Leu Leu Pro Ser Ser Pro Leu Asp Ala Gly Arg His Gln Val
            170                 175                 180

gcc aac gtt ttg ggg atc gca gct agt gtg ctg gaa gac gtg gca gct   691
Ala Asn Val Leu Gly Ile Ala Ala Ser Val Leu Glu Asp Val Ala Ala
        185                 190                 195

tcc cta aaa gcc aag gat gca gcc aaa ctc aac aat gct ttg gaa gca   739
Ser Leu Lys Ala Lys Asp Ala Ala Lys Leu Asn Asn Ala Leu Glu Ala
    200                 205                 210

ttg aga agg tcg cag gcg tcg gtg aac aag ctg gaa act gcg gca tct   787
Leu Arg Arg Ser Gln Ala Ser Val Asn Lys Leu Glu Thr Ala Ala Ser
215                 220                 225

tca ggc aag gaa gca acc acc gta tcg cca ttt tta tgg gga gat agg   835
Ser Gly Lys Glu Ala Thr Thr Val Ser Pro Phe Leu Trp Gly Asp Arg
230                 235                 240                 245

gcc cgc gtg aga tcg ctg tat cgc att ctg gcg cca gtg gac aac gtc   883
Ala Arg Val Arg Ser Leu Tyr Arg Ile Leu Ala Pro Val Asp Asn Val
            250                 255                 260

atc cga aat gct cga gtc ctt gcg cga cgg gca gtg gtg ctg acc gaa   931
Ile Arg Asn Ala Arg Val Leu Ala Arg Arg Ala Val Val Leu Thr Glu
        265                 270                 275
```

```
gac aat gac acc gtc agt gat gaa caa atc cac gtg att gag gaa atc   979
Asp Asn Asp Thr Val Ser Asp Glu Gln Ile His Val Ile Glu Glu Ile
        280                 285                 290

gca gac att gca ctg cga ctg tca gac ctt tat gag cac cac aaa gaa   1027
Ala Asp Ile Ala Leu Arg Leu Ser Asp Leu Tyr Glu His His Lys Glu
    295                 300                 305

atc agt gaa gca ctg gaa att cct gag ttg gtt aac cga ctg cgt caa   1075
Ile Ser Glu Ala Leu Glu Ile Pro Glu Leu Val Asn Arg Leu Arg Gln
310                 315                 320                 325

ctg ggc agt gaa gtg ggc gag gac atc gcc gaa gat cga gtg cta tcc   1123
Leu Gly Ser Glu Val Gly Glu Asp Ile Ala Glu Asp Arg Val Leu Ser
                330                 335                 340

gca caa gta att ttg gcg caa tcg cga tcc atc att gtg gac ctg ttg   1171
Ala Gln Val Ile Leu Ala Gln Ser Arg Ser Ile Ile Val Asp Leu Leu
            345                 350                 355

cag atc tgc ggc atg tcc agg gaa tct gcg gtg gca gtg ttg gtt ccg   1219
Gln Ile Cys Gly Met Ser Arg Glu Ser Ala Val Ala Val Leu Val Pro
        360                 365                 370

acc tca gag agt ccg gct tac cct ccg gag ctg tgg gat gac gaa gac   1267
Thr Ser Glu Ser Pro Ala Tyr Pro Pro Glu Leu Trp Asp Asp Glu Asp
    375                 380                 385

tagcctttta tcgcggttcg gtt                                        1290


<210> 630
<211> 389
<212> PRT
<213> Corynebacterium glutamicum

<400> 630
Met Ala Lys Lys Lys Leu Gly Thr Val Ala Arg Leu Ser Glu Leu Asp
  1               5                  10                  15

Lys Ser Leu Arg Asn Arg Leu Leu Arg Val Arg Ser Arg Leu Leu Phe
             20                  25                  30

Ile Val His Ser Ala Ile Gly Ala Gly Val Ala Tyr Trp Ile Ala Val
         35                  40                  45

Glu Val Ile Lys His Gly Gln Pro Phe Phe Ala Pro Met Ser Ala Val
     50                  55                  60

Ile Ile Leu Gly Leu Ser Gly Gly Asp Arg Ile Lys Arg Ala Thr Glu
 65                  70                  75                  80

Leu Thr Leu Gly Cys Ala Leu Gly Val Gly Leu Gly Asp Leu Leu Ile
                 85                  90                  95

Met Gln Ile Gly Thr Gly Tyr Trp Gln Ile Phe Val Val Val Gly Leu
            100                 105                 110

Ala Leu Leu Val Ala Ser Phe Val Ser Pro Ala Pro Leu Val Ser Asn
        115                 120                 125
```

```
Gln Met Ala Ile Gly Gly Ile Leu Ile Ala Thr Met Phe Pro Pro Gly
    130                 135                 140

Asp Gly Gly Ser Ile Asp Arg Met Ile Asp Ala Phe Ile Gly Gly Gly
145                 150                 155                 160

Val Gly Ile Leu Val Ile Ala Leu Leu Pro Ser Ser Pro Leu Asp Ala
                165                 170                 175

Gly Arg His Gln Val Ala Asn Val Leu Gly Ile Ala Ala Ser Val Leu
            180                 185                 190

Glu Asp Val Ala Ala Ser Leu Lys Ala Lys Asp Ala Ala Lys Leu Asn
        195                 200                 205

Asn Ala Leu Glu Ala Leu Arg Arg Ser Gln Ala Ser Val Asn Lys Leu
    210                 215                 220

Glu Thr Ala Ala Ser Ser Gly Lys Glu Ala Thr Thr Val Ser Pro Phe
225                 230                 235                 240

Leu Trp Gly Asp Arg Ala Arg Val Arg Ser Leu Tyr Arg Ile Leu Ala
                245                 250                 255

Pro Val Asp Asn Val Ile Arg Asn Ala Arg Val Leu Ala Arg Arg Ala
            260                 265                 270

Val Val Leu Thr Glu Asp Asn Asp Thr Val Ser Asp Glu Gln Ile His
        275                 280                 285

Val Ile Glu Glu Ile Ala Asp Ile Ala Leu Arg Leu Ser Asp Leu Tyr
    290                 295                 300

Glu His His Lys Glu Ile Ser Glu Ala Leu Glu Ile Pro Glu Leu Val
305                 310                 315                 320

Asn Arg Leu Arg Gln Leu Gly Ser Glu Val Gly Glu Asp Ile Ala Glu
                325                 330                 335

Asp Arg Val Leu Ser Ala Gln Val Ile Leu Ala Gln Ser Arg Ser Ile
            340                 345                 350

Ile Val Asp Leu Leu Gln Ile Cys Gly Met Ser Arg Glu Ser Ala Val
        355                 360                 365

Ala Val Leu Val Pro Thr Ser Glu Ser Pro Ala Tyr Pro Pro Glu Leu
    370                 375                 380

Trp Asp Asp Glu Asp
385
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<210> 631
<211> 842
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (40)..(819)
<223> FRXA01448

<400> 631
gcctcgtttg tttcaccggc accgttggtg agtaatcagatg gcc att ggt ggc att 57
Met Ala Ile Gly Gly Ile
1 5

ttg att gcc acg atg ttc ccg cca ggt gat ggt gga agc att gac cgt 105
Leu Ile Ala Thr Met Phe Pro Pro Gly Asp Gly Gly Ser Ile Asp Arg
10 15 20

atg atc gac gcc ttc att ggt ggt ggc gtg gga att ttg gtc atc gca 153
Met Ile Asp Ala Phe Ile Gly Gly Gly Val Gly Ile Leu Val Ile Ala
25 30 35

ctt ctt ccc tca tct cct ctt gac gca ggc cgg cat caa gtg gcc aac 201
Leu Leu Pro Ser Ser Pro Leu Asp Ala Gly Arg His Gln Val Ala Asn
40 45 50

gtt ttg ggg atc gca gct agt gtg ctg gaa gac gtg gca gct tcc cta 249
Val Leu Gly Ile Ala Ala Ser Val Leu Glu Asp Val Ala Ala Ser Leu
55 60 65 70

aaa gcc aag gat gca gcc aaa ctc aac aat gct ttg gaa gca ttg aga 297
Lys Ala Lys Asp Ala Ala Lys Leu Asn Asn Ala Leu Glu Ala Leu Arg
75 80 85

agg tcg cag gcg tcg gtg aac aag ctg gaa act gcg gca tct tca ggc 345
Arg Ser Gln Ala Ser Val Asn Lys Leu Glu Thr Ala Ala Ser Ser Gly
90 95 100

aag gaa gca acc acc gta tcg cca ttt tta tgg gga gat agg gcc cgc 393
Lys Glu Ala Thr Thr Val Ser Pro Phe Leu Trp Gly Asp Arg Ala Arg
105 110 115

gtg aga tcg ctg tat cgc att ctg gcg cca gtg gac aac gtc atc cga 441
Val Arg Ser Leu Tyr Arg Ile Leu Ala Pro Val Asp Asn Val Ile Arg
120 125 130

aat gct cga gtc ctt gcg cga cgg gca gtg gtg ctg acc gaa gac aat 489
Asn Ala Arg Val Leu Ala Arg Arg Ala Val Val Leu Thr Glu Asp Asn
135 140 145 150

gac acc gtc agt gat gaa caa atc cac gtg att gag gaa atc gca gac 537
Asp Thr Val Ser Asp Glu Gln Ile His Val Ile Glu Glu Ile Ala Asp
155 160 165

att gca ctg cga ctg tca gac ctt tat gag cac cac aaa gaa atc agt 585
Ile Ala Leu Arg Leu Ser Asp Leu Tyr Glu His His Lys Glu Ile Ser
170 175 180

gaa gca ctg gaa att cct gag ttg gtt aac cga ctg cgt caa ctg ggc 633
Glu Ala Leu Glu Ile Pro Glu Leu Val Asn Arg Leu Arg Gln Leu Gly
185 190 195

agt gaa gtg ggc gag gac atc gcc gaa gat cga gtg cta tcc gca caa 681
Ser Glu Val Gly Glu Asp Ile Ala Glu Asp Arg Val Leu Ser Ala Gln
200 205 210

gta att ttg gcg caa tcg cga tcc atc att gtg gac ctg ttg cag atc 729
Val Ile Leu Ala Gln Ser Arg Ser Ile Ile Val Asp Leu Leu Gln Ile
215 220 225 230

```
tgc ggc atg tcc agg gaa tct gcg gtg gca gtg ttg gtt ccg acc tca   777
Cys Gly Met Ser Arg Glu Ser Ala Val Ala Val Leu Val Pro Thr Ser
                235                 240                 245

gag agt ccg gct tac cct ccg gag ctg tgg gat gac gaa gac           819
Glu Ser Pro Ala Tyr Pro Pro Glu Leu Trp Asp Asp Glu Asp
            250                 255                 260

tagcctttta tcgcggttcg gtt                                        842


<210> 632
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

<400> 632
Met Ala Ile Gly Gly Ile Leu Ile Ala Thr Met Phe Pro Pro Gly Asp
  1               5                  10                  15

Gly Gly Ser Ile Asp Arg Met Ile Asp Ala Phe Ile Gly Gly Gly Val
             20                  25                  30

Gly Ile Leu Val Ile Ala Leu Leu Pro Ser Ser Pro Leu Asp Ala Gly
         35                  40                  45

Arg His Gln Val Ala Asn Val Leu Gly Ile Ala Ala Ser Val Leu Glu
     50                  55                  60

Asp Val Ala Ala Ser Leu Lys Ala Lys Asp Ala Ala Lys Leu Asn Asn
 65                  70                  75                  80

Ala Leu Glu Ala Leu Arg Arg Ser Gln Ala Ser Val Asn Lys Leu Glu
                 85                  90                  95

Thr Ala Ala Ser Ser Gly Lys Glu Ala Thr Thr Val Ser Pro Phe Leu
            100                 105                 110

Trp Gly Asp Arg Ala Arg Val Arg Ser Leu Tyr Arg Ile Leu Ala Pro
        115                 120                 125

Val Asp Asn Val Ile Arg Asn Ala Arg Val Leu Ala Arg Arg Ala Val
    130                 135                 140

Val Leu Thr Glu Asp Asn Asp Thr Val Ser Asp Glu Gln Ile His Val
145                 150                 155                 160

Ile Glu Glu Ile Ala Asp Ile Ala Leu Arg Leu Ser Asp Leu Tyr Glu
                165                 170                 175

His His Lys Glu Ile Ser Glu Ala Leu Glu Ile Pro Glu Leu Val Asn
            180                 185                 190

Arg Leu Arg Gln Leu Gly Ser Glu Val Gly Glu Asp Ile Ala Glu Asp
        195                 200                 205

Arg Val Leu Ser Ala Gln Val Ile Leu Ala Gln Ser Arg Ser Ile Ile
    210                 215                 220

Val Asp Leu Leu Gln Ile Cys Gly Met Ser Arg Glu Ser Ala Val Ala
```

```
225                 230                 235                 240

Val Leu Val Pro Thr Ser Glu Ser Pro Ala Tyr Pro Pro Glu Leu Trp
                245                 250                 255

Asp Asp Glu Asp
            260


<210> 633
<211> 933
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(910)
<223> RXN01459

<400> 633
gattcggcga ttcacgaata tccaccctac aacctgtgtt cgcttacagc gttgttcgga 60

tcgtagcaat aggaaatagt tgccttgtag attggtaaat atg aac tct aat ggc   115
                                        Met Asn Ser Asn Gly
                                          1               5

ttt ggt ttc tct ttt ggc aac aac gat gac gac gat gac aaa aac cgc   163
Phe Gly Phe Ser Phe Gly Asn Asn Asp Asp Asp Asp Asp Lys Asn Arg
                10                  15                  20

aac aac gac cca ttc ggc ctt ttc ggt ggc aac ttc gga ttc gga gga   211
Asn Asn Asp Pro Phe Gly Leu Phe Gly Gly Asn Phe Gly Phe Gly Gly
            25                  30                  35

caa ggt ggc gct ggt ggc ccc ggc gga tta ggc gat att tta aac cag   259
Gln Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly Asp Ile Leu Asn Gln
        40                  45                  50

ttc ggc cag atg ctg tcc gga atg gga gat tcg atg aac tcc ccc gaa   307
Phe Gly Gln Met Leu Ser Gly Met Gly Asp Ser Met Asn Ser Pro Glu
    55                  60                  65

gca gca ggc ccg gtt aat tat gat tta gca gca cgc atc gcc cgc cag   355
Ala Ala Gly Pro Val Asn Tyr Asp Leu Ala Ala Arg Ile Ala Arg Gln
70                  75                  80                  85

cag att ggt cgc gta gcg ccg gtg aag gat tct gag aag gaa gca gtc   403
Gln Ile Gly Arg Val Ala Pro Val Lys Asp Ser Glu Lys Glu Ala Val
                90                  95                  100

gaa gag tcc ctt cgc ctt gct gaa ctc tgg ctc gat aac gcc acc cag   451
Glu Glu Ser Leu Arg Leu Ala Glu Leu Trp Leu Asp Asn Ala Thr Gln
            105                 110                 115

ctc ccc act tcc ggg cac cgc gtc gaa gcg tgg aat cca gaa aac tgg   499
Leu Pro Thr Ser Gly His Arg Val Glu Ala Trp Asn Pro Glu Asn Trp
        120                 125                 130

tta gaa aac acc ctg cct gtg tgg aag cgt ctt gtc tcc cct gtt gcg   547
Leu Glu Asn Thr Leu Pro Val Trp Lys Arg Leu Val Ser Pro Val Ala
    135                 140                 145
```

```
gag caa atg aac aaa gcc caa tta gaa aac ctc cct gaa gaa gcc cgc   595
Glu Gln Met Asn Lys Ala Gln Leu Glu Asn Leu Pro Glu Glu Ala Arg
150                 155                 160                 165

gag atg atg ggc ccg atg tct tct ttg atg aac tcc atg tct tcg atg   643
Glu Met Met Gly Pro Met Ser Ser Leu Met Asn Ser Met Ser Ser Met
                170                 175                 180

aac ttc gga gtt caa tta gga aat gcg ctg ggc gac ctc gca aag cag   691
Asn Phe Gly Val Gln Leu Gly Asn Ala Leu Gly Asp Leu Ala Lys Gln
            185                 190                 195

acc ctc acc ggc tct gac ttc ggt ttg cct atc tcc cca gtc ggc gta   739
Thr Leu Thr Gly Ser Asp Phe Gly Leu Pro Ile Ser Pro Val Gly Val
        200                 205                 210

tct gcc gtc ctg ccc ggc aac atc gcc gaa gca tcc aaa ggc ctc aac   787
Ser Ala Val Leu Pro Gly Asn Ile Ala Glu Ala Ser Lys Gly Leu Asn
    215                 220                 225

gtg gca ccg caa gaa atg ctc gtt tac atc tgt gcc cgc gaa gcc gcc   835
Val Ala Pro Gln Glu Met Leu Val Tyr Ile Cys Ala Arg Glu Ala Ala
230                 235                 240                 245

gcc aac gcc tct tca agc acg tgc cgt ggc ttg tcg agc gcc tcg ttt   883
Ala Asn Ala Ser Ser Ser Thr Cys Arg Gly Leu Ser Ser Ala Ser Phe
                250                 255                 260

cct ccg ttg agg aat acg ccg tcg gcc tagaaatcga cacctcacac         930
Pro Pro Leu Arg Asn Thr Pro Ser Ala
            265                 270

att                                                               933


<210> 634
<211> 270
<212> PRT
<213> Corynebacterium glutamicum

<400> 634
Met Asn Ser Asn Gly Phe Gly Phe Ser Phe Gly Asn Asn Asp Asp Asp
  1               5                  10                  15

Asp Asp Lys Asn Arg Asn Asn Asp Pro Phe Gly Leu Phe Gly Gly Asn
             20                  25                  30

Phe Gly Phe Gly Gly Gln Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly
         35                  40                  45

Asp Ile Leu Asn Gln Phe Gly Gln Met Leu Ser Gly Met Gly Asp Ser
     50                  55                  60

Met Asn Ser Pro Glu Ala Ala Gly Pro Val Asn Tyr Asp Leu Ala Ala
 65                  70                  75                  80

Arg Ile Ala Arg Gln Gln Ile Gly Arg Val Ala Pro Val Lys Asp Ser
                 85                  90                  95

Glu Lys Glu Ala Val Glu Glu Ser Leu Arg Leu Ala Glu Leu Trp Leu
```

```
            100                 105                 110

Asp Asn Ala Thr Gln Leu Pro Thr Ser Gly His Arg Val Glu Ala Trp
        115                 120                 125

Asn Pro Glu Asn Trp Leu Glu Asn Thr Leu Pro Val Trp Lys Arg Leu
    130                 135                 140

Val Ser Pro Val Ala Glu Gln Met Asn Lys Ala Gln Leu Glu Asn Leu
145                 150                 155                 160

Pro Glu Glu Ala Arg Glu Met Met Gly Pro Met Ser Ser Leu Met Asn
                165                 170                 175

Ser Met Ser Ser Met Asn Phe Gly Val Gln Leu Gly Asn Ala Leu Gly
            180                 185                 190

Asp Leu Ala Lys Gln Thr Leu Thr Gly Ser Asp Phe Gly Leu Pro Ile
        195                 200                 205

Ser Pro Val Gly Val Ser Ala Val Leu Pro Gly Asn Ile Ala Glu Ala
    210                 215                 220

Ser Lys Gly Leu Asn Val Ala Pro Gln Glu Met Leu Val Tyr Ile Cys
225                 230                 235                 240

Ala Arg Glu Ala Ala Ala Asn Ala Ser Ser Ser Thr Cys Arg Gly Leu
                245                 250                 255

Ser Ser Ala Ser Phe Pro Pro Leu Arg Asn Thr Pro Ser Ala
            260                 265                 270


<210> 635
<211> 933
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(910)
<223> FRXA01459

<400> 635
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tcgtagcaat aggaaatagt tgccttgtag attggtaaat atg aac tct aat ggc   115
                                        Met Asn Ser Asn Gly
                                          1               5

ttt ggt ttc tct ttt ggc aac aac gat gac gac gat gac aaa aac cgc   163
Phe Gly Phe Ser Phe Gly Asn Asn Asp Asp Asp Asp Asp Lys Asn Arg
                  10                  15                  20

aac aac gac cca ttc ggc ctt ttc ggt ggc aac ttc gga ttc gga gga   211
Asn Asn Asp Pro Phe Gly Leu Phe Gly Gly Asn Phe Gly Phe Gly Gly
              25                  30                  35

caa ggt ggc gct ggt ggc ccc ggc gga tta ggc gat att tta aac cag   259
Gln Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly Asp Ile Leu Asn Gln
          40                  45                  50
```

```
ttc ggc cag atg ctg tcc gga atg gga gat tcg atg aac tcc ccc gaa   307
Phe Gly Gln Met Leu Ser Gly Met Gly Asp Ser Met Asn Ser Pro Glu
     55                  60                  65

gca gca ggc ccg gtt aat tat gat tta gca gca cgc atc gcc cgc cag   355
Ala Ala Gly Pro Val Asn Tyr Asp Leu Ala Ala Arg Ile Ala Arg Gln
 70                  75                  80                  85

cag att ggt cgc gta gcg ccg gtg aag gat tct gag aag gaa gca gtc   403
Gln Ile Gly Arg Val Ala Pro Val Lys Asp Ser Glu Lys Glu Ala Val
                 90                  95                 100

gaa gag tcc ctt cgc ctt gct gaa ctc tgg ctc gat aac gcc acc cag   451
Glu Glu Ser Leu Arg Leu Ala Glu Leu Trp Leu Asp Asn Ala Thr Gln
            105                 110                 115

ctc ccc act tcc ggg cac cgc gtc gaa gcg tgg aat cca gaa aac tgg   499
Leu Pro Thr Ser Gly His Arg Val Glu Ala Trp Asn Pro Glu Asn Trp
        120                 125                 130

tta gaa aac acc ctg cct gtg tgg aag cgt ctt gtc tcc cct gtt gcg   547
Leu Glu Asn Thr Leu Pro Val Trp Lys Arg Leu Val Ser Pro Val Ala
    135                 140                 145

gag caa atg aac aaa gcc caa tta gaa aac ctc cct gaa gaa gcc cgc   595
Glu Gln Met Asn Lys Ala Gln Leu Glu Asn Leu Pro Glu Glu Ala Arg
150                 155                 160                 165

gag atg atg ggc ccg atg tct tct ttg atg aac tcc atg tct tcg atg   643
Glu Met Met Gly Pro Met Ser Ser Leu Met Asn Ser Met Ser Ser Met
                170                 175                 180

aac ttc gga gtt caa tta gga aat gcg ctg ggc gac ctc gca aag cag   691
Asn Phe Gly Val Gln Leu Gly Asn Ala Leu Gly Asp Leu Ala Lys Gln
            185                 190                 195

acc ctc acc ggc tct gac ttc ggt ttg cct atc tcc cca gtc ggc gta   739
Thr Leu Thr Gly Ser Asp Phe Gly Leu Pro Ile Ser Pro Val Gly Val
        200                 205                 210

tct gcc gtc ctg ccc ggc aac atc gcc gaa gca tcc aaa ggc ctc aac   787
Ser Ala Val Leu Pro Gly Asn Ile Ala Glu Ala Ser Lys Gly Leu Asn
    215                 220                 225

gtg gca ccg caa gaa atg ctc gtt tac atc tgt gcc cgc gaa gcc gcc   835
Val Ala Pro Gln Glu Met Leu Val Tyr Ile Cys Ala Arg Glu Ala Ala
230                 235                 240                 245

gcc aac gcc tct tca agc acg tgc cgt ggc ttg tcg agc gcc tcg ttt   883
Ala Asn Ala Ser Ser Ser Thr Cys Arg Gly Leu Ser Ser Ala Ser Phe
                250                 255                 260

cct ccg ttg agg aat acg ccg tcg gcc tagaaatcga cacctcacac         930
Pro Pro Leu Arg Asn Thr Pro Ser Ala
            265                 270

att                                                               933
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<210> 636

<211> 270
<212> PRT
<213> Corynebacterium glutamicum

<400> 636

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Met Asn Ser Asn Gly Phe Gly Phe Ser Phe Gly Asn Asn Asp Asp Asp
  1               5                  10                  15

Asp Asp Lys Asn Arg Asn Asn Asp Pro Phe Gly Leu Phe Gly Gly Asn
             20                  25                  30

Phe Gly Phe Gly Gly Gln Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly
         35                  40                  45

Asp Ile Leu Asn Gln Phe Gly Gln Met Leu Ser Gly Met Gly Asp Ser
     50                  55                  60

Met Asn Ser Pro Glu Ala Ala Gly Pro Val Asn Tyr Asp Leu Ala Ala
 65                  70                  75                  80

Arg Ile Ala Arg Gln Gln Ile Gly Arg Val Ala Pro Val Lys Asp Ser
                 85                  90                  95

Glu Lys Glu Ala Val Glu Glu Ser Leu Arg Leu Ala Glu Leu Trp Leu
            100                 105                 110

Asp Asn Ala Thr Gln Leu Pro Thr Ser Gly His Arg Val Glu Ala Trp
        115                 120                 125

Asn Pro Glu Asn Trp Leu Glu Asn Thr Leu Pro Val Trp Lys Arg Leu
    130                 135                 140

Val Ser Pro Val Ala Glu Gln Met Asn Lys Ala Gln Leu Glu Asn Leu
145                 150                 155                 160

Pro Glu Glu Ala Arg Glu Met Met Gly Pro Met Ser Ser Leu Met Asn
                165                 170                 175

Ser Met Ser Ser Met Asn Phe Gly Val Gln Leu Gly Asn Ala Leu Gly
            180                 185                 190

Asp Leu Ala Lys Gln Thr Leu Thr Gly Ser Asp Phe Gly Leu Pro Ile
        195                 200                 205

Ser Pro Val Gly Val Ser Ala Val Leu Pro Gly Asn Ile Ala Glu Ala
    210                 215                 220

Ser Lys Gly Leu Asn Val Ala Pro Gln Glu Met Leu Val Tyr Ile Cys
225                 230                 235                 240

Ala Arg Glu Ala Ala Ala Asn Ala Ser Ser Ser Thr Cys Arg Gly Leu
                245                 250                 255

Ser Ser Ala Ser Phe Pro Pro Leu Arg Asn Thr Pro Ser Ala
            260                 265                 270
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<210> 637
<211> 417
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(394)
<223> RXN01460

<400> 637
gcaacatcgc cgaagcatcc aaaggcctca acgtggcacc gcaagaaatg ctcgtttaca 60

tctgtgcccg cgaagccgcc gccaacgcct cttcaagcac gtg ccg tgg ctt gtc 115
Val Pro Trp Leu Val
1 5

gag cgc ctc gtt tcc tcc gtt gag gaa tac gcc gtc ggc cta gaa atc 163
Glu Arg Leu Val Ser Ser Val Glu Glu Tyr Ala Val Gly Leu Glu Ile
10 15 20

gac acc tca cac att caa gag gcc atg ggc aac ttc caa atg gac aac 211
Asp Thr Ser His Ile Gln Glu Ala Met Gly Asn Phe Gln Met Asp Asn
25 30 35

cca gat cct gaa cgc ctc cag gaa atg atg aac gaa ctc caa ggt atg 259
Pro Asp Pro Glu Arg Leu Gln Glu Met Met Asn Glu Leu Gln Gly Met
40 45 50

gac ctg tcc cca cgc atc gga tcc cgc aac gcc aac gca gta tcc cgc 307
Asp Leu Ser Pro Arg Ile Gly Ser Arg Asn Ala Asn Ala Val Ser Arg
55 60 65

ctg gaa act ctc ctc gca ctc gtc gaa ggc tgg gtc gac atc gta gtt 355
Leu Glu Thr Leu Leu Ala Leu Val Glu Gly Trp Val Asp Ile Val Val
70 75 80 85

acc caa gcc ctg agc gaa cgc att cca tca ccg acg cca tgaacgaagc 404
Thr Gln Ala Leu Ser Glu Arg Ile Pro Ser Pro Thr Pro
90 95

ctggaagcgc cgc 417

<210> 638
<211> 98
<212> PRT
<213> Corynebacterium glutamicum

<400> 638
Val Pro Trp Leu Val Glu Arg Leu Val Ser Ser Val Glu Glu Tyr Ala
1 5 10 15

Val Gly Leu Glu Ile Asp Thr Ser His Ile Gln Glu Ala Met Gly Asn
20 25 30

Phe Gln Met Asp Asn Pro Asp Pro Glu Arg Leu Gln Glu Met Met Asn
35 40 45

Glu Leu Gln Gly Met Asp Leu Ser Pro Arg Ile Gly Ser Arg Asn Ala
50 55 60

Asn Ala Val Ser Arg Leu Glu Thr Leu Leu Ala Leu Val Glu Gly Trp
65 70 75 80

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Val Asp Ile Val Val Thr Gln Ala Leu Ser Glu Arg Ile Pro Ser Pro
                 85                  90                  95

Thr Pro



<210> 639
<211> 417
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(394)
<223> FRXA01460

<400> 639
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tctgtgcccg cgaagccgcc gccaacgcct cttcaagcac gtg ccg tgg ctt gtc   115
                                            Val Pro Trp Leu Val
                                              1               5

gag cgc ctc gtt tcc tcc gtt gag gaa tac gcc gtc ggc cta gaa atc   163
Glu Arg Leu Val Ser Ser Val Glu Glu Tyr Ala Val Gly Leu Glu Ile
                10                  15                  20

gac acc tca cac att caa gag gcc atg ggc aac ttc caa atg gac aac   211
Asp Thr Ser His Ile Gln Glu Ala Met Gly Asn Phe Gln Met Asp Asn
            25                  30                  35

cca gat cct gaa cgc ctc cag gaa atg atg aac gaa ctc caa ggt atg   259
Pro Asp Pro Glu Arg Leu Gln Glu Met Met Asn Glu Leu Gln Gly Met
        40                  45                  50

gac ctg tcc cca cgc atc gga tcc cgc aac gcc aac gca gta tcc cgc   307
Asp Leu Ser Pro Arg Ile Gly Ser Arg Asn Ala Asn Ala Val Ser Arg
    55                  60                  65

ctg gaa act ctc ctc gca ctc gtc gaa ggc tgg gtc gac atc gta gtt   355
Leu Glu Thr Leu Leu Ala Leu Val Glu Gly Trp Val Asp Ile Val Val
70                  75                  80                  85

acc caa gcc ctg agc gaa cgc att cca tca ccg acg cca tgaacgaagc    404
Thr Gln Ala Leu Ser Glu Arg Ile Pro Ser Pro Thr Pro
                90                  95

ctggaagcgc cgc                                                   417


<210> 640
<211> 98
<212> PRT
<213> Corynebacterium glutamicum

<400> 640
Val Pro Trp Leu Val Glu Arg Leu Val Ser Ser Val Glu Glu Tyr Ala
  1               5                  10                  15

Val Gly Leu Glu Ile Asp Thr Ser His Ile Gln Glu Ala Met Gly Asn
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            20                  25                  30

Phe Gln Met Asp Asn Pro Asp Pro Glu Arg Leu Gln Glu Met Met Asn
         35                  40                  45

Glu Leu Gln Gly Met Asp Leu Ser Pro Arg Ile Gly Ser Arg Asn Ala
     50                  55                  60

Asn Ala Val Ser Arg Leu Glu Thr Leu Leu Ala Leu Val Glu Gly Trp
 65                  70                  75                  80

Val Asp Ile Val Val Thr Gln Ala Leu Ser Glu Arg Ile Pro Ser Pro
                 85                  90                  95

Thr Pro
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<210> 641
<211> 930
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(907)
<223> RXN01471

<400> 641

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cctccaacca gagctataaa aaaggttgta gaagaaattt cttaacatac atcgttgtgt 60

tgccaggggt ttaacagatt agttgctaag gtctgtctcc atg cag agt ttt aag   115
                                           Met Gln Ser Phe Lys
                                             1               5

acg ctt gaa tct tgg cct gtc gac aat gtt tcg gcc agt gtc atc tcc   163
Thr Leu Glu Ser Trp Pro Val Asp Asn Val Ser Ala Ser Val Ile Ser
                 10                  15                  20

gac ggc gcc gtg cac ttt tac ggc gac gtc gat cgt gtt ttt gaa ctc   211
Asp Gly Ala Val His Phe Tyr Gly Asp Val Asp Arg Val Phe Glu Leu
             25                  30                  35

atg agt gtg aca aaa ctc ctg gcc acc tac ggt ttc ctt gtt gcc atc   259
Met Ser Val Thr Lys Leu Leu Ala Thr Tyr Gly Phe Leu Val Ala Ile
         40                  45                  50

gaa gaa ggt gtt ttt gag ctc gat tca ccg atg ggt cct gaa gga tcc   307
Glu Glu Gly Val Phe Glu Leu Asp Ser Pro Met Gly Pro Glu Gly Ser
     55                  60                  65

aca gtg agg cat ctg ctc tca cat gct tcc ggc gtg gca ttc gat aag   355
Thr Val Arg His Leu Leu Ser His Ala Ser Gly Val Ala Phe Asp Lys
 70                  75                  80                  85

ccg gta gcg gaa aag gga gtg ggg gag cgc cgc att tac tcc tct gct   403
Pro Val Ala Glu Lys Gly Val Gly Glu Arg Arg Ile Tyr Ser Ser Ala
                 90                  95                 100

ggc atg gac atc ttg gcg gat gct gtt gcc gct gaa gct gaa atg ccg   451
Gly Met Asp Ile Leu Ala Asp Ala Val Ala Ala Glu Ala Glu Met Pro
```

```
            105                 110                 115

ttt gca gag tat ctc cgc gag gct gtg ttc gag cct ttg gga atg gag   499
Phe Ala Glu Tyr Leu Arg Glu Ala Val Phe Glu Pro Leu Gly Met Glu
        120                 125                 130

aac tct gaa cta tgg ggt tct gcg ggc cac gag gcg cgc agc aca gtg   547
Asn Ser Glu Leu Trp Gly Ser Ala Gly His Glu Ala Arg Ser Thr Val
    135                 140                 145

gct gat ctg acc aag ttc ggc caa gag ctc acc gca cca act ctg atc   595
Ala Asp Leu Thr Lys Phe Gly Gln Glu Leu Thr Ala Pro Thr Leu Ile
150                 155                 160                 165

tca cca gaa acc ctt gca gag gct ttc cag gtg caa ttc ccg gaa ctg   643
Ser Pro Glu Thr Leu Ala Glu Ala Phe Gln Val Gln Phe Pro Glu Leu
                170                 175                 180

att ggc acc gtc ccc ggt tat ggc atg cag aag ccg tgt ccg tgg gga   691
Ile Gly Thr Val Pro Gly Tyr Gly Met Gln Lys Pro Cys Pro Trp Gly
            185                 190                 195

ttg ggc ttt gaa att aag gga cag aag tcg ccg cac tgg aca ggt gac   739
Leu Gly Phe Glu Ile Lys Gly Gln Lys Ser Pro His Trp Thr Gly Asp
        200                 205                 210

ttg atg ccg gag aac act gct gga cac ttt gga cag tcg gga aca ttc   787
Leu Met Pro Glu Asn Thr Ala Gly His Phe Gly Gln Ser Gly Thr Phe
    215                 220                 225

ttt tgg act gtt cca ggc tca ggt caa gtc ggg gtt gtt ttg act gac   835
Phe Trp Thr Val Pro Gly Ser Gly Gln Val Gly Val Val Leu Thr Asp
230                 235                 240                 245

cga aat ttc ggt cct tgg gct aaa ccg ttg tgg act gcc ttc aat gac   883
Arg Asn Phe Gly Pro Trp Ala Lys Pro Leu Trp Thr Ala Phe Asn Asp
                250                 255                 260

gaa gtc tgg gcc gag tta aat tca taaacttttg ccgtaattac ggt         930
Glu Val Trp Ala Glu Leu Asn Ser
            265
```

<210> 642
<211> 269
<212> PRT
<213> Corynebacterium glutamicum

<400> 642

```
Met Gln Ser Phe Lys Thr Leu Glu Ser Trp Pro Val Asp Asn Val Ser
  1               5                  10                  15

Ala Ser Val Ile Ser Asp Gly Ala Val His Phe Tyr Gly Asp Val Asp
             20                  25                  30

Arg Val Phe Glu Leu Met Ser Val Thr Lys Leu Leu Ala Thr Tyr Gly
         35                  40                  45

Phe Leu Val Ala Ile Glu Glu Gly Val Phe Glu Leu Asp Ser Pro Met
     50                  55                  60
```

```
Gly Pro Glu Gly Ser Thr Val Arg His Leu Leu Ser His Ala Ser Gly
 65                  70                  75                  80

Val Ala Phe Asp Lys Pro Val Ala Glu Lys Gly Val Gly Glu Arg Arg
                 85                  90                  95

Ile Tyr Ser Ser Ala Gly Met Asp Ile Leu Ala Asp Ala Val Ala Ala
            100                 105                 110

Glu Ala Glu Met Pro Phe Ala Glu Tyr Leu Arg Glu Ala Val Phe Glu
        115                 120                 125

Pro Leu Gly Met Glu Asn Ser Glu Leu Trp Gly Ser Ala Gly His Glu
    130                 135                 140

Ala Arg Ser Thr Val Ala Asp Leu Thr Lys Phe Gly Gln Glu Leu Thr
145                 150                 155                 160

Ala Pro Thr Leu Ile Ser Pro Glu Thr Leu Ala Glu Ala Phe Gln Val
                165                 170                 175

Gln Phe Pro Glu Leu Ile Gly Thr Val Pro Gly Tyr Gly Met Gln Lys
            180                 185                 190

Pro Cys Pro Trp Gly Leu Gly Phe Glu Ile Lys Gly Gln Lys Ser Pro
        195                 200                 205

His Trp Thr Gly Asp Leu Met Pro Glu Asn Thr Ala Gly His Phe Gly
    210                 215                 220

Gln Ser Gly Thr Phe Phe Trp Thr Val Pro Gly Ser Gly Gln Val Gly
225                 230                 235                 240

Val Val Leu Thr Asp Arg Asn Phe Gly Pro Trp Ala Lys Pro Leu Trp
                245                 250                 255

Thr Ala Phe Asn Asp Glu Val Trp Ala Glu Leu Asn Ser
            260                 265
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<210> 643
<211> 930
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(907)
<223> FRXA01471

<400> 643
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tgccaggggt ttaacagatt agttgctaag gtctgtctcc atg cag agt ttt aag 115
                                            Met Gln Ser Phe Lys
                                              1   5

acg ctt gaa tct tgg cct gtc gac aat gtt tcg gcc agt gtc atc tcc 163
Thr Leu Glu Ser Trp Pro Val Asp Asn Val Ser Ala Ser Val Ile Ser
                 10   15   20

```
gac ggc gcc gtg cac ttt tac ggc gac gtc gat cgt gtt ttt gaa ctc   211
Asp Gly Ala Val His Phe Tyr Gly Asp Val Asp Arg Val Phe Glu Leu
            25                  30                  35

atg agt gtg aca aaa ctc ctg gcc acc tac ggt ttc ctt gtt gcc atc   259
Met Ser Val Thr Lys Leu Leu Ala Thr Tyr Gly Phe Leu Val Ala Ile
        40                  45                  50

gaa gaa ggt gtt ttt gag ctc gat tca ccg atg ggt cct gaa gga tcc   307
Glu Glu Gly Val Phe Glu Leu Asp Ser Pro Met Gly Pro Glu Gly Ser
    55                  60                  65

aca gtg agg cat ctg ctc tca cat gct tcc ggc gtg gca ttc gat aag   355
Thr Val Arg His Leu Leu Ser His Ala Ser Gly Val Ala Phe Asp Lys
70                  75                  80                  85

ccg gta gcg gaa aag gga gtg ggg gag cgc cgc att tac tcc tct gct   403
Pro Val Ala Glu Lys Gly Val Gly Glu Arg Arg Ile Tyr Ser Ser Ala
                90                  95                  100

ggc atg gac atc ttg gcg gat gct gtt gcc gct gaa gct gaa atg ccg   451
Gly Met Asp Ile Leu Ala Asp Ala Val Ala Ala Glu Ala Glu Met Pro
            105                 110                 115

ttt gca gag tat ctc cgc gag gct gtg ttc gag cct ttg gga atg gag   499
Phe Ala Glu Tyr Leu Arg Glu Ala Val Phe Glu Pro Leu Gly Met Glu
        120                 125                 130

aac tct gaa cta tgg ggt tct gcg ggc cac gag gcg cgc agc aca gtg   547
Asn Ser Glu Leu Trp Gly Ser Ala Gly His Glu Ala Arg Ser Thr Val
    135                 140                 145

gct gat ctg acc aag ttc ggc caa gag ctc acc gca cca act ctg atc   595
Ala Asp Leu Thr Lys Phe Gly Gln Glu Leu Thr Ala Pro Thr Leu Ile
150                 155                 160                 165

tca cca gaa acc ctt gca gag gct ttc cag gtg caa ttc ccg gaa ctg   643
Ser Pro Glu Thr Leu Ala Glu Ala Phe Gln Val Gln Phe Pro Glu Leu
                170                 175                 180

att ggc acc gtc ccc ggt tat ggc atg cag aag ccg tgt ccg tgg gga   691
Ile Gly Thr Val Pro Gly Tyr Gly Met Gln Lys Pro Cys Pro Trp Gly
            185                 190                 195

ttg ggc ttt gaa att aag gga cag aag tcg ccg cac tgg aca ggt gac   739
Leu Gly Phe Glu Ile Lys Gly Gln Lys Ser Pro His Trp Thr Gly Asp
        200                 205                 210

ttg atg ccg gag aac act gct gga cac ttt gga cag tcg gga aca ttc   787
Leu Met Pro Glu Asn Thr Ala Gly His Phe Gly Gln Ser Gly Thr Phe
    215                 220                 225

ttt tgg act gtt cca ggc tca ggt caa gtc ggg gtt gtt ttg act gac   835
Phe Trp Thr Val Pro Gly Ser Gly Gln Val Gly Val Val Leu Thr Asp
230                 235                 240                 245

cga aat ttc ggt cct tgg gct aaa ccg ttg tgg act gcc ttc aat gac   883
Arg Asn Phe Gly Pro Trp Ala Lys Pro Leu Trp Thr Ala Phe Asn Asp
                250                 255                 260

gaa gtc tgg gcc gag tta aat tca taaacttttg ccgtaattac ggt         930
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Glu Val Trp Ala Glu Leu Asn Ser
            265


<210> 644
<211> 269
<212> PRT
<213> Corynebacterium glutamicum

<400> 644
Met Gln Ser Phe Lys Thr Leu Glu Ser Trp Pro Val Asp Asn Val Ser
  1               5                  10                  15

Ala Ser Val Ile Ser Asp Gly Ala Val His Phe Tyr Gly Asp Val Asp
             20                  25                  30

Arg Val Phe Glu Leu Met Ser Val Thr Lys Leu Leu Ala Thr Tyr Gly
         35                  40                  45

Phe Leu Val Ala Ile Glu Glu Gly Val Phe Glu Leu Asp Ser Pro Met
     50                  55                  60

Gly Pro Glu Gly Ser Thr Val Arg His Leu Leu Ser His Ala Ser Gly
 65                  70                  75                  80

Val Ala Phe Asp Lys Pro Val Ala Glu Lys Gly Val Gly Glu Arg Arg
                 85                  90                  95

Ile Tyr Ser Ser Ala Gly Met Asp Ile Leu Ala Asp Ala Val Ala Ala
            100                 105                 110

Glu Ala Glu Met Pro Phe Ala Glu Tyr Leu Arg Glu Ala Val Phe Glu
        115                 120                 125

Pro Leu Gly Met Glu Asn Ser Glu Leu Trp Gly Ser Ala Gly His Glu
    130                 135                 140

Ala Arg Ser Thr Val Ala Asp Leu Thr Lys Phe Gly Gln Glu Leu Thr
145                 150                 155                 160

Ala Pro Thr Leu Ile Ser Pro Glu Thr Leu Ala Glu Ala Phe Gln Val
                165                 170                 175

Gln Phe Pro Glu Leu Ile Gly Thr Val Pro Gly Tyr Gly Met Gln Lys
            180                 185                 190

Pro Cys Pro Trp Gly Leu Gly Phe Glu Ile Lys Gly Gln Lys Ser Pro
        195                 200                 205

His Trp Thr Gly Asp Leu Met Pro Glu Asn Thr Ala Gly His Phe Gly
    210                 215                 220

Gln Ser Gly Thr Phe Phe Trp Thr Val Pro Gly Ser Gly Gln Val Gly
225                 230                 235                 240

Val Val Leu Thr Asp Arg Asn Phe Gly Pro Trp Ala Lys Pro Leu Trp
                245                 250                 255

Thr Ala Phe Asn Asp Glu Val Trp Ala Glu Leu Asn Ser
            260                 265
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<210> 645
<211> 363
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(340)
<223> RXN01479

<400> 645
agcgctgccc gtgccataaa tttcgaagaa gcgcgaaaca ggtagagtct aaggtgtcat 60

tcttggtaca agttttatat ttagggagag ttatccacac atg atc cag tta gtg 115
Met Ile Gln Leu Val
1 5

ata ggc gct gca gca ggc tac gtg ctt ggc aca aag gcc ggc cgc aag 163
Ile Gly Ala Ala Ala Gly Tyr Val Leu Gly Thr Lys Ala Gly Arg Lys
10 15 20

cgt tac cac cag atc aaa aag gga tat gag gca gcg att aac tcc cct 211
Arg Tyr His Gln Ile Lys Lys Gly Tyr Glu Ala Ala Ile Asn Ser Pro
25 30 35

gcc acc aaa tct gca gta aac gcc gcc cgc aaa gcc att gcc aac aag 259
Ala Thr Lys Ser Ala Val Asn Ala Ala Arg Lys Ala Ile Ala Asn Lys
40 45 50

ctg gat ccg cag ccc cgc atg aag gaa gta aaa aac ctg cgg act gcg 307
Leu Asp Pro Gln Pro Arg Met Lys Glu Val Lys Asn Leu Arg Thr Ala
55 60 65

gac ggg cat gaa gtc ctc gag caa gac cag gac taaattaccc tctaaacgcc 360
Asp Gly His Glu Val Leu Glu Gln Asp Gln Asp
70 75 80

cgg 363

<210> 646
<211> 80
<212> PRT
<213> Corynebacterium glutamicum

<400> 646
Met Ile Gln Leu Val Ile Gly Ala Ala Ala Gly Tyr Val Leu Gly Thr
1 5 10 15

Lys Ala Gly Arg Lys Arg Tyr His Gln Ile Lys Lys Gly Tyr Glu Ala
20 25 30

Ala Ile Asn Ser Pro Ala Thr Lys Ser Ala Val Asn Ala Ala Arg Lys
35 40 45

Ala Ile Ala Asn Lys Leu Asp Pro Gln Pro Arg Met Lys Glu Val Lys
50 55 60

Asn Leu Arg Thr Ala Asp Gly His Glu Val Leu Glu Gln Asp Gln Asp
65 70 75 80

<210> 647
<211> 351
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(328)
<223> FRXA01479

<400> 647
gccataaatt tcgaagaagc gcgaaacagg tagagtctaa ggtgtcattc ttggtacaag 60

ttttatattt agggagagtt atccacacat gatccagtta gtg ata ggc gct gca 115
Val Ile Gly Ala Ala
1 5

gca ggc tac gtg ctt ggc aca aag gcc ggc cgc aag cgt tac cac cag 163
Ala Gly Tyr Val Leu Gly Thr Lys Ala Gly Arg Lys Arg Tyr His Gln
10 15 20

atc aaa aag gga tat gag gca gcg att aac tcc cct gcc acc aaa tct 211
Ile Lys Lys Gly Tyr Glu Ala Ala Ile Asn Ser Pro Ala Thr Lys Ser
25 30 35

gca gta aac gcc gcc cgc aaa gcc att gcc aac aag ctg gat ccg cag 259
Ala Val Asn Ala Ala Arg Lys Ala Ile Ala Asn Lys Leu Asp Pro Gln
40 45 50

ccc cgc atg aag gaa gta aaa aac ctg cgg act gcg gac ggg cat gaa 307
Pro Arg Met Lys Glu Val Lys Asn Leu Arg Thr Ala Asp Gly His Glu
55 60 65

gtc ctc gag caa gac cag gac taaattaccc tctaaacgcc cgg 351
Val Leu Glu Gln Asp Gln Asp
70 75

<210> 648
<211> 76
<212> PRT
<213> Corynebacterium glutamicum

<400> 648
Val Ile Gly Ala Ala Ala Gly Tyr Val Leu Gly Thr Lys Ala Gly Arg
1 5 10 15

Lys Arg Tyr His Gln Ile Lys Lys Gly Tyr Glu Ala Ala Ile Asn Ser
20 25 30

Pro Ala Thr Lys Ser Ala Val Asn Ala Ala Arg Lys Ala Ile Ala Asn
35 40 45

Lys Leu Asp Pro Gln Pro Arg Met Lys Glu Val Lys Asn Leu Arg Thr
50 55 60

```
Ala Asp Gly His Glu Val Leu Glu Gln Asp Gln Asp
 65                  70                  75


<210> 649
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(646)
<223> RXN01484

<400> 649
gagtttactc ttaaccgcag tagtgcagcc agccctgagg gtggtggcgt attcgatgct 60

cagaacgcct aataatcggc acaaaattga ttcaattttg gtg ttg ggc aca gct   115
                                            Val Leu Gly Thr Ala
                                              1               5

caa tat gat gga gtt cca tcg agg cag ttt gct gct cgt ttg agg cat   163
Gln Tyr Asp Gly Val Pro Ser Arg Gln Phe Ala Ala Arg Leu Arg His
                 10                  15                  20

gcc gcg aag ctg tgg cgt ctt cat gaa atc cag cat gta tat act gtc   211
Ala Ala Lys Leu Trp Arg Leu His Glu Ile Gln His Val Tyr Thr Val
             25                  30                  35

ggc gga aaa ctt cct ggc gat cgt ttc acc gaa gca gaa gtc gcg cgg   259
Gly Gly Lys Leu Pro Gly Asp Arg Phe Thr Glu Ala Glu Val Ala Arg
         40                  45                  50

gag tat ttg atc aaa gag ggc gtg gat ccg gat ctg att ttt gtc tct   307
Glu Tyr Leu Ile Lys Glu Gly Val Asp Pro Asp Leu Ile Phe Val Ser
     55                  60                  65

gca gtt ggc aat gac act gtc tcc tcc tat gag gcg ctt gat ccg gaa   355
Ala Val Gly Asn Asp Thr Val Ser Ser Tyr Glu Ala Leu Asp Pro Glu
 70                  75                  80                  85

aag ctt ggt cgg gtg ctg att gtt act gat ccg aac cat tcg tat cgg   403
Lys Leu Gly Arg Val Leu Ile Val Thr Asp Pro Asn His Ser Tyr Arg
                 90                  95                 100

gcg gtg cgc atc gcg cga cgc atg ggc ttt gac gcg aaa cct tcc ccg   451
Ala Val Arg Ile Ala Arg Arg Met Gly Phe Asp Ala Lys Pro Ser Pro
            105                 110                 115

aca acc tat agt ccc gcg aag ttt ccg tcg ata gtt tat ttt ctg acc   499
Thr Thr Tyr Ser Pro Ala Lys Phe Pro Ser Ile Val Tyr Phe Leu Thr
        120                 125                 130

ttg tcc cat gag tgg ggc ggg gta gta gta cag gac gtg tcg cgg ctc   547
Leu Ser His Glu Trp Gly Gly Val Val Val Gln Asp Val Ser Arg Leu
    135                 140                 145

ttg ggt gaa cgg gtg ccc gat aag gtg aag cat ctt tgc gcg caa tcc   595
Leu Gly Glu Arg Val Pro Asp Lys Val Lys His Leu Cys Ala Gln Ser
150                 155                 160                 165
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```
aag gtc tgc tgc gcc ctt cgc ggc gtg cac gcc atg agc aac ttc gga   643
Lys Val Cys Cys Ala Leu Arg Gly Val His Ala Met Ser Asn Phe Gly
                170                 175                 180

ggc tgaaaaagta gatgtacccc tat                                     669
Gly
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<210> 650
<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 650

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Val Leu Gly Thr Ala Gln Tyr Asp Gly Val Pro Ser Arg Gln Phe Ala
  1               5                  10                  15

Ala Arg Leu Arg His Ala Ala Lys Leu Trp Arg Leu His Glu Ile Gln
             20                  25                  30

His Val Tyr Thr Val Gly Gly Lys Leu Pro Gly Asp Arg Phe Thr Glu
         35                  40                  45

Ala Glu Val Ala Arg Glu Tyr Leu Ile Lys Glu Gly Val Asp Pro Asp
     50                  55                  60

Leu Ile Phe Val Ser Ala Val Gly Asn Asp Thr Val Ser Ser Tyr Glu
 65                  70                  75                  80

Ala Leu Asp Pro Glu Lys Leu Gly Arg Val Leu Ile Val Thr Asp Pro
                 85                  90                  95

Asn His Ser Tyr Arg Ala Val Arg Ile Ala Arg Arg Met Gly Phe Asp
            100                 105                 110

Ala Lys Pro Ser Pro Thr Thr Tyr Ser Pro Ala Lys Phe Pro Ser Ile
        115                 120                 125

Val Tyr Phe Leu Thr Leu Ser His Glu Trp Gly Gly Val Val Val Gln
    130                 135                 140

Asp Val Ser Arg Leu Leu Gly Glu Arg Val Pro Asp Lys Val Lys His
145                 150                 155                 160

Leu Cys Ala Gln Ser Lys Val Cys Cys Ala Leu Arg Gly Val His Ala
                165                 170                 175

Met Ser Asn Phe Gly Gly
            180
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<210> 651
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
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<223> FRXA01484

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cagaacgcct aataatcggc acaaaattga ttcaattttg gtg ttg ggc aca gct 115
Val Leu Gly Thr Ala
1 5

caa tat gat gga gtt cca tcg agg cag ttt gct gct cgt ttg agg cat 163
Gln Tyr Asp Gly Val Pro Ser Arg Gln Phe Ala Ala Arg Leu Arg His
10 15 20

gcc gcg aag ctg tgg cgt ctt cat gaa atc cag cat gta tat act gtc 211
Ala Ala Lys Leu Trp Arg Leu His Glu Ile Gln His Val Tyr Thr Val
25 30 35

ggc gga aaa ctt cct ggc gat cgt ttc acc gaa gca gaa gtc gcg cgg 259
Gly Gly Lys Leu Pro Gly Asp Arg Phe Thr Glu Ala Glu Val Ala Arg
40 45 50

gag tat ttg atc aaa gag ggc gtg gat ccg gat ctg att ttt gtc tct 307
Glu Tyr Leu Ile Lys Glu Gly Val Asp Pro Asp Leu Ile Phe Val Ser
55 60 65

gca gtt ggc aat gac act gtc tcc tcc tat gag gcg ctt gat ccg gaa 355
Ala Val Gly Asn Asp Thr Val Ser Ser Tyr Glu Ala Leu Asp Pro Glu
70 75 80 85

aag ctt ggt cgg gtg ctg att gtt act gat ccg aac cat tcg tat cgg 403
Lys Leu Gly Arg Val Leu Ile Val Thr Asp Pro Asn His Ser Tyr Arg
90 95 100

gcg gtg cgc atc gcg cga cgc atg ggc ttt gac gcg aaa cct tcc ccg 451
Ala Val Arg Ile Ala Arg Arg Met Gly Phe Asp Ala Lys Pro Ser Pro
105 110 115

aca acc tat agt ccc gcg aag ttt ccg tcg ata gtt tat ttt ctg acc 499
Thr Thr Tyr Ser Pro Ala Lys Phe Pro Ser Ile Val Tyr Phe Leu Thr
120 125 130

ttg tcc cat gag tgg ggc ggg gta gta gta cag gac gtg tcg cgg ctc 547
Leu Ser His Glu Trp Gly Gly Val Val Val Gln Asp Val Ser Arg Leu
135 140 145

ttg ggt gaa cgg gtg ccc gat aag gtg aag cat ctt tgc gcg caa tcc 595
Leu Gly Glu Arg Val Pro Asp Lys Val Lys His Leu Cys Ala Gln Ser
150 155 160 165

aag gtc tgc tgc gcc ctt cgc ggc gtg cac gcc atg agc aac ttc gga 643
Lys Val Cys Cys Ala Leu Arg Gly Val His Ala Met Ser Asn Phe Gly
170 175 180

ggc tgaaaaagta gatgtacccc tat 669
Gly

<210> 652
<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 652
Val Leu Gly Thr Ala Gln Tyr Asp Gly Val Pro Ser Arg Gln Phe Ala
1 5 10 15

Ala Arg Leu Arg His Ala Ala Lys Leu Trp Arg Leu His Glu Ile Gln
20 25 30

His Val Tyr Thr Val Gly Gly Lys Leu Pro Gly Asp Arg Phe Thr Glu
35 40 45

Ala Glu Val Ala Arg Glu Tyr Leu Ile Lys Glu Gly Val Asp Pro Asp
50 55 60

Leu Ile Phe Val Ser Ala Val Gly Asn Asp Thr Val Ser Ser Tyr Glu
65 70 75 80

Ala Leu Asp Pro Glu Lys Leu Gly Arg Val Leu Ile Val Thr Asp Pro
85 90 95

Asn His Ser Tyr Arg Ala Val Arg Ile Ala Arg Arg Met Gly Phe Asp
100 105 110

Ala Lys Pro Ser Pro Thr Thr Tyr Ser Pro Ala Lys Phe Pro Ser Ile
115 120 125

Val Tyr Phe Leu Thr Leu Ser His Glu Trp Gly Gly Val Val Val Gln
130 135 140

Asp Val Ser Arg Leu Leu Gly Glu Arg Val Pro Asp Lys Val Lys His
145 150 155 160

Leu Cys Ala Gln Ser Lys Val Cys Cys Ala Leu Arg Gly Val His Ala
165 170 175

Met Ser Asn Phe Gly Gly
180

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<211> 2175
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<213> Corynebacterium glutamicum

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<222> (101)..(2152)
<223> RXN01485

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ttaactagtg tgccagctgg actcgtctaa ggtggggacc atg aac ttt agt ttg 115
Met Asn Phe Ser Leu
1 5

gtg cat ctt cgg gaa aac gtc cgc cgt gta tcg gtc act gtg gca att 163
Val His Leu Arg Glu Asn Val Arg Arg Val Ser Val Thr Val Ala Ile
10 15 20

gga gct ggc gcg ctc ctt atc agt gga cca ttt ttt act gct cac act 211

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Gly Ala Gly Ala Leu Leu Ile Ser Gly Pro Phe Phe Thr Ala His Thr
            25                  30                  35

gca gaa gcc aca gaa aca tat gtc ttg gct gaa tca cca gaa ttt tac   259
Ala Glu Ala Thr Glu Thr Tyr Val Leu Ala Glu Ser Pro Glu Phe Tyr
        40                  45                  50

caa gac aat gtc act gac tac acc ggc cag att tcc tcg tcc gat atc   307
Gln Asp Asn Val Thr Asp Tyr Thr Gly Gln Ile Ser Ser Ser Asp Ile
    55                  60                  65

acc aac att cag gct gcc atc gat gat gta aag gca tct gaa caa aag   355
Thr Asn Ile Gln Ala Ala Ile Asp Asp Val Lys Ala Ser Glu Gln Lys
70                  75                  80                  85

gtt att ttc gtt gtt ttc cta agc tct ttc gac gga gtt gac cct gaa   403
Val Ile Phe Val Val Phe Leu Ser Ser Phe Asp Gly Val Asp Pro Glu
                90                  95                  100

acg tgg acg cag caa gca ctc caa gcc aac ggc ggc gga aac gtc ttg   451
Thr Trp Thr Gln Gln Ala Leu Gln Ala Asn Gly Gly Gly Asn Val Leu
            105                 110                 115

att tat gca ctc gct ccc gag gaa cgg cag tac ggc atc caa ggt ggt   499
Ile Tyr Ala Leu Ala Pro Glu Glu Arg Gln Tyr Gly Ile Gln Gly Gly
        120                 125                 130

act caa tgg acc gac gct gaa ctc gac gcc gcc aac aac gct gct ttc   547
Thr Gln Trp Thr Asp Ala Glu Leu Asp Ala Ala Asn Asn Ala Ala Phe
    135                 140                 145

cag gca ctt tcc caa gaa gat tgg gca ggc tct gca cta gcg ctg gca   595
Gln Ala Leu Ser Gln Glu Asp Trp Ala Gly Ser Ala Leu Ala Leu Ala
150                 155                 160                 165

gaa tca gtt ggt tct agt tct tcc agc tct tcg ggc tcg tcc agc tct   643
Glu Ser Val Gly Ser Ser Ser Ser Ser Ser Ser Gly Ser Ser Ser Ser
                170                 175                 180

tcc gat ttt tcc ggc gct tgg ttg gct gct gcg ggc gtt ggc aca gtg   691
Ser Asp Phe Ser Gly Ala Trp Leu Ala Ala Ala Gly Val Gly Thr Val
            185                 190                 195

gcc gct ggt ggc gga att tgg gcc tat tcc cgc agc cgc aag aag aaa   739
Ala Ala Gly Gly Gly Ile Trp Ala Tyr Ser Arg Ser Arg Lys Lys Lys
        200                 205                 210

aca agt gct gca acc ttg gaa gat gca cgc gaa atc gac ccg cgc gat   787
Thr Ser Ala Ala Thr Leu Glu Asp Ala Arg Glu Ile Asp Pro Arg Asp
    215                 220                 225

acc aac cgc ctc atg cag ctt ccc atg gaa act ctc gaa cac ctt gcc   835
Thr Asn Arg Leu Met Gln Leu Pro Met Glu Thr Leu Glu His Leu Ala
230                 235                 240                 245

caa gaa gag ctc acc tcc act gat gac tcc atc cgt cgc gga aaa gaa   883
Gln Glu Glu Leu Thr Ser Thr Asp Asp Ser Ile Arg Arg Gly Lys Glu
                250                 255                 260

gag ctc gct atc gct acc tcc gag ttc gga cca gag cgc acc cgc agc   931
Glu Leu Ala Ile Ala Thr Ser Glu Phe Gly Pro Glu Arg Thr Arg Ser
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            265                 270                 275

ttc aac cgc gcc atg aac cac tcc acc ggc acc ctg caa aaa gcc ttt   979
Phe Asn Arg Ala Met Asn His Ser Thr Gly Thr Leu Gln Lys Ala Phe
        280                 285                 290

gag att cag cag cgc ctc aac gat tct atc cca gaa tcc gaa gcc gaa   1027
Glu Ile Gln Gln Arg Leu Asn Asp Ser Ile Pro Glu Ser Glu Ala Glu
    295                 300                 305

cgt caa tcc atg ctg gta gaa atc att tca tcc tgt ggc caa gcc gac   1075
Arg Gln Ser Met Leu Val Glu Ile Ile Ser Ser Cys Gly Gln Ala Asp
310                 315                 320                 325

gat gcc ctc gac gcc gaa gcc caa aac ttt gcc gat atg cgc aac ctg   1123
Asp Ala Leu Asp Ala Glu Ala Gln Asn Phe Ala Asp Met Arg Asn Leu
                330                 335                 340

ctg atc aac gcg ggc agc aaa ttg gat gct ctc acc caa aaa tcc gtc   1171
Leu Ile Asn Ala Gly Ser Lys Leu Asp Ala Leu Thr Gln Lys Ser Val
            345                 350                 355

gac ctg cgc acc cgc ctc ccc aag gcc caa gaa aca ctc gct ggc ctg   1219
Asp Leu Arg Thr Arg Leu Pro Lys Ala Gln Glu Thr Leu Ala Gly Leu
        360                 365                 370

cgc act cgc tac tca gca gag gtc ctt gaa agc atc gac gac aac gtc   1267
Arg Thr Arg Tyr Ser Ala Glu Val Leu Glu Ser Ile Asp Asp Asn Val
    375                 380                 385

gac ctc gcc agc gct tcg ctc gac gaa gca gaa gaa gtc ctg cca cag   1315
Asp Leu Ala Ser Ala Ser Leu Asp Glu Ala Glu Glu Val Leu Pro Gln
390                 395                 400                 405

gcg tac gag ata gag tcc atg ccc gca ggc gag cag ggc ggg ctt atc   1363
Ala Tyr Glu Ile Glu Ser Met Pro Ala Gly Glu Gln Gly Gly Leu Ile
                410                 415                 420

gac gcg atc cgt cac atc gag cac gcc atc act acc gca gac aaa ctc   1411
Asp Ala Ile Arg His Ile Glu His Ala Ile Thr Thr Ala Asp Lys Leu
            425                 430                 435

ctc gcg ggc gtc gag cat gcc gat gaa aac atc tcc aca gcc aaa gca   1459
Leu Ala Gly Val Glu His Ala Asp Glu Asn Ile Ser Thr Ala Lys Ala
        440                 445                 450

aac gtt gcc gat ctg atc caa gaa atc tca gac gaa atc aac gaa gcc   1507
Asn Val Ala Asp Leu Ile Gln Glu Ile Ser Asp Glu Ile Asn Glu Ala
    455                 460                 465

ggc caa ctc aaa caa agc gca gga gcc gac ggt gcc cgt gcc gac tgg   1555
Gly Gln Leu Lys Gln Ser Ala Gly Ala Asp Gly Ala Arg Ala Asp Trp
470                 475                 480                 485

gcc tcc ctc gac gat gct gtc cgc gca gcc agc gca gca cta atc acc   1603
Ala Ser Leu Asp Asp Ala Val Arg Ala Ala Ser Ala Ala Leu Ile Thr
                490                 495                 500

gca tca gca gac gcc gaa aag gat ccg ctc gga acc tac aca gaa ctt   1651
Ala Ser Ala Asp Ala Glu Lys Asp Pro Leu Gly Thr Tyr Thr Glu Leu
            505                 510                 515
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gtc gat gtc gac tcc gcc ctc gac act caa ctt gac aca ctt cgc gcc   1699
Val Asp Val Asp Ser Ala Leu Asp Thr Gln Leu Asp Thr Leu Arg Ala
        520                 525                 530

acc gca gct gat caa gcc cgc cag cta cgc gta ttc gac caa cag ctg   1747
Thr Ala Ala Asp Gln Ala Arg Gln Leu Arg Val Phe Asp Gln Gln Leu
    535                 540                 545

caa tct gca aga agc caa atc caa aag gcc gaa gac ctc atc tcc acc   1795
Gln Ser Ala Arg Ser Gln Ile Gln Lys Ala Glu Asp Leu Ile Ser Thr
550                 555                 560                 565

cgc ggt cgc atc gta aaa tcc gaa gcc cgc acc cac ctg gcc aac gca   1843
Arg Gly Arg Ile Val Lys Ser Glu Ala Arg Thr His Leu Ala Asn Ala
                570                 575                 580

caa aag ctg tac gcc atg gca caa caa aac cgc acc cgc gac acc cgt   1891
Gln Lys Leu Tyr Ala Met Ala Gln Gln Asn Arg Thr Arg Asp Thr Arg
            585                 590                 595

gca gga att gat tac gga cgt caa gca gca gtc gca gcc caa cgc gcc   1939
Ala Gly Ile Asp Tyr Gly Arg Gln Ala Ala Val Ala Ala Gln Arg Ala
        600                 605                 610

agc aag tca gca caa aac gac atc acc acc tac aac aat cgc cac aat   1987
Ser Lys Ser Ala Gln Asn Asp Ile Thr Thr Tyr Asn Asn Arg His Asn
    615                 620                 625

tcc ggt ggc gga acc acc ggt gcg att gtc acc ggc atg gtg atc aac   2035
Ser Gly Gly Gly Thr Thr Gly Ala Ile Val Thr Gly Met Val Ile Asn
630                 635                 640                 645

tcg att ctc aac agc ggc cgc ggt ggc ggt ttc tgt gga ggc gga ggc   2083
Ser Ile Leu Asn Ser Gly Arg Gly Gly Gly Phe Cys Gly Gly Gly Gly
                650                 655                 660

ttt ggt gga ggc ggt ggc ggc ttc agc ggt ggt ggc ggt ggc gga gga   2131
Phe Gly Gly Gly Gly Gly Gly Phe Ser Gly Gly Gly Gly Gly Gly Gly
            665                 670                 675

ggg ttc cgc gga ggc cgc ttc tagcctgaaa cgagcaaaac caa             2175
Gly Phe Arg Gly Gly Arg Phe
        680
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<213> Corynebacterium glutamicum

<400> 654

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Met Asn Phe Ser Leu Val His Leu Arg Glu Asn Val Arg Arg Val Ser
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Val Thr Val Ala Ile Gly Ala Gly Ala Leu Leu Ile Ser Gly Pro Phe
             20                  25                  30

Phe Thr Ala His Thr Ala Glu Ala Thr Glu Thr Tyr Val Leu Ala Glu
         35                  40                  45
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Ser Pro Glu Phe Tyr Gln Asp Asn Val Thr Asp Tyr Thr Gly Gln Ile
     50                  55                  60

Ser Ser Ser Asp Ile Thr Asn Ile Gln Ala Ala Ile Asp Asp Val Lys
 65                  70                  75                  80

Ala Ser Glu Gln Lys Val Ile Phe Val Val Phe Leu Ser Ser Phe Asp
                 85                  90                  95

Gly Val Asp Pro Glu Thr Trp Thr Gln Gln Ala Leu Gln Ala Asn Gly
            100                 105                 110

Gly Gly Asn Val Leu Ile Tyr Ala Leu Ala Pro Glu Glu Arg Gln Tyr
        115                 120                 125

Gly Ile Gln Gly Gly Thr Gln Trp Thr Asp Ala Glu Leu Asp Ala Ala
    130                 135                 140

Asn Asn Ala Ala Phe Gln Ala Leu Ser Gln Glu Asp Trp Ala Gly Ser
145                 150                 155                 160

Ala Leu Ala Leu Ala Glu Ser Val Gly Ser Ser Ser Ser Ser Ser Ser
                165                 170                 175

Gly Ser Ser Ser Ser Ser Asp Phe Ser Gly Ala Trp Leu Ala Ala Ala
            180                 185                 190

Gly Val Gly Thr Val Ala Ala Gly Gly Gly Ile Trp Ala Tyr Ser Arg
        195                 200                 205

Ser Arg Lys Lys Lys Thr Ser Ala Ala Thr Leu Glu Asp Ala Arg Glu
    210                 215                 220

Ile Asp Pro Arg Asp Thr Asn Arg Leu Met Gln Leu Pro Met Glu Thr
225                 230                 235                 240

Leu Glu His Leu Ala Gln Glu Glu Leu Thr Ser Thr Asp Asp Ser Ile
                245                 250                 255

Arg Arg Gly Lys Glu Glu Leu Ala Ile Ala Thr Ser Glu Phe Gly Pro
            260                 265                 270

Glu Arg Thr Arg Ser Phe Asn Arg Ala Met Asn His Ser Thr Gly Thr
        275                 280                 285

Leu Gln Lys Ala Phe Glu Ile Gln Gln Arg Leu Asn Asp Ser Ile Pro
    290                 295                 300

Glu Ser Glu Ala Glu Arg Gln Ser Met Leu Val Glu Ile Ile Ser Ser
305                 310                 315                 320

Cys Gly Gln Ala Asp Asp Ala Leu Asp Ala Glu Ala Gln Asn Phe Ala
                325                 330                 335

Asp Met Arg Asn Leu Leu Ile Asn Ala Gly Ser Lys Leu Asp Ala Leu
            340                 345                 350

Thr Gln Lys Ser Val Asp Leu Arg Thr Arg Leu Pro Lys Ala Gln Glu
        355                 360                 365

Thr Leu Ala Gly Leu Arg Thr Arg Tyr Ser Ala Glu Val Leu Glu Ser
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370 375 380

Ile Asp Asp Asn Val Asp Leu Ala Ser Ala Ser Leu Asp Glu Ala Glu
385 390 395 400

Glu Val Leu Pro Gln Ala Tyr Glu Ile Glu Ser Met Pro Ala Gly Glu
405 410 415

Gln Gly Gly Leu Ile Asp Ala Ile Arg His Ile Glu His Ala Ile Thr
420 425 430

Thr Ala Asp Lys Leu Leu Ala Gly Val Glu His Ala Asp Glu Asn Ile
435 440 445

Ser Thr Ala Lys Ala Asn Val Ala Asp Leu Ile Gln Glu Ile Ser Asp
450 455 460

Glu Ile Asn Glu Ala Gly Gln Leu Lys Gln Ser Ala Gly Ala Asp Gly
465 470 475 480

Ala Arg Ala Asp Trp Ala Ser Leu Asp Asp Ala Val Arg Ala Ala Ser
485 490 495

Ala Ala Leu Ile Thr Ala Ser Ala Asp Ala Glu Lys Asp Pro Leu Gly
500 505 510

Thr Tyr Thr Glu Leu Val Asp Val Asp Ser Ala Leu Asp Thr Gln Leu
515 520 525

Asp Thr Leu Arg Ala Thr Ala Ala Asp Gln Ala Arg Gln Leu Arg Val
530 535 540

Phe Asp Gln Gln Leu Gln Ser Ala Arg Ser Gln Ile Gln Lys Ala Glu
545 550 555 560

Asp Leu Ile Ser Thr Arg Gly Arg Ile Val Lys Ser Glu Ala Arg Thr
565 570 575

His Leu Ala Asn Ala Gln Lys Leu Tyr Ala Met Ala Gln Gln Asn Arg
580 585 590

Thr Arg Asp Thr Arg Ala Gly Ile Asp Tyr Gly Arg Gln Ala Ala Val
595 600 605

Ala Ala Gln Arg Ala Ser Lys Ser Ala Gln Asn Asp Ile Thr Thr Tyr
610 615 620

Asn Asn Arg His Asn Ser Gly Gly Gly Thr Thr Gly Ala Ile Val Thr
625 630 635 640

Gly Met Val Ile Asn Ser Ile Leu Asn Ser Gly Arg Gly Gly Gly Phe
645 650 655

Cys Gly Gly Gly Gly Phe Gly Gly Gly Gly Gly Gly Phe Ser Gly Gly
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Gly Gly Gly Gly Gly Gly Phe Arg Gly Gly Arg Phe
675 680

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<211> 2175
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(2152)
<223> FRXA01485

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ttaactagtg tgccagctgg actcgtctaa ggtggggacc atg aac ttt agt ttg 115
Met Asn Phe Ser Leu
1 5

gtg cat ctt cgg gaa aac gtc cgc cgt gta tcg gtc act gtg gca att 163
Val His Leu Arg Glu Asn Val Arg Arg Val Ser Val Thr Val Ala Ile
10 15 20

gga gct ggc gcg ctc ctt atc agt gga cca ttt ttt act gct cac act 211
Gly Ala Gly Ala Leu Leu Ile Ser Gly Pro Phe Phe Thr Ala His Thr
25 30 35

gca gaa gcc aca gaa aca tat gtc ttg gct gaa tca cca gaa ttt tac 259
Ala Glu Ala Thr Glu Thr Tyr Val Leu Ala Glu Ser Pro Glu Phe Tyr
40 45 50

caa gac aat gtc act gac tac acc ggc cag att tcc tcg tcc gat atc 307
Gln Asp Asn Val Thr Asp Tyr Thr Gly Gln Ile Ser Ser Ser Asp Ile
55 60 65

acc aac att cag gct gcc atc gat gat gta aag gca tct gaa caa aag 355
Thr Asn Ile Gln Ala Ala Ile Asp Asp Val Lys Ala Ser Glu Gln Lys
70 75 80 85

gtt att ttc gtt gtt ttc cta agc tct ttc gac gga gtt gac cct gaa 403
Val Ile Phe Val Val Phe Leu Ser Ser Phe Asp Gly Val Asp Pro Glu
90 95 100

acg tgg acg cag caa gca ctc caa gcc aac ggc ggc gga aac gtc ttg 451
Thr Trp Thr Gln Gln Ala Leu Gln Ala Asn Gly Gly Gly Asn Val Leu
105 110 115

att tat gca ctc gct ccc gag gaa cgg cag tac ggc atc caa ggt ggt 499
Ile Tyr Ala Leu Ala Pro Glu Glu Arg Gln Tyr Gly Ile Gln Gly Gly
120 125 130

act caa tgg acc gac gct gaa ctc gac gcc gcc aac aac gct gct ttc 547
Thr Gln Trp Thr Asp Ala Glu Leu Asp Ala Ala Asn Asn Ala Ala Phe
135 140 145

cag gca ctt tcc caa gaa gat tgg gca ggc tct gca cta gcg ctg gca 595
Gln Ala Leu Ser Gln Glu Asp Trp Ala Gly Ser Ala Leu Ala Leu Ala
150 155 160 165

gaa tca gtt ggt tct agt tct tcc agc tct tcg ggc tcg tcc agc tct 643
Glu Ser Val Gly Ser Ser Ser Ser Ser Ser Ser Gly Ser Ser Ser Ser
170 175 180

tcc gat ttt tcc ggc gct tgg ttg gct gct gcg ggc gtt ggc aca gtg 691

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Ser Asp Phe Ser Gly Ala Trp Leu Ala Ala Ala Gly Val Gly Thr Val
            185                 190                 195

gcc gct ggt ggc gga att tgg gcc tat tcc cgc agc cgc aag aag aaa   739
Ala Ala Gly Gly Gly Ile Trp Ala Tyr Ser Arg Ser Arg Lys Lys Lys
        200                 205                 210

aca agt gct gca acc ttg gaa gat gca cgc gaa atc gac ccg cgc gat   787
Thr Ser Ala Ala Thr Leu Glu Asp Ala Arg Glu Ile Asp Pro Arg Asp
    215                 220                 225

acc aac cgc ctc atg cag ctt ccc atg gaa act ctc gaa cac ctt gcc   835
Thr Asn Arg Leu Met Gln Leu Pro Met Glu Thr Leu Glu His Leu Ala
230                 235                 240                 245

caa gaa gag ctc acc tcc act gat gac tcc atc cgt cgc gga aaa gaa   883
Gln Glu Glu Leu Thr Ser Thr Asp Asp Ser Ile Arg Arg Gly Lys Glu
                250                 255                 260

gag ctc gct atc gct acc tcc gag ttc gga cca gag cgc acc cgc agc   931
Glu Leu Ala Ile Ala Thr Ser Glu Phe Gly Pro Glu Arg Thr Arg Ser
            265                 270                 275

ttc aac cgc gcc atg aac cac tcc acc ggc acc ctg caa aaa gcc ttt   979
Phe Asn Arg Ala Met Asn His Ser Thr Gly Thr Leu Gln Lys Ala Phe
        280                 285                 290

gag att cag cag cgc ctc aac gat tct atc cca gaa tcc gaa gcc gaa   1027
Glu Ile Gln Gln Arg Leu Asn Asp Ser Ile Pro Glu Ser Glu Ala Glu
    295                 300                 305

cgt caa tcc atg ctg gta gaa atc att tca tcc tgt ggc caa gcc gac   1075
Arg Gln Ser Met Leu Val Glu Ile Ile Ser Ser Cys Gly Gln Ala Asp
310                 315                 320                 325

gat gcc ctc gac gcc gaa gcc caa aac ttt gcc gat atg cgc aac ctg   1123
Asp Ala Leu Asp Ala Glu Ala Gln Asn Phe Ala Asp Met Arg Asn Leu
                330                 335                 340

ctg atc aac gcg ggc agc aaa ttg gat gct ctc acc caa aaa tcc gtc   1171
Leu Ile Asn Ala Gly Ser Lys Leu Asp Ala Leu Thr Gln Lys Ser Val
            345                 350                 355

gac ctg cgc acc cgc ctc ccc aag gcc caa gaa aca ctc gct ggc ctg   1219
Asp Leu Arg Thr Arg Leu Pro Lys Ala Gln Glu Thr Leu Ala Gly Leu
        360                 365                 370

cgc act cgc tac tca gca gag gtc ctt gaa agc atc gac gac aac gtc   1267
Arg Thr Arg Tyr Ser Ala Glu Val Leu Glu Ser Ile Asp Asp Asn Val
    375                 380                 385

gac ctc gcc agc gct tcg ctc gac gaa gca gaa gaa gtc ctg cca cag   1315
Asp Leu Ala Ser Ala Ser Leu Asp Glu Ala Glu Glu Val Leu Pro Gln
390                 395                 400                 405

gcg tac gag ata gag tcc atg ccc gca ggc gag cag ggc ggg ctt atc   1363
Ala Tyr Glu Ile Glu Ser Met Pro Ala Gly Glu Gln Gly Gly Leu Ile
                410                 415                 420

gac gcg atc cgt cac atc gag cac gcc atc act acc gca gac aaa ctc   1411
Asp Ala Ile Arg His Ile Glu His Ala Ile Thr Thr Ala Asp Lys Leu
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                425                 430                 435

ctc gcg ggc gtc gag cat gcc gat gaa aac atc tcc aca gcc aaa gca   1459
Leu Ala Gly Val Glu His Ala Asp Glu Asn Ile Ser Thr Ala Lys Ala
        440                 445                 450

aac gtt gcc gat ctg atc caa gaa atc tca gac gaa atc aac gaa gcc   1507
Asn Val Ala Asp Leu Ile Gln Glu Ile Ser Asp Glu Ile Asn Glu Ala
    455                 460                 465

ggc caa ctc aaa caa agc gca gga gcc gac ggt gcc cgt gcc gac tgg   1555
Gly Gln Leu Lys Gln Ser Ala Gly Ala Asp Gly Ala Arg Ala Asp Trp
470                 475                 480                 485

gcc tcc ctc gac gat gct gtc cgc gca gcc agc gca gca cta atc acc   1603
Ala Ser Leu Asp Asp Ala Val Arg Ala Ala Ser Ala Ala Leu Ile Thr
                490                 495                 500

gca tca gca gac gcc gaa aag gat ccg ctc gga acc tac aca gaa ctt   1651
Ala Ser Ala Asp Ala Glu Lys Asp Pro Leu Gly Thr Tyr Thr Glu Leu
            505                 510                 515

gtc gat gtc gac tcc gcc ctc gac act caa ctt gac aca ctt cgc gcc   1699
Val Asp Val Asp Ser Ala Leu Asp Thr Gln Leu Asp Thr Leu Arg Ala
        520                 525                 530

acc gca gct gat caa gcc cgc cag cta cgc gta ttc gac caa cag ctg   1747
Thr Ala Ala Asp Gln Ala Arg Gln Leu Arg Val Phe Asp Gln Gln Leu
    535                 540                 545

caa tct gca aga agc caa atc caa aag gcc gaa gac ctc atc tcc acc   1795
Gln Ser Ala Arg Ser Gln Ile Gln Lys Ala Glu Asp Leu Ile Ser Thr
550                 555                 560                 565

cgc ggt cgc atc gta aaa tcc gaa gcc cgc acc cac ctg gcc aac gca   1843
Arg Gly Arg Ile Val Lys Ser Glu Ala Arg Thr His Leu Ala Asn Ala
                570                 575                 580

caa aag ctg tac gcc atg gca caa caa aac cgc acc cgc gac acc cgt   1891
Gln Lys Leu Tyr Ala Met Ala Gln Gln Asn Arg Thr Arg Asp Thr Arg
            585                 590                 595

gca gga att gat tac gga cgt caa gca gca gtc gca gcc caa cgc gcc   1939
Ala Gly Ile Asp Tyr Gly Arg Gln Ala Ala Val Ala Ala Gln Arg Ala
        600                 605                 610

agc aag tca gca caa aac gac atc acc acc tac aac aat cgc cac aat   1987
Ser Lys Ser Ala Gln Asn Asp Ile Thr Thr Tyr Asn Asn Arg His Asn
    615                 620                 625

tcc ggt ggc gga acc acc ggt gcg att gtc acc ggc atg gtg atc aac   2035
Ser Gly Gly Gly Thr Thr Gly Ala Ile Val Thr Gly Met Val Ile Asn
630                 635                 640                 645

tcg att ctc aac agc ggc cgc ggt ggc ggt ttc tgt gga ggc gga ggc   2083
Ser Ile Leu Asn Ser Gly Arg Gly Gly Gly Phe Cys Gly Gly Gly Gly
                650                 655                 660

ttt ggt gga ggc ggt ggc ggc ttc agc ggt ggt ggc ggt ggc gga gga   2131
Phe Gly Gly Gly Gly Gly Gly Phe Ser Gly Gly Gly Gly Gly Gly Gly
            665                 670                 675
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ggg ttc cgc gga ggc cgc ttc tagcctgaaa cgagcaaaac caa 2175
Gly Phe Arg Gly Gly Arg Phe
680

<210> 656
<211> 684
<212> PRT
<213> Corynebacterium glutamicum

<400> 656
Met Asn Phe Ser Leu Val His Leu Arg Glu Asn Val Arg Arg Val Ser
1 5 10 15

Val Thr Val Ala Ile Gly Ala Gly Ala Leu Leu Ile Ser Gly Pro Phe
20 25 30

Phe Thr Ala His Thr Ala Glu Ala Thr Glu Thr Tyr Val Leu Ala Glu
35 40 45

Ser Pro Glu Phe Tyr Gln Asp Asn Val Thr Asp Tyr Thr Gly Gln Ile
50 55 60

Ser Ser Ser Asp Ile Thr Asn Ile Gln Ala Ala Ile Asp Asp Val Lys
65 70 75 80

Ala Ser Glu Gln Lys Val Ile Phe Val Val Phe Leu Ser Ser Phe Asp
85 90 95

Gly Val Asp Pro Glu Thr Trp Thr Gln Gln Ala Leu Gln Ala Asn Gly
100 105 110

Gly Gly Asn Val Leu Ile Tyr Ala Leu Ala Pro Glu Glu Arg Gln Tyr
115 120 125

Gly Ile Gln Gly Gly Thr Gln Trp Thr Asp Ala Glu Leu Asp Ala Ala
130 135 140

Asn Asn Ala Ala Phe Gln Ala Leu Ser Gln Glu Asp Trp Ala Gly Ser
145 150 155 160

Ala Leu Ala Leu Ala Glu Ser Val Gly Ser Ser Ser Ser Ser Ser Ser
165 170 175

Gly Ser Ser Ser Ser Ser Asp Phe Ser Gly Ala Trp Leu Ala Ala Ala
180 185 190

Gly Val Gly Thr Val Ala Ala Gly Gly Gly Ile Trp Ala Tyr Ser Arg
195 200 205

Ser Arg Lys Lys Lys Thr Ser Ala Ala Thr Leu Glu Asp Ala Arg Glu
210 215 220

Ile Asp Pro Arg Asp Thr Asn Arg Leu Met Gln Leu Pro Met Glu Thr
225 230 235 240

Leu Glu His Leu Ala Gln Glu Glu Leu Thr Ser Thr Asp Asp Ser Ile
245 250 255

Arg Arg Gly Lys Glu Glu Leu Ala Ile Ala Thr Ser Glu Phe Gly Pro

```
            260                 265                 270

Glu Arg Thr Arg Ser Phe Asn Arg Ala Met Asn His Ser Thr Gly Thr
        275                 280                 285

Leu Gln Lys Ala Phe Glu Ile Gln Gln Arg Leu Asn Asp Ser Ile Pro
    290                 295                 300

Glu Ser Glu Ala Glu Arg Gln Ser Met Leu Val Glu Ile Ile Ser Ser
305                 310                 315                 320

Cys Gly Gln Ala Asp Asp Ala Leu Asp Ala Glu Ala Gln Asn Phe Ala
                325                 330                 335

Asp Met Arg Asn Leu Leu Ile Asn Ala Gly Ser Lys Leu Asp Ala Leu
            340                 345                 350

Thr Gln Lys Ser Val Asp Leu Arg Thr Arg Leu Pro Lys Ala Gln Glu
        355                 360                 365

Thr Leu Ala Gly Leu Arg Thr Arg Tyr Ser Ala Glu Val Leu Glu Ser
    370                 375                 380

Ile Asp Asp Asn Val Asp Leu Ala Ser Ala Ser Leu Asp Glu Ala Glu
385                 390                 395                 400

Glu Val Leu Pro Gln Ala Tyr Glu Ile Glu Ser Met Pro Ala Gly Glu
                405                 410                 415

Gln Gly Gly Leu Ile Asp Ala Ile Arg His Ile Glu His Ala Ile Thr
            420                 425                 430

Thr Ala Asp Lys Leu Leu Ala Gly Val Glu His Ala Asp Glu Asn Ile
        435                 440                 445

Ser Thr Ala Lys Ala Asn Val Ala Asp Leu Ile Gln Glu Ile Ser Asp
    450                 455                 460

Glu Ile Asn Glu Ala Gly Gln Leu Lys Gln Ser Ala Gly Ala Asp Gly
465                 470                 475                 480

Ala Arg Ala Asp Trp Ala Ser Leu Asp Asp Ala Val Arg Ala Ala Ser
                485                 490                 495

Ala Ala Leu Ile Thr Ala Ser Ala Asp Ala Glu Lys Asp Pro Leu Gly
            500                 505                 510

Thr Tyr Thr Glu Leu Val Asp Val Asp Ser Ala Leu Asp Thr Gln Leu
        515                 520                 525

Asp Thr Leu Arg Ala Thr Ala Ala Asp Gln Ala Arg Gln Leu Arg Val
    530                 535                 540

Phe Asp Gln Gln Leu Gln Ser Ala Arg Ser Gln Ile Gln Lys Ala Glu
545                 550                 555                 560

Asp Leu Ile Ser Thr Arg Gly Arg Ile Val Lys Ser Glu Ala Arg Thr
                565                 570                 575

His Leu Ala Asn Ala Gln Lys Leu Tyr Ala Met Ala Gln Gln Asn Arg
            580                 585                 590
```

Thr Arg Asp Thr Arg Ala Gly Ile Asp Tyr Gly Arg Gln Ala Ala Val
595 600 605

Ala Ala Gln Arg Ala Ser Lys Ser Ala Gln Asn Asp Ile Thr Thr Tyr
610 615 620

Asn Asn Arg His Asn Ser Gly Gly Gly Thr Thr Gly Ala Ile Val Thr
625 630 635 640

Gly Met Val Ile Asn Ser Ile Leu Asn Ser Gly Arg Gly Gly Gly Phe
645 650 655

Cys Gly Gly Gly Gly Phe Gly Gly Gly Gly Gly Gly Phe Ser Gly Gly
660 665 670

Gly Gly Gly Gly Gly Gly Phe Arg Gly Gly Arg Phe
675 680

<210> 657
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> RXN01492

<400> 657
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tggacaaaga cttttagcaa caactatgtg gaggtgacag gtg acc aca act ctg 115
Val Thr Thr Thr Leu
1 5

tgg gcg gtt tct gac ctc cat gca gcg gtg aaa gct aac gct gat cca 163
Trp Ala Val Ser Asp Leu His Ala Ala Val Lys Ala Asn Ala Asp Pro
10 15 20

att gag aat att cag cct aag gat ccg tct gac tgg ttg att gtt gca 211
Ile Glu Asn Ile Gln Pro Lys Asp Pro Ser Asp Trp Leu Ile Val Ala
25 30 35

ggt gac gtg gcg gaa cgt acc gaa ttg gtg ctg gaa att ttg gca cgt 259
Gly Asp Val Ala Glu Arg Thr Glu Leu Val Leu Glu Ile Leu Ala Arg
40 45 50

ttg cgc agg cgc ttt gcc aag gtg atc tgg gtt ccg ggt aac cat gag 307
Leu Arg Arg Arg Phe Ala Lys Val Ile Trp Val Pro Gly Asn His Glu
55 60 65

ttg ttt tct cgc tcc gcg gac cgc tat cag ggg cgc gat aag tac tct 355
Leu Phe Ser Arg Ser Ala Asp Arg Tyr Gln Gly Arg Asp Lys Tyr Ser
70 75 80 85

gaa ctc gtt gaa ggc tgc cgc aag att gat gtg ttg act ccg gag gac 403
Glu Leu Val Glu Gly Cys Arg Lys Ile Asp Val Leu Thr Pro Glu Asp
90 95 100

```
cct tac tta acc ttt ggt ggg gtt act atc gtt ccg ttg ttt aca ctc   451
Pro Tyr Leu Thr Phe Gly Gly Val Thr Ile Val Pro Leu Phe Thr Leu
            105                 110                 115

tat gac tac tcg ttc cgt cga cct ggt ttc acc gtg gag cag gct gtg   499
Tyr Asp Tyr Ser Phe Arg Arg Pro Gly Phe Thr Val Glu Gln Ala Val
        120                 125                 130

caa gcg gcg cgg gat cgt caa gtg atg atg act gat gag ttt tct att   547
Gln Ala Ala Arg Asp Arg Gln Val Met Met Thr Asp Glu Phe Ser Ile
    135                 140                 145

gcg cct ttt gtt gat atc cga gcg tgg tgc tgg gat cgc tta gcc tat   595
Ala Pro Phe Val Asp Ile Arg Ala Trp Cys Trp Asp Arg Leu Ala Tyr
150                 155                 160                 165

tcc att aag cgt ttg agc aag atc aac ggg cca aca att ttg att aac   643
Ser Ile Lys Arg Leu Ser Lys Ile Asn Gly Pro Thr Ile Leu Ile Asn
                170                 175                 180

cac tgg ccg ctg gtg gtg gaa ccg act tat cag atg cgc tgg cag gaa   691
His Trp Pro Leu Val Val Glu Pro Thr Tyr Gln Met Arg Trp Gln Glu
            185                 190                 195

ctt gca ttg tgg tgc ggt act cgc cac acc agg gga tgg gcc gaa cgc   739
Leu Ala Leu Trp Cys Gly Thr Arg His Thr Arg Gly Trp Ala Glu Arg
        200                 205                 210

tac aac gcg gaa gcc gtt att tac ggt cat ctg cat atg ccc gga ata   787
Tyr Asn Ala Glu Ala Val Ile Tyr Gly His Leu His Met Pro Gly Ile
    215                 220                 225

acc aac gtc aac ggt gtg aaa cac att gaa gtg tcg ttg ggt tat ccg   835
Thr Asn Val Asn Gly Val Lys His Ile Glu Val Ser Leu Gly Tyr Pro
230                 235                 240                 245

cgc gaa tgg gag cat tgg tct ggg cag cat gtg tgg cca tat cca gtg   883
Arg Glu Trp Glu His Trp Ser Gly Gln His Val Trp Pro Tyr Pro Val
                250                 255                 260

atg gag gtg gac aat gct gga tgagtctttg tttccaaatt cgg             927
Met Glu Val Asp Asn Ala Gly
            265
```

<210> 658
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 658

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Val Thr Thr Thr Leu Trp Ala Val Ser Asp Leu His Ala Ala Val Lys
  1               5                  10                  15

Ala Asn Ala Asp Pro Ile Glu Asn Ile Gln Pro Lys Asp Pro Ser Asp
            20                  25                  30

Trp Leu Ile Val Ala Gly Asp Val Ala Glu Arg Thr Glu Leu Val Leu
        35                  40                  45

Glu Ile Leu Ala Arg Leu Arg Arg Arg Phe Ala Lys Val Ile Trp Val
```

```
     50                  55                  60

Pro Gly Asn His Glu Leu Phe Ser Arg Ser Ala Asp Arg Tyr Gln Gly
 65                  70                  75                  80

Arg Asp Lys Tyr Ser Glu Leu Val Glu Gly Cys Arg Lys Ile Asp Val
                 85                  90                  95

Leu Thr Pro Glu Asp Pro Tyr Leu Thr Phe Gly Gly Val Thr Ile Val
            100                 105                 110

Pro Leu Phe Thr Leu Tyr Asp Tyr Ser Phe Arg Arg Pro Gly Phe Thr
        115                 120                 125

Val Glu Gln Ala Val Gln Ala Ala Arg Asp Arg Gln Val Met Met Thr
    130                 135                 140

Asp Glu Phe Ser Ile Ala Pro Phe Val Asp Ile Arg Ala Trp Cys Trp
145                 150                 155                 160

Asp Arg Leu Ala Tyr Ser Ile Lys Arg Leu Ser Lys Ile Asn Gly Pro
                165                 170                 175

Thr Ile Leu Ile Asn His Trp Pro Leu Val Val Glu Pro Thr Tyr Gln
            180                 185                 190

Met Arg Trp Gln Glu Leu Ala Leu Trp Cys Gly Thr Arg His Thr Arg
        195                 200                 205

Gly Trp Ala Glu Arg Tyr Asn Ala Glu Ala Val Ile Tyr Gly His Leu
    210                 215                 220

His Met Pro Gly Ile Thr Asn Val Asn Gly Val Lys His Ile Glu Val
225                 230                 235                 240

Ser Leu Gly Tyr Pro Arg Glu Trp Glu His Trp Ser Gly Gln His Val
                245                 250                 255

Trp Pro Tyr Pro Val Met Glu Val Asp Asn Ala Gly
            260                 265
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09607307.090705

<210> 659
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> FRXA01492

<400> 659
tgaagtgggc gcgttagctt cggcgcgtgg caaaccacat ttgctggact gcaggcataa 60

tggacaaaga cttttagcaa caactatgtg gaggtgacag gtg acc aca act ctg 115
                                              Val Thr Thr Thr Leu
                                                1   5

tgg gcg gtt tct gac ctc cat gca gcg gtg aaa gct aac gct gat cca 163
Trp Ala Val Ser Asp Leu His Ala Ala Val Lys Ala Asn Ala Asp Pro

```
                  10                  15                  20

att gag aat att cag cct aag gat ccg tct gac tgg ttg att gtt gca   211
Ile Glu Asn Ile Gln Pro Lys Asp Pro Ser Asp Trp Leu Ile Val Ala
            25                  30                  35

ggt gac gtg gcg gaa cgt acc gaa ttg gtg ctg gaa att ttg gca cgt   259
Gly Asp Val Ala Glu Arg Thr Glu Leu Val Leu Glu Ile Leu Ala Arg
        40                  45                  50

ttg cgc agg cgc ttt gcc aag gtg atc tgg gtt ccg ggt aac cat gag   307
Leu Arg Arg Arg Phe Ala Lys Val Ile Trp Val Pro Gly Asn His Glu
    55                  60                  65

ttg ttt tct cgc tcc gcg gac cgc tat cag ggg cgc gat aag tac tct   355
Leu Phe Ser Arg Ser Ala Asp Arg Tyr Gln Gly Arg Asp Lys Tyr Ser
70                  75                  80                  85

gaa ctc gtt gaa ggc tgc cgc aag att gat gtg ttg act ccg gag gac   403
Glu Leu Val Glu Gly Cys Arg Lys Ile Asp Val Leu Thr Pro Glu Asp
                90                  95                  100

cct tac tta acc ttt ggt ggg gtt act atc gtt ccg ttg ttt aca ctc   451
Pro Tyr Leu Thr Phe Gly Gly Val Thr Ile Val Pro Leu Phe Thr Leu
            105                 110                 115

tat gac tac tcg ttc cgt cga cct ggt ttc acc gtg gag cag gct gtg   499
Tyr Asp Tyr Ser Phe Arg Arg Pro Gly Phe Thr Val Glu Gln Ala Val
        120                 125                 130

caa gcg gcg cgg gat cgt caa gtg atg atg act gat gag ttt tct att   547
Gln Ala Ala Arg Asp Arg Gln Val Met Met Thr Asp Glu Phe Ser Ile
    135                 140                 145

gcg cct ttt gtt gat atc cga gcg tgg tgc tgg gat cgc tta gcc tat   595
Ala Pro Phe Val Asp Ile Arg Ala Trp Cys Trp Asp Arg Leu Ala Tyr
150                 155                 160                 165

tcc att aag cgt ttg agc aag atc aac ggg cca aca att ttg att aac   643
Ser Ile Lys Arg Leu Ser Lys Ile Asn Gly Pro Thr Ile Leu Ile Asn
                170                 175                 180

cac tgg ccg ctg gtg gtg gaa ccg act tat cag atg cgc tgg cag gaa   691
His Trp Pro Leu Val Val Glu Pro Thr Tyr Gln Met Arg Trp Gln Glu
            185                 190                 195

ctt gca ttg tgg tgc ggt act cgc cac acc agg gga tgg gcc gaa cgc   739
Leu Ala Leu Trp Cys Gly Thr Arg His Thr Arg Gly Trp Ala Glu Arg
        200                 205                 210

tac aac gcg gaa gcc gtt att tac ggt cat ctg cat atg ccc gga ata   787
Tyr Asn Ala Glu Ala Val Ile Tyr Gly His Leu His Met Pro Gly Ile
    215                 220                 225

acc aac gtc aac ggt gtg aaa cac att gaa gtg tcg ttg ggt tat ccg   835
Thr Asn Val Asn Gly Val Lys His Ile Glu Val Ser Leu Gly Tyr Pro
230                 235                 240                 245

cgc gaa tgg gag cat tgg tct ggg cag cat gtg tgg cca tat cca gtg   883
Arg Glu Trp Glu His Trp Ser Gly Gln His Val Trp Pro Tyr Pro Val
                250                 255                 260
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atg gag gtg gac aat gct gga tgagtctttg tttccaaatt cgg 927
Met Glu Val Asp Asn Ala Gly
265

<210> 660
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 660
Val Thr Thr Thr Leu Trp Ala Val Ser Asp Leu His Ala Ala Val Lys
1 5 10 15

Ala Asn Ala Asp Pro Ile Glu Asn Ile Gln Pro Lys Asp Pro Ser Asp
20 25 30

Trp Leu Ile Val Ala Gly Asp Val Ala Glu Arg Thr Glu Leu Val Leu
35 40 45

Glu Ile Leu Ala Arg Leu Arg Arg Arg Phe Ala Lys Val Ile Trp Val
50 55 60

Pro Gly Asn His Glu Leu Phe Ser Arg Ser Ala Asp Arg Tyr Gln Gly
65 70 75 80

Arg Asp Lys Tyr Ser Glu Leu Val Glu Gly Cys Arg Lys Ile Asp Val
85 90 95

Leu Thr Pro Glu Asp Pro Tyr Leu Thr Phe Gly Gly Val Thr Ile Val
100 105 110

Pro Leu Phe Thr Leu Tyr Asp Tyr Ser Phe Arg Arg Pro Gly Phe Thr
115 120 125

Val Glu Gln Ala Val Gln Ala Ala Arg Asp Arg Gln Val Met Met Thr
130 135 140

Asp Glu Phe Ser Ile Ala Pro Phe Val Asp Ile Arg Ala Trp Cys Trp
145 150 155 160

Asp Arg Leu Ala Tyr Ser Ile Lys Arg Leu Ser Lys Ile Asn Gly Pro
165 170 175

Thr Ile Leu Ile Asn His Trp Pro Leu Val Val Glu Pro Thr Tyr Gln
180 185 190

Met Arg Trp Gln Glu Leu Ala Leu Trp Cys Gly Thr Arg His Thr Arg
195 200 205

Gly Trp Ala Glu Arg Tyr Asn Ala Glu Ala Val Ile Tyr Gly His Leu
210 215 220

His Met Pro Gly Ile Thr Asn Val Asn Gly Val Lys His Ile Glu Val
225 230 235 240

Ser Leu Gly Tyr Pro Arg Glu Trp Glu His Trp Ser Gly Gln His Val
245 250 255

Trp Pro Tyr Pro Val Met Glu Val Asp Asn Ala Gly

260 265

<210> 661
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> RXN01518

<400> 661
agcagaacct gatgccgtcc tgcacggcac gaccattgca gaacatgtgg ataatcttga 60

tcccacagac attgaaggtg tcaccaagat ttaaggagtc gtg gct ttc atg cag 115
Val Ala Phe Met Gln
1 5

aaa acg tca gcg ggt tgg ttg atc gca acg gga ggt ttc ctc gcc gct 163
Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala
10 15 20

gtg tcc gcc att ttg acg tgg cgt ttt tat gga tcc atg acc tct att 211
Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly Ser Met Thr Ser Ile
25 30 35

tcc atc acg gta tcc atc act ttt tgg ttg ttg gcc gtg gtg tgt ggt 259
Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu Ala Val Val Cys Gly
40 45 50

ttc gca ggt gtg aag gtc caa ggt cgc ctc gat gag ggg ctg atc ggc 307
Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp Glu Gly Leu Ile Gly
55 60 65

cag gac aaa tcc caa atg aac ccc gtg acc att gcc tat ctg gcc atg 355
Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile Ala Tyr Leu Ala Met
70 75 80 85

ctg ggt cga gcg tgt gcg tgg ggt ggc gca att ttc ggc ggc gtt tat 403
Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile Phe Gly Gly Val Tyr
90 95 100

gtg gga att ggc agt tat gta atc cca cgc gcc ggt gag ttg tcc gca 451
Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala Gly Glu Leu Ser Ala
105 110 115

gca tcg aat gat ctt ccg gga gtt att gcc tgt gcg ctg ggc gga atc 499
Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys Ala Leu Gly Gly Ile
120 125 130

gca ctc tca gct gcc gga ctt tat tta gag cga agc tgt gag gct ccg 547
Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg Ser Cys Glu Ala Pro
135 140 145

cct ccc caa tct ggc gaa gcg atc agc tagattggaa ttcatgaatc 594
Pro Pro Gln Ser Gly Glu Ala Ile Ser
150 155

aag 597

<210> 662
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 662
Val Ala Phe Met Gln Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly
1 5 10 15

Gly Phe Leu Ala Ala Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly
20 25 30

Ser Met Thr Ser Ile Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu
35 40 45

Ala Val Val Cys Gly Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp
50 55 60

Glu Gly Leu Ile Gly Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile
65 70 75 80

Ala Tyr Leu Ala Met Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile
85 90 95

Phe Gly Gly Val Tyr Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala
100 105 110

Gly Glu Leu Ser Ala Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys
115 120 125

Ala Leu Gly Gly Ile Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg
130 135 140

Ser Cys Glu Ala Pro Pro Pro Gln Ser Gly Glu Ala Ile Ser
145 150 155

<210> 663
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> FRXA01518

<400> 663
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tcccacagac attgaaggtg tcaccaagat ttaaggagtc gtg gct ttc atg cag 115
Val Ala Phe Met Gln
1 5

aaa acg tca gcg ggt tgg ttg atc gca acg gga ggt ttc ctc gcc gct 163
Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala
10 15 20

gtg tcc gcc att ttg acg tgg cgt ttt tat gga tcc atg acc tct att 211

```
Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly Ser Met Thr Ser Ile
            25                  30                  35

tcc atc acg gta tcc atc act ttt tgg ttg ttg gcc gtg gtg tgt ggt   259
Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu Ala Val Val Cys Gly
        40                  45                  50

ttc gca ggt gtg aag gtc caa ggt cgc ctc gat gag ggg ctg atc ggc   307
Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp Glu Gly Leu Ile Gly
    55                  60                  65

cag gac aaa tcc caa atg aac ccc gtg acc att gcc tat ctg gcc atg   355
Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile Ala Tyr Leu Ala Met
70                  75                  80                  85

ctg ggt cga gcg tgt gcg tgg ggt ggc gca att ttc ggc ggc gtt tat   403
Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile Phe Gly Gly Val Tyr
                90                  95                  100

gtg gga att ggc agt tat gta atc cca cgc gcc ggt gag ttg tcc gca   451
Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala Gly Glu Leu Ser Ala
            105                 110                 115

gca tcg aat gat ctt ccg gga gtt att gcc tgt gcg ctg ggc gga atc   499
Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys Ala Leu Gly Gly Ile
        120                 125                 130

gca ctc tca gct gcc gga ctt tat tta gag cga agc tgt gag gct ccg   547
Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg Ser Cys Glu Ala Pro
    135                 140                 145

cct ccc caa tct ggc gaa gcg atc agc tagattggaa ttcatgaatc         594
Pro Pro Gln Ser Gly Glu Ala Ile Ser
150                 155

aag                                                               597


<210> 664
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 664
Val Ala Phe Met Gln Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly
  1               5                  10                  15

Gly Phe Leu Ala Ala Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly
            20                  25                  30

Ser Met Thr Ser Ile Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu
        35                  40                  45

Ala Val Val Cys Gly Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp
    50                  55                  60

Glu Gly Leu Ile Gly Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile
65                  70                  75                  80

Ala Tyr Leu Ala Met Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile
                85                  90                  95
```

```
Phe Gly Gly Val Tyr Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala
      100                 105                 110

Gly Glu Leu Ser Ala Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys
        115                 120                 125

Ala Leu Gly Gly Ile Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg
    130                 135                 140

Ser Cys Glu Ala Pro Pro Pro Gln Ser Gly Glu Ala Ile Ser
145                 150                 155


<210> 665
<211> 1727
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (46)..(1704)
<223> RXN01549

<400> 665
tgaattccgt ttctagattt tttttattga ttgtgagagt gcattgtg gct aat gat  57
                                                Val Ala Asn Asp
                                                  1

ttt ata gaa cca aat gat gcc ccc gat gca cct gat aat ggt gac tcg  105
Phe Ile Glu Pro Asn Asp Ala Pro Asp Ala Pro Asp Asn Gly Asp Ser
  5                  10                  15                  20

gga agc tcg ggg ttt gtt gat gaa gca aaa gat aag acc cgc tca gct  153
Gly Ser Ser Gly Phe Val Asp Glu Ala Lys Asp Lys Thr Arg Ser Ala
                 25                  30                  35

gca caa ggc tta ggt tat ggc gca cta cgt gta ggt ttt ggt act gca  201
Ala Gln Gly Leu Gly Tyr Gly Ala Leu Arg Val Gly Phe Gly Thr Ala
             40                  45                  50

gca ctt gca gcc aat ggt gct cgc tct atg ggt aat ttg gct aaa aac  249
Ala Leu Ala Ala Asn Gly Ala Arg Ser Met Gly Asn Leu Ala Lys Asn
         55                  60                  65

ctg tgg aca cga atg atg ggg ctt gcc ctg tct gcc ggt act ggt atc  297
Leu Trp Thr Arg Met Met Gly Leu Ala Leu Ser Ala Gly Thr Gly Ile
     70                  75                  80

tct gct gcc aca ggt ggc atg atc act gca cgt gta ggc gca atg ctg  345
Ser Ala Ala Thr Gly Gly Met Ile Thr Ala Arg Val Gly Ala Met Leu
 85                  90                  95                 100

gca ggt aca ggc tcg gtg ttg tcg tcg gtg acg act att gcg ttg att  393
Ala Gly Thr Gly Ser Val Leu Ser Ser Val Thr Thr Ile Ala Leu Ile
                105                 110                 115

gtg tcg atg att gtg gtg ccg gca ggt cga aaa gac ggc att atc gag  441
Val Ser Met Ile Val Val Pro Ala Gly Arg Lys Asp Gly Ile Ile Glu
            120                 125                 130
```

```
ttg tgt gag ccg cca gta acg gcc aac ccg ttt acc att gac gca ggt   489
Leu Cys Glu Pro Pro Val Thr Ala Asn Pro Phe Thr Ile Asp Ala Gly
        135                 140                 145

gat atg act gag aac gcg aag ttg gtg tac ggt gcg ctg tcg tat ctt   537
Asp Met Thr Glu Asn Ala Lys Leu Val Tyr Gly Ala Leu Ser Tyr Leu
    150                 155                 160

ggg atg aat gat caa aat atc gcc ggt gtc ttg ggc aac ttt gag aca   585
Gly Met Asn Asp Gln Asn Ile Ala Gly Val Leu Gly Asn Phe Glu Thr
165                 170                 175                 180

gaa tca ggt atc gac ccg act gcg gtg gag ggt att ttt gat gaa cca   633
Glu Ser Gly Ile Asp Pro Thr Ala Val Glu Gly Ile Phe Asp Glu Pro
                185                 190                 195

aat acc atc ggt cct cgg aag aga gct gcg tgg gat aag aac ttt gaa   681
Asn Thr Ile Gly Pro Arg Lys Arg Ala Ala Trp Asp Lys Asn Phe Glu
            200                 205                 210

cct cag ccg atg ggt att ggg ctt ggg cag tgg aca gca ggg cgc aca   729
Pro Gln Pro Met Gly Ile Gly Leu Gly Gln Trp Thr Ala Gly Arg Thr
        215                 220                 225

cag atg ttg cta gat ttt gcc gcc gat aga aac cga gac tgg cat tac   777
Gln Met Leu Leu Asp Phe Ala Ala Asp Arg Asn Arg Asp Trp His Tyr
    230                 235                 240

atc gac gtg cag ctt gca ttt gct att agt ggc gat aat gaa agc gat   825
Ile Asp Val Gln Leu Ala Phe Ala Ile Ser Gly Asp Asn Glu Ser Asp
245                 250                 255                 260

cgc aag gtt ttt ctg gaa atg gtt gat aat aaa aac tcc agt agc aat   873
Arg Lys Val Phe Leu Glu Met Val Asp Asn Lys Asn Ser Ser Ser Asn
                265                 270                 275

agc ccc acc gca gcg tcc gag tac ttc ctg cgt gag tgg gag cgc ccg   921
Ser Pro Thr Ala Ala Ser Glu Tyr Phe Leu Arg Glu Trp Glu Arg Pro
            280                 285                 290

gca gat gtc gca ggt aat gca ccc att cgt gca gag caa gca tct aag   969
Ala Asp Val Ala Gly Asn Ala Pro Ile Arg Ala Glu Gln Ala Ser Lys
        295                 300                 305

tgg tac gcg cag atg ggt ggt tgg caa aag aac tca acc ttg ggt gag   1017
Trp Tyr Ala Gln Met Gly Gly Trp Gln Lys Asn Ser Thr Leu Gly Glu
    310                 315                 320

tct gtg atc gct atg gct gat ggt gca gca gca aaa tcc acg gcg cgt   1065
Ser Val Ile Ala Met Ala Asp Gly Ala Ala Ala Lys Ser Thr Ala Arg
325                 330                 335                 340

gat gag cag gat gct ctt aat gat tgt cct gaa gag gac cgc acc tca   1113
Asp Glu Gln Asp Ala Leu Asn Asp Cys Pro Glu Glu Asp Arg Thr Ser
                345                 350                 355

ggt gga aat acg tcc gct gca gaa gca atg gtg act att tca cat cct   1161
Gly Gly Asn Thr Ser Ala Ala Glu Ala Met Val Thr Ile Ser His Pro
            360                 365                 370

tat ctg gct gat tct cgt ggc aat gac ggt act gat att tac cgc tat   1209
```

```
Tyr Leu Ala Asp Ser Arg Gly Asn Asp Gly Thr Asp Ile Tyr Arg Tyr
        375                 380                 385

atc cat gat gaa gtg ctc acc ggt gat ccg tat tac gca tcc tgt gac   1257
Ile His Asp Glu Val Leu Thr Gly Asp Pro Tyr Tyr Ala Ser Cys Asp
    390                 395                 400

cgt ggc gtt gct acc gct att cgc tgg tcg ggc acg gat gat acg ttc   1305
Arg Gly Val Ala Thr Ala Ile Arg Trp Ser Gly Thr Asp Asp Thr Phe
405                 410                 415                 420

cca gca ggt cca aca gca gca cag tat gaa tac gtt gtg ggc aca gga   1353
Pro Ala Gly Pro Thr Ala Ala Gln Tyr Glu Tyr Val Val Gly Thr Gly
                425                 430                 435

tcg ggc cgt tgg gag gaa atc ggc aat ctt gcc acc atg tca gag aac   1401
Ser Gly Arg Trp Glu Glu Ile Gly Asn Leu Ala Thr Met Ser Glu Asn
            440                 445                 450

gat ttg tta cct ggc gat gtg ctt ctt ggt gca ccg aat cac gtt gcg   1449
Asp Leu Leu Pro Gly Asp Val Leu Leu Gly Ala Pro Asn His Val Ala
        455                 460                 465

atg tat gtc agc aat gag gtt gtt gtg gac atg ttg ggc cct ggt aat   1497
Met Tyr Val Ser Asn Glu Val Val Val Asp Met Leu Gly Pro Gly Asn
    470                 475                 480

gca gag cct aat gca gct att ggt cat gca tcg ttg aat gac cgc tca   1545
Ala Glu Pro Asn Ala Ala Ile Gly His Ala Ser Leu Asn Asp Arg Ser
485                 490                 495                 500

cct ggt ctg gat acc ttg agt ctg gat gga tgg ggc gtg aac ttc aag   1593
Pro Gly Leu Asp Thr Leu Ser Leu Asp Gly Trp Gly Val Asn Phe Lys
                505                 510                 515

gtg ttc cgc aac acc cag gct gag aca aac tca gtg ttc tct ggt gta   1641
Val Phe Arg Asn Thr Gln Ala Glu Thr Asn Ser Val Phe Ser Gly Val
            520                 525                 530

cag att ccg gct ggt aaa gaa att ggc gaa atg act aac cca act cga   1689
Gln Ile Pro Ala Gly Lys Glu Ile Gly Glu Met Thr Asn Pro Thr Arg
        535                 540                 545

act act cct gca gga taagtttttt tcatcgctgg gtt                    1727
Thr Thr Pro Ala Gly
    550
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<210> 666
<211> 553
<212> PRT
<213> Corynebacterium glutamicum

<400> 666

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Val Ala Asn Asp Phe Ile Glu Pro Asn Asp Ala Pro Asp Ala Pro Asp
  1               5                  10                  15

Asn Gly Asp Ser Gly Ser Ser Gly Phe Val Asp Glu Ala Lys Asp Lys
            20                  25                  30

Thr Arg Ser Ala Ala Gln Gly Leu Gly Tyr Gly Ala Leu Arg Val Gly
```

```
         35                  40                  45

Phe Gly Thr Ala Ala Leu Ala Ala Asn Gly Ala Arg Ser Met Gly Asn
     50                  55                  60

Leu Ala Lys Asn Leu Trp Thr Arg Met Met Gly Leu Ala Leu Ser Ala
 65                  70                  75                  80

Gly Thr Gly Ile Ser Ala Ala Thr Gly Gly Met Ile Thr Ala Arg Val
                 85                  90                  95

Gly Ala Met Leu Ala Gly Thr Gly Ser Val Leu Ser Ser Val Thr Thr
            100                 105                 110

Ile Ala Leu Ile Val Ser Met Ile Val Val Pro Ala Gly Arg Lys Asp
        115                 120                 125

Gly Ile Ile Glu Leu Cys Glu Pro Pro Val Thr Ala Asn Pro Phe Thr
    130                 135                 140

Ile Asp Ala Gly Asp Met Thr Glu Asn Ala Lys Leu Val Tyr Gly Ala
145                 150                 155                 160

Leu Ser Tyr Leu Gly Met Asn Asp Gln Asn Ile Ala Gly Val Leu Gly
                165                 170                 175

Asn Phe Glu Thr Glu Ser Gly Ile Asp Pro Thr Ala Val Glu Gly Ile
            180                 185                 190

Phe Asp Glu Pro Asn Thr Ile Gly Pro Arg Lys Arg Ala Ala Trp Asp
        195                 200                 205

Lys Asn Phe Glu Pro Gln Pro Met Gly Ile Gly Leu Gly Gln Trp Thr
    210                 215                 220

Ala Gly Arg Thr Gln Met Leu Leu Asp Phe Ala Ala Asp Arg Asn Arg
225                 230                 235                 240

Asp Trp His Tyr Ile Asp Val Gln Leu Ala Phe Ala Ile Ser Gly Asp
                245                 250                 255

Asn Glu Ser Asp Arg Lys Val Phe Leu Glu Met Val Asp Asn Lys Asn
            260                 265                 270

Ser Ser Ser Asn Ser Pro Thr Ala Ala Ser Glu Tyr Phe Leu Arg Glu
        275                 280                 285

Trp Glu Arg Pro Ala Asp Val Ala Gly Asn Ala Pro Ile Arg Ala Glu
    290                 295                 300

Gln Ala Ser Lys Trp Tyr Ala Gln Met Gly Gly Trp Gln Lys Asn Ser
305                 310                 315                 320

Thr Leu Gly Glu Ser Val Ile Ala Met Ala Asp Gly Ala Ala Ala Lys
                325                 330                 335

Ser Thr Ala Arg Asp Glu Gln Asp Ala Leu Asn Asp Cys Pro Glu Glu
            340                 345                 350

Asp Arg Thr Ser Gly Gly Asn Thr Ser Ala Ala Glu Ala Met Val Thr
        355                 360                 365
```

```
Ile Ser His Pro Tyr Leu Ala Asp Ser Arg Gly Asn Asp Gly Thr Asp
    370                 375                 380

Ile Tyr Arg Tyr Ile His Asp Glu Val Leu Thr Gly Asp Pro Tyr Tyr
385                 390                 395                 400

Ala Ser Cys Asp Arg Gly Val Ala Thr Ala Ile Arg Trp Ser Gly Thr
                405                 410                 415

Asp Asp Thr Phe Pro Ala Gly Pro Thr Ala Ala Gln Tyr Glu Tyr Val
            420                 425                 430

Val Gly Thr Gly Ser Gly Arg Trp Glu Glu Ile Gly Asn Leu Ala Thr
        435                 440                 445

Met Ser Glu Asn Asp Leu Leu Pro Gly Asp Val Leu Leu Gly Ala Pro
    450                 455                 460

Asn His Val Ala Met Tyr Val Ser Asn Glu Val Val Val Asp Met Leu
465                 470                 475                 480

Gly Pro Gly Asn Ala Glu Pro Asn Ala Ala Ile Gly His Ala Ser Leu
                485                 490                 495

Asn Asp Arg Ser Pro Gly Leu Asp Thr Leu Ser Leu Asp Gly Trp Gly
            500                 505                 510

Val Asn Phe Lys Val Phe Arg Asn Thr Gln Ala Glu Thr Asn Ser Val
        515                 520                 525

Phe Ser Gly Val Gln Ile Pro Ala Gly Lys Glu Ile Gly Glu Met Thr
    530                 535                 540

Asn Pro Thr Arg Thr Thr Pro Ala Gly
545                 550
```

<210> 667
<211> 942
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (59)..(919)
<223> FRXA01549

<400> 667

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cagcttgcat ttgctattag tggcgataat gaaagcgatc gcaaggtttt tctggaaaatg 61
                                                                 Met
                                                                   1

gtt gat aat aaa aac tcc agt agc aat agc ccc acc gca gcg tcc gag   109
Val Asp Asn Lys Asn Ser Ser Ser Asn Ser Pro Thr Ala Ala Ser Glu
  1               5                  10                  15

tac ttc ctg cgt gag tgg gag cgc ccg gca gat gtc gca ggt aat gca   157
Tyr Phe Leu Arg Glu Trp Glu Arg Pro Ala Asp Val Ala Gly Asn Ala
            20                  25                  30
```

```
ccc att cgt gca gag caa gca tct aag tgg tac gcg cag atg ggt ggt   205
Pro Ile Arg Ala Glu Gln Ala Ser Lys Trp Tyr Ala Gln Met Gly Gly
     35                  40                  45

tgg caa aag aac tca acc ttg ggt gag tct gtg atc gct atg gct gat   253
Trp Gln Lys Asn Ser Thr Leu Gly Glu Ser Val Ile Ala Met Ala Asp
 50                  55                  60                  65

ggt gca gca gca aaa tcc acg gcg cgt gat gag cag gat gct ctt aat   301
Gly Ala Ala Ala Lys Ser Thr Ala Arg Asp Glu Gln Asp Ala Leu Asn
                 70                  75                  80

gat tgt cct gaa gag gac cgc acc tca ggt gga aat acg tcc gct gca   349
Asp Cys Pro Glu Glu Asp Arg Thr Ser Gly Gly Asn Thr Ser Ala Ala
             85                  90                  95

gaa gca atg gtg act att tca cat cct tat ctg gct gat tct cgt ggc   397
Glu Ala Met Val Thr Ile Ser His Pro Tyr Leu Ala Asp Ser Arg Gly
        100                 105                 110

aat gac ggt act gat att tac cgc tat atc cat gat gaa gtg ctc acc   445
Asn Asp Gly Thr Asp Ile Tyr Arg Tyr Ile His Asp Glu Val Leu Thr
    115                 120                 125

ggt gat ccg tat tac gca tcc tgt gac cgt ggc gtt gct acc gct att   493
Gly Asp Pro Tyr Tyr Ala Ser Cys Asp Arg Gly Val Ala Thr Ala Ile
130                 135                 140                 145

cgc tgg tcg ggc acg gat gat acg ttc cca gca ggt cca aca gca gca   541
Arg Trp Ser Gly Thr Asp Asp Thr Phe Pro Ala Gly Pro Thr Ala Ala
                150                 155                 160

cag tat gaa tac gtt gtg ggc aca gga tcg ggc cgt tgg gag gaa atc   589
Gln Tyr Glu Tyr Val Val Gly Thr Gly Ser Gly Arg Trp Glu Glu Ile
            165                 170                 175

ggc aat ctt gcc acc atg tca gag aac gat ttg tta cct ggc gat gtg   637
Gly Asn Leu Ala Thr Met Ser Glu Asn Asp Leu Leu Pro Gly Asp Val
        180                 185                 190

ctt ctt ggt gca ccg aat cac gtt gcg atg tat gtc agc aat gag gtt   685
Leu Leu Gly Ala Pro Asn His Val Ala Met Tyr Val Ser Asn Glu Val
    195                 200                 205

gtt gtg gac atg ttg ggc cct ggt aat gca gag cct aat gca gct att   733
Val Val Asp Met Leu Gly Pro Gly Asn Ala Glu Pro Asn Ala Ala Ile
210                 215                 220                 225

ggt cat gca tcg ttg aat gac cgc tca cct ggt ctg gat acc ttg agt   781
Gly His Ala Ser Leu Asn Asp Arg Ser Pro Gly Leu Asp Thr Leu Ser
                230                 235                 240

ctg gat gga tgg ggc gtg aac ttc aag gtg ttc cgc aac acc cag gct   829
Leu Asp Gly Trp Gly Val Asn Phe Lys Val Phe Arg Asn Thr Gln Ala
            245                 250                 255

gag aca aac tca gtg ttc tct ggt gta cag att ccg gct ggt aaa gaa   877
Glu Thr Asn Ser Val Phe Ser Gly Val Gln Ile Pro Ala Gly Lys Glu
        260                 265                 270

att ggc gaa atg act aac cca act cga act act cct gca gga           919
```

```
Ile Gly Glu Met Thr Asn Pro Thr Arg Thr Thr Pro Ala Gly
    275                 280                 285

taagtttttt tcatcgctgg gtt                                              942


<210> 668
<211> 287
<212> PRT
<213> Corynebacterium glutamicum

<400> 668
Met Val Asp Asn Lys Asn Ser Ser Ser Asn Ser Pro Thr Ala Ala Ser
  1               5                  10                  15

Glu Tyr Phe Leu Arg Glu Trp Glu Arg Pro Ala Asp Val Ala Gly Asn
             20                  25                  30

Ala Pro Ile Arg Ala Glu Gln Ala Ser Lys Trp Tyr Ala Gln Met Gly
         35                  40                  45

Gly Trp Gln Lys Asn Ser Thr Leu Gly Glu Ser Val Ile Ala Met Ala
     50                  55                  60

Asp Gly Ala Ala Ala Lys Ser Thr Ala Arg Asp Glu Gln Asp Ala Leu
 65                  70                  75                  80

Asn Asp Cys Pro Glu Glu Asp Arg Thr Ser Gly Gly Asn Thr Ser Ala
                 85                  90                  95

Ala Glu Ala Met Val Thr Ile Ser His Pro Tyr Leu Ala Asp Ser Arg
            100                 105                 110

Gly Asn Asp Gly Thr Asp Ile Tyr Arg Tyr Ile His Asp Glu Val Leu
        115                 120                 125

Thr Gly Asp Pro Tyr Tyr Ala Ser Cys Asp Arg Gly Val Ala Thr Ala
    130                 135                 140

Ile Arg Trp Ser Gly Thr Asp Asp Thr Phe Pro Ala Gly Pro Thr Ala
145                 150                 155                 160

Ala Gln Tyr Glu Tyr Val Val Gly Thr Gly Ser Gly Arg Trp Glu Glu
                165                 170                 175

Ile Gly Asn Leu Ala Thr Met Ser Glu Asn Asp Leu Leu Pro Gly Asp
            180                 185                 190

Val Leu Leu Gly Ala Pro Asn His Val Ala Met Tyr Val Ser Asn Glu
        195                 200                 205

Val Val Val Asp Met Leu Gly Pro Gly Asn Ala Glu Pro Asn Ala Ala
    210                 215                 220

Ile Gly His Ala Ser Leu Asn Asp Arg Ser Pro Gly Leu Asp Thr Leu
225                 230                 235                 240

Ser Leu Asp Gly Trp Gly Val Asn Phe Lys Val Phe Arg Asn Thr Gln
                245                 250                 255

Ala Glu Thr Asn Ser Val Phe Ser Gly Val Gln Ile Pro Ala Gly Lys
```

```
            260                 265                 270

Glu Ile Gly Glu Met Thr Asn Pro Thr Arg Thr Thr Pro Ala Gly
        275                 280                 285


<210> 669
<211> 363
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (46)..(363)
<223> FRXA02011

<400> 669
tgaattccgt ttctagattt tttttattga ttgtgagagt gcattgtg gct aat gat  57
                                                Val Ala Asn Asp
                                                  1

ttt ata gaa cca aat gat gcc ccc gat gca cct gat aat ggt gac tcg  105
Phe Ile Glu Pro Asn Asp Ala Pro Asp Ala Pro Asp Asn Gly Asp Ser
  5                  10                  15                  20

gga agc tcg ggg ttt gtt gat gaa gca aaa gat aag acc cgc tca gct  153
Gly Ser Ser Gly Phe Val Asp Glu Ala Lys Asp Lys Thr Arg Ser Ala
                 25                  30                  35

gca caa ggc tta ggt tat ggc gca cta cgt gta ggt ttt ggt act gca  201
Ala Gln Gly Leu Gly Tyr Gly Ala Leu Arg Val Gly Phe Gly Thr Ala
             40                  45                  50

gca ctt gca gcc aat ggt gct cgc tct atg ggt aat ttg gct aaa aac  249
Ala Leu Ala Ala Asn Gly Ala Arg Ser Met Gly Asn Leu Ala Lys Asn
         55                  60                  65

ctg tgg aca cca atg atg ggg ctt gcc ctg tct gcc ggt act ggt atc  297
Leu Trp Thr Pro Met Met Gly Leu Ala Leu Ser Ala Gly Thr Gly Ile
     70                  75                  80

tct gct gcc aca ggt ggc atg atc act gca cgt gta ggc gca atg ctg  345
Ser Ala Ala Thr Gly Gly Met Ile Thr Ala Arg Val Gly Ala Met Leu
 85                  90                  95                 100

gca ggt aca ggc tcg gcg                                      363
Ala Gly Thr Gly Ser Ala
                105


<210> 670
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 670
Val Ala Asn Asp Phe Ile Glu Pro Asn Asp Ala Pro Asp Ala Pro Asp
  1               5                  10                  15

Asn Gly Asp Ser Gly Ser Ser Gly Phe Val Asp Glu Ala Lys Asp Lys
             20                  25                  30
```

```
Thr Arg Ser Ala Ala Gln Gly Leu Gly Tyr Gly Ala Leu Arg Val Gly
         35                  40                  45

Phe Gly Thr Ala Ala Leu Ala Ala Asn Gly Ala Arg Ser Met Gly Asn
     50                  55                  60

Leu Ala Lys Asn Leu Trp Thr Pro Met Met Gly Leu Ala Leu Ser Ala
 65                  70                  75                  80

Gly Thr Gly Ile Ser Ala Ala Thr Gly Gly Met Ile Thr Ala Arg Val
                 85                  90                  95

Gly Ala Met Leu Ala Gly Thr Gly Ser Ala
            100                 105


<210> 671
<211> 939
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(916)
<223> RXN01557

<400> 671
taaaggtgtg aaaatagttc ctcacgtggg gaactatact gatccttgat gcgttaactt 60

gattgacgac gaaaaatcaa ttgaaaggat cggggactcc gtg cga agc agc aat   115
                                            Val Arg Ser Ser Asn
                                              1               5

ccc gtt ttt agt tcc ctt aag gaa act caa cgt cca caa ggc cag aac   163
Pro Val Phe Ser Ser Leu Lys Glu Thr Gln Arg Pro Gln Gly Gln Asn
                 10                  15                  20

cca tac ggt ggt tac gac aac ttc ggt ggt gtc tac cag caa aac gta   211
Pro Tyr Gly Gly Tyr Asp Asn Phe Gly Gly Val Tyr Gln Gln Asn Val
             25                  30                  35

gct cca cag aag gcg gag cgc cca atg act gtg gat gat gtg atc acc   259
Ala Pro Gln Lys Ala Glu Arg Pro Met Thr Val Asp Asp Val Ile Thr
         40                  45                  50

aag act ggt atc act ctc gcg gtt att atc gtt ttt gca ttg gtc acc   307
Lys Thr Gly Ile Thr Leu Ala Val Ile Ile Val Phe Ala Leu Val Thr
     55                  60                  65

ttt ggc gtg tgg ttg gtt agc ccc ggc ctc gga atg atc ttg acc ctt   355
Phe Gly Val Trp Leu Val Ser Pro Gly Leu Gly Met Ile Leu Thr Leu
 70                  75                  80                  85

gtt ggt gcc atc ggt ggt ttc atc acc gtt ctg gtc agc acc ttc ggc   403
Val Gly Ala Ile Gly Gly Phe Ile Thr Val Leu Val Ser Thr Phe Gly
                 90                  95                 100

aag aag tac gga tct gcg gca gtc act ttg att tac gca gta ttc gaa   451
Lys Lys Tyr Gly Ser Ala Ala Val Thr Leu Ile Tyr Ala Val Phe Glu
            105                 110                 115
```

```
ggc ctc ttc gtc ggc gga att tcc ctt ctg ctg tcc ggc ttc aca gtt   499
Gly Leu Phe Val Gly Gly Ile Ser Leu Leu Leu Ser Gly Phe Thr Val
        120                 125                 130

ggt aac gcc aac gca ggt ggc ctc att ggc cag gca gtc ctt ggc acc   547
Gly Asn Ala Asn Ala Gly Gly Leu Ile Gly Gln Ala Val Leu Gly Thr
    135                 140                 145

atc ggt gta ttc att ggc atg ctg ttt gta tac aag act ggc gct atc   595
Ile Gly Val Phe Ile Gly Met Leu Phe Val Tyr Lys Thr Gly Ala Ile
150                 155                 160                 165

aag gtc act cct aag ttc aac cgc atc ctc acc ggc atg atg gtt ggc   643
Lys Val Thr Pro Lys Phe Asn Arg Ile Leu Thr Gly Met Met Val Gly
                170                 175                 180

gtc ctg gtt ctt gtc ctg ggc aac gtt gta tgg gca ctg ttc act ggt   691
Val Leu Val Leu Val Leu Gly Asn Val Val Trp Ala Leu Phe Thr Gly
            185                 190                 195

ggc gca agc cca ctg cgt gac ggt gga atc atc gcg att atc ttc tcc   739
Gly Ala Ser Pro Leu Arg Asp Gly Gly Ile Ile Ala Ile Ile Phe Ser
        200                 205                 210

ctc ttc tgc atc ggc ctg gca gca ttc agc ttc ctc tcc gac ttc gat   787
Leu Phe Cys Ile Gly Leu Ala Ala Phe Ser Phe Leu Ser Asp Phe Asp
    215                 220                 225

gca gct gac cgc ctc gtc cgc gaa ggt gca cct tcc aag atg gca tgg   835
Ala Ala Asp Arg Leu Val Arg Glu Gly Ala Pro Ser Lys Met Ala Trp
230                 235                 240                 245

ggc gtt gcg ctt ggt ctt gca gtg acc ttg gtc tgg ctc tac acc gaa   883
Gly Val Ala Leu Gly Leu Ala Val Thr Leu Val Trp Leu Tyr Thr Glu
                250                 255                 260

atc cta cgt ctg ctt agc tac ttc caa aac cgc tagtttacgc agcacaagac 936
Ile Leu Arg Leu Leu Ser Tyr Phe Gln Asn Arg
            265                 270

ccc                                                               939
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<210> 672
<211> 272
<212> PRT
<213> Corynebacterium glutamicum

<400> 672

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Val Arg Ser Ser Asn Pro Val Phe Ser Ser Leu Lys Glu Thr Gln Arg
  1               5                  10                  15

Pro Gln Gly Gln Asn Pro Tyr Gly Gly Tyr Asp Asn Phe Gly Gly Val
             20                  25                  30

Tyr Gln Gln Asn Val Ala Pro Gln Lys Ala Glu Arg Pro Met Thr Val
         35                  40                  45

Asp Asp Val Ile Thr Lys Thr Gly Ile Thr Leu Ala Val Ile Ile Val
     50                  55                  60
```

```
Phe Ala Leu Val Thr Phe Gly Val Trp Leu Val Ser Pro Gly Leu Gly
 65                  70                  75                  80

Met Ile Leu Thr Leu Val Gly Ala Ile Gly Gly Phe Ile Thr Val Leu
                 85                  90                  95

Val Ser Thr Phe Gly Lys Lys Tyr Gly Ser Ala Ala Val Thr Leu Ile
            100                 105                 110

Tyr Ala Val Phe Glu Gly Leu Phe Val Gly Gly Ile Ser Leu Leu Leu
        115                 120                 125

Ser Gly Phe Thr Val Gly Asn Ala Asn Ala Gly Gly Leu Ile Gly Gln
    130                 135                 140

Ala Val Leu Gly Thr Ile Gly Val Phe Ile Gly Met Leu Phe Val Tyr
145                 150                 155                 160

Lys Thr Gly Ala Ile Lys Val Thr Pro Lys Phe Asn Arg Ile Leu Thr
                165                 170                 175

Gly Met Met Val Gly Val Leu Val Leu Val Leu Gly Asn Val Val Trp
            180                 185                 190

Ala Leu Phe Thr Gly Gly Ala Ser Pro Leu Arg Asp Gly Gly Ile Ile
        195                 200                 205

Ala Ile Ile Phe Ser Leu Phe Cys Ile Gly Leu Ala Ala Phe Ser Phe
    210                 215                 220

Leu Ser Asp Phe Asp Ala Ala Asp Arg Leu Val Arg Glu Gly Ala Pro
225                 230                 235                 240

Ser Lys Met Ala Trp Gly Val Ala Leu Gly Leu Ala Val Thr Leu Val
                245                 250                 255

Trp Leu Tyr Thr Glu Ile Leu Arg Leu Leu Ser Tyr Phe Gln Asn Arg
            260                 265                 270
```

Sequence Listing

<210> 673
<211> 939
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(916)
<223> FRXA01557

<400> 673
taaaggtgtg aaaatagttc ctcacgtggg gaactatact gatccttgat gcgttaactt 60

gattgacgac gaaaaatcaa ttgaaaggat cggggactcc gtg cga agc agc aat 115
                                                Val Arg Ser Ser Asn
                                                  1   5

```
ccc gtt ttt agt tcc ctt aag gaa act caa cgt cca caa ggc cag aac   163
Pro Val Phe Ser Ser Leu Lys Glu Thr Gln Arg Pro Gln Gly Gln Asn
                 10                  15                  20

cca tac ggt ggt tac gac aac ttc ggt ggt gtc tac cag caa aac gta   211
Pro Tyr Gly Gly Tyr Asp Asn Phe Gly Gly Val Tyr Gln Gln Asn Val
             25                  30                  35

gct cca cag aag gcg gag cgc cca atg act gtg gat gat gtg atc acc   259
Ala Pro Gln Lys Ala Glu Arg Pro Met Thr Val Asp Asp Val Ile Thr
         40                  45                  50

aag act ggt atc act ctc gcg gtt att atc gtt ttt gca ttg gtc acc   307
Lys Thr Gly Ile Thr Leu Ala Val Ile Ile Val Phe Ala Leu Val Thr
     55                  60                  65

ttt ggc gtg tgg ttg gtt agc ccc ggc ctc gga atg atc ttg acc ctt   355
Phe Gly Val Trp Leu Val Ser Pro Gly Leu Gly Met Ile Leu Thr Leu
 70                  75                  80                  85

gtt ggt gcc atc ggt ggt ttc atc acc gtt ctg gtc agc acc ttc ggc   403
Val Gly Ala Ile Gly Gly Phe Ile Thr Val Leu Val Ser Thr Phe Gly
                 90                  95                 100

aag aag tac gga tct gcg gca gtc act ttg att tac gca gta ttc gaa   451
Lys Lys Tyr Gly Ser Ala Ala Val Thr Leu Ile Tyr Ala Val Phe Glu
             105                 110                 115

ggc ctc ttc gtc ggc gga att tcc ctt ctg ctg tcc ggc ttc aca gtt   499
Gly Leu Phe Val Gly Gly Ile Ser Leu Leu Leu Ser Gly Phe Thr Val
         120                 125                 130

ggt aac gcc aac gca ggt ggc ctc att ggc cag gca gtc ctt ggc acc   547
Gly Asn Ala Asn Ala Gly Gly Leu Ile Gly Gln Ala Val Leu Gly Thr
     135                 140                 145

atc ggt gta ttc att ggc atg ctg ttt gta tac aag act ggc gct atc   595
Ile Gly Val Phe Ile Gly Met Leu Phe Val Tyr Lys Thr Gly Ala Ile
150                 155                 160                 165

aag gtc act cct aag ttc aac cgc atc ctc acc ggc atg atg gtt ggc   643
Lys Val Thr Pro Lys Phe Asn Arg Ile Leu Thr Gly Met Met Val Gly
                 170                 175                 180

gtc ctg gtt ctt gtc ctg ggc aac gtt gta tgg gca ctg ttc act ggt   691
Val Leu Val Leu Val Leu Gly Asn Val Val Trp Ala Leu Phe Thr Gly
             185                 190                 195

ggc gca agc cca ctg cgt gac ggt gga atc atc gcg att atc ttc tcc   739
Gly Ala Ser Pro Leu Arg Asp Gly Gly Ile Ile Ala Ile Ile Phe Ser
         200                 205                 210

ctc ttc tgc atc ggc ctg gca gca ttc agc ttc ctc tcc gac ttc gat   787
Leu Phe Cys Ile Gly Leu Ala Ala Phe Ser Phe Leu Ser Asp Phe Asp
     215                 220                 225

gca gct gac cgc ctc gtc cgc gaa ggt gca cct tcc aag atg gca tgg   835
Ala Ala Asp Arg Leu Val Arg Glu Gly Ala Pro Ser Lys Met Ala Trp
230                 235                 240                 245

ggc gtt gcg ctt ggt ctt gca gtg acc ttg gtc tgg ctc tac acc gaa   883
```

```
Gly Val Ala Leu Gly Leu Ala Val Thr Leu Val Trp Leu Tyr Thr Glu
                250                 255                 260

atc cta cgt ctg ctt agc tac ttc caa aac cgc tagtttacgc agcacaagac 936
Ile Leu Arg Leu Leu Ser Tyr Phe Gln Asn Arg
            265                 270

ccc                                                               939


<210> 674
<211> 272
<212> PRT
<213> Corynebacterium glutamicum

<400> 674
Val Arg Ser Ser Asn Pro Val Phe Ser Ser Leu Lys Glu Thr Gln Arg
  1               5                  10                  15

Pro Gln Gly Gln Asn Pro Tyr Gly Gly Tyr Asp Asn Phe Gly Gly Val
             20                  25                  30

Tyr Gln Gln Asn Val Ala Pro Gln Lys Ala Glu Arg Pro Met Thr Val
         35                  40                  45

Asp Asp Val Ile Thr Lys Thr Gly Ile Thr Leu Ala Val Ile Ile Val
     50                  55                  60

Phe Ala Leu Val Thr Phe Gly Val Trp Leu Val Ser Pro Gly Leu Gly
 65                  70                  75                  80

Met Ile Leu Thr Leu Val Gly Ala Ile Gly Gly Phe Ile Thr Val Leu
                 85                  90                  95

Val Ser Thr Phe Gly Lys Lys Tyr Gly Ser Ala Ala Val Thr Leu Ile
            100                 105                 110

Tyr Ala Val Phe Glu Gly Leu Phe Val Gly Gly Ile Ser Leu Leu Leu
        115                 120                 125

Ser Gly Phe Thr Val Gly Asn Ala Asn Ala Gly Gly Leu Ile Gly Gln
    130                 135                 140

Ala Val Leu Gly Thr Ile Gly Val Phe Ile Gly Met Leu Phe Val Tyr
145                 150                 155                 160

Lys Thr Gly Ala Ile Lys Val Thr Pro Lys Phe Asn Arg Ile Leu Thr
                165                 170                 175

Gly Met Met Val Gly Val Leu Val Leu Val Leu Gly Asn Val Val Trp
            180                 185                 190

Ala Leu Phe Thr Gly Gly Ala Ser Pro Leu Arg Asp Gly Gly Ile Ile
        195                 200                 205

Ala Ile Ile Phe Ser Leu Phe Cys Ile Gly Leu Ala Ala Phe Ser Phe
    210                 215                 220

Leu Ser Asp Phe Asp Ala Ala Asp Arg Leu Val Arg Glu Gly Ala Pro
225                 230                 235                 240
```

```
Ser Lys Met Ala Trp Gly Val Ala Leu Gly Leu Ala Val Thr Leu Val
                245                 250                 255

Trp Leu Tyr Thr Glu Ile Leu Arg Leu Leu Ser Tyr Phe Gln Asn Arg
            260                 265                 270
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<210> 675
<211> 1158
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1135)
<223> RXN01574

<400> 675

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aaaaatccgc acaccccaca ttgctcaaag gaattgacaa ggcgcttcgc aaggccgagt 60

aaggtgggca acgagtcggt gagagtatga ggaatatttg atg agc aac aaa cgc   115
                                              Met Ser Asn Lys Arg
                                                1               5

atc ggt gta gtg atc gtt tcc tac gga cac gaa caa gat gtt gcc aac   163
Ile Gly Val Val Ile Val Ser Tyr Gly His Glu Gln Asp Val Ala Asn
                10                  15                  20

ctg gta gac aca ttt gca gat cag ctg aaa act ggt gac cgc gta gtt   211
Leu Val Asp Thr Phe Ala Asp Gln Leu Lys Thr Gly Asp Arg Val Val
            25                  30                  35

gtc gtg gac aac cgc aaa cct tgg gtg tta aaa gac gcc gtg ggg gag   259
Val Val Asp Asn Arg Lys Pro Trp Val Leu Lys Asp Ala Val Gly Glu
        40                  45                  50

cgc ctg gaa aaa cac ggc gca gag atc atc aac cac gac aac ggt ggt   307
Arg Leu Glu Lys His Gly Ala Glu Ile Ile Asn His Asp Asn Gly Gly
    55                  60                  65

ttc gcc gct ggc tgc aac gtg ggc gca gcg cac atc gtg gat gac gtt   355
Phe Ala Ala Gly Cys Asn Val Gly Ala Ala His Ile Val Asp Asp Val
70                  75                  80                  85

gac ctg ctg ttc ttc ctc aac ccc gac aca gtg atc gac gat ccc acc   403
Asp Leu Leu Phe Phe Leu Asn Pro Asp Thr Val Ile Asp Asp Pro Thr
                90                  95                  100

ctg ttc aat tcg ctg aga cgc gtc gat gaa cag tgg gca gca ttc atg   451
Leu Phe Asn Ser Leu Arg Arg Val Asp Glu Gln Trp Ala Ala Phe Met
            105                 110                 115

ccg tac ctg ctg ctt cct gac agc acc att aac tcc gca ggc aac gcc   499
Pro Tyr Leu Leu Leu Pro Asp Ser Thr Ile Asn Ser Ala Gly Asn Ala
        120                 125                 130

ctg cat att tcc gga ctg tcg tgg gtg act ggt ctg gat gaa aaa cca   547
Leu His Ile Ser Gly Leu Ser Trp Val Thr Gly Leu Asp Glu Lys Pro
```

```
    135                 140                 145

gtt gaa ggc tca tct gaa gtt acc gat att tcc att gcc tct ggc gcc   595
Val Glu Gly Ser Ser Glu Val Thr Asp Ile Ser Ile Ala Ser Gly Ala
150                 155                 160                 165

tgc ctt gcc gtg cgc gtg gac tgg tgg aaa cgc ctc ggt ggc atg gaa   643
Cys Leu Ala Val Arg Val Asp Trp Trp Lys Arg Leu Gly Gly Met Glu
                170                 175                 180

gaa ctg tat ttc atg tac cac gaa gac act gac ttc tcc gcc cgc ttg   691
Glu Leu Tyr Phe Met Tyr His Glu Asp Thr Asp Phe Ser Ala Arg Leu
            185                 190                 195

ctg ctg gcc ggc ggt cga att ggt ctc ctg cat tcc gcg tat gtc acc   739
Leu Leu Ala Gly Gly Arg Ile Gly Leu Leu His Ser Ala Tyr Val Thr
        200                 205                 210

cac cat tac gac tac gcc aag ggt gac tac aag tgg att tac atc gaa   787
His His Tyr Asp Tyr Ala Lys Gly Asp Tyr Lys Trp Ile Tyr Ile Glu
    215                 220                 225

cga aac cga cac gtt ttg ctg ctc agc gtg ctg ccg ctt cca ttg ctg   835
Arg Asn Arg His Val Leu Leu Leu Ser Val Leu Pro Leu Pro Leu Leu
230                 235                 240                 245

ttc gtg ctg atc ccg cag atc ctc ggt gtg aac ctg gga ctg tgg gcg   883
Phe Val Leu Ile Pro Gln Ile Leu Gly Val Asn Leu Gly Leu Trp Ala
                250                 255                 260

att gcc gca aag gaa aag agg gtc gga ctc aag gtg aag tcc ctt cgc   931
Ile Ala Ala Lys Glu Lys Arg Val Gly Leu Lys Val Lys Ser Leu Arg
            265                 270                 275

ctc ctg atc cgc gat cta cca gcg att ttc aaa ctg cgt agg agc acg   979
Leu Leu Ile Arg Asp Leu Pro Ala Ile Phe Lys Leu Arg Arg Ser Thr
        280                 285                 290

cag gag ctt gcc gaa ctc aca cca tcg caa tat ctg gca aaa atg gaa   1027
Gln Glu Leu Ala Glu Leu Thr Pro Ser Gln Tyr Leu Ala Lys Met Glu
    295                 300                 305

tgg cgc cta gac aat ccc aac cta ggc aac att gga tcc aac aag att   1075
Trp Arg Leu Asp Asn Pro Asn Leu Gly Asn Ile Gly Ser Asn Lys Ile
310                 315                 320                 325

gtt gcg act gga tat aag acc tat tac aag ttg tgt atg agt atc ctg   1123
Val Ala Thr Gly Tyr Lys Thr Tyr Tyr Lys Leu Cys Met Ser Ile Leu
                330                 335                 340

aaa ttg ctc gct taacacccca taaagagggt gaa                        1158
Lys Leu Leu Ala
            345
```

<210> 676
<211> 345
<212> PRT
<213> Corynebacterium glutamicum

<400> 676

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Met Ser Asn Lys Arg Ile Gly Val Val Ile Val Ser Tyr Gly His Glu
 1               5                  10                  15

Gln Asp Val Ala Asn Leu Val Asp Thr Phe Ala Asp Gln Leu Lys Thr
            20                  25                  30

Gly Asp Arg Val Val Val Val Asp Asn Arg Lys Pro Trp Val Leu Lys
        35                  40                  45

Asp Ala Val Gly Glu Arg Leu Glu Lys His Gly Ala Glu Ile Ile Asn
    50                  55                  60

His Asp Asn Gly Gly Phe Ala Ala Gly Cys Asn Val Gly Ala Ala His
65                  70                  75                  80

Ile Val Asp Asp Val Asp Leu Leu Phe Phe Leu Asn Pro Asp Thr Val
                85                  90                  95

Ile Asp Asp Pro Thr Leu Phe Asn Ser Leu Arg Arg Val Asp Glu Gln
            100                 105                 110

Trp Ala Ala Phe Met Pro Tyr Leu Leu Leu Pro Asp Ser Thr Ile Asn
        115                 120                 125

Ser Ala Gly Asn Ala Leu His Ile Ser Gly Leu Ser Trp Val Thr Gly
    130                 135                 140

Leu Asp Glu Lys Pro Val Glu Gly Ser Ser Glu Val Thr Asp Ile Ser
145                 150                 155                 160

Ile Ala Ser Gly Ala Cys Leu Ala Val Arg Val Asp Trp Trp Lys Arg
                165                 170                 175

Leu Gly Gly Met Glu Glu Leu Tyr Phe Met Tyr His Glu Asp Thr Asp
            180                 185                 190

Phe Ser Ala Arg Leu Leu Leu Ala Gly Gly Arg Ile Gly Leu Leu His
        195                 200                 205

Ser Ala Tyr Val Thr His His Tyr Asp Tyr Ala Lys Gly Asp Tyr Lys
    210                 215                 220

Trp Ile Tyr Ile Glu Arg Asn Arg His Val Leu Leu Leu Ser Val Leu
225                 230                 235                 240

Pro Leu Pro Leu Leu Phe Val Leu Ile Pro Gln Ile Leu Gly Val Asn
                245                 250                 255

Leu Gly Leu Trp Ala Ile Ala Ala Lys Glu Lys Arg Val Gly Leu Lys
            260                 265                 270

Val Lys Ser Leu Arg Leu Leu Ile Arg Asp Leu Pro Ala Ile Phe Lys
        275                 280                 285

Leu Arg Arg Ser Thr Gln Glu Leu Ala Glu Leu Thr Pro Ser Gln Tyr
    290                 295                 300

Leu Ala Lys Met Glu Trp Arg Leu Asp Asn Pro Asn Leu Gly Asn Ile
305                 310                 315                 320

Gly Ser Asn Lys Ile Val Ala Thr Gly Tyr Lys Thr Tyr Tyr Lys Leu
```

```
                325                 330                 335

Cys Met Ser Ile Leu Lys Leu Leu Ala
            340                 345


<210> 677
<211> 1158
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1135)
<223> FRXA01574

<400> 677
aaaaatccgc acaccccaca ttgctcaaag gaattgacaa ggcgcttcgc aaggccgagt 60

aaggtgggca acgagtcggt gagagtatga ggaatatttg atg agc aac aaa cgc   115
                                              Met Ser Asn Lys Arg
                                                1               5

atc ggt gta gtg atc gtt tcc tac gga cac gaa caa gat gtt gcc aac   163
Ile Gly Val Val Ile Val Ser Tyr Gly His Glu Gln Asp Val Ala Asn
                10                  15                  20

ctg gta gac aca ttt gca gat cag ctg aaa act ggt gac cgc gta gtt   211
Leu Val Asp Thr Phe Ala Asp Gln Leu Lys Thr Gly Asp Arg Val Val
            25                  30                  35

gtc gtg gac aac cgc aaa cct tgg gtg tta aaa gac gcc gtg ggg gag   259
Val Val Asp Asn Arg Lys Pro Trp Val Leu Lys Asp Ala Val Gly Glu
        40                  45                  50

cgc ctg gaa aaa cac ggc gca gag atc atc aac cac gac aac ggt ggt   307
Arg Leu Glu Lys His Gly Ala Glu Ile Ile Asn His Asp Asn Gly Gly
    55                  60                  65

ttc gcc gct ggc tgc aac gtg ggc gca gcg cac atc gtg gat gac gtt   355
Phe Ala Ala Gly Cys Asn Val Gly Ala Ala His Ile Val Asp Asp Val
70                  75                  80                  85

gac ctg ctg ttc ttc ctc aac ccc gac aca gtg atc gac gat ccc acc   403
Asp Leu Leu Phe Phe Leu Asn Pro Asp Thr Val Ile Asp Asp Pro Thr
                90                  95                  100

ctg ttc aat tcg ctg aga cgc gtc gat gaa cag tgg gca gca ttc atg   451
Leu Phe Asn Ser Leu Arg Arg Val Asp Glu Gln Trp Ala Ala Phe Met
            105                 110                 115

ccg tac ctg ctg ctt cct gac agc acc att aac tcc gca ggc aac gcc   499
Pro Tyr Leu Leu Leu Pro Asp Ser Thr Ile Asn Ser Ala Gly Asn Ala
        120                 125                 130

ctg cat att tcc gga ctg tcg tgg gtg act ggt ctg gat gaa aaa cca   547
Leu His Ile Ser Gly Leu Ser Trp Val Thr Gly Leu Asp Glu Lys Pro
    135                 140                 145

gtt gaa ggc tca tct gaa gtt acc gat att tcc att gcc tct ggc gcc   595
Val Glu Gly Ser Ser Glu Val Thr Asp Ile Ser Ile Ala Ser Gly Ala
```

```
150                 155                 160                 165

tgc ctt gcc gtg cgc gtg gac tgg tgg aaa cgc ctc ggt ggc atg gaa   643
Cys Leu Ala Val Arg Val Asp Trp Trp Lys Arg Leu Gly Gly Met Glu
                170                 175                 180

gaa ctg tat ttc atg tac cac gaa gac act gac ttc tcc gcc cgc ttg   691
Glu Leu Tyr Phe Met Tyr His Glu Asp Thr Asp Phe Ser Ala Arg Leu
            185                 190                 195

ctg ctg gcc ggc ggt cga att ggt ctc ctg cat tcc gcg tat gtc acc   739
Leu Leu Ala Gly Gly Arg Ile Gly Leu Leu His Ser Ala Tyr Val Thr
        200                 205                 210

cac cat tac gac tac gcc aag ggt gac tac aag tgg att tac atc gaa   787
His His Tyr Asp Tyr Ala Lys Gly Asp Tyr Lys Trp Ile Tyr Ile Glu
    215                 220                 225

cga aac cga cac gtt ttg ctg ctc agc gtg ctg ccg ctt cca ttg ctg   835
Arg Asn Arg His Val Leu Leu Leu Ser Val Leu Pro Leu Pro Leu Leu
230                 235                 240                 245

ttc gtg ctg atc ccg cag atc ctc ggt gtg aac ctg gga ctg tgg gcg   883
Phe Val Leu Ile Pro Gln Ile Leu Gly Val Asn Leu Gly Leu Trp Ala
                250                 255                 260

att gcc gca aag gaa aag agg gtc gga ctc aag gtg aag tcc ctt cgc   931
Ile Ala Ala Lys Glu Lys Arg Val Gly Leu Lys Val Lys Ser Leu Arg
            265                 270                 275

ctc ctg atc cgc gat cta cca gcg att ttc aaa ctg cgt agg agc acg   979
Leu Leu Ile Arg Asp Leu Pro Ala Ile Phe Lys Leu Arg Arg Ser Thr
        280                 285                 290

cag gag ctt gcc gaa ctc aca cca tcg caa tat ctg gca aaa atg gaa   1027
Gln Glu Leu Ala Glu Leu Thr Pro Ser Gln Tyr Leu Ala Lys Met Glu
    295                 300                 305

tgg cgc cta gac aat ccc aac cta ggc aac att gga tcc aac aag att   1075
Trp Arg Leu Asp Asn Pro Asn Leu Gly Asn Ile Gly Ser Asn Lys Ile
310                 315                 320                 325

gtt gcg act gga tat aag acc tat tac aag ttg tgt atg agt atc ctg   1123
Val Ala Thr Gly Tyr Lys Thr Tyr Tyr Lys Leu Cys Met Ser Ile Leu
                330                 335                 340

aaa ttg ctc gct taacacccca taaagagggt gaa                        1158
Lys Leu Leu Ala
            345
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Sequence Listing

<210> 678
<211> 345
<212> PRT
<213> Corynebacterium glutamicum

<400> 678

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Met Ser Asn Lys Arg Ile Gly Val Val Ile Val Ser Tyr Gly His Glu
  1               5                  10                  15

Gln Asp Val Ala Asn Leu Val Asp Thr Phe Ala Asp Gln Leu Lys Thr
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                20                  25                  30

Gly Asp Arg Val Val Val Val Asp Asn Arg Lys Pro Trp Val Leu Lys
          35                  40                  45

Asp Ala Val Gly Glu Arg Leu Glu Lys His Gly Ala Glu Ile Ile Asn
      50                  55                  60

His Asp Asn Gly Gly Phe Ala Ala Gly Cys Asn Val Gly Ala Ala His
 65                  70                  75                  80

Ile Val Asp Asp Val Asp Leu Leu Phe Phe Leu Asn Pro Asp Thr Val
                 85                  90                  95

Ile Asp Asp Pro Thr Leu Phe Asn Ser Leu Arg Arg Val Asp Glu Gln
            100                 105                 110

Trp Ala Ala Phe Met Pro Tyr Leu Leu Leu Pro Asp Ser Thr Ile Asn
        115                 120                 125

Ser Ala Gly Asn Ala Leu His Ile Ser Gly Leu Ser Trp Val Thr Gly
    130                 135                 140

Leu Asp Glu Lys Pro Val Glu Gly Ser Ser Glu Val Thr Asp Ile Ser
145                 150                 155                 160

Ile Ala Ser Gly Ala Cys Leu Ala Val Arg Val Asp Trp Trp Lys Arg
                165                 170                 175

Leu Gly Gly Met Glu Glu Leu Tyr Phe Met Tyr His Glu Asp Thr Asp
            180                 185                 190

Phe Ser Ala Arg Leu Leu Leu Ala Gly Gly Arg Ile Gly Leu Leu His
        195                 200                 205

Ser Ala Tyr Val Thr His His Tyr Asp Tyr Ala Lys Gly Asp Tyr Lys
    210                 215                 220

Trp Ile Tyr Ile Glu Arg Asn Arg His Val Leu Leu Leu Ser Val Leu
225                 230                 235                 240

Pro Leu Pro Leu Leu Phe Val Leu Ile Pro Gln Ile Leu Gly Val Asn
                245                 250                 255

Leu Gly Leu Trp Ala Ile Ala Ala Lys Glu Lys Arg Val Gly Leu Lys
            260                 265                 270

Val Lys Ser Leu Arg Leu Leu Ile Arg Asp Leu Pro Ala Ile Phe Lys
        275                 280                 285

Leu Arg Arg Ser Thr Gln Glu Leu Ala Glu Leu Thr Pro Ser Gln Tyr
    290                 295                 300

Leu Ala Lys Met Glu Trp Arg Leu Asp Asn Pro Asn Leu Gly Asn Ile
305                 310                 315                 320

Gly Ser Asn Lys Ile Val Ala Thr Gly Tyr Lys Thr Tyr Tyr Lys Leu
                325                 330                 335

Cys Met Ser Ile Leu Lys Leu Leu Ala
            340                 345
```

<210> 679
<211> 1143
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1120)
<223> RXN01589

<400> 679
agggatgtag atgcgccctc atattggtac aaaaatataa attatcagca tgatttggac 60

gctttaattc aaaaattgta agctgttagg aggtccacaa atg gta gaa caa ata 115
Met Val Glu Gln Ile
1 5

aaa gat aaa cta gga cgt ccc atc cgt gac tta cgg tta tct gtg aca 163
Lys Asp Lys Leu Gly Arg Pro Ile Arg Asp Leu Arg Leu Ser Val Thr
10 15 20

gat cgg tgt aac ttt agg tgt gat tat tgc atg cct aaa gag gta ttt 211
Asp Arg Cys Asn Phe Arg Cys Asp Tyr Cys Met Pro Lys Glu Val Phe
25 30 35

gga gat gat ttc gta ttt tta cct aaa aat gaa ctg tta acg ttt gat 259
Gly Asp Asp Phe Val Phe Leu Pro Lys Asn Glu Leu Leu Thr Phe Asp
40 45 50

gaa atg gct aga atc gct aag gta tat gca gaa tta ggt gta aaa aaa 307
Glu Met Ala Arg Ile Ala Lys Val Tyr Ala Glu Leu Gly Val Lys Lys
55 60 65

ata cgc att aca ggt gga gaa cca ttg atg cga cgc gat tta gat gta 355
Ile Arg Ile Thr Gly Gly Glu Pro Leu Met Arg Arg Asp Leu Asp Val
70 75 80 85

ctt ata gct aaa tta aat caa atc gat ggt att gaa gat att ggt ttg 403
Leu Ile Ala Lys Leu Asn Gln Ile Asp Gly Ile Glu Asp Ile Gly Leu
90 95 100

act aca aat ggt ttg tta tta aaa aag cat gga caa aag tta tat gat 451
Thr Thr Asn Gly Leu Leu Leu Lys Lys His Gly Gln Lys Leu Tyr Asp
105 110 115

gct ggg cta cgc aga att aat gtc agt ttg gat gct att gat gat acg 499
Ala Gly Leu Arg Arg Ile Asn Val Ser Leu Asp Ala Ile Asp Asp Thr
120 125 130

cta ttt caa tca atc aat aat cgt aat att aaa gcg act acg att tta 547
Leu Phe Gln Ser Ile Asn Asn Arg Asn Ile Lys Ala Thr Thr Ile Leu
135 140 145

gaa caa att gat tac gcg acg tct att ggt ttg aat gta aaa gta aat 595
Glu Gln Ile Asp Tyr Ala Thr Ser Ile Gly Leu Asn Val Lys Val Asn
150 155 160 165

gtt gtt ata caa aaa ggt att aac gat gat caa atc ata cca atg ctt 643
Val Val Ile Gln Lys Gly Ile Asn Asp Asp Gln Ile Ile Pro Met Leu

```
                  170                 175                 180

gaa tat ttt aaa gat aaa cat ata gag att cga ttt ata gaa ttt atg   691
Glu Tyr Phe Lys Asp Lys His Ile Glu Ile Arg Phe Ile Glu Phe Met
            185                 190                 195

gat gtt ggt aat gat aat gga tgg gat ttc agt aaa gtt gta act aaa   739
Asp Val Gly Asn Asp Asn Gly Trp Asp Phe Ser Lys Val Val Thr Lys
        200                 205                 210

gat gaa atg ctt aca atg ata gag cag cac ttt gaa atc gat cct gta   787
Asp Glu Met Leu Thr Met Ile Glu Gln His Phe Glu Ile Asp Pro Val
    215                 220                 225

gaa cca aaa tat ttt ggg gaa gta gca aaa tat tat cgc cat aag gat   835
Glu Pro Lys Tyr Phe Gly Glu Val Ala Lys Tyr Tyr Arg His Lys Asp
230                 235                 240                 245

aat ggt gtt caa ttt ggt ttg att aca agt gtt tca caa tca ttt tgt   883
Asn Gly Val Gln Phe Gly Leu Ile Thr Ser Val Ser Gln Ser Phe Cys
                250                 255                 260

tct aca tgt aca cgc gca agg ctg tca tca gat ggg aag ttt tac gga   931
Ser Thr Cys Thr Arg Ala Arg Leu Ser Ser Asp Gly Lys Phe Tyr Gly
            265                 270                 275

tgt tta ttt gca act gtc gat gga ttt aac gtt aaa gcg ttt att cgt   979
Cys Leu Phe Ala Thr Val Asp Gly Phe Asn Val Lys Ala Phe Ile Arg
        280                 285                 290

tct ggc gtg acc gac gaa gaa tta aaa gaa caa ttt aaa gct tta tgg   1027
Ser Gly Val Thr Asp Glu Glu Leu Lys Glu Gln Phe Lys Ala Leu Trp
    295                 300                 305

caa ata aga gat gat cga tat tca gat gag aga act gct caa aca gtt   1075
Gln Ile Arg Asp Asp Arg Tyr Ser Asp Glu Arg Thr Ala Gln Thr Val
310                 315                 320                 325

gcc aat cgt caa cgt aaa aag ata aac atg aat tat att ggt ggt       1120
Ala Asn Arg Gln Arg Lys Lys Ile Asn Met Asn Tyr Ile Gly Gly
                330                 335                 340

taatgtgtag ggaccactac ata                                       1143
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<210> 680
<211> 340
<212> PRT
<213> Corynebacterium glutamicum

<400> 680

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Met Val Glu Gln Ile Lys Asp Lys Leu Gly Arg Pro Ile Arg Asp Leu
  1               5                  10                  15

Arg Leu Ser Val Thr Asp Arg Cys Asn Phe Arg Cys Asp Tyr Cys Met
             20                  25                  30

Pro Lys Glu Val Phe Gly Asp Asp Phe Val Phe Leu Pro Lys Asn Glu
         35                  40                  45

Leu Leu Thr Phe Asp Glu Met Ala Arg Ile Ala Lys Val Tyr Ala Glu
```

```
     50                  55                  60

Leu Gly Val Lys Lys Ile Arg Ile Thr Gly Gly Glu Pro Leu Met Arg
 65                  70                  75                  80

Arg Asp Leu Asp Val Leu Ile Ala Lys Leu Asn Gln Ile Asp Gly Ile
                 85                  90                  95

Glu Asp Ile Gly Leu Thr Thr Asn Gly Leu Leu Leu Lys Lys His Gly
            100                 105                 110

Gln Lys Leu Tyr Asp Ala Gly Leu Arg Arg Ile Asn Val Ser Leu Asp
        115                 120                 125

Ala Ile Asp Asp Thr Leu Phe Gln Ser Ile Asn Asn Arg Asn Ile Lys
    130                 135                 140

Ala Thr Thr Ile Leu Glu Gln Ile Asp Tyr Ala Thr Ser Ile Gly Leu
145                 150                 155                 160

Asn Val Lys Val Asn Val Val Ile Gln Lys Gly Ile Asn Asp Asp Gln
                165                 170                 175

Ile Ile Pro Met Leu Glu Tyr Phe Lys Asp Lys His Ile Glu Ile Arg
            180                 185                 190

Phe Ile Glu Phe Met Asp Val Gly Asn Asp Asn Gly Trp Asp Phe Ser
        195                 200                 205

Lys Val Val Thr Lys Asp Glu Met Leu Thr Met Ile Glu Gln His Phe
    210                 215                 220

Glu Ile Asp Pro Val Glu Pro Lys Tyr Phe Gly Glu Val Ala Lys Tyr
225                 230                 235                 240

Tyr Arg His Lys Asp Asn Gly Val Gln Phe Gly Leu Ile Thr Ser Val
                245                 250                 255

Ser Gln Ser Phe Cys Ser Thr Cys Thr Arg Ala Arg Leu Ser Ser Asp
            260                 265                 270

Gly Lys Phe Tyr Gly Cys Leu Phe Ala Thr Val Asp Gly Phe Asn Val
        275                 280                 285

Lys Ala Phe Ile Arg Ser Gly Val Thr Asp Glu Glu Leu Lys Glu Gln
    290                 295                 300

Phe Lys Ala Leu Trp Gln Ile Arg Asp Asp Arg Tyr Ser Asp Glu Arg
305                 310                 315                 320

Thr Ala Gln Thr Val Ala Asn Arg Gln Arg Lys Lys Ile Asn Met Asn
                325                 330                 335

Tyr Ile Gly Gly
            340
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<210> 681
<211> 1425
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1402)
<223> RXN01592

<400> 681
gattcaatgg tagaggtatt tcatttcctc ccattggatc acactctttt tgtcgttcta 60

taataaagtc tttacccggt tctcaacatc aaggaacaac atg gct gat aac ttc 115
Met Ala Asp Asn Phe
1 5

gac cgc tct cgt gac aac gat cgc tca agc gac cgc act cct cgt gga 163
Asp Arg Ser Arg Asp Asn Asp Arg Ser Ser Asp Arg Thr Pro Arg Gly
10 15 20

gac cgc ggc gat cgc ggt ggc tac cga aac tcc cgc ggc aac gat gac 211
Asp Arg Gly Asp Arg Gly Gly Tyr Arg Asn Ser Arg Gly Asn Asp Asp
25 30 35

cgc gga aac tac cgt caa aac cga gat ggt gaa tca cga gat cgc ggc 259
Arg Gly Asn Tyr Arg Gln Asn Arg Asp Gly Glu Ser Arg Asp Arg Gly
40 45 50

gga tac ctc ggt gac cgt cgc gac aac cgc tca ggt gaa tat cgt caa 307
Gly Tyr Leu Gly Asp Arg Arg Asp Asn Arg Ser Gly Glu Tyr Arg Gln
55 60 65

cgt gac gat agg cgt gac gat cgt agg gac aac cga agc gat gac cgc 355
Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asn Arg Ser Asp Asp Arg
70 75 80 85

cgc ggt ggt tac cgc tcc gat cgc aac ttt gac gat cgc aac agc aac 403
Arg Gly Gly Tyr Arg Ser Asp Arg Asn Phe Asp Asp Arg Asn Ser Asn
90 95 100

atg cgt gat gat cgt cgc ggc ggc gac cgt tca tac agc cgt aat gat 451
Met Arg Asp Asp Arg Arg Gly Gly Asp Arg Ser Tyr Ser Arg Asn Asp
105 110 115

cgc tcc gat cgt ggc tat cgt agc aat gac cgc tac gac cgt aat gat 499
Arg Ser Asp Arg Gly Tyr Arg Ser Asn Asp Arg Tyr Asp Arg Asn Asp
120 125 130

cgt cgc gat gac aac agg gac acc agg ggt ggc gat cgc gga gac cgt 547
Arg Arg Asp Asp Asn Arg Asp Thr Arg Gly Gly Asp Arg Gly Asp Arg
135 140 145

cgc tac gac agg cgc gat gac cga cgt gat gat cgt cgc gat gat cgt 595
Arg Tyr Asp Arg Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asp Arg
150 155 160 165

cgt ggc gga cag ggc cag ggg cgt cca ggt gga gat cgt cga cat gcg 643
Arg Gly Gly Gln Gly Gln Gly Arg Pro Gly Gly Asp Arg Arg His Ala
170 175 180

aac cgt gca ggt gca ggt cgc gat cag cag cgt gat tcg ctg cat cca 691
Asn Arg Ala Gly Ala Gly Arg Asp Gln Gln Arg Asp Ser Leu His Pro
185 190 195

```
cag cgc gct ggt ttc cgt gaa gag cgc ttg aac act cgt ctc aat gag   739
Gln Arg Ala Gly Phe Arg Glu Glu Arg Leu Asn Thr Arg Leu Asn Glu
        200                 205                 210

cct gat ttg ccg ggc gat att gat atc aag gac ttg gat cct ttg gtc   787
Pro Asp Leu Pro Gly Asp Ile Asp Ile Lys Asp Leu Asp Pro Leu Val
    215                 220                 225

ctg cag gat ttg aag gtt ttg tct aag gac aac gca gat gcc gtc gca   835
Leu Gln Asp Leu Lys Val Leu Ser Lys Asp Asn Ala Asp Ala Val Ala
230                 235                 240                 245

aag cat atg atc atg gct gcg acc tgg ctg gcc gac gat cct caa ttg   883
Lys His Met Ile Met Ala Ala Thr Trp Leu Ala Asp Asp Pro Gln Leu
                250                 255                 260

gca ctg cgc cac gcc cgt gct gcg aag gat cgc gcg gga cgc gtg tcc   931
Ala Leu Arg His Ala Arg Ala Ala Lys Asp Arg Ala Gly Arg Val Ser
            265                 270                 275

gtc gtg cgt gag acg aac ggc att gct gct tac cat gct ggt gag tgg   979
Val Val Arg Glu Thr Asn Gly Ile Ala Ala Tyr His Ala Gly Glu Trp
        280                 285                 290

aag gaa gct ctt tcg gag ctt cgt gct gcg cgc cgc atg tcg ggt ggt   1027
Lys Glu Ala Leu Ser Glu Leu Arg Ala Ala Arg Arg Met Ser Gly Gly
    295                 300                 305

cct ggt ttg att gct gtg atg gct gac tgt gag cgt ggc ttg ggt cgt   1075
Pro Gly Leu Ile Ala Val Met Ala Asp Cys Glu Arg Gly Leu Gly Arg
310                 315                 320                 325

cct gag aag gcg att gag ctg gct cga gaa gag gat ttg agc tct ttg   1123
Pro Glu Lys Ala Ile Glu Leu Ala Arg Glu Glu Asp Leu Ser Ser Leu
                330                 335                 340

gat cag gat aac ctg atc gag tta gcg att gtt gtt gct gga gca cgc   1171
Asp Gln Asp Asn Leu Ile Glu Leu Ala Ile Val Val Ala Gly Ala Arg
            345                 350                 355

cat gat ttg ggt cag cat gac tct gcg att gtg gaa ttg cag aag gtt   1219
His Asp Leu Gly Gln His Asp Ser Ala Ile Val Glu Leu Gln Lys Val
        360                 365                 370

aat cca agc ttg aag agc acc ggt ttc acc cat tct cgt ttg tct tac   1267
Asn Pro Ser Leu Lys Ser Thr Gly Phe Thr His Ser Arg Leu Ser Tyr
    375                 380                 385

gct tac gcc gat gcg ctt gtt ttg gct ggt cgt ggc gat gaa gca cgt   1315
Ala Tyr Ala Asp Ala Leu Val Leu Ala Gly Arg Gly Asp Glu Ala Arg
390                 395                 400                 405

gag tgg ttc cag cac gct gcc acc ttg gat gag gac ggc tac ctc gat   1363
Glu Trp Phe Gln His Ala Ala Thr Leu Asp Glu Asp Gly Tyr Leu Asp
                410                 415                 420

gca gag gag cgt atc gag cag ctc gat aat ggg aac aac tagactattg    1412
Ala Glu Glu Arg Ile Glu Gln Leu Asp Asn Gly Asn Asn
            425                 430

gtctagagtg taa                                                   1425
```

<210> 682
<211> 434
<212> PRT
<213> Corynebacterium glutamicum

<400> 682

```
Met Ala Asp Asn Phe Asp Arg Ser Arg Asp Asn Asp Arg Ser Ser Asp
  1               5                  10                  15

Arg Thr Pro Arg Gly Asp Arg Gly Asp Arg Gly Gly Tyr Arg Asn Ser
             20                  25                  30

Arg Gly Asn Asp Asp Arg Gly Asn Tyr Arg Gln Asn Arg Asp Gly Glu
         35                  40                  45

Ser Arg Asp Arg Gly Gly Tyr Leu Gly Asp Arg Arg Asp Asn Arg Ser
     50                  55                  60

Gly Glu Tyr Arg Gln Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asn
 65                  70                  75                  80

Arg Ser Asp Asp Arg Arg Gly Gly Tyr Arg Ser Asp Arg Asn Phe Asp
                 85                  90                  95

Asp Arg Asn Ser Asn Met Arg Asp Asp Arg Arg Gly Gly Asp Arg Ser
            100                 105                 110

Tyr Ser Arg Asn Asp Arg Ser Asp Arg Gly Tyr Arg Ser Asn Asp Arg
        115                 120                 125

Tyr Asp Arg Asn Asp Arg Arg Asp Asp Asn Arg Asp Thr Arg Gly Gly
    130                 135                 140

Asp Arg Gly Asp Arg Arg Tyr Asp Arg Arg Asp Asp Arg Arg Asp Asp
145                 150                 155                 160

Arg Arg Asp Asp Arg Arg Gly Gly Gln Gly Gln Gly Arg Pro Gly Gly
                165                 170                 175

Asp Arg Arg His Ala Asn Arg Ala Gly Ala Gly Arg Asp Gln Gln Arg
            180                 185                 190

Asp Ser Leu His Pro Gln Arg Ala Gly Phe Arg Glu Glu Arg Leu Asn
        195                 200                 205

Thr Arg Leu Asn Glu Pro Asp Leu Pro Gly Asp Ile Asp Ile Lys Asp
    210                 215                 220

Leu Asp Pro Leu Val Leu Gln Asp Leu Lys Val Leu Ser Lys Asp Asn
225                 230                 235                 240

Ala Asp Ala Val Ala Lys His Met Ile Met Ala Ala Thr Trp Leu Ala
                245                 250                 255

Asp Asp Pro Gln Leu Ala Leu Arg His Ala Arg Ala Ala Lys Asp Arg
            260                 265                 270

Ala Gly Arg Val Ser Val Val Arg Glu Thr Asn Gly Ile Ala Ala Tyr
        275                 280                 285
```

```
His Ala Gly Glu Trp Lys Glu Ala Leu Ser Glu Leu Arg Ala Ala Arg
    290                 295                 300

Arg Met Ser Gly Gly Pro Gly Leu Ile Ala Val Met Ala Asp Cys Glu
305                 310                 315                 320

Arg Gly Leu Gly Arg Pro Glu Lys Ala Ile Glu Leu Ala Arg Glu Glu
                325                 330                 335

Asp Leu Ser Ser Leu Asp Gln Asp Asn Leu Ile Glu Leu Ala Ile Val
            340                 345                 350

Val Ala Gly Ala Arg His Asp Leu Gly Gln His Asp Ser Ala Ile Val
        355                 360                 365

Glu Leu Gln Lys Val Asn Pro Ser Leu Lys Ser Thr Gly Phe Thr His
    370                 375                 380

Ser Arg Leu Ser Tyr Ala Tyr Ala Asp Ala Leu Val Leu Ala Gly Arg
385                 390                 395                 400

Gly Asp Glu Ala Arg Glu Trp Phe Gln His Ala Ala Thr Leu Asp Glu
                405                 410                 415

Asp Gly Tyr Leu Asp Ala Glu Glu Arg Ile Glu Gln Leu Asp Asn Gly
            420                 425                 430

Asn Asn
```

09/05/2005 09:09:09

<210> 683
<211> 1316
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1293)
<223> FRXA01592

<400> 683

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aac ttc gac cgc tct cgt gac aac gat cgc tca agc gcc cgc act cct   48
Asn Phe Asp Arg Ser Arg Asp Asn Asp Arg Ser Ser Ala Arg Thr Pro
  1               5                  10                  15

cgt gga gac cgc ggc gat cgc ggt ggc tac cga aac tcc cgc ggc aac   96
Arg Gly Asp Arg Gly Asp Arg Gly Gly Tyr Arg Asn Ser Arg Gly Asn
             20                  25                  30

gat gac cgc gga aac tac cgt caa aac cga gat ggt gaa tca cga gat   144
Asp Asp Arg Gly Asn Tyr Arg Gln Asn Arg Asp Gly Glu Ser Arg Asp
         35                  40                  45

cgc ggc gga tac ctc ggt gac cgt cgc gac aac cgc tca ggt gaa tat   192
Arg Gly Gly Tyr Leu Gly Asp Arg Arg Asp Asn Arg Ser Gly Glu Tyr
     50                  55                  60

cgt caa cgt gac gat agg cgt gac gat cgt agg gac aac cga agc gat   240
Arg Gln Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asn Arg Ser Asp
```

```
 65                  70                  75                  80

gac cgc cgc ggt ggt tac cgc tcc gat cgc aac ttt gac gat cgc aac   288
Asp Arg Arg Gly Gly Tyr Arg Ser Asp Arg Asn Phe Asp Asp Arg Asn
                 85                  90                  95

agc aac atg cgt gat gat cgt cgc ggc ggc gac cgt tca tac agc cgt   336
Ser Asn Met Arg Asp Asp Arg Arg Gly Gly Asp Arg Ser Tyr Ser Arg
            100                 105                 110

aat gat cgc tcc gat cgt ggc tat cgt agc aat gac cgc tac gac cgt   384
Asn Asp Arg Ser Asp Arg Gly Tyr Arg Ser Asn Asp Arg Tyr Asp Arg
        115                 120                 125

aat gat cgt cgc gat gac aac agg gac acc agg ggt ggc gat cgc gga   432
Asn Asp Arg Arg Asp Asp Asn Arg Asp Thr Arg Gly Gly Asp Arg Gly
    130                 135                 140

gac cgt cgc tac gac agg cgc gat gac cga cgt gat gat cgt cgc gat   480
Asp Arg Arg Tyr Asp Arg Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp
145                 150                 155                 160

gat cgt cgt ggc gga cag ggc cag ggg cgt cca ggt gga gat cgt cga   528
Asp Arg Arg Gly Gly Gln Gly Gln Gly Arg Pro Gly Gly Asp Arg Arg
                165                 170                 175

cat gcg aac cgt gca ggt gca ggt cgc gat cag cag cgt gat tcg ctg   576
His Ala Asn Arg Ala Gly Ala Gly Arg Asp Gln Gln Arg Asp Ser Leu
            180                 185                 190

cat cca cag cgc gct ggt ttc cgt gaa gag cgc ttg aac act cgt ctc   624
His Pro Gln Arg Ala Gly Phe Arg Glu Glu Arg Leu Asn Thr Arg Leu
        195                 200                 205

aat gag cct gat ttg ccg ggc gat att gat atc aag gac ttg gat cct   672
Asn Glu Pro Asp Leu Pro Gly Asp Ile Asp Ile Lys Asp Leu Asp Pro
    210                 215                 220

ttg gtc ctg cag gat ttg aag gtt ttg tct aag gac aac gca gat gcc   720
Leu Val Leu Gln Asp Leu Lys Val Leu Ser Lys Asp Asn Ala Asp Ala
225                 230                 235                 240

gtc gca aag cat atg atc atg gct gcg acc tgg ctg gcc gac gat cct   768
Val Ala Lys His Met Ile Met Ala Ala Thr Trp Leu Ala Asp Asp Pro
                245                 250                 255

caa ttg gca ctg cgc cac gcc cgt gct gcg aag gat cgc gcg gga cgc   816
Gln Leu Ala Leu Arg His Ala Arg Ala Ala Lys Asp Arg Ala Gly Arg
            260                 265                 270

gtg tcc gtc gtg cgt gag acg aac ggc att gct gct tac cat gct ggt   864
Val Ser Val Val Arg Glu Thr Asn Gly Ile Ala Ala Tyr His Ala Gly
        275                 280                 285

gag tgg aag gaa gct ctt tcg gag ctt cgt gct gcg cgc cgc atg tcg   912
Glu Trp Lys Glu Ala Leu Ser Glu Leu Arg Ala Ala Arg Arg Met Ser
    290                 295                 300

ggt ggt cct ggt ttg att gct gtg atg gct gac tgt gag cgt ggc ttg   960
Gly Gly Pro Gly Leu Ile Ala Val Met Ala Asp Cys Glu Arg Gly Leu
305                 310                 315                 320
```

```
ggt cgt cct gag aag gcg att gag ctg gct cga gaa gag gat ttg agc   1008
Gly Arg Pro Glu Lys Ala Ile Glu Leu Ala Arg Glu Glu Asp Leu Ser
                325                 330                 335

tct ttg gat cag gat aac ctg atc gag tta gcg att gtt gtt gct gga   1056
Ser Leu Asp Gln Asp Asn Leu Ile Glu Leu Ala Ile Val Val Ala Gly
            340                 345                 350

gca cgc cat gat ttg ggt cag cat gac tct gcg att gtg gaa ttg cag   1104
Ala Arg His Asp Leu Gly Gln His Asp Ser Ala Ile Val Glu Leu Gln
        355                 360                 365

aag gtt aat cca agc ttg aag agc acc ggt ttc acc cat tct cgt ttg   1152
Lys Val Asn Pro Ser Leu Lys Ser Thr Gly Phe Thr His Ser Arg Leu
    370                 375                 380

tct tac gct tac gcc gat gcg ctt gtt ttg gct ggt cgt ggc gat gaa   1200
Ser Tyr Ala Tyr Ala Asp Ala Leu Val Leu Ala Gly Arg Gly Asp Glu
385                 390                 395                 400

gca cgt gag tgg ttc cag cac gct gcc acc ttg gat gag gac ggc tac   1248
Ala Arg Glu Trp Phe Gln His Ala Ala Thr Leu Asp Glu Asp Gly Tyr
                405                 410                 415

ctc gat gca gag gag cgt atc gag cag ctc gat aat ggg aac aac       1293
Leu Asp Ala Glu Glu Arg Ile Glu Gln Leu Asp Asn Gly Asn Asn
            420                 425                 430

tagactattg gtctagagtg taa                                        1316
```

<210> 684
<211> 431
<212> PRT
<213> Corynebacterium glutamicum

<400> 684

```
Asn Phe Asp Arg Ser Arg Asp Asn Asp Arg Ser Ser Ala Arg Thr Pro
  1               5                  10                  15

Arg Gly Asp Arg Gly Asp Arg Gly Gly Tyr Arg Asn Ser Arg Gly Asn
             20                  25                  30

Asp Asp Arg Gly Asn Tyr Arg Gln Asn Arg Asp Gly Glu Ser Arg Asp
         35                  40                  45

Arg Gly Gly Tyr Leu Gly Asp Arg Arg Asp Asn Arg Ser Gly Glu Tyr
     50                  55                  60

Arg Gln Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asn Arg Ser Asp
 65                  70                  75                  80

Asp Arg Arg Gly Gly Tyr Arg Ser Asp Arg Asn Phe Asp Asp Arg Asn
                 85                  90                  95

Ser Asn Met Arg Asp Asp Arg Arg Gly Gly Asp Arg Ser Tyr Ser Arg
            100                 105                 110

Asn Asp Arg Ser Asp Arg Gly Tyr Arg Ser Asn Asp Arg Tyr Asp Arg
        115                 120                 125
```

```
Asn Asp Arg Arg Asp Asp Asn Arg Asp Thr Arg Gly Gly Asp Arg Gly
    130                 135                 140

Asp Arg Arg Tyr Asp Arg Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp
145                 150                 155                 160

Asp Arg Arg Gly Gly Gln Gly Gln Gly Arg Pro Gly Gly Asp Arg Arg
                165                 170                 175

His Ala Asn Arg Ala Gly Ala Gly Arg Asp Gln Gln Arg Asp Ser Leu
            180                 185                 190

His Pro Gln Arg Ala Gly Phe Arg Glu Glu Arg Leu Asn Thr Arg Leu
        195                 200                 205

Asn Glu Pro Asp Leu Pro Gly Asp Ile Asp Ile Lys Asp Leu Asp Pro
    210                 215                 220

Leu Val Leu Gln Asp Leu Lys Val Leu Ser Lys Asp Asn Ala Asp Ala
225                 230                 235                 240

Val Ala Lys His Met Ile Met Ala Ala Thr Trp Leu Ala Asp Asp Pro
                245                 250                 255

Gln Leu Ala Leu Arg His Ala Arg Ala Ala Lys Asp Arg Ala Gly Arg
            260                 265                 270

Val Ser Val Val Arg Glu Thr Asn Gly Ile Ala Ala Tyr His Ala Gly
        275                 280                 285

Glu Trp Lys Glu Ala Leu Ser Glu Leu Arg Ala Ala Arg Arg Met Ser
    290                 295                 300

Gly Gly Pro Gly Leu Ile Ala Val Met Ala Asp Cys Glu Arg Gly Leu
305                 310                 315                 320

Gly Arg Pro Glu Lys Ala Ile Glu Leu Ala Arg Glu Glu Asp Leu Ser
                325                 330                 335

Ser Leu Asp Gln Asp Asn Leu Ile Glu Leu Ala Ile Val Val Ala Gly
            340                 345                 350

Ala Arg His Asp Leu Gly Gln His Asp Ser Ala Ile Val Glu Leu Gln
        355                 360                 365

Lys Val Asn Pro Ser Leu Lys Ser Thr Gly Phe Thr His Ser Arg Leu
    370                 375                 380

Ser Tyr Ala Tyr Ala Asp Ala Leu Val Leu Ala Gly Arg Gly Asp Glu
385                 390                 395                 400

Ala Arg Glu Trp Phe Gln His Ala Ala Thr Leu Asp Glu Asp Gly Tyr
                405                 410                 415

Leu Asp Ala Glu Glu Arg Ile Glu Gln Leu Asp Asn Gly Asn Asn
            420                 425                 430
```

<210> 685
<211> 1305

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1282)
<223> RXN01597

<400> 685
gagtagaacc acttctcgcc gccagtgcat aagagttttc ttggaatttt ttaggcgcgc 60

ctccaccaaa ggttgagact ttggttccac aatgggctgc atg agt ctg ttc aac 115
Met Ser Leu Phe Asn
1 5

cgc aaa gcc gac ctg ccc ggc ctg caa ggt gcc acc cga atc tgc acc 163
Arg Lys Ala Asp Leu Pro Gly Leu Gln Gly Ala Thr Arg Ile Cys Thr
10 15 20

ccg cag ggc aaa ggg cta aag cgc ctg tcc gaa ggc gat ctc gca atc 211
Pro Gln Gly Lys Gly Leu Lys Arg Leu Ser Glu Gly Asp Leu Ala Ile
25 30 35

att gat gca cca gat cta tcc agg acc ttc gcc caa cga ttg cta gca 259
Ile Asp Ala Pro Asp Leu Ser Arg Thr Phe Ala Gln Arg Leu Leu Ala
40 45 50

gca aaa ccc gcc gca gtc ctc aac gtt tcc cgg ttc acc acc gga tcg 307
Ala Lys Pro Ala Ala Val Leu Asn Val Ser Arg Phe Thr Thr Gly Ser
55 60 65

gtg ccc aac ttt gga ccg caa atg ctt atc gac ggc ggc atc cag ctc 355
Val Pro Asn Phe Gly Pro Gln Met Leu Ile Asp Gly Gly Ile Gln Leu
70 75 80 85

gtg gaa ggc ttt ggc cag gag ctg ctc gac ggc acc aaa gac ggt aag 403
Val Glu Gly Phe Gly Gln Glu Leu Leu Asp Gly Thr Lys Asp Gly Lys
90 95 100

aaa ggt cgc ctg aca gaa gat gga cag ctc ttc tac ggc gaa cga ctg 451
Lys Gly Arg Leu Thr Glu Asp Gly Gln Leu Phe Tyr Gly Glu Arg Leu
105 110 115

atc tct aac ggc agt gtt ctc agt gga cct gcg gct gaa aat gca ttt 499
Ile Ser Asn Gly Ser Val Leu Ser Gly Pro Ala Ala Glu Asn Ala Phe
120 125 130

gca gac gcc cag caa tca ctg ctg gac cgc atg gaa gcc tat ttc ggc 547
Ala Asp Ala Gln Gln Ser Leu Leu Asp Arg Met Glu Ala Tyr Phe Gly
135 140 145

aac acc att cag ttc att cac tca gaa gca ccg ctc ctg atc gat ggc 595
Asn Thr Ile Gln Phe Ile His Ser Glu Ala Pro Leu Leu Ile Asp Gly
150 155 160 165

ctc ggc att ccc gat acc gga aat gcc att gaa ggc cgc aaa gtt ctc 643
Leu Gly Ile Pro Asp Thr Gly Asn Ala Ile Glu Gly Arg Lys Val Leu
170 175 180

att gcc tca cca ggg gat aac cac cgc agc agg ctc aaa gaa ctc cgc 691
Ile Ala Ser Pro Gly Asp Asn His Arg Ser Arg Leu Lys Glu Leu Arg

```
            185                 190                 195

agc ttc atc cgc gaa tac gat cca gta ctc atc ggt gtc gat ggg gca   739
Ser Phe Ile Arg Glu Tyr Asp Pro Val Leu Ile Gly Val Asp Gly Ala
        200                 205                 210

gca gac acc ttg gtg gaa ttg ggg tac aag ccc gcg ctg atc gtc ggc   787
Ala Asp Thr Leu Val Glu Leu Gly Tyr Lys Pro Ala Leu Ile Val Gly
    215                 220                 225

aat ccc act ggt atc ggc gca gat gcg ctg cgc agt ggc gcc aac gta   835
Asn Pro Thr Gly Ile Gly Ala Asp Ala Leu Arg Ser Gly Ala Asn Val
230                 235                 240                 245

att ttg cca gct gat cca gac ggc cac gct gtt ggt ctg gag cgc atc   883
Ile Leu Pro Ala Asp Pro Asp Gly His Ala Val Gly Leu Glu Arg Ile
                250                 255                 260

cag gat ctt ggc atc ggt gcg atg acc ttc cca tcc tca gta aat tcc   931
Gln Asp Leu Gly Ile Gly Ala Met Thr Phe Pro Ser Ser Val Asn Ser
            265                 270                 275

tcc acg gat ctg gcg ctc ctg ctt gcg gat ttc cac aac ccg cag atg   979
Ser Thr Asp Leu Ala Leu Leu Leu Ala Asp Phe His Asn Pro Gln Met
        280                 285                 290

atc gtc aac gtc ggc ggt cct gtc acc ctt gat ggt gtt ttt gaa aac   1027
Ile Val Asn Val Gly Gly Pro Val Thr Leu Asp Gly Val Phe Glu Asn
    295                 300                 305

cga gaa gat tcc gat ccc gcg gcg ctt ttg acg cgc gcc aag cta ggc   1075
Arg Glu Asp Ser Asp Pro Ala Ala Leu Leu Thr Arg Ala Lys Leu Gly
310                 315                 320                 325

acc aag ctt gtc gac gga tcc gtc atc gca agt ctt tac aca gtg cgc   1123
Thr Lys Leu Val Asp Gly Ser Val Ile Ala Ser Leu Tyr Thr Val Arg
                330                 335                 340

agc tcc agc aac ctt gga tgg atg tgg gca ctg tta gcc att ttg gtg   1171
Ser Ser Ser Asn Leu Gly Trp Met Trp Ala Leu Leu Ala Ile Leu Val
            345                 350                 355

gtt ctt gca gtc gtg att gtt atc gct ggc acc gca gga tca ggc tct   1219
Val Leu Ala Val Val Ile Val Ile Ala Gly Thr Ala Gly Ser Gly Ser
        360                 365                 370

ttt acc gac aac ctc att gac acc tgg aac agc ttc gcg ctg aca gtg   1267
Phe Thr Asp Asn Leu Ile Asp Thr Trp Asn Ser Phe Ala Leu Thr Val
    375                 380                 385

cag ggt tgg ttc aaa taggaaggca acatggctaa acg                    1305
Gln Gly Trp Phe Lys
390
```

<210> 686
<211> 394
<212> PRT
<213> Corynebacterium glutamicum

<400> 686

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Met Ser Leu Phe Asn Arg Lys Ala Asp Leu Pro Gly Leu Gln Gly Ala
 1               5                  10                  15

Thr Arg Ile Cys Thr Pro Gln Gly Lys Gly Leu Lys Arg Leu Ser Glu
            20                  25                  30

Gly Asp Leu Ala Ile Ile Asp Ala Pro Asp Leu Ser Arg Thr Phe Ala
        35                  40                  45

Gln Arg Leu Leu Ala Ala Lys Pro Ala Ala Val Leu Asn Val Ser Arg
    50                  55                  60

Phe Thr Thr Gly Ser Val Pro Asn Phe Gly Pro Gln Met Leu Ile Asp
65                  70                  75                  80

Gly Gly Ile Gln Leu Val Glu Gly Phe Gly Gln Glu Leu Leu Asp Gly
                85                  90                  95

Thr Lys Asp Gly Lys Lys Gly Arg Leu Thr Glu Asp Gly Gln Leu Phe
            100                 105                 110

Tyr Gly Glu Arg Leu Ile Ser Asn Gly Ser Val Leu Ser Gly Pro Ala
        115                 120                 125

Ala Glu Asn Ala Phe Ala Asp Ala Gln Gln Ser Leu Leu Asp Arg Met
    130                 135                 140

Glu Ala Tyr Phe Gly Asn Thr Ile Gln Phe Ile His Ser Glu Ala Pro
145                 150                 155                 160

Leu Leu Ile Asp Gly Leu Gly Ile Pro Asp Thr Gly Asn Ala Ile Glu
                165                 170                 175

Gly Arg Lys Val Leu Ile Ala Ser Pro Gly Asp Asn His Arg Ser Arg
            180                 185                 190

Leu Lys Glu Leu Arg Ser Phe Ile Arg Glu Tyr Asp Pro Val Leu Ile
        195                 200                 205

Gly Val Asp Gly Ala Ala Asp Thr Leu Val Glu Leu Gly Tyr Lys Pro
    210                 215                 220

Ala Leu Ile Val Gly Asn Pro Thr Gly Ile Gly Ala Asp Ala Leu Arg
225                 230                 235                 240

Ser Gly Ala Asn Val Ile Leu Pro Ala Asp Pro Asp Gly His Ala Val
                245                 250                 255

Gly Leu Glu Arg Ile Gln Asp Leu Gly Ile Gly Ala Met Thr Phe Pro
            260                 265                 270

Ser Ser Val Asn Ser Ser Thr Asp Leu Ala Leu Leu Leu Ala Asp Phe
        275                 280                 285

His Asn Pro Gln Met Ile Val Asn Val Gly Gly Pro Val Thr Leu Asp
    290                 295                 300

Gly Val Phe Glu Asn Arg Glu Asp Ser Asp Pro Ala Ala Leu Leu Thr
305                 310                 315                 320

Arg Ala Lys Leu Gly Thr Lys Leu Val Asp Gly Ser Val Ile Ala Ser
```

```
                325                 330                 335

Leu Tyr Thr Val Arg Ser Ser Ser Asn Leu Gly Trp Met Trp Ala Leu
            340                 345                 350

Leu Ala Ile Leu Val Val Leu Ala Val Val Ile Val Ile Ala Gly Thr
        355                 360                 365

Ala Gly Ser Gly Ser Phe Thr Asp Asn Leu Ile Asp Thr Trp Asn Ser
    370                 375                 380

Phe Ala Leu Thr Val Gln Gly Trp Phe Lys
385                 390


<210> 687
<211> 1305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1282)
<223> FRXA01597

<400> 687
gagtagaacc acttctcgcc gccagtgcat aagagttttc ttggaatttt ttaggcgcgc 60

ctccaccaaa ggttgagact ttggttccac aatgggctgc atg agt ctg ttc aac   115
                                            Met Ser Leu Phe Asn
                                              1               5

cgc aaa gcc gac ctg ccc ggc ctg caa ggt gcc acc cga atc tgc acc   163
Arg Lys Ala Asp Leu Pro Gly Leu Gln Gly Ala Thr Arg Ile Cys Thr
                10                  15                  20

ccg cag ggc aaa ggg cta aag cgc ctg tcc gaa ggc gat ctc gca atc   211
Pro Gln Gly Lys Gly Leu Lys Arg Leu Ser Glu Gly Asp Leu Ala Ile
            25                  30                  35

att gat gca cca gat cta tcc agg acc ttc gcc caa cga ttg cta gca   259
Ile Asp Ala Pro Asp Leu Ser Arg Thr Phe Ala Gln Arg Leu Leu Ala
        40                  45                  50

gca aaa ccc gcc gca gtc ctc aac gtt tcc cgg ttc acc acc gga tcg   307
Ala Lys Pro Ala Ala Val Leu Asn Val Ser Arg Phe Thr Thr Gly Ser
    55                  60                  65

gtg ccc aac ttt gga ccg caa atg ctt atc gac ggc ggc atc cag ctc   355
Val Pro Asn Phe Gly Pro Gln Met Leu Ile Asp Gly Gly Ile Gln Leu
70                  75                  80                  85

gtg gaa ggc ttt ggc cag gag ctg ctc gac ggc acc aaa gac ggt aag   403
Val Glu Gly Phe Gly Gln Glu Leu Leu Asp Gly Thr Lys Asp Gly Lys
                90                  95                  100

aaa ggt cgc ctg aca gaa gat gga cag ctc ttc tac ggc gaa cga ctg   451
Lys Gly Arg Leu Thr Glu Asp Gly Gln Leu Phe Tyr Gly Glu Arg Leu
            105                 110                 115

atc tct aac ggc agt gtt ctc agt gga cct gcg gct gaa aat gca ttt   499
```

```
Ile Ser Asn Gly Ser Val Leu Ser Gly Pro Ala Ala Glu Asn Ala Phe
        120                 125                 130

gca gac gcc cag caa tca ctg ctg gac cgc atg gaa gcc tat ttc ggc   547
Ala Asp Ala Gln Gln Ser Leu Leu Asp Arg Met Glu Ala Tyr Phe Gly
    135                 140                 145

aac acc att cag ttc att cac tca gaa gca ccg ctc ctg atc gat ggc   595
Asn Thr Ile Gln Phe Ile His Ser Glu Ala Pro Leu Leu Ile Asp Gly
150                 155                 160                 165

ctc ggc att ccc gat acc gga aat gcc att gaa ggc cgc aaa gtt ctc   643
Leu Gly Ile Pro Asp Thr Gly Asn Ala Ile Glu Gly Arg Lys Val Leu
                170                 175                 180

att gcc tca cca ggg gat aac cac cgc agc agg ctc aaa gaa ctc cgc   691
Ile Ala Ser Pro Gly Asp Asn His Arg Ser Arg Leu Lys Glu Leu Arg
            185                 190                 195

agc ttc atc cgc gaa tac gat cca gta ctc atc ggt gtc gat ggg gca   739
Ser Phe Ile Arg Glu Tyr Asp Pro Val Leu Ile Gly Val Asp Gly Ala
        200                 205                 210

gca gac acc ttg gtg gaa ttg ggg tac aag ccc gcg ctg atc gtc ggc   787
Ala Asp Thr Leu Val Glu Leu Gly Tyr Lys Pro Ala Leu Ile Val Gly
    215                 220                 225

aat ccc act ggt atc ggc gca gat gcg ctg cgc agt ggc gcc aac gta   835
Asn Pro Thr Gly Ile Gly Ala Asp Ala Leu Arg Ser Gly Ala Asn Val
230                 235                 240                 245

att ttg cca gct gat cca gac ggc cac gct gtt ggt ctg gag cgc atc   883
Ile Leu Pro Ala Asp Pro Asp Gly His Ala Val Gly Leu Glu Arg Ile
                250                 255                 260

cag gat ctt ggc atc ggt gcg atg acc ttc cca tcc tca gta aat tcc   931
Gln Asp Leu Gly Ile Gly Ala Met Thr Phe Pro Ser Ser Val Asn Ser
            265                 270                 275

tcc acg gat ctg gcg ctc ctg ctt gcg gat ttc cac aac ccg cag atg   979
Ser Thr Asp Leu Ala Leu Leu Leu Ala Asp Phe His Asn Pro Gln Met
        280                 285                 290

atc gtc aac gtc ggc ggt cct gtc acc ctt gat ggt gtt ttt gaa aac   1027
Ile Val Asn Val Gly Gly Pro Val Thr Leu Asp Gly Val Phe Glu Asn
    295                 300                 305

cga gaa gat tcc gat ccc gcg gcg ctt ttg acg cgc gcc aag cta ggc   1075
Arg Glu Asp Ser Asp Pro Ala Ala Leu Leu Thr Arg Ala Lys Leu Gly
310                 315                 320                 325

acc aag ctt gtc gac gga tcc gtc atc gca agt ctt tac aca gtg cgc   1123
Thr Lys Leu Val Asp Gly Ser Val Ile Ala Ser Leu Tyr Thr Val Arg
                330                 335                 340

agc tcc agc aac ctt gga tgg atg tgg gca ctg tta gcc att ttg gtg   1171
Ser Ser Ser Asn Leu Gly Trp Met Trp Ala Leu Leu Ala Ile Leu Val
            345                 350                 355

gtt ctt gca gtc gtg att gtt atc gct ggc acc gca gga tca ggc tct   1219
Val Leu Ala Val Val Ile Val Ile Ala Gly Thr Ala Gly Ser Gly Ser
```

```
        360                 365                 370

ttt acc gac aac ctc att gac acc tgg aac agc ttc gcg ctg aca gtg   1267
Phe Thr Asp Asn Leu Ile Asp Thr Trp Asn Ser Phe Ala Leu Thr Val
    375                 380                 385

cag ggt tgg ttc aaa taggaaggca acatggctaa acg                     1305
Gln Gly Trp Phe Lys
390
```

<210> 688
<211> 394
<212> PRT
<213> Corynebacterium glutamicum

<400> 688

```
Met Ser Leu Phe Asn Arg Lys Ala Asp Leu Pro Gly Leu Gln Gly Ala
  1               5                  10                  15

Thr Arg Ile Cys Thr Pro Gln Gly Lys Gly Leu Lys Arg Leu Ser Glu
             20                  25                  30

Gly Asp Leu Ala Ile Ile Asp Ala Pro Asp Leu Ser Arg Thr Phe Ala
         35                  40                  45

Gln Arg Leu Leu Ala Ala Lys Pro Ala Ala Val Leu Asn Val Ser Arg
     50                  55                  60

Phe Thr Thr Gly Ser Val Pro Asn Phe Gly Pro Gln Met Leu Ile Asp
 65                  70                  75                  80

Gly Gly Ile Gln Leu Val Glu Gly Phe Gly Gln Glu Leu Leu Asp Gly
                 85                  90                  95

Thr Lys Asp Gly Lys Lys Gly Arg Leu Thr Glu Asp Gly Gln Leu Phe
            100                 105                 110

Tyr Gly Glu Arg Leu Ile Ser Asn Gly Ser Val Leu Ser Gly Pro Ala
        115                 120                 125

Ala Glu Asn Ala Phe Ala Asp Ala Gln Gln Ser Leu Leu Asp Arg Met
    130                 135                 140

Glu Ala Tyr Phe Gly Asn Thr Ile Gln Phe Ile His Ser Glu Ala Pro
145                 150                 155                 160

Leu Leu Ile Asp Gly Leu Gly Ile Pro Asp Thr Gly Asn Ala Ile Glu
                165                 170                 175

Gly Arg Lys Val Leu Ile Ala Ser Pro Gly Asp Asn His Arg Ser Arg
            180                 185                 190

Leu Lys Glu Leu Arg Ser Phe Ile Arg Glu Tyr Asp Pro Val Leu Ile
        195                 200                 205

Gly Val Asp Gly Ala Ala Asp Thr Leu Val Glu Leu Gly Tyr Lys Pro
    210                 215                 220

Ala Leu Ile Val Gly Asn Pro Thr Gly Ile Gly Ala Asp Ala Leu Arg
225                 230                 235                 240
```

```
Ser Gly Ala Asn Val Ile Leu Pro Ala Asp Pro Asp Gly His Ala Val
                245                 250                 255

Gly Leu Glu Arg Ile Gln Asp Leu Gly Ile Gly Ala Met Thr Phe Pro
            260                 265                 270

Ser Ser Val Asn Ser Ser Thr Asp Leu Ala Leu Leu Leu Ala Asp Phe
        275                 280                 285

His Asn Pro Gln Met Ile Val Asn Val Gly Gly Pro Val Thr Leu Asp
    290                 295                 300

Gly Val Phe Glu Asn Arg Glu Asp Ser Asp Pro Ala Ala Leu Leu Thr
305                 310                 315                 320

Arg Ala Lys Leu Gly Thr Lys Leu Val Asp Gly Ser Val Ile Ala Ser
                325                 330                 335

Leu Tyr Thr Val Arg Ser Ser Ser Asn Leu Gly Trp Met Trp Ala Leu
            340                 345                 350

Leu Ala Ile Leu Val Val Leu Ala Val Val Ile Val Ile Ala Gly Thr
        355                 360                 365

Ala Gly Ser Gly Ser Phe Thr Asp Asn Leu Ile Asp Thr Trp Asn Ser
    370                 375                 380

Phe Ala Leu Thr Val Gln Gly Trp Phe Lys
385                 390


<210> 689
<211> 1086
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1063)
<223> RXN01598

<400> 689
cgctggcacc gcaggatcag gctcttttac cgacaacctc attgacacct ggaacagctt 60

cgcgctgaca gtgcagggtt ggttcaaata ggaaggcaac atg gct aaa cga cgt   115
                                            Met Ala Lys Arg Arg
                                              1               5

gga aga ggc gcc gca acc ttc gcc gca ctg gga ttt ggt gca gca gcc   163
Gly Arg Gly Ala Ala Thr Phe Ala Ala Leu Gly Phe Gly Ala Ala Ala
                  10                  15                  20

ggc att gcc ttt gga act tat gtg ctt gca ccc aac ctt cct gaa aac   211
Gly Ile Ala Phe Gly Thr Tyr Val Leu Ala Pro Asn Leu Pro Glu Asn
              25                  30                  35

att gac cca aat gca cca aca tca gct gaa tta gtc gag gca gag acc   259
Ile Asp Pro Asn Ala Pro Thr Ser Ala Glu Leu Val Glu Ala Glu Thr
          40                  45                  50
```

```
ttg gct gag gtt aat gcg gtg cag gcc gat caa gca gac agc atc att   307
Leu Ala Glu Val Asn Ala Val Gln Ala Asp Gln Ala Asp Ser Ile Ile
     55                  60                  65

gac cac atc gtg gaa gac gtg gtg gct ggc aca ctg acc gat cgc ccc   355
Asp His Ile Val Glu Asp Val Val Ala Gly Thr Leu Thr Asp Arg Pro
 70                  75                  80                  85

gta ctg gtg atg cgc acc gct gac gct gaa gaa tca gac gtt gcc gat   403
Val Leu Val Met Arg Thr Ala Asp Ala Glu Glu Ser Asp Val Ala Asp
                90                  95                 100

gtg tca tgg ctg ttg cag caa gca gga gct att aat gct gga tcc att   451
Val Ser Trp Leu Leu Gln Gln Ala Gly Ala Ile Asn Ala Gly Ser Ile
            105                 110                 115

aca ctt gag gag aat ttc ttc tcc caa gac ggc gcg gac cag ctg aaa   499
Thr Leu Glu Glu Asn Phe Phe Ser Gln Asp Gly Ala Asp Gln Leu Lys
        120                 125                 130

tca atc gtg gca aat acg ttg cct gca ggc gct cag ctt tct gaa acc   547
Ser Ile Val Ala Asn Thr Leu Pro Ala Gly Ala Gln Leu Ser Glu Thr
    135                 140                 145

caa ctg gat cca gga act cac gct ggc gag gca ctt ggt gcc gct ttg   595
Gln Leu Asp Pro Gly Thr His Ala Gly Glu Ala Leu Gly Ala Ala Leu
150                 155                 160                 165

ctg ctc aac cct gaa act ggt gaa cca cta gcc agc act gca gag cgc   643
Leu Leu Asn Pro Glu Thr Gly Glu Pro Leu Ala Ser Thr Ala Glu Arg
                170                 175                 180

gga cta ttg ctc aac gtg ctg cgc gac aac ggt tac atc tcg tac gaa   691
Gly Leu Leu Leu Asn Val Leu Arg Asp Asn Gly Tyr Ile Ser Tyr Glu
            185                 190                 195

gac ggc acc att ttg cca ggc cag gtc atc gtg atg att act ggc gat   739
Asp Gly Thr Ile Leu Pro Gly Gln Val Ile Val Met Ile Thr Gly Asp
        200                 205                 210

agc gac ggc tca ggt gat ggt gcc ttc gct gca gaa aca caa tcg ctg   787
Ser Asp Gly Ser Gly Asp Gly Ala Phe Ala Ala Glu Thr Gln Ser Leu
    215                 220                 225

ttt gct cgc gca ctt gac gcc caa gga tca ggc gtg gtg gtt gca gga   835
Phe Ala Arg Ala Leu Asp Ala Gln Gly Ser Gly Val Val Val Ala Gly
230                 235                 240                 245

cgt att cac act gct gct gat act gga gtt att gga cgg ctt cgt gcc   883
Arg Ile His Thr Ala Ala Asp Thr Gly Val Ile Gly Arg Leu Arg Ala
                250                 255                 260

aac cct gat gct gca gaa aac gtc tct aca att gat tcc gtg aat cgt   931
Asn Pro Asp Ala Ala Glu Asn Val Ser Thr Ile Asp Ser Val Asn Arg
            265                 270                 275

act tgg ggc aag atg gct acc gtg cta tca gtt cgt gag gaa cta gcc   979
Thr Trp Gly Lys Met Ala Thr Val Leu Ser Val Arg Glu Glu Leu Ala
        280                 285                 290

ggt agg tct gga gcg ttt ggt tcc gct gcc tcc gca gac gcg gca agt   1027
```

```
Gly Arg Ser Gly Ala Phe Gly Ser Ala Ala Ser Ala Asp Ala Ala Ser
    295                 300                 305

ccg tct ctc gat gga act gca gca gcg cca gcg cag taggttttcc        1073
Pro Ser Leu Asp Gly Thr Ala Ala Ala Pro Ala Gln
310                 315                 320

aagcctttaa aac                                                    1086


<210> 690
<211> 321
<212> PRT
<213> Corynebacterium glutamicum

<400> 690
Met Ala Lys Arg Arg Gly Arg Gly Ala Ala Thr Phe Ala Ala Leu Gly
  1               5                  10                  15

Phe Gly Ala Ala Ala Gly Ile Ala Phe Gly Thr Tyr Val Leu Ala Pro
             20                  25                  30

Asn Leu Pro Glu Asn Ile Asp Pro Asn Ala Pro Thr Ser Ala Glu Leu
         35                  40                  45

Val Glu Ala Glu Thr Leu Ala Glu Val Asn Ala Val Gln Ala Asp Gln
     50                  55                  60

Ala Asp Ser Ile Ile Asp His Ile Val Glu Asp Val Val Ala Gly Thr
 65                  70                  75                  80

Leu Thr Asp Arg Pro Val Leu Val Met Arg Thr Ala Asp Ala Glu Glu
                 85                  90                  95

Ser Asp Val Ala Asp Val Ser Trp Leu Leu Gln Gln Ala Gly Ala Ile
            100                 105                 110

Asn Ala Gly Ser Ile Thr Leu Glu Glu Asn Phe Phe Ser Gln Asp Gly
        115                 120                 125

Ala Asp Gln Leu Lys Ser Ile Val Ala Asn Thr Leu Pro Ala Gly Ala
    130                 135                 140

Gln Leu Ser Glu Thr Gln Leu Asp Pro Gly Thr His Ala Gly Glu Ala
145                 150                 155                 160

Leu Gly Ala Ala Leu Leu Leu Asn Pro Glu Thr Gly Glu Pro Leu Ala
                165                 170                 175

Ser Thr Ala Glu Arg Gly Leu Leu Leu Asn Val Leu Arg Asp Asn Gly
            180                 185                 190

Tyr Ile Ser Tyr Glu Asp Gly Thr Ile Leu Pro Gly Gln Val Ile Val
        195                 200                 205

Met Ile Thr Gly Asp Ser Asp Gly Ser Gly Asp Gly Ala Phe Ala Ala
    210                 215                 220

Glu Thr Gln Ser Leu Phe Ala Arg Ala Leu Asp Ala Gln Gly Ser Gly
225                 230                 235                 240
```

```
Val Val Val Ala Gly Arg Ile His Thr Ala Ala Asp Thr Gly Val Ile
                245                 250                 255

Gly Arg Leu Arg Ala Asn Pro Asp Ala Ala Glu Asn Val Ser Thr Ile
            260                 265                 270

Asp Ser Val Asn Arg Thr Trp Gly Lys Met Ala Thr Val Leu Ser Val
        275                 280                 285

Arg Glu Glu Leu Ala Gly Arg Ser Gly Ala Phe Gly Ser Ala Ala Ser
    290                 295                 300

Ala Asp Ala Ala Ser Pro Ser Leu Asp Gly Thr Ala Ala Ala Pro Ala
305                 310                 315                 320

Gln
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<210> 691
<211> 1086
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1063)
<223> FRXA01598

<400> 691

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cgctggcacc gcaggatcag gctcttttac cgacaacctc attgacacct ggaacagctt 60

cgcgctgaca gtgcagggtt ggttcaaata ggaaggcaac atg gct aaa cga cgt   115
                                            Met Ala Lys Arg Arg
                                              1               5

gga aga ggc gcc gca acc ttc gcc gca ctg gga ttt ggt gca gca gcc   163
Gly Arg Gly Ala Ala Thr Phe Ala Ala Leu Gly Phe Gly Ala Ala Ala
                  10                  15                  20

ggc att gcc ttt gga act tat gtg ctt gca ccc aac ctt cct gaa aac   211
Gly Ile Ala Phe Gly Thr Tyr Val Leu Ala Pro Asn Leu Pro Glu Asn
              25                  30                  35

att gac cca aat gca cca aca tca gct gaa tta gtc gag gca gag acc   259
Ile Asp Pro Asn Ala Pro Thr Ser Ala Glu Leu Val Glu Ala Glu Thr
          40                  45                  50

ttg gct gag gtt aat gcg gtg cag gcc gat caa gca gac agc atc att   307
Leu Ala Glu Val Asn Ala Val Gln Ala Asp Gln Ala Asp Ser Ile Ile
      55                  60                  65

gac cac atc gtg gaa gac gtg gtg gct ggc aca ctg acc gat cgc ccc   355
Asp His Ile Val Glu Asp Val Val Ala Gly Thr Leu Thr Asp Arg Pro
  70                  75                  80                  85

gta ctg gtg atg cgc acc gct gac gct gaa gaa tca gac gtt gcc gat   403
Val Leu Val Met Arg Thr Ala Asp Ala Glu Glu Ser Asp Val Ala Asp
                  90                  95                 100

gtg tca tgg ctg ttg cag caa gca gga gct att aat gct gga tcc att   451
```

```
Val Ser Trp Leu Leu Gln Gln Ala Gly Ala Ile Asn Ala Gly Ser Ile
            105                 110                 115

aca ctt gag gag aat ttc ttc tcc caa gac ggc gcg gac cag ctg aaa   499
Thr Leu Glu Glu Asn Phe Phe Ser Gln Asp Gly Ala Asp Gln Leu Lys
        120                 125                 130

tca atc gtg gca aat acg ttg cct gca ggc gct cag ctt tct gaa acc   547
Ser Ile Val Ala Asn Thr Leu Pro Ala Gly Ala Gln Leu Ser Glu Thr
    135                 140                 145

caa ctg gat cca gga act cac gct ggc gag gca ctt ggt gcc gct ttg   595
Gln Leu Asp Pro Gly Thr His Ala Gly Glu Ala Leu Gly Ala Ala Leu
150                 155                 160                 165

ctg ctc aac cct gaa act ggt gaa cca cta gcc agc act gca gag cgc   643
Leu Leu Asn Pro Glu Thr Gly Glu Pro Leu Ala Ser Thr Ala Glu Arg
                170                 175                 180

gga cta ttg ctc aac gtg ctg cgc gac aac ggt tac atc tcg tac gaa   691
Gly Leu Leu Leu Asn Val Leu Arg Asp Asn Gly Tyr Ile Ser Tyr Glu
            185                 190                 195

gac ggc acc att ttg cca ggc cag gtc atc gtg atg att act ggc gat   739
Asp Gly Thr Ile Leu Pro Gly Gln Val Ile Val Met Ile Thr Gly Asp
        200                 205                 210

agc gac ggc tca ggt gat ggt gcc ttc gct gca gaa aca caa tcg ctg   787
Ser Asp Gly Ser Gly Asp Gly Ala Phe Ala Ala Glu Thr Gln Ser Leu
    215                 220                 225

ttt gct cgc gca ctt gac gcc caa gga tca ggc gtg gtg gtt gca gga   835
Phe Ala Arg Ala Leu Asp Ala Gln Gly Ser Gly Val Val Val Ala Gly
230                 235                 240                 245

cgt att cac act gct gct gat act gga gtt att gga cgg ctt cgt gcc   883
Arg Ile His Thr Ala Ala Asp Thr Gly Val Ile Gly Arg Leu Arg Ala
                250                 255                 260

aac cct gat gct gca gaa aac gtc tct aca att gat tcc gtg aat cgt   931
Asn Pro Asp Ala Ala Glu Asn Val Ser Thr Ile Asp Ser Val Asn Arg
            265                 270                 275

act tgg ggc aag atg gct acc gtg cta tca gtt cgt gag gaa cta gcc   979
Thr Trp Gly Lys Met Ala Thr Val Leu Ser Val Arg Glu Glu Leu Ala
        280                 285                 290

ggt agg tct gga gcg ttt ggt tcc gct gcc tcc gca gac gcg gca agt   1027
Gly Arg Ser Gly Ala Phe Gly Ser Ala Ala Ser Ala Asp Ala Ala Ser
    295                 300                 305

ccg tct ctc gat gga act gca gca gcg cca gcg cag taggttttcc        1073
Pro Ser Leu Asp Gly Thr Ala Ala Ala Pro Ala Gln
310                 315                 320

aagcctttaa aac                                                   1086
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<210> 692
<211> 321
<212> PRT

<213> Corynebacterium glutamicum

<400> 692

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Met Ala Lys Arg Arg Gly Arg Gly Ala Ala Thr Phe Ala Ala Leu Gly
  1               5                  10                  15

Phe Gly Ala Ala Ala Gly Ile Ala Phe Gly Thr Tyr Val Leu Ala Pro
             20                  25                  30

Asn Leu Pro Glu Asn Ile Asp Pro Asn Ala Pro Thr Ser Ala Glu Leu
         35                  40                  45

Val Glu Ala Glu Thr Leu Ala Glu Val Asn Ala Val Gln Ala Asp Gln
     50                  55                  60

Ala Asp Ser Ile Ile Asp His Ile Val Glu Asp Val Val Ala Gly Thr
 65                  70                  75                  80

Leu Thr Asp Arg Pro Val Leu Val Met Arg Thr Ala Asp Ala Glu Glu
                 85                  90                  95

Ser Asp Val Ala Asp Val Ser Trp Leu Leu Gln Gln Ala Gly Ala Ile
            100                 105                 110

Asn Ala Gly Ser Ile Thr Leu Glu Glu Asn Phe Phe Ser Gln Asp Gly
        115                 120                 125

Ala Asp Gln Leu Lys Ser Ile Val Ala Asn Thr Leu Pro Ala Gly Ala
    130                 135                 140

Gln Leu Ser Glu Thr Gln Leu Asp Pro Gly Thr His Ala Gly Glu Ala
145                 150                 155                 160

Leu Gly Ala Ala Leu Leu Leu Asn Pro Glu Thr Gly Glu Pro Leu Ala
                165                 170                 175

Ser Thr Ala Glu Arg Gly Leu Leu Leu Asn Val Leu Arg Asp Asn Gly
            180                 185                 190

Tyr Ile Ser Tyr Glu Asp Gly Thr Ile Leu Pro Gly Gln Val Ile Val
        195                 200                 205

Met Ile Thr Gly Asp Ser Asp Gly Ser Gly Asp Gly Ala Phe Ala Ala
    210                 215                 220

Glu Thr Gln Ser Leu Phe Ala Arg Ala Leu Asp Ala Gln Gly Ser Gly
225                 230                 235                 240

Val Val Val Ala Gly Arg Ile His Thr Ala Ala Asp Thr Gly Val Ile
                245                 250                 255

Gly Arg Leu Arg Ala Asn Pro Asp Ala Ala Glu Asn Val Ser Thr Ile
            260                 265                 270

Asp Ser Val Asn Arg Thr Trp Gly Lys Met Ala Thr Val Leu Ser Val
        275                 280                 285

Arg Glu Glu Leu Ala Gly Arg Ser Gly Ala Phe Gly Ser Ala Ala Ser
    290                 295                 300

Ala Asp Ala Ala Ser Pro Ser Leu Asp Gly Thr Ala Ala Ala Pro Ala
```

305 310 315 320

Gln

<210> 693
<211> 507
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(484)
<223> RXN01618

<400> 693
ggccgtgcgc gcctccagcg agcctggccg tgccggaaaa gtgctcattc gtttctaaac 60

gtttaaggcc cattagaccc ctgatttaaa aggatctcac atg atc att atc gga 115
Met Ile Ile Ile Gly
1 5

gca gtt ttc gcc atc ctc gca gtt cta ctg cat gtt ttc atc ttc tac 163
Ala Val Phe Ala Ile Leu Ala Val Leu Leu His Val Phe Ile Phe Tyr
10 15 20

atg gaa tca ttc gca tgg act agt gag aaa gca cgt gga gtt ttc ggc 211
Met Glu Ser Phe Ala Trp Thr Ser Glu Lys Ala Arg Gly Val Phe Gly
25 30 35

acc acc gaa atc gac gcc gaa aac acc aag gag atg gcc tac aac caa 259
Thr Thr Glu Ile Asp Ala Glu Asn Thr Lys Glu Met Ala Tyr Asn Gln
40 45 50

ggc ttc tac aac ttc ttc ctg gca gtc atc gcc ggc gtg ggt gtt gcg 307
Gly Phe Tyr Asn Phe Phe Leu Ala Val Ile Ala Gly Val Gly Val Ala
55 60 65

ttc ctc ttc gct ggt tca act ggc atc ggc gca gcc ctc gca ctc gct 355
Phe Leu Phe Ala Gly Ser Thr Gly Ile Gly Ala Ala Leu Ala Leu Ala
70 75 80 85

ggc acc ggt tcc atg ctg gca gcc gct gca gtg ttg gct ttg agc tca 403
Gly Thr Gly Ser Met Leu Ala Ala Ala Ala Val Leu Ala Leu Ser Ser
90 95 100

ccc gac aag cgt ggt gca gcc ttc aag caa ggc acg ttc ccg ctg ctc 451
Pro Asp Lys Arg Gly Ala Ala Phe Lys Gln Gly Thr Phe Pro Leu Leu
105 110 115

gca gtg gtg ttc ctt gtg att gga ttg ctg gtt taagcagttt tttaaaggaa 504
Ala Val Val Phe Leu Val Ile Gly Leu Leu Val
120 125

ctt 507

<210> 694
<211> 128
<212> PRT

<213> Corynebacterium glutamicum

<400> 694

```
Met Ile Ile Ile Gly Ala Val Phe Ala Ile Leu Ala Val Leu Leu His
  1               5                  10                  15

Val Phe Ile Phe Tyr Met Glu Ser Phe Ala Trp Thr Ser Glu Lys Ala
             20                  25                  30

Arg Gly Val Phe Gly Thr Thr Glu Ile Asp Ala Glu Asn Thr Lys Glu
         35                  40                  45

Met Ala Tyr Asn Gln Gly Phe Tyr Asn Phe Phe Leu Ala Val Ile Ala
     50                  55                  60

Gly Val Gly Val Ala Phe Leu Phe Ala Gly Ser Thr Gly Ile Gly Ala
 65                  70                  75                  80

Ala Leu Ala Leu Ala Gly Thr Gly Ser Met Leu Ala Ala Ala Ala Val
                 85                  90                  95

Leu Ala Leu Ser Ser Pro Asp Lys Arg Gly Ala Ala Phe Lys Gln Gly
            100                 105                 110

Thr Phe Pro Leu Leu Ala Val Val Phe Leu Val Ile Gly Leu Leu Val
        115                 120                 125
```

<210> 695
<211> 507
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(484)
<223> FRXA01618

<400> 695

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ggccgtgcgc gcctccagcg agcctggccg tgccggaaaa gtgctcattc gtttctaaac 60

gtttaaggcc cattagaccc ctgatttaaa aggatctcac atg atc att atc gga   115
                                            Met Ile Ile Ile Gly
                                              1               5

gca gtt ttc gcc atc ctc gca gtt cta ctg cat gtt ttc atc ttc tac   163
Ala Val Phe Ala Ile Leu Ala Val Leu Leu His Val Phe Ile Phe Tyr
                 10                  15                  20

atg gaa tca ttc gca tgg act agt gag aaa gca cgt gga gtt ttc ggc   211
Met Glu Ser Phe Ala Trp Thr Ser Glu Lys Ala Arg Gly Val Phe Gly
             25                  30                  35

acc acc gaa atc gac gcc gaa aac acc aag gag atg gcc tac aac caa   259
Thr Thr Glu Ile Asp Ala Glu Asn Thr Lys Glu Met Ala Tyr Asn Gln
         40                  45                  50

ggc ttc tac aac ttc ttc ctg gca gtc atc gcc ggc gtg ggt gtt gcg   307
```

```
Gly Phe Tyr Asn Phe Phe Leu Ala Val Ile Ala Gly Val Gly Val Ala
     55                  60                  65

ttc ctc ttc gct ggt tca act ggc atc ggc gca gcc ctc gca ctc gct   355
Phe Leu Phe Ala Gly Ser Thr Gly Ile Gly Ala Ala Leu Ala Leu Ala
 70                  75                  80                  85

ggc acc ggt tcc atg ctg gca gcc gct gca gtg ttg gct ttg agc tca   403
Gly Thr Gly Ser Met Leu Ala Ala Ala Ala Val Leu Ala Leu Ser Ser
                 90                  95                 100

ccc gac aag cgt ggt gca gcc ttc aag caa ggc acg ttc ccg ctg ctc   451
Pro Asp Lys Arg Gly Ala Ala Phe Lys Gln Gly Thr Phe Pro Leu Leu
            105                 110                 115

gca gtg gtg ttc ctt gtg att gga ttg ctg gtt taagcagttt tttaaaggaa 504
Ala Val Val Phe Leu Val Ile Gly Leu Leu Val
        120                 125

ctt                                                               507
```

<210> 696
<211> 128
<212> PRT
<213> Corynebacterium glutamicum

<400> 696

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Met Ile Ile Ile Gly Ala Val Phe Ala Ile Leu Ala Val Leu Leu His
  1               5                  10                  15

Val Phe Ile Phe Tyr Met Glu Ser Phe Ala Trp Thr Ser Glu Lys Ala
             20                  25                  30

Arg Gly Val Phe Gly Thr Thr Glu Ile Asp Ala Glu Asn Thr Lys Glu
         35                  40                  45

Met Ala Tyr Asn Gln Gly Phe Tyr Asn Phe Phe Leu Ala Val Ile Ala
     50                  55                  60

Gly Val Gly Val Ala Phe Leu Phe Ala Gly Ser Thr Gly Ile Gly Ala
 65                  70                  75                  80

Ala Leu Ala Leu Ala Gly Thr Gly Ser Met Leu Ala Ala Ala Ala Val
                 85                  90                  95

Leu Ala Leu Ser Ser Pro Asp Lys Arg Gly Ala Ala Phe Lys Gln Gly
            100                 105                 110

Thr Phe Pro Leu Leu Ala Val Val Phe Leu Val Ile Gly Leu Leu Val
        115                 120                 125
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<210> 697
<211> 675
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(652)
<223> RXN01634

<400> 697
attggatcta ggaaaaatta tgaacatctc aaagctcgga ctgaggatcg cggtcacagc 60

aacggcgacc acaacggcgc ttgccctcgg tggcacgcac atg gca gtt ggt caa 115
Met Ala Val Gly Gln
1 5

gaa act gat ctg ctc aac gct atg gaa aca ctc gct ggg gtt ccc tca 163
Glu Thr Asp Leu Leu Asn Ala Met Glu Thr Leu Ala Gly Val Pro Ser
10 15 20

gac ttg gtg gtc act gaa atc ctc ccc gat acc acc agc tat gac aat 211
Asp Leu Val Val Thr Glu Ile Leu Pro Asp Thr Thr Ser Tyr Asp Asn
25 30 35

ttt gaa ttc ttt gaa gtt cac aac acc ggc agt gca ccc gtg acc att 259
Phe Glu Phe Phe Glu Val His Asn Thr Gly Ser Ala Pro Val Thr Ile
40 45 50

ggg gaa ggg gag tac acc ttc gcc tat tcc ttt gac gat tcc gcc gat 307
Gly Glu Gly Glu Tyr Thr Phe Ala Tyr Ser Phe Asp Asp Ser Ala Asp
55 60 65

acg tcc cgc gac aag gca ctg gat ctt ggc ggg gaa gtc acg gta gat 355
Thr Ser Arg Asp Lys Ala Leu Asp Leu Gly Gly Glu Val Thr Val Asp
70 75 80 85

gca ggc gaa acc att gtg gtg tgg att gag tac tcc agt tca act gtt 403
Ala Gly Glu Thr Ile Val Val Trp Ile Glu Tyr Ser Ser Ser Thr Val
90 95 100

gat acc gct gcg ttt agt gag caa gac ttc cgt gat ttc tac ggc atg 451
Asp Thr Ala Ala Phe Ser Glu Gln Asp Phe Arg Asp Phe Tyr Gly Met
105 110 115

gat tcc tca gcc cgc atc ttc cga gca act ggc cag gcg ggt ctc gct 499
Asp Ser Ser Ala Arg Ile Phe Arg Ala Thr Gly Gln Ala Gly Leu Ala
120 125 130

aac ggt ggt gat cgt ggc atc cga gtt ctg tac aat ggt gaa gtt tct 547
Asn Gly Gly Asp Arg Gly Ile Arg Val Leu Tyr Asn Gly Glu Val Ser
135 140 145

ggt tgg tcc cac tac cca tca gat agc gca gcg gtt caa aag gga att 595
Gly Trp Ser His Tyr Pro Ser Asp Ser Ala Ala Val Gln Lys Gly Ile
150 155 160 165

gac ttc gcg ctg cca aaa gta ggg gag cag gcc agc att gca agt gcg 643
Asp Phe Ala Leu Pro Lys Val Gly Glu Gln Ala Ser Ile Ala Ser Ala
170 175 180

cac caa aac tgatccaact ccaggatcaa tta 675
His Gln Asn

<210> 698
<211> 184
<212> PRT
<213> Corynebacterium glutamicum

<400> 698
Met Ala Val Gly Gln Glu Thr Asp Leu Leu Asn Ala Met Glu Thr Leu
1 5 10 15

Ala Gly Val Pro Ser Asp Leu Val Val Thr Glu Ile Leu Pro Asp Thr
20 25 30

Thr Ser Tyr Asp Asn Phe Glu Phe Phe Glu Val His Asn Thr Gly Ser
35 40 45

Ala Pro Val Thr Ile Gly Glu Gly Glu Tyr Thr Phe Ala Tyr Ser Phe
50 55 60

Asp Asp Ser Ala Asp Thr Ser Arg Asp Lys Ala Leu Asp Leu Gly Gly
65 70 75 80

Glu Val Thr Val Asp Ala Gly Glu Thr Ile Val Val Trp Ile Glu Tyr
85 90 95

Ser Ser Ser Thr Val Asp Thr Ala Ala Phe Ser Glu Gln Asp Phe Arg
100 105 110

Asp Phe Tyr Gly Met Asp Ser Ser Ala Arg Ile Phe Arg Ala Thr Gly
115 120 125

Gln Ala Gly Leu Ala Asn Gly Gly Asp Arg Gly Ile Arg Val Leu Tyr
130 135 140

Asn Gly Glu Val Ser Gly Trp Ser His Tyr Pro Ser Asp Ser Ala Ala
145 150 155 160

Val Gln Lys Gly Ile Asp Phe Ala Leu Pro Lys Val Gly Glu Gln Ala
165 170 175

Ser Ile Ala Ser Ala His Gln Asn
180

<210> 699
<211> 675
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(652)
<223> FRXA01634

<400> 699
attggatcta ggaaaaatta tgaacatctc aaagctcgga ctgaggatcg cggtcacagc 60

aacggcgacc acaacggcgc ttgccctcgg tggcacgcac atg gca gtt ggt caa 115
Met Ala Val Gly Gln
1 5

gaa act gat ctg ctc aac gct atg gaa aca ctc gct ggg gtt ccc tca 163

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Glu Thr Asp Leu Leu Asn Ala Met Glu Thr Leu Ala Gly Val Pro Ser
                10                  15                  20

gac ttg gtg gtc act gaa atc ctc ccc gat acc acc agc tat gac aat   211
Asp Leu Val Val Thr Glu Ile Leu Pro Asp Thr Thr Ser Tyr Asp Asn
            25                  30                  35

ttt gaa ttc ttt gaa gtt cac aac acc ggc agt gca ccc gtg acc att   259
Phe Glu Phe Phe Glu Val His Asn Thr Gly Ser Ala Pro Val Thr Ile
        40                  45                  50

ggg gaa ggg gag tac acc ttc gcc tat tcc ttt gac gat tcc gcc gat   307
Gly Glu Gly Glu Tyr Thr Phe Ala Tyr Ser Phe Asp Asp Ser Ala Asp
    55                  60                  65

acg tcc cgc gac aag gca ctg gat ctt ggc ggg gaa gtc acg gta gat   355
Thr Ser Arg Asp Lys Ala Leu Asp Leu Gly Gly Glu Val Thr Val Asp
70                  75                  80                  85

gca ggc gaa acc att gtg gtg tgg att gag tac tcc agt tca act gtt   403
Ala Gly Glu Thr Ile Val Val Trp Ile Glu Tyr Ser Ser Ser Thr Val
                90                  95                  100

gat acc gct gcg ttt agt gag caa gac ttc cgt gat ttc tac ggc atg   451
Asp Thr Ala Ala Phe Ser Glu Gln Asp Phe Arg Asp Phe Tyr Gly Met
            105                 110                 115

gat tcc tca gcc cgc atc ttc cga gca act ggc cag gcg ggt ctc gct   499
Asp Ser Ser Ala Arg Ile Phe Arg Ala Thr Gly Gln Ala Gly Leu Ala
        120                 125                 130

aac ggt ggt gat cgt ggc atc cga gtt ctg tac aat ggt gaa gtt tct   547
Asn Gly Gly Asp Arg Gly Ile Arg Val Leu Tyr Asn Gly Glu Val Ser
    135                 140                 145

ggt tgg tcc cac tac cca tca gat agc gca gcg gtt caa aag gga att   595
Gly Trp Ser His Tyr Pro Ser Asp Ser Ala Ala Val Gln Lys Gly Ile
150                 155                 160                 165

gac ttc gcg ctg cca aaa gta ggg gag cag gcc agc att gca agt gcg   643
Asp Phe Ala Leu Pro Lys Val Gly Glu Gln Ala Ser Ile Ala Ser Ala
                170                 175                 180

cac caa aac tgatccaact ccaggatcaa tta                            675
His Gln Asn
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Sequence Listing

<210> 700
<211> 184
<212> PRT
<213> Corynebacterium glutamicum

<400> 700

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Met Ala Val Gly Gln Glu Thr Asp Leu Leu Asn Ala Met Glu Thr Leu
  1               5                  10                  15

Ala Gly Val Pro Ser Asp Leu Val Val Thr Glu Ile Leu Pro Asp Thr
            20                  25                  30

Thr Ser Tyr Asp Asn Phe Glu Phe Phe Glu Val His Asn Thr Gly Ser
```

```
         35                  40                  45

Ala Pro Val Thr Ile Gly Glu Gly Glu Tyr Thr Phe Ala Tyr Ser Phe
     50                  55                  60

Asp Asp Ser Ala Asp Thr Ser Arg Asp Lys Ala Leu Asp Leu Gly Gly
 65                  70                  75                  80

Glu Val Thr Val Asp Ala Gly Glu Thr Ile Val Val Trp Ile Glu Tyr
                 85                  90                  95

Ser Ser Ser Thr Val Asp Thr Ala Ala Phe Ser Glu Gln Asp Phe Arg
            100                 105                 110

Asp Phe Tyr Gly Met Asp Ser Ser Ala Arg Ile Phe Arg Ala Thr Gly
        115                 120                 125

Gln Ala Gly Leu Ala Asn Gly Gly Asp Arg Gly Ile Arg Val Leu Tyr
    130                 135                 140

Asn Gly Glu Val Ser Gly Trp Ser His Tyr Pro Ser Asp Ser Ala Ala
145                 150                 155                 160

Val Gln Lys Gly Ile Asp Phe Ala Leu Pro Lys Val Gly Glu Gln Ala
                165                 170                 175

Ser Ile Ala Ser Ala His Gln Asn
            180


<210> 701
<211> 864
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(841)
<223> RXN01635

<400> 701
agggaattga cttcgcgctg ccaaaagtag gggagcaggc cagcattgca agtgcgcacc 60

aaaactgatc caactccagg atcaattact tctgatcaag ttg att cct ggc gga   115
                                        Leu Ile Pro Gly Gly
                                          1               5

ttg gac act cca gaa gag cct gaa gcc cct gaa gac tct ctt ttt gaa   163
Leu Asp Thr Pro Glu Glu Pro Glu Ala Pro Glu Asp Ser Leu Phe Glu
                 10                  15                  20

ggg cgc act ccc cct agg gat gca agc acc cgc ttg atc ctc act gaa   211
Gly Arg Thr Pro Pro Arg Asp Ala Ser Thr Arg Leu Ile Leu Thr Glu
            25                  30                  35

cta atg gtc aac tcc acc aac atg ggc agt tct gat ggt ttt gag tat   259
Leu Met Val Asn Ser Thr Asn Met Gly Ser Ser Asp Gly Phe Glu Tyr
        40                  45                  50

gtg gaa atc acc aac act act gcc gaa ccc atc gat ttt tcc gat tac   307
Val Glu Ile Thr Asn Thr Thr Ala Glu Pro Ile Asp Phe Ser Asp Tyr
```

```
     55                  60                  65

acc ttg aac tac ctg tac ccg cag gat gag ttc acc aac acc aac gaa   355
Thr Leu Asn Tyr Leu Tyr Pro Gln Asp Glu Phe Thr Asn Thr Asn Glu
 70                  75                  80                  85

gcc gtc tgg gct gcg gaa cct ggt gat gtc att att cag cct gga aaa   403
Ala Val Trp Ala Ala Glu Pro Gly Asp Val Ile Ile Gln Pro Gly Lys
                90                  95                 100

tct ctc gtg ttt tgg atc aaa aat ggc ccc aat gat gag gca acc gca   451
Ser Leu Val Phe Trp Ile Lys Asn Gly Pro Asn Asp Glu Ala Thr Ala
            105                 110                 115

gca gat ttc aat gca gaa tat ggc acc aac ctg gag gct gga aaa gac   499
Ala Asp Phe Asn Ala Glu Tyr Gly Thr Asn Leu Glu Ala Gly Lys Asp
        120                 125                 130

ctt gtt gaa atc tcc tca ggt ggg atg gcc aat ggt act gcc aga gga   547
Leu Val Glu Ile Ser Ser Gly Gly Met Ala Asn Gly Thr Ala Arg Gly
    135                 140                 145

atg cag att cag acc aac act ggc cac ata gtc aac cgt ggt ttc tac   595
Met Gln Ile Gln Thr Asn Thr Gly His Ile Val Asn Arg Gly Phe Tyr
150                 155                 160                 165

aac atg gct ggc gct tct gat gtg aaa gcc aac gag ggt ctt cat ttc   643
Asn Met Ala Gly Ala Ser Asp Val Lys Ala Asn Glu Gly Leu His Phe
                170                 175                 180

gca gtg gat gag tct gat ctt ctg aag caa acg ctt gtc ggc agc ggt   691
Ala Val Asp Glu Ser Asp Leu Leu Lys Gln Thr Leu Val Gly Ser Gly
            185                 190                 195

gcg cca acc ccg ggc act gtg tac act tcg cag att cct aat cca ctg   739
Ala Pro Thr Pro Gly Thr Val Tyr Thr Ser Gln Ile Pro Asn Pro Leu
        200                 205                 210

tct gcc gtt atc gct gat tct tct gta cca ctc atc aca gat aat acc   787
Ser Ala Val Ile Ala Asp Ser Ser Val Pro Leu Ile Thr Asp Asn Thr
    215                 220                 225

gca acc agt atc aac cct gcg gag ccg ttt acc ttc gcc ttc aaa tat   835
Ala Thr Ser Ile Asn Pro Ala Glu Pro Phe Thr Phe Ala Phe Lys Tyr
230                 235                 240                 245

cac cga tgatgtccag gtgcgcacgg caa                                 864
His Arg
```

US20090176274A1

<210> 702
<211> 247
<212> PRT
<213> Corynebacterium glutamicum

<400> 702

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Leu Ile Pro Gly Gly Leu Asp Thr Pro Glu Glu Pro Glu Ala Pro Glu
  1               5                  10                  15

Asp Ser Leu Phe Glu Gly Arg Thr Pro Pro Arg Asp Ala Ser Thr Arg
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            20                  25                  30

Leu Ile Leu Thr Glu Leu Met Val Asn Ser Thr Asn Met Gly Ser Ser
         35                  40                  45

Asp Gly Phe Glu Tyr Val Glu Ile Thr Asn Thr Thr Ala Glu Pro Ile
     50                  55                  60

Asp Phe Ser Asp Tyr Thr Leu Asn Tyr Leu Tyr Pro Gln Asp Glu Phe
 65                  70                  75                  80

Thr Asn Thr Asn Glu Ala Val Trp Ala Ala Glu Pro Gly Asp Val Ile
                 85                  90                  95

Ile Gln Pro Gly Lys Ser Leu Val Phe Trp Ile Lys Asn Gly Pro Asn
            100                 105                 110

Asp Glu Ala Thr Ala Ala Asp Phe Asn Ala Glu Tyr Gly Thr Asn Leu
        115                 120                 125

Glu Ala Gly Lys Asp Leu Val Glu Ile Ser Ser Gly Gly Met Ala Asn
    130                 135                 140

Gly Thr Ala Arg Gly Met Gln Ile Gln Thr Asn Thr Gly His Ile Val
145                 150                 155                 160

Asn Arg Gly Phe Tyr Asn Met Ala Gly Ala Ser Asp Val Lys Ala Asn
                165                 170                 175

Glu Gly Leu His Phe Ala Val Asp Glu Ser Asp Leu Leu Lys Gln Thr
            180                 185                 190

Leu Val Gly Ser Gly Ala Pro Thr Pro Gly Thr Val Tyr Thr Ser Gln
        195                 200                 205

Ile Pro Asn Pro Leu Ser Ala Val Ile Ala Asp Ser Ser Val Pro Leu
    210                 215                 220

Ile Thr Asp Asn Thr Ala Thr Ser Ile Asn Pro Ala Glu Pro Phe Thr
225                 230                 235                 240

Phe Ala Phe Lys Tyr His Arg
                245
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Sequence Listing

<210> 703
<211> 864
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(841)
<223> FRXA01635

<400> 703
agggaattga cttcgcgctg ccaaaagtag gggagcaggc cagcattgca agtgcgcacc 60

aaaactgatc caactccagg atcaattact tctgatcaag ttg att cct ggc gga 115
                                        Leu Ile Pro Gly Gly
                                          1   5

```
ttg gac act cca gaa gag cct gaa gcc cct gaa gac tct ctt ttt gaa   163
Leu Asp Thr Pro Glu Glu Pro Glu Ala Pro Glu Asp Ser Leu Phe Glu
                10                  15                  20

ggg cgc act ccc cct agg gat gca agc acc cgc ttg atc ctc act gaa   211
Gly Arg Thr Pro Pro Arg Asp Ala Ser Thr Arg Leu Ile Leu Thr Glu
            25                  30                  35

cta atg gtc aac tcc acc aac atg ggc agt tct gat ggt ttt gag tat   259
Leu Met Val Asn Ser Thr Asn Met Gly Ser Ser Asp Gly Phe Glu Tyr
        40                  45                  50

gtg gaa atc acc aac act act gcc gaa ccc atc gat ttt tcc gat tac   307
Val Glu Ile Thr Asn Thr Thr Ala Glu Pro Ile Asp Phe Ser Asp Tyr
    55                  60                  65

acc ttg aac tac ctg tac ccg cag gat gag ttc acc aac acc aac gaa   355
Thr Leu Asn Tyr Leu Tyr Pro Gln Asp Glu Phe Thr Asn Thr Asn Glu
70                  75                  80                  85

gcc gtc tgg gct gcg gaa cct ggt gat gtc att att cag cct gga aaa   403
Ala Val Trp Ala Ala Glu Pro Gly Asp Val Ile Ile Gln Pro Gly Lys
                90                  95                  100

tct ctc gtg ttt tgg atc aaa aat ggc ccc aat gat gag gca acc gca   451
Ser Leu Val Phe Trp Ile Lys Asn Gly Pro Asn Asp Glu Ala Thr Ala
            105                 110                 115

gca gat ttc aat gca gaa tat ggc acc aac ctg gag gct gga aaa gac   499
Ala Asp Phe Asn Ala Glu Tyr Gly Thr Asn Leu Glu Ala Gly Lys Asp
        120                 125                 130

ctt gtt gaa atc tcc tca ggt ggg atg gcc aat ggt act gcc aga gga   547
Leu Val Glu Ile Ser Ser Gly Gly Met Ala Asn Gly Thr Ala Arg Gly
    135                 140                 145

atg cag att cag acc aac act ggc cac ata gtc aac cgt ggt ttc tac   595
Met Gln Ile Gln Thr Asn Thr Gly His Ile Val Asn Arg Gly Phe Tyr
150                 155                 160                 165

aac atg gct ggc gct tct gat gtg aaa gcc aac gag ggt ctt cat ttc   643
Asn Met Ala Gly Ala Ser Asp Val Lys Ala Asn Glu Gly Leu His Phe
                170                 175                 180

gca gtg gat gag tct gat ctt ctg aag caa acg ctt gtc ggc agc ggt   691
Ala Val Asp Glu Ser Asp Leu Leu Lys Gln Thr Leu Val Gly Ser Gly
            185                 190                 195

gcg cca acc ccg ggc act gtg tac act tcg cag att cct aat cca ctg   739
Ala Pro Thr Pro Gly Thr Val Tyr Thr Ser Gln Ile Pro Asn Pro Leu
        200                 205                 210

tct gcc gtt atc gct gat tct tct gta cca ctc atc aca gat aat acc   787
Ser Ala Val Ile Ala Asp Ser Ser Val Pro Leu Ile Thr Asp Asn Thr
    215                 220                 225

gca acc agt atc aac cct gcg gag ccg ttt acc ttc gcc ttc aaa tat   835
Ala Thr Ser Ile Asn Pro Ala Glu Pro Phe Thr Phe Ala Phe Lys Tyr
230                 235                 240                 245
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cac cga tgatgtccag gtgcgcacgg caa 864
His Arg

<210> 704
<211> 247
<212> PRT
<213> Corynebacterium glutamicum

<400> 704
Leu Ile Pro Gly Gly Leu Asp Thr Pro Glu Glu Pro Glu Ala Pro Glu
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Asp Ser Leu Phe Glu Gly Arg Thr Pro Pro Arg Asp Ala Ser Thr Arg
20 25 30

Leu Ile Leu Thr Glu Leu Met Val Asn Ser Thr Asn Met Gly Ser Ser
35 40 45

Asp Gly Phe Glu Tyr Val Glu Ile Thr Asn Thr Thr Ala Glu Pro Ile
50 55 60

Asp Phe Ser Asp Tyr Thr Leu Asn Tyr Leu Tyr Pro Gln Asp Glu Phe
65 70 75 80

Thr Asn Thr Asn Glu Ala Val Trp Ala Ala Glu Pro Gly Asp Val Ile
85 90 95

Ile Gln Pro Gly Lys Ser Leu Val Phe Trp Ile Lys Asn Gly Pro Asn
100 105 110

Asp Glu Ala Thr Ala Ala Asp Phe Asn Ala Glu Tyr Gly Thr Asn Leu
115 120 125

Glu Ala Gly Lys Asp Leu Val Glu Ile Ser Ser Gly Gly Met Ala Asn
130 135 140

Gly Thr Ala Arg Gly Met Gln Ile Gln Thr Asn Thr Gly His Ile Val
145 150 155 160

Asn Arg Gly Phe Tyr Asn Met Ala Gly Ala Ser Asp Val Lys Ala Asn
165 170 175

Glu Gly Leu His Phe Ala Val Asp Glu Ser Asp Leu Leu Lys Gln Thr
180 185 190

Leu Val Gly Ser Gly Ala Pro Thr Pro Gly Thr Val Tyr Thr Ser Gln
195 200 205

Ile Pro Asn Pro Leu Ser Ala Val Ile Ala Asp Ser Ser Val Pro Leu
210 215 220

Ile Thr Asp Asn Thr Ala Thr Ser Ile Asn Pro Ala Glu Pro Phe Thr
225 230 235 240

Phe Ala Phe Lys Tyr His Arg
245

<210> 705

<211> 1293
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1270)
<223> RXN01647

<400> 705
gctgggggaa tacatggctg aaggcatgtt gatgcccacg acatcggcgc aggtgtcggg 60

gcataaattt ctggtgcggc gcatcgaaca tgggttggtg atg ggc gat gtg cgc 115
Met Gly Asp Val Arg
1 5

atg att cat gat cca ctt ggt agg cgc cgg cgg gcg ttg gtg ttt ggg 163
Met Ile His Asp Pro Leu Gly Arg Arg Arg Arg Ala Leu Val Phe Gly
10 15 20

gtg gtg gcg tgc gtg atg ttg gcg gtg gga tca ttg gcg ttg gct att 211
Val Val Ala Cys Val Met Leu Ala Val Gly Ser Leu Ala Leu Ala Ile
25 30 35

ttt cga ccc gcg aag gat ccg gcc gat gcg ccg ttg atc cgc tct gaa 259
Phe Arg Pro Ala Lys Asp Pro Ala Asp Ala Pro Leu Ile Arg Ser Glu
40 45 50

tcc ggc gcg ctc ttt gtg cag ctg gat ggg tcg gtg cat ccg gtg gct 307
Ser Gly Ala Leu Phe Val Gln Leu Asp Gly Ser Val His Pro Val Ala
55 60 65

aat gtg gcc tcg gct cgg ttg att gtg ggg gag ccg gtg gat ccg gtg 355
Asn Val Ala Ser Ala Arg Leu Ile Val Gly Glu Pro Val Asp Pro Val
70 75 80 85

aac gcc agc gat gcg atc atc gcg ggc atg ccg cgc gga gtg ccg gtg 403
Asn Ala Ser Asp Ala Ile Ile Ala Gly Met Pro Arg Gly Val Pro Val
90 95 100

ggg gtt cct gat gcg ccg ggg ctt ttc agc agc acc gaa gaa ccc gag 451
Gly Val Pro Asp Ala Pro Gly Leu Phe Ser Ser Thr Glu Glu Pro Glu
105 110 115

caa gat tgg ttt gtg tgc cag gat gtc ggc act ggg gat cta cac att 499
Gln Asp Trp Phe Val Cys Gln Asp Val Gly Thr Gly Asp Leu His Ile
120 125 130

acg gtt cct agg ggc gga cta ggg ccc acc ctg att gcg gaa gga aat 547
Thr Val Pro Arg Gly Gly Leu Gly Pro Thr Leu Ile Ala Glu Gly Asn
135 140 145

ggg tgg ctg ggg gcg tcg aaa agc gaa acc ggc gag gtc acc tgg aac 595
Gly Trp Leu Gly Ala Ser Lys Ser Glu Thr Gly Glu Val Thr Trp Asn
150 155 160 165

ctg att acc gcg gac ggg cgc cgc gaa ctg ccg gcg tgg ggc agc gaa 643
Leu Ile Thr Ala Asp Gly Arg Arg Glu Leu Pro Ala Trp Gly Ser Glu
170 175 180

cat ggg cgc att atg cgc cgc cac ctg ggg att tcc gag gac acc ccg 691

```
His Gly Arg Ile Met Arg Arg His Leu Gly Ile Ser Glu Asp Thr Pro
            185                 190                 195

cgc gta tac ctg acc act gag ctg ctc aac gcg atc ccc gag cac gac   739
Arg Val Tyr Leu Thr Thr Glu Leu Leu Asn Ala Ile Pro Glu His Asp
        200                 205                 210

gcg gtc cgc ttc cca gcc ccg ctg ccc gag ctt gtc gac gcc tcc acc   787
Ala Val Arg Phe Pro Ala Pro Leu Pro Glu Leu Val Asp Ala Ser Thr
    215                 220                 225

cgc aac tgg tta cgg ctc gac ggg gcg ctc gcc gaa atc acg ccg cta   835
Arg Asn Trp Leu Arg Leu Asp Gly Ala Leu Ala Glu Ile Thr Pro Leu
230                 235                 240                 245

cag cgc ggg ttg ctt atc gac gcc ggt tcc ggt gtt ttc ccc gac ccc   883
Gln Arg Gly Leu Leu Ile Asp Ala Gly Ser Gly Val Phe Pro Asp Pro
                250                 255                 260

acc gcg ctt ctt ggt gtg cat gaa gaa aca gcc aac acc ttg acg ctg   931
Thr Ala Leu Leu Gly Val His Glu Glu Thr Ala Asn Thr Leu Thr Leu
            265                 270                 275

ccc gag caa aca gtt tct tgg caa gat ctg gac ggt ggt ttt gcc tgc   979
Pro Glu Gln Thr Val Ser Trp Gln Asp Leu Asp Gly Gly Phe Ala Cys
        280                 285                 290

gcg gat ggt gaa ggc cag atc ggt ttc ctg gaa act ctg gaa tcg ggg   1027
Ala Asp Gly Glu Gly Gln Ile Gly Phe Leu Glu Thr Leu Glu Ser Gly
    295                 300                 305

gtg gcg cta tct ggt gat tcc agg gcg aaa agt ttc agc aca aac gct   1075
Val Ala Leu Ser Gly Asp Ser Arg Ala Lys Ser Phe Ser Thr Asn Ala
310                 315                 320                 325

ggt ggg gca gtg ggc gtg gac agt ggc ttt ggc tac tat gtg gtc tct   1123
Gly Gly Ala Val Gly Val Asp Ser Gly Phe Gly Tyr Tyr Val Val Ser
                330                 335                 340

gat ttt ggg ctg atg cac cct gtt tct act ggt gaa tcg atg gtt gcc   1171
Asp Phe Gly Leu Met His Pro Val Ser Thr Gly Glu Ser Met Val Ala
            345                 350                 355

cta gga atc act gac gtg cag gtc gtg ccg tgg agc gtg ctg cga ttg   1219
Leu Gly Ile Thr Asp Val Gln Val Val Pro Trp Ser Val Leu Arg Leu
        360                 365                 370

ttg ccg cag gga agt gaa tta gca aaa gag aca gcg ctc gcg ccc acc   1267
Leu Pro Gln Gly Ser Glu Leu Ala Lys Glu Thr Ala Leu Ala Pro Thr
    375                 380                 385

tat taaggagtat ggtggcctta cat                                    1293
Tyr
390
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<210> 706
<211> 390
<212> PRT
<213> Corynebacterium glutamicum

<400> 706

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Met Gly Asp Val Arg Met Ile His Asp Pro Leu Gly Arg Arg Arg Arg
  1               5                  10                  15

Ala Leu Val Phe Gly Val Val Ala Cys Val Met Leu Ala Val Gly Ser
             20                  25                  30

Leu Ala Leu Ala Ile Phe Arg Pro Ala Lys Asp Pro Ala Asp Ala Pro
         35                  40                  45

Leu Ile Arg Ser Glu Ser Gly Ala Leu Phe Val Gln Leu Asp Gly Ser
     50                  55                  60

Val His Pro Val Ala Asn Val Ala Ser Ala Arg Leu Ile Val Gly Glu
 65                  70                  75                  80

Pro Val Asp Pro Val Asn Ala Ser Asp Ala Ile Ile Ala Gly Met Pro
                 85                  90                  95

Arg Gly Val Pro Val Gly Val Pro Asp Ala Pro Gly Leu Phe Ser Ser
            100                 105                 110

Thr Glu Glu Pro Glu Gln Asp Trp Phe Val Cys Gln Asp Val Gly Thr
        115                 120                 125

Gly Asp Leu His Ile Thr Val Pro Arg Gly Gly Leu Gly Pro Thr Leu
    130                 135                 140

Ile Ala Glu Gly Asn Gly Trp Leu Gly Ala Ser Lys Ser Glu Thr Gly
145                 150                 155                 160

Glu Val Thr Trp Asn Leu Ile Thr Ala Asp Gly Arg Arg Glu Leu Pro
                165                 170                 175

Ala Trp Gly Ser Glu His Gly Arg Ile Met Arg Arg His Leu Gly Ile
            180                 185                 190

Ser Glu Asp Thr Pro Arg Val Tyr Leu Thr Thr Glu Leu Leu Asn Ala
        195                 200                 205

Ile Pro Glu His Asp Ala Val Arg Phe Pro Ala Pro Leu Pro Glu Leu
    210                 215                 220

Val Asp Ala Ser Thr Arg Asn Trp Leu Arg Leu Asp Gly Ala Leu Ala
225                 230                 235                 240

Glu Ile Thr Pro Leu Gln Arg Gly Leu Leu Ile Asp Ala Gly Ser Gly
                245                 250                 255

Val Phe Pro Asp Pro Thr Ala Leu Leu Gly Val His Glu Glu Thr Ala
            260                 265                 270

Asn Thr Leu Thr Leu Pro Glu Gln Thr Val Ser Trp Gln Asp Leu Asp
        275                 280                 285

Gly Gly Phe Ala Cys Ala Asp Gly Glu Gly Gln Ile Gly Phe Leu Glu
    290                 295                 300

Thr Leu Glu Ser Gly Val Ala Leu Ser Gly Asp Ser Arg Ala Lys Ser
305                 310                 315                 320
```

```
Phe Ser Thr Asn Ala Gly Gly Ala Val Gly Val Asp Ser Gly Phe Gly
                325                 330                 335

Tyr Tyr Val Val Ser Asp Phe Gly Leu Met His Pro Val Ser Thr Gly
            340                 345                 350

Glu Ser Met Val Ala Leu Gly Ile Thr Asp Val Gln Val Val Pro Trp
        355                 360                 365

Ser Val Leu Arg Leu Leu Pro Gln Gly Ser Glu Leu Ala Lys Glu Thr
    370                 375                 380

Ala Leu Ala Pro Thr Tyr
385                 390


<210> 707
<211> 911
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(888)
<223> FRXA01647

<400> 707
atg ccg cgc gga gtg ccg gtg ggg gtt cct gat gcg ccg ggg ctt ttc   48
Met Pro Arg Gly Val Pro Val Gly Val Pro Asp Ala Pro Gly Leu Phe
  1               5                  10                  15

agc agc acc gaa gaa ccc gag caa gat tgg ttt gtg tgc cag gat gtc   96
Ser Ser Thr Glu Glu Pro Glu Gln Asp Trp Phe Val Cys Gln Asp Val
             20                  25                  30

ggc act ggg gat cta cac att acg gtt cct agg ggc gga cta ggg ccc   144
Gly Thr Gly Asp Leu His Ile Thr Val Pro Arg Gly Gly Leu Gly Pro
         35                  40                  45

acc ctg att gcg gaa gga aat ggg tgg ctg ggg gcg tcg aaa agc gaa   192
Thr Leu Ile Ala Glu Gly Asn Gly Trp Leu Gly Ala Ser Lys Ser Glu
     50                  55                  60

acc ggc gag gtc acc tgg aac ctg att acc gcg gac ggg cgc cgc gaa   240
Thr Gly Glu Val Thr Trp Asn Leu Ile Thr Ala Asp Gly Arg Arg Glu
 65                  70                  75                  80

ctg ccg gcg tgg ggc agc gaa cat ggg cgc att atg cgc cgc cac ctg   288
Leu Pro Ala Trp Gly Ser Glu His Gly Arg Ile Met Arg Arg His Leu
                 85                  90                  95

ggg att tcc gag gac acc ccg cgc gta tac ctg acc act gag ctg ctc   336
Gly Ile Ser Glu Asp Thr Pro Arg Val Tyr Leu Thr Thr Glu Leu Leu
            100                 105                 110

aac gcg atc ccc gag cac gac gcg gtc cgc ttc cca gcc ccg ctg ccc   384
Asn Ala Ile Pro Glu His Asp Ala Val Arg Phe Pro Ala Pro Leu Pro
        115                 120                 125

gag ctt gtc gac gcc tcc acc cgc aac tgg tta cgg ctc gac ggg gcg   432
Glu Leu Val Asp Ala Ser Thr Arg Asn Trp Leu Arg Leu Asp Gly Ala
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```
    130                 135                 140

ctc gcc gaa atc acg ccg cta cag cgc ggg ttg ctt atc gac gcc ggt   480
Leu Ala Glu Ile Thr Pro Leu Gln Arg Gly Leu Leu Ile Asp Ala Gly
145                 150                 155                 160

tcc ggt gtt ttc ccc gac ccc acc gcg ctt ctt ggt gtg cat gaa gaa   528
Ser Gly Val Phe Pro Asp Pro Thr Ala Leu Leu Gly Val His Glu Glu
                165                 170                 175

aca gcc aac acc ttg acg ctg ccc gag caa aca gtt tct tgg caa gat   576
Thr Ala Asn Thr Leu Thr Leu Pro Glu Gln Thr Val Ser Trp Gln Asp
            180                 185                 190

ctg gac ggt ggt ttt gcc tgc gcg gat ggt gaa ggc cag atc ggt ttc   624
Leu Asp Gly Gly Phe Ala Cys Ala Asp Gly Glu Gly Gln Ile Gly Phe
        195                 200                 205

ctg gaa act ctg gaa tcg ggg gtg gcg cta tct ggt gat tcc agg gcg   672
Leu Glu Thr Leu Glu Ser Gly Val Ala Leu Ser Gly Asp Ser Arg Ala
    210                 215                 220

aaa agt ttc agc aca aac gct ggt ggg gca gtg ggc gtg gac agt ggc   720
Lys Ser Phe Ser Thr Asn Ala Gly Gly Ala Val Gly Val Asp Ser Gly
225                 230                 235                 240

ttt ggc tac tat gtg gtc tct gat ttt ggg ctg atg cac cct gtt tct   768
Phe Gly Tyr Tyr Val Val Ser Asp Phe Gly Leu Met His Pro Val Ser
                245                 250                 255

act ggt gaa tcg atg gtt gcc cta gga atc act gac gtg cag gtc gtg   816
Thr Gly Glu Ser Met Val Ala Leu Gly Ile Thr Asp Val Gln Val Val
            260                 265                 270

ccg tgg agc gtg ctg cga ttg ttg ccg cag gga agt gaa tta gca aaa   864
Pro Trp Ser Val Leu Arg Leu Leu Pro Gln Gly Ser Glu Leu Ala Lys
        275                 280                 285

gag aca gcg ctc gcg ccc acc tat taaggagtat ggtggcctta cat         911
Glu Thr Ala Leu Ala Pro Thr Tyr
    290                 295
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```
Thr Gly Glu Val Thr Trp Asn Leu Ile Thr Ala Asp Gly Arg Arg Glu
 65                  70                  75                  80

Leu Pro Ala Trp Gly Ser Glu His Gly Arg Ile Met Arg Arg His Leu
                 85                  90                  95

Gly Ile Ser Glu Asp Thr Pro Arg Val Tyr Leu Thr Thr Glu Leu Leu
            100                 105                 110

Asn Ala Ile Pro Glu His Asp Ala Val Arg Phe Pro Ala Pro Leu Pro
        115                 120                 125

Glu Leu Val Asp Ala Ser Thr Arg Asn Trp Leu Arg Leu Asp Gly Ala
    130                 135                 140

Leu Ala Glu Ile Thr Pro Leu Gln Arg Gly Leu Leu Ile Asp Ala Gly
145                 150                 155                 160

Ser Gly Val Phe Pro Asp Pro Thr Ala Leu Leu Gly Val His Glu Glu
                165                 170                 175

Thr Ala Asn Thr Leu Thr Leu Pro Glu Gln Thr Val Ser Trp Gln Asp
            180                 185                 190

Leu Asp Gly Gly Phe Ala Cys Ala Asp Gly Glu Gly Gln Ile Gly Phe
        195                 200                 205

Leu Glu Thr Leu Glu Ser Gly Val Ala Leu Ser Gly Asp Ser Arg Ala
    210                 215                 220

Lys Ser Phe Ser Thr Asn Ala Gly Gly Ala Val Gly Val Asp Ser Gly
225                 230                 235                 240

Phe Gly Tyr Tyr Val Val Ser Asp Phe Gly Leu Met His Pro Val Ser
                245                 250                 255

Thr Gly Glu Ser Met Val Ala Leu Gly Ile Thr Asp Val Gln Val Val
            260                 265                 270

Pro Trp Ser Val Leu Arg Leu Leu Pro Gln Gly Ser Glu Leu Ala Lys
        275                 280                 285

Glu Thr Ala Leu Ala Pro Thr Tyr
    290                 295
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<210> 709
<211> 1856
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1833)
<223> RXN01658

<400> 709

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gat cca cag atc ctg tca cca acc ttc acc cag caa cag cag ctg cga   48
Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Leu Arg
  1               5                  10                  15
```

```
aac ttc tac ggt ttc cca gac cag ctg gcg atg gac cgc ttt gaa gta   96
Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val
             20                  25                  30

gat ggc aaa ctc cgc gac ttt gtt gtg gca gca cgt gag ctc gat cca  144
Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro
         35                  40                  45

aac gcc ctg cag caa aac cag cag gac tgg att aac cgt cac act gtt  192
Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
     50                  55                  60

tat acc cac ggc aac ggc ttc att gca gct caa gca aac cag gtg gat  240
Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp
 65                  70                  75                  80

gag gtc gcc cgc gac gtc gga tcc act cgt ggt ggt tac cct gtc tac  288
Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr
                 85                  90                  95

acc gtc tct gat ttg cag tcg aat gct cgt gct gca gaa agc gaa gat  336
Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp
            100                 105                 110

gct gag gag ctt ggc atc aag gtt gat gag cct cgt gtg tac tac gga  384
Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly
        115                 120                 125

cca ctg att gct tct gcg act gat ggt gct gac tac gca att gtc ggt  432
Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly
    130                 135                 140

gac acc ggc gat ggc cca gtc gag tac gac act gac acc tcc agc tac  480
Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr
145                 150                 155                 160

acc tac gaa ggt gct ggc ggc gtg gac att gga aac atg gtc aac cgt  528
Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg
                165                 170                 175

gcg atg ttt gca ttg cgc tac cag gaa atg aac atg ctc ctg tct gat  576
Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp
            180                 185                 190

cgt gtt ggt tcc gaa tcc aag atc cta ttt gag cgc gat cct cgt tcc  624
Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser
        195                 200                 205

cgt gtg gaa aag gtt gca cct tgg ttg acc act gac tcc aag acc tac  672
Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr
    210                 215                 220

cca act gtg att gat ggt cgc atc aag tgg atc gtc gat ggc tac acc  720
Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr
225                 230                 235                 240

acc ttg gat agt ctt ccg tac tcc acg cgc acc tca ctg acg gaa gcg  768
Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala
                245                 250                 255

act cag gat gct gtc atg cct gac ggc acc cca cag cca ctg atc aca  816
```

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Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr
            260                 265                 270

gat agg gtc ggt tac atc cgc aac tcc gtg aag gct gtt gtt gat gcg   864
Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala
        275                 280                 285

tac gac gga act gtt gaa ctc tac gaa ttc gac acc gaa gat cct gtt   912
Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val
    290                 295                 300

ctg aag gca tgg cgt ggc gtg ttc cca gac acc gtg aag gac ggg tcg   960
Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser
305                 310                 315                 320

gag att tcc gat gag ctt cgc gca cac ctg cgt tac cca gaa gat ttg  1008
Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu
                325                 330                 335

ttc aag gtc cag cgt gac atg ctg gcc aag tac aac gtt gat gat tct  1056
Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser
            340                 345                 350

gga aca ttc ttc acc aac gat gcg ttc tgg tct gtc cca ggt gac cca  1104
Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro
        355                 360                 365

act gca gcg gag ggc cgc cag gaa ctt aag cag cct cct tac tac gtg  1152
Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val
    370                 375                 380

gtg gca gca gac cca gag acc ggt gag tcc agc ttc cag ctg atc acc  1200
Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr
385                 390                 395                 400

ccg ttc cgt gga ctt cag cgc gag tac ctc tct gca cac atg tct gcg  1248
Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala
                405                 410                 415

tcg tct gat cca gtt acc tac ggt gaa atc act gtt cgt gtg ctg cct  1296
Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro
            420                 425                 430

acc gat tct gtg acc cag ggt cca aag cag gcc cag gat gcg atg atg  1344
Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met
        435                 440                 445

tca tct gac cag gtt gct cag gac caa aca ctg tgg cgt gga tcg aac  1392
Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn
    450                 455                 460

gat ctg cac aac gga aac ctg ttg acc ttg cca gtt ggt ggc gga gag  1440
Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu
465                 470                 475                 480

atc ctc tac gtt gag ccg att tac tcg cag cgc aag gat cag gca tcg  1488
Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala Ser
                485                 490                 495

gcc ttc ccg aag ctt ctg cgc gtg ctg gtc ttc tac aag ggt cag gtt  1536
Ala Phe Pro Lys Leu Leu Arg Val Leu Val Phe Tyr Lys Gly Gln Val
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            500                 505                 510

ggt tac gca cca acg atc gct gaa gcc cta tcg cag gtc ggc att gat   1584
Gly Tyr Ala Pro Thr Ile Ala Glu Ala Leu Ser Gln Val Gly Ile Asp
        515                 520                 525

ccg aag gaa gcg cag gac atc gaa gag gta gat ggc acc gct acg acg   1632
Pro Lys Glu Ala Gln Asp Ile Glu Glu Val Asp Gly Thr Ala Thr Thr
    530                 535                 540

cca tcg act gat gag act gac act gac act gat cag cct gca acc gaa   1680
Pro Ser Thr Asp Glu Thr Asp Thr Asp Thr Asp Gln Pro Ala Thr Glu
545                 550                 555                 560

acc cca act gca cca gtg agt gag gcg gaa gga atc gcg gcc atc aac   1728
Thr Pro Thr Ala Pro Val Ser Glu Ala Glu Gly Ile Ala Ala Ile Asn
                565                 570                 575

gat gcg ttg agc aac ctt gaa gct gct cgc gat agc tct ttc gaa gag   1776
Asp Ala Leu Ser Asn Leu Glu Ala Ala Arg Asp Ser Ser Phe Glu Glu
            580                 585                 590

tat ggt cgt gca ctc gat gcg ctt gat cgt gcc gtc gat agc tac cag   1824
Tyr Gly Arg Ala Leu Asp Ala Leu Asp Arg Ala Val Asp Ser Tyr Gln
        595                 600                 605

tcc gca cag tagcgtttga gtaaacagcc cga                            1856
Ser Ala Gln
    610


<210> 710
<211> 611
<212> PRT
<213> Corynebacterium glutamicum

<400> 710
Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Gln Leu Arg
  1               5                  10                  15

Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val
             20                  25                  30

Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro
         35                  40                  45

Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
     50                  55                  60

Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp
 65                  70                  75                  80

Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr
                 85                  90                  95

Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp
            100                 105                 110

Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly
        115                 120                 125
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Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly
    130                 135                 140

Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr
145                 150                 155                 160

Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg
                165                 170                 175

Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp
            180                 185                 190

Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser
        195                 200                 205

Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr
    210                 215                 220

Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr
225                 230                 235                 240

Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala
                245                 250                 255

Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr
            260                 265                 270

Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala
        275                 280                 285

Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val
    290                 295                 300

Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser
305                 310                 315                 320

Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu
                325                 330                 335

Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser
            340                 345                 350

Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro
        355                 360                 365

Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val
    370                 375                 380

Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr
385                 390                 395                 400

Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala
                405                 410                 415

Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro
            420                 425                 430

Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met
        435                 440                 445

Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn
```

```
    450                 455                 460

Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu
465                 470                 475                 480

Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala Ser
                485                 490                 495

Ala Phe Pro Lys Leu Leu Arg Val Leu Val Phe Tyr Lys Gly Gln Val
            500                 505                 510

Gly Tyr Ala Pro Thr Ile Ala Glu Ala Leu Ser Gln Val Gly Ile Asp
        515                 520                 525

Pro Lys Glu Ala Gln Asp Ile Glu Glu Val Asp Gly Thr Ala Thr Thr
    530                 535                 540

Pro Ser Thr Asp Glu Thr Asp Thr Asp Thr Asp Gln Pro Ala Thr Glu
545                 550                 555                 560

Thr Pro Thr Ala Pro Val Ser Glu Ala Glu Gly Ile Ala Ala Ile Asn
                565                 570                 575

Asp Ala Leu Ser Asn Leu Glu Ala Ala Arg Asp Ser Ser Phe Glu Glu
            580                 585                 590

Tyr Gly Arg Ala Leu Asp Ala Leu Asp Arg Ala Val Asp Ser Tyr Gln
        595                 600                 605

Ser Ala Gln
    610


<210> 711
<211> 1485
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1485)
<223> FRXA01658

<400> 711
gat cca cag atc ctg tca cca acc ttc acc cag caa cag cag ctg cga   48
Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Gln Leu Arg
  1               5                  10                  15

aac ttc tac ggt ttc cca gac cag ctg gcg atg gac cgc ttt gaa gta   96
Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val
             20                  25                  30

gat ggc aaa ctc cgc gac ttt gtt gtg gca gca cgt gag ctc gat cca   144
Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro
         35                  40                  45

aac gcc ctg cag caa aac cag cag gac tgg att aac cgt cac act gtt   192
Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
     50                  55                  60

tat acc cac ggc aac ggc ttc att gca gct caa gca aac cag gtg gat   240
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```
Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp
 65                  70                  75                  80

gag gtc gcc cgc gac gtc gga tcc act cgt ggt ggt tac cct gtc tac   288
Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr
                 85                  90                  95

acc gtc tct gat ttg cag tcg aat gct cgt gct gca gaa agc gaa gat   336
Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp
            100                 105                 110

gct gag gag ctt ggc atc aag gtt gat gag cct cgt gtg tac tac gga   384
Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly
        115                 120                 125

cca ctg att gct tct gcg act gat ggt gct gac tac gca att gtc ggt   432
Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly
    130                 135                 140

gac acc ggc gat ggc cca gtc gag tac gac act gac acc tcc agc tac   480
Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr
145                 150                 155                 160

acc tac gaa ggt gct ggc ggc gtg gac att gga aac atg gtc aac cgt   528
Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg
                165                 170                 175

gcg atg ttt gca ttg cgc tac cag gaa atg aac atg ctc ctg tct gat   576
Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp
            180                 185                 190

cgt gtt ggt tcc gaa tcc aag atc cta ttt gag cgc gat cct cgt tcc   624
Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser
        195                 200                 205

cgt gtg gaa aag gtt gca cct tgg ttg acc act gac tcc aag acc tac   672
Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr
    210                 215                 220

cca act gtg att gat ggt cgc atc aag tgg atc gtc gat ggc tac acc   720
Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr
225                 230                 235                 240

acc ttg gat agt ctt ccg tac tcc acg cgc acc tca ctg acg gaa gcg   768
Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala
                245                 250                 255

act cag gat gct gtc atg cct gac ggc acc cca cag cca ctg atc aca   816
Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr
            260                 265                 270

gat agg gtc ggt tac atc cgc aac tcc gtg aag gct gtt gtt gat gcg   864
Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala
        275                 280                 285

tac gac gga act gtt gaa ctc tac gaa ttc gac acc gaa gat cct gtt   912
Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val
    290                 295                 300

ctg aag gca tgg cgt ggc gtg ttc cca gac acc gtg aag gac ggg tcg   960
Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser
```

```
305                 310                 315                 320

gag att tcc gat gag ctt cgc gca cac ctg cgt tac cca gaa gat ttg   1008
Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu
                325                 330                 335

ttc aag gtc cag cgt gac atg ctg gcc aag tac aac gtt gat gat tct   1056
Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser
            340                 345                 350

gga aca ttc ttc acc aac gat gcg ttc tgg tct gtc cca ggt gac cca   1104
Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro
        355                 360                 365

act gca gcg gag ggc cgc cag gaa ctt aag cag cct cct tac tac gtg   1152
Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val
    370                 375                 380

gtg gca gca gac cca gag acc ggt gag tcc agc ttc cag ctg atc acc   1200
Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr
385                 390                 395                 400

ccg ttc cgt gga ctt cag cgc gag tac ctc tct gca cac atg tct gcg   1248
Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala
                405                 410                 415

tcg tct gat cca gtt acc tac ggt gaa atc act gtt cgt gtg ctg cct   1296
Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro
            420                 425                 430

acc gat tct gtg acc cag ggt cca aag cag gcc cag gat gcg atg atg   1344
Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met
        435                 440                 445

tca tct gac cag gtt gct cag gac caa aca ctg tgg cgt gga tcg aac   1392
Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn
    450                 455                 460

gat ctg cac aac gga aac ctg ttg acc ttg cca gtt ggt ggc gga gag   1440
Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu
465                 470                 475                 480

atc ctc tac gtt gag ccg att tac tcg cag cgc aag gat cag gca       1485
Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala
                485                 490                 495
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<210> 712
<211> 495
<212> PRT
<213> Corynebacterium glutamicum

<400> 712

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Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Gln Leu Arg
  1               5                  10                  15

Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val
            20                  25                  30

Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro
        35                  40                  45
```

```
Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
     50                  55                  60

Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp
 65                  70                  75                  80

Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr
                 85                  90                  95

Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp
            100                 105                 110

Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly
        115                 120                 125

Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly
    130                 135                 140

Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr
145                 150                 155                 160

Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg
                165                 170                 175

Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp
            180                 185                 190

Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser
        195                 200                 205

Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr
    210                 215                 220

Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr
225                 230                 235                 240

Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala
                245                 250                 255

Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr
            260                 265                 270

Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala
        275                 280                 285

Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val
    290                 295                 300

Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser
305                 310                 315                 320

Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu
                325                 330                 335

Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser
            340                 345                 350

Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro
        355                 360                 365
```

```
Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val
    370                 375                 380

Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr
385                 390                 395                 400

Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala
                405                 410                 415

Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro
            420                 425                 430

Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met
        435                 440                 445

Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn
    450                 455                 460

Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu
465                 470                 475                 480

Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala
                485                 490                 495
```

20040259 20040259 20040259

<210> 713
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(646)
<223> RXN01659

<400> 713

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ttgatgcgcg ccgcggtgag cagcctgccg atccagagcg tgaagaatct gatgatttag 60

tcgagattga taccgtctct ggattccgcc tgctcagtac gtg gcg ggg gtt gcg   115
                                              Val Ala Gly Val Ala
                                                1               5

cag cgt ttt gtc gac gag cgc att cac gtc ggt ttg gat tcc atg cca   163
Gln Arg Phe Val Asp Glu Arg Ile His Val Gly Leu Asp Ser Met Pro
                10                  15                  20

gaa gct gtg act gct gtg tgg atg gaa tct gat tgg gtg ttg gcg gaa   211
Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala Glu
            25                  30                  35

acc atc aag ggt tcc acg cct tcc gat tgg gaa gag att ttg cgg ccg   259
Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg Pro
        40                  45                  50

ttg gcg ctg ctc acg gac gcg tct ttc acg ttg cca cct cgt tcc acg   307
Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser Thr
    55                  60                  65

cgt gcg caa acc ttg gat ttg aag cat ttg gaa cca agc cgt ctg aag   355
Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu Lys
70                  75                  80                  85
```

```
ccg gag cag cca gaa aag cca gcg ttt act ccc aat gct tcg gaa gaa   403
Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu Glu
                 90                  95                 100

gat ttg tct cag ccg ttg gtg atc cgc ccc gag gag ccg ttg cag atg   451
Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln Met
            105                 110                 115

ccg gtt cgc ggt gtg cag gaa agc cgc gga gtg gtc gag cca cgg tca   499
Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg Ser
        120                 125                 130

ttg ggt gcg gat gat gtg gag tcg att gcg gag ggc gat cca gag cgt   547
Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu Arg
    135                 140                 145

ccg agc gat ctt tat ggc acg cgt gtg ctg cgt gat ctc aat ggt cag   595
Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly Gln
150                 155                 160                 165

tcc agt att ttc caa gat tcc acc gac gcg gat gag cca cca aaa aag   643
Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys Lys
                170                 175                 180

tgg tagaaaactg gtgtttttcg gcc                                    669
Trp
```

09/30/2004 09:54:00 AM

<210> 714
<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 714

```
Val Ala Gly Val Ala Gln Arg Phe Val Asp Glu Arg Ile His Val Gly
  1               5                  10                  15

Leu Asp Ser Met Pro Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp
            20                  25                  30

Trp Val Leu Ala Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu
        35                  40                  45

Glu Ile Leu Arg Pro Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu
    50                  55                  60

Pro Pro Arg Ser Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu
65                  70                  75                  80

Pro Ser Arg Leu Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro
                85                  90                  95

Asn Ala Ser Glu Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu
            100                 105                 110

Glu Pro Leu Gln Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val
        115                 120                 125

Val Glu Pro Arg Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu
```

```
    130                 135                 140

Gly Asp Pro Glu Arg Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg
145                 150                 155                 160

Asp Leu Asn Gly Gln Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp
                165                 170                 175

Glu Pro Pro Lys Lys Trp
            180
```

<210> 715
<211> 509
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(486)
<223> FRXA01659

<400> 715

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cca gaa gct gtg act gct gtg tgg atg gaa tct gat tgg gtg ttg gcg   48
Pro Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala
  1               5                  10                  15

gaa acc atc aag ggt tcc acg cct tcc gat tgg gaa gag att ttg cgg   96
Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg
             20                  25                  30

ccg ttg gcg ctg ctc acg gac gcg tct ttc acg ttg cca cct cgt tcc   144
Pro Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser
         35                  40                  45

acg cgt gcg caa acc ttg gat ttg aag cat ttg gaa cca agc cgt ctg   192
Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu
     50                  55                  60

aag ccg gag cag cca gaa aag cca gcg ttt act ccc aat gct tcg gaa   240
Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu
 65                  70                  75                  80

gaa gat ttg tct cag ccg ttg gtg atc cgc ccc gag gag ccg ttg cag   288
Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln
                 85                  90                  95

atg ccg gtt cgc ggt gtg cag gaa agc cgc gga gtg gtc gag cca cgg   336
Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg
            100                 105                 110

tca ttg ggt gcg gat gat gtg gag tcg att gcg gag ggc gat cca gag   384
Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu
        115                 120                 125

cgt ccg agc gat ctt tat ggc acg cgt gtg ctg cgt gat ctc aat ggt   432
Arg Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly
    130                 135                 140

cag tcc agt att ttc caa gat tcc acc gac gcg gat gag cca cca aaa   480
Gln Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys
```

```
145                 150                 155                 160

aag tgg tagaaaactg gtgtttttcg gcc                                   509
Lys Trp


<210> 716
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 716
Pro Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala
  1               5                  10                  15

Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg
             20                  25                  30

Pro Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser
         35                  40                  45

Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu
     50                  55                  60

Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu
 65                  70                  75                  80

Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln
                 85                  90                  95

Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg
            100                 105                 110

Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu
        115                 120                 125

Arg Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly
    130                 135                 140

Gln Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys
145                 150                 155                 160

Lys Trp


<210> 717
<211> 981
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(958)
<223> RXN01663

<400> 717
tattttgctg gttggtcaca gtggagcgct aaccccgaga atcctatcga ggcctaaaat 60

cgtggcttga gtacgcactg ccagtaaggt gtgtgatgtg atg gaa ata agt gtc   115
```

```
                                                    Met Glu Ile Ser Val
                                                      1               5

ttg atc atc gcc gca ctg atc ttg gtg gca ggc atc gta ctg tgg cgc   163
Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly Ile Val Leu Trp Arg
                  10                  15                  20

gcg gac tcg tct aaa cag gca gct aaa aag gct gaa tca cct gtg ggc   211
Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala Glu Ser Pro Val Gly
              25                  30                  35

tca gtc gca cct gcg ccc gtg ctg gtt gaa gaa gag ccg gac cct gag   259
Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu Glu Pro Asp Pro Glu
          40                  45                  50

ttt gag cca gaa ctg gac cct gaa cca gaa gcg caa cca gaa cca gag   307
Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala Gln Pro Glu Pro Glu
      55                  60                  65

ctg gaa gtt gcg cct aga ttt gcg cca gaa cca gtt caa gat ctt gag   355
Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro Val Gln Asp Leu Glu
  70                  75                  80                  85

ccg gat cag gct gag gac att tat ttt gat gat tcc cct gaa ctc gat   403
Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp Ser Pro Glu Leu Asp
                  90                  95                 100

gct gat gtt gaa aat gcc ttg gct gag ctt act gag gta gaa gac tac   451
Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr Glu Val Glu Asp Tyr
              105                 110                 115

ccg gaa gag cca gtg cag tct gag caa cct caa gcc cct gcc acg gcg   499
Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln Ala Pro Ala Thr Ala
          120                 125                 130

gag gta gct gcg gac gag gag caa cgg ggc gtc gat aag cat tcg ttt   547
Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val Asp Lys His Ser Phe
      135                 140                 145

ttg agc tct ttg cct ggt tcg cag cgc cgg gag cgc cga aac tgg gcg   595
Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu Arg Arg Asn Trp Ala
150                 155                 160                 165

gcg aag cac cac ttc gat ttc atc aag gaa gat gcc ttt ttg acc gat   643
Ala Lys His His Phe Asp Phe Ile Lys Glu Asp Ala Phe Leu Thr Asp
                  170                 175                 180

gaa tgg tca agg ggt gcg gca tcg act ggt gcc gtt gca cgt gat gtg   691
Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala Val Ala Arg Asp Val
              185                 190                 195

gtc agt ggc atg gct gaa gga tat gaa acg cat ctg gtg gat ttg gcg   739
Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His Leu Val Asp Leu Ala
          200                 205                 210

ggc gtg ccc gtg atg gcg atg cgc cgt gga att acc tct gac gtg gtc   787
Gly Val Pro Val Met Ala Met Arg Arg Gly Ile Thr Ser Asp Val Val
      215                 220                 225

att gat gcg cgc cgc ggt gag cag cct gcc gat cca gag cgt gaa gaa   835
Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp Pro Glu Arg Glu Glu
```

```
230                 235                 240                 245

tct gat gat tta gtc gag att gat acc gtc tct gga ttc cgc ctg ctc   883
Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser Gly Phe Arg Leu Leu
                250                 255                 260

agt acg tgg cgg ggg ttg cgc agc gtt ttg tcg acg agc gca ttc acg   931
Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser Thr Ser Ala Phe Thr
            265                 270                 275

tcg gtt tgg att cca tgc cag aag ctg tgactgctgt gtggatggaa         978
Ser Val Trp Ile Pro Cys Gln Lys Leu
        280                 285

tct                                                               981


<210> 718
<211> 286
<212> PRT
<213> Corynebacterium glutamicum

<400> 718
Met Glu Ile Ser Val Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly
  1               5                  10                  15

Ile Val Leu Trp Arg Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala
             20                  25                  30

Glu Ser Pro Val Gly Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu
         35                  40                  45

Glu Pro Asp Pro Glu Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala
     50                  55                  60

Gln Pro Glu Pro Glu Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro
 65                  70                  75                  80

Val Gln Asp Leu Glu Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp
                 85                  90                  95

Ser Pro Glu Leu Asp Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr
            100                 105                 110

Glu Val Glu Asp Tyr Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln
        115                 120                 125

Ala Pro Ala Thr Ala Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val
    130                 135                 140

Asp Lys His Ser Phe Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu
145                 150                 155                 160

Arg Arg Asn Trp Ala Ala Lys His His Phe Asp Phe Ile Lys Glu Asp
                165                 170                 175

Ala Phe Leu Thr Asp Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala
            180                 185                 190

Val Ala Arg Asp Val Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His
        195                 200                 205
```

```
Leu Val Asp Leu Ala Gly Val Pro Val Met Ala Met Arg Arg Gly Ile
    210                 215                 220

Thr Ser Asp Val Val Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp
225                 230                 235                 240

Pro Glu Arg Glu Glu Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser
                245                 250                 255

Gly Phe Arg Leu Leu Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser
            260                 265                 270

Thr Ser Ala Phe Thr Ser Val Trp Ile Pro Cys Gln Lys Leu
        275                 280                 285


<210> 719
<211> 535
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(535)
<223> FRXA01663

<400> 719
tattttgctg gttggtcaca gtggagcgct aaccccgaga atcctatcga ggcctaaaat 60

cgtggcttga gtacgcactg ccagtaaggt gtgtgatgtg atg gaa ata agt gtc   115
                                          Met Glu Ile Ser Val
                                            1               5

ttg atc atc gcc gca ctg atc ttg gtg gca ggc atc gta ctg tgg cgc   163
Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly Ile Val Leu Trp Arg
                10                  15                  20

gcg gac tcg tct aaa cag gca gct aaa aag gct gaa tca cct gtg ggc   211
Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala Glu Ser Pro Val Gly
            25                  30                  35

tca gtc gca cct gcg ccc gtg ctg gtt gaa gaa gag ccg gac cct gag   259
Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu Glu Pro Asp Pro Glu
        40                  45                  50

ttt gag cca gaa ctg gac cct gaa cca gaa gcg caa cca gaa cca gag   307
Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala Gln Pro Glu Pro Glu
    55                  60                  65

ctg gaa gtt gcg cct aga ttt gcg cca gaa cca gtt caa gat ctt gag   355
Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro Val Gln Asp Leu Glu
70                  75                  80                  85

ccg gat cag gct gag gac att tat ttt gat gat tcc cct gaa ctc gat   403
Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp Ser Pro Glu Leu Asp
                90                  95                  100

gct gat gtt gaa aat gcc ttg gct gag ctt act gag gta gaa gac tac   451
Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr Glu Val Glu Asp Tyr
            105                 110                 115
```

```
ccg gaa gag cca gtg cag tct gag caa cct caa gcc cct gcc acg gcg   499
Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln Ala Pro Ala Thr Ala
        120                 125                 130

gag gta gct gcg gac gag gag caa cgg ggc gtc gat                   535
Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val Asp
    135                 140                 145


<210> 720
<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 720
Met Glu Ile Ser Val Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly
  1               5                  10                  15

Ile Val Leu Trp Arg Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala
             20                  25                  30

Glu Ser Pro Val Gly Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu
         35                  40                  45

Glu Pro Asp Pro Glu Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala
     50                  55                  60

Gln Pro Glu Pro Glu Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro
 65                  70                  75                  80

Val Gln Asp Leu Glu Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp
                 85                  90                  95

Ser Pro Glu Leu Asp Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr
            100                 105                 110

Glu Val Glu Asp Tyr Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln
        115                 120                 125

Ala Pro Ala Thr Ala Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val
    130                 135                 140

Asp
145


<210> 721
<211> 1038
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1015)
<223> RXN01669

<400> 721
cacccacagt caccaagaac atagccactc cacacacaac cactccacac acaaccacga 60

gggtcacgac caccatcacc ccaccggatt caaaggattt ttg tac gag att ttc   115
```

```
                                                    Leu Tyr Glu Ile Phe
                                                      1               5

gtt cca cac tcc cat gac acc gcc gac tcg att gat gat gct atg gag   163
Val Pro His Ser His Asp Thr Ala Asp Ser Ile Asp Asp Ala Met Glu
                 10                  15                  20

gcg aac tca gag ggt att cga gcg ctg aag ttt agc ctt gta ttg atg   211
Ala Asn Ser Glu Gly Ile Arg Ala Leu Lys Phe Ser Leu Val Leu Met
             25                  30                  35

ctg ctc acg acg gtt ttg cag gct atc att gtg tct ttt tct gga tct   259
Leu Leu Thr Thr Val Leu Gln Ala Ile Ile Val Ser Phe Ser Gly Ser
         40                  45                  50

gtt gca ctg ttg gcg gat acg gtt cac aac ctt tcc gac gca ttg act   307
Val Ala Leu Leu Ala Asp Thr Val His Asn Leu Ser Asp Ala Leu Thr
     55                  60                  65

gcg att cct ctt tgg att gct ttc ata ctt tcc cgg cgc gca gcg act   355
Ala Ile Pro Leu Trp Ile Ala Phe Ile Leu Ser Arg Arg Ala Ala Thr
 70                  75                  80                  85

caa aaa tat acg tat gga ttc aat cgt gca gag gat tta gcg ggg ttg   403
Gln Lys Tyr Thr Tyr Gly Phe Asn Arg Ala Glu Asp Leu Ala Gly Leu
                 90                  95                 100

ttt att gtc gcg atg att gct ctt tcg gcg att gtt gct gca tgg cag   451
Phe Ile Val Ala Met Ile Ala Leu Ser Ala Ile Val Ala Ala Trp Gln
             105                 110                 115

gcg atc gac cgg atg att aat cct cgc ccg atg gag aat att gaa tgg   499
Ala Ile Asp Arg Met Ile Asn Pro Arg Pro Met Glu Asn Ile Glu Trp
         120                 125                 130

gtg att gcg gca ggt gtt att ggt ttc tta gga aat gag gct gtg gca   547
Val Ile Ala Ala Gly Val Ile Gly Phe Leu Gly Asn Glu Ala Val Ala
     135                 140                 145

atg tat cgc att cgg gtt ggt aag agg att ggc tcg gct gct ttg gtt   595
Met Tyr Arg Ile Arg Val Gly Lys Arg Ile Gly Ser Ala Ala Leu Val
150                 155                 160                 165

gca gat ggc gtt cat gct cgc acg gat ggt ttt act tca ctt gca gtt   643
Ala Asp Gly Val His Ala Arg Thr Asp Gly Phe Thr Ser Leu Ala Val
                 170                 175                 180

gtc gca ggt ggt gtt gga gtt ttt ctg gga ttc ccc ctg gct gac cca   691
Val Ala Gly Gly Val Gly Val Phe Leu Gly Phe Pro Leu Ala Asp Pro
             185                 190                 195

att atc gga ttg atc att tct gcg atg att gcc acc ctt ctt gtt ggt   739
Ile Ile Gly Leu Ile Ile Ser Ala Met Ile Ala Thr Leu Leu Val Gly
         200                 205                 210

acg atc cgt tcg gtt ggc aga cgc ctc atg gat gga att gag ccg gag   787
Thr Ile Arg Ser Val Gly Arg Arg Leu Met Asp Gly Ile Glu Pro Glu
     215                 220                 225

ttg gta gag aag gct acg cac gcg atc tgg cat gtg aag gaa att gag   835
Leu Val Glu Lys Ala Thr His Ala Ile Trp His Val Lys Glu Ile Glu
```

```
230                 235                 240                 245

tcg att gat cga ctg agg ttg agg tgg gtt gga cac cgt ctt cac ggc   883
Ser Ile Asp Arg Leu Arg Leu Arg Trp Val Gly His Arg Leu His Gly
                250                 255                 260

gat gcc acg gtc agc act tct aca tca tcg cta tcg gaa gcc acc gca   931
Asp Ala Thr Val Ser Thr Ser Thr Ser Ser Leu Ser Glu Ala Thr Ala
            265                 270                 275

atc gcc ctt gag gct gag ctt tcc gtc aaa caa cat ctt ccc aat gtg   979
Ile Ala Leu Glu Ala Glu Leu Ser Val Lys Gln His Leu Pro Asn Val
        280                 285                 290

gat gaa atg act gtg acc atc acc cct tcc aaa cct tgagtcccgt        1025
Asp Glu Met Thr Val Thr Ile Thr Pro Ser Lys Pro
    295                 300                 305

gatacaattg ttg                                                   1038


<210> 722
<211> 305
<212> PRT
<213> Corynebacterium glutamicum

<400> 722
Leu Tyr Glu Ile Phe Val Pro His Ser His Asp Thr Ala Asp Ser Ile
  1               5                  10                  15

Asp Asp Ala Met Glu Ala Asn Ser Glu Gly Ile Arg Ala Leu Lys Phe
             20                  25                  30

Ser Leu Val Leu Met Leu Leu Thr Thr Val Leu Gln Ala Ile Ile Val
         35                  40                  45

Ser Phe Ser Gly Ser Val Ala Leu Leu Ala Asp Thr Val His Asn Leu
     50                  55                  60

Ser Asp Ala Leu Thr Ala Ile Pro Leu Trp Ile Ala Phe Ile Leu Ser
 65                  70                  75                  80

Arg Arg Ala Ala Thr Gln Lys Tyr Thr Tyr Gly Phe Asn Arg Ala Glu
                 85                  90                  95

Asp Leu Ala Gly Leu Phe Ile Val Ala Met Ile Ala Leu Ser Ala Ile
            100                 105                 110

Val Ala Ala Trp Gln Ala Ile Asp Arg Met Ile Asn Pro Arg Pro Met
        115                 120                 125

Glu Asn Ile Glu Trp Val Ile Ala Ala Gly Val Ile Gly Phe Leu Gly
    130                 135                 140

Asn Glu Ala Val Ala Met Tyr Arg Ile Arg Val Gly Lys Arg Ile Gly
145                 150                 155                 160

Ser Ala Ala Leu Val Ala Asp Gly Val His Ala Arg Thr Asp Gly Phe
                165                 170                 175

Thr Ser Leu Ala Val Val Ala Gly Gly Val Gly Val Phe Leu Gly Phe
```

```
            180                 185                 190

Pro Leu Ala Asp Pro Ile Ile Gly Leu Ile Ile Ser Ala Met Ile Ala
        195                 200                 205

Thr Leu Leu Val Gly Thr Ile Arg Ser Val Gly Arg Arg Leu Met Asp
    210                 215                 220

Gly Ile Glu Pro Glu Leu Val Glu Lys Ala Thr His Ala Ile Trp His
225                 230                 235                 240

Val Lys Glu Ile Glu Ser Ile Asp Arg Leu Arg Leu Arg Trp Val Gly
                245                 250                 255

His Arg Leu His Gly Asp Ala Thr Val Ser Thr Ser Thr Ser Ser Leu
            260                 265                 270

Ser Glu Ala Thr Ala Ile Ala Leu Glu Ala Glu Leu Ser Val Lys Gln
        275                 280                 285

His Leu Pro Asn Val Asp Glu Met Thr Val Thr Ile Thr Pro Ser Lys
    290                 295                 300

Pro
305
```

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<210> 723
<211> 755
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(732)
<223> FRXA01669

<400> 723

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cac aac ctt tcc gac gca ttg act gcg att cct ctt tgg att gct ttc   48
His Asn Leu Ser Asp Ala Leu Thr Ala Ile Pro Leu Trp Ile Ala Phe
  1               5                  10                  15

ata ctt tcc cgg cgc gca gcg act caa aaa tat acg tat gga ttc aat   96
Ile Leu Ser Arg Arg Ala Ala Thr Gln Lys Tyr Thr Tyr Gly Phe Asn
             20                  25                  30

cgt gca gag gat tta gcg ggg ttg ttt att gtc gcg atg att gct ctt   144
Arg Ala Glu Asp Leu Ala Gly Leu Phe Ile Val Ala Met Ile Ala Leu
         35                  40                  45

tcg gcg att gtt gct gca tgg cag gcg atc gac cgg atg att aat cct   192
Ser Ala Ile Val Ala Ala Trp Gln Ala Ile Asp Arg Met Ile Asn Pro
     50                  55                  60

cgc ccg atg gag aat att gaa tgg gtg att gcg gca ggt gtt att ggt   240
Arg Pro Met Glu Asn Ile Glu Trp Val Ile Ala Ala Gly Val Ile Gly
 65                  70                  75                  80

ttc tta gga aat gag gct gtg gca atg tat cgc att cgg gtt ggt aag   288
Phe Leu Gly Asn Glu Ala Val Ala Met Tyr Arg Ile Arg Val Gly Lys
                 85                  90                  95
```

```
agg att ggc tcg gct gct ttg gtt gca gat ggc gtt cat gct cgc acg   336
Arg Ile Gly Ser Ala Ala Leu Val Ala Asp Gly Val His Ala Arg Thr
            100                 105                 110

gat ggt ttt act tca ctt gca gtt gtc gca ggt ggt gtt gga gtt ttt   384
Asp Gly Phe Thr Ser Leu Ala Val Val Ala Gly Gly Val Gly Val Phe
        115                 120                 125

ctg gga ttc ccc ctg gct gac cca att atc gga ttg atc att tct gcg   432
Leu Gly Phe Pro Leu Ala Asp Pro Ile Ile Gly Leu Ile Ile Ser Ala
    130                 135                 140

atg att gcc acc ctt ctt gtt ggt acg atc cgt tcg gtt ggc aga cgc   480
Met Ile Ala Thr Leu Leu Val Gly Thr Ile Arg Ser Val Gly Arg Arg
145                 150                 155                 160

ctc atg gat gga att gag ccg gag ttg gta gag aag gct acg cac gcg   528
Leu Met Asp Gly Ile Glu Pro Glu Leu Val Glu Lys Ala Thr His Ala
                165                 170                 175

atc tgg cat gtg aag gaa att gag tcg att gat cga ctg agg ttg agg   576
Ile Trp His Val Lys Glu Ile Glu Ser Ile Asp Arg Leu Arg Leu Arg
            180                 185                 190

tgg gtt gga cac cgt ctt cac ggc gat gcc acg gtc agc act tct aca   624
Trp Val Gly His Arg Leu His Gly Asp Ala Thr Val Ser Thr Ser Thr
        195                 200                 205

tca tcg cta tcg gaa gcc acc gca atc gcc ctt gag gct gag ctt tcc   672
Ser Ser Leu Ser Glu Ala Thr Ala Ile Ala Leu Glu Ala Glu Leu Ser
    210                 215                 220

gtc aaa caa cat ctt ccc aat gtg gat gaa atg act gtg acc atc acc   720
Val Lys Gln His Leu Pro Asn Val Asp Glu Met Thr Val Thr Ile Thr
225                 230                 235                 240

cct tcc aaa cct tgagtcccgt gatacaattg ttg                        755
Pro Ser Lys Pro
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Sequence Listing

<210> 724
<211> 244
<212> PRT
<213> Corynebacterium glutamicum

<400> 724

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His Asn Leu Ser Asp Ala Leu Thr Ala Ile Pro Leu Trp Ile Ala Phe
  1               5                  10                  15

Ile Leu Ser Arg Arg Ala Ala Thr Gln Lys Tyr Thr Tyr Gly Phe Asn
             20                  25                  30

Arg Ala Glu Asp Leu Ala Gly Leu Phe Ile Val Ala Met Ile Ala Leu
         35                  40                  45

Ser Ala Ile Val Ala Ala Trp Gln Ala Ile Asp Arg Met Ile Asn Pro
     50                  55                  60

Arg Pro Met Glu Asn Ile Glu Trp Val Ile Ala Ala Gly Val Ile Gly
```

```
 65                  70                  75                  80

Phe Leu Gly Asn Glu Ala Val Ala Met Tyr Arg Ile Arg Val Gly Lys
                85                  90                  95

Arg Ile Gly Ser Ala Ala Leu Val Ala Asp Gly Val His Ala Arg Thr
            100                 105                 110

Asp Gly Phe Thr Ser Leu Ala Val Val Ala Gly Gly Val Gly Val Phe
        115                 120                 125

Leu Gly Phe Pro Leu Ala Asp Pro Ile Ile Gly Leu Ile Ile Ser Ala
    130                 135                 140

Met Ile Ala Thr Leu Leu Val Gly Thr Ile Arg Ser Val Gly Arg Arg
145                 150                 155                 160

Leu Met Asp Gly Ile Glu Pro Glu Leu Val Glu Lys Ala Thr His Ala
                165                 170                 175

Ile Trp His Val Lys Glu Ile Glu Ser Ile Asp Arg Leu Arg Leu Arg
            180                 185                 190

Trp Val Gly His Arg Leu His Gly Asp Ala Thr Val Ser Thr Ser Thr
        195                 200                 205

Ser Ser Leu Ser Glu Ala Thr Ala Ile Ala Leu Glu Ala Glu Leu Ser
    210                 215                 220

Val Lys Gln His Leu Pro Asn Val Asp Glu Met Thr Val Thr Ile Thr
225                 230                 235                 240

Pro Ser Lys Pro
```

US20050059090A1

<210> 725
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXN01672

<400> 725

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agtagcaaag ggtgcagtcg aaggaccagc atccaagact gctgccgaag aaaccgactc 60

cgttgacaac ggatccgacg aaaacggcga ggaataattt atg gca tcc cga gaa   115
                                              Met Ala Ser Arg Glu
                                                1               5

gta tcc atc acc cga atc tca cca cta gca acc ttc cga gtt gca ctg   163
Val Ser Ile Thr Arg Ile Ser Pro Leu Ala Thr Phe Arg Val Ala Leu
                10                  15                  20

gca atg tcc atc atc gga ctc gtg gcg tgg atc atc tgc gta acc gtc   211
Ala Met Ser Ile Ile Gly Leu Val Ala Trp Ile Ile Cys Val Thr Val
            25                  30                  35
```

```
ctc tat ttc gga ctt aac gtg gct ggc gtc tgg cag aac ttc aac gat   259
Leu Tyr Phe Gly Leu Asn Val Ala Gly Val Trp Gln Asn Phe Asn Asp
         40                  45                  50

gtc atc ggc ggt gtt ggt gca gaa caa acc atc acc ttc ggg ctc gtc   307
Val Ile Gly Gly Val Gly Ala Glu Gln Thr Ile Thr Phe Gly Leu Val
     55                  60                  65

ctg agc att tcc gca ctt ctg gga gct atc gga gcg att acc gtc gct   355
Leu Ser Ile Ser Ala Leu Leu Gly Ala Ile Gly Ala Ile Thr Val Ala
 70                  75                  80                  85

gtg ctt gca cca ttg tgt gca atc atc tac aac tcg att gtt gac ctc   403
Val Leu Ala Pro Leu Cys Ala Ile Ile Tyr Asn Ser Ile Val Asp Leu
                 90                  95                 100

ttc ggt gga ctg cag att caa ctg caa gaa gaa gta gac taacctctga   452
Phe Gly Gly Leu Gln Ile Gln Leu Gln Glu Glu Val Asp
            105                 110

aacacaaacc cct                                                   465
```

<210> 726
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 726

```
Met Ala Ser Arg Glu Val Ser Ile Thr Arg Ile Ser Pro Leu Ala Thr
  1               5                  10                  15

Phe Arg Val Ala Leu Ala Met Ser Ile Ile Gly Leu Val Ala Trp Ile
             20                  25                  30

Ile Cys Val Thr Val Leu Tyr Phe Gly Leu Asn Val Ala Gly Val Trp
         35                  40                  45

Gln Asn Phe Asn Asp Val Ile Gly Gly Val Gly Ala Glu Gln Thr Ile
     50                  55                  60

Thr Phe Gly Leu Val Leu Ser Ile Ser Ala Leu Leu Gly Ala Ile Gly
 65                  70                  75                  80

Ala Ile Thr Val Ala Val Leu Ala Pro Leu Cys Ala Ile Ile Tyr Asn
                 85                  90                  95

Ser Ile Val Asp Leu Phe Gly Gly Leu Gln Ile Gln Leu Gln Glu Glu
            100                 105                 110

Val Asp
```

<210> 727
<211> 332
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (1)..(309)
<223> FRXA01672

<400> 727
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tca cca cta gca acc ttc cga gtt gca ctg gca atg tcc atc atc gga   48
Ser Pro Leu Ala Thr Phe Arg Val Ala Leu Ala Met Ser Ile Ile Gly
  1               5                  10                  15

ctc gtg gcg tgg atc atc tgc gta acc gtc ctc tat ttc gga ctt aac   96
Leu Val Ala Trp Ile Ile Cys Val Thr Val Leu Tyr Phe Gly Leu Asn
             20                  25                  30

gtg gct ggc gtc tgg cag aac ttc aac gat gtc atc ggc ggt gtt ggt   144
Val Ala Gly Val Trp Gln Asn Phe Asn Asp Val Ile Gly Gly Val Gly
         35                  40                  45

gca gaa caa acc atc acc ttc ggg ctc gtc ctg agc att tcc gca ctt   192
Ala Glu Gln Thr Ile Thr Phe Gly Leu Val Leu Ser Ile Ser Ala Leu
     50                  55                  60

ctg gga gct atc gga gcg att acc gtc gct gtg ctt gca cca ttg tgt   240
Leu Gly Ala Ile Gly Ala Ile Thr Val Ala Val Leu Ala Pro Leu Cys
 65                  70                  75                  80

gca atc atc tac aac tcg att gtt gac ctc ttc ggt gga ctg cag att   288
Ala Ile Ile Tyr Asn Ser Ile Val Asp Leu Phe Gly Gly Leu Gln Ile
                 85                  90                  95

caa ctg caa gaa gaa gta gac taacctctga aacacaaacc cct             332
Gln Leu Gln Glu Glu Val Asp
            100
```

<210> 728
<211> 103
<212> PRT
<213> Corynebacterium glutamicum

<400> 728
```
Ser Pro Leu Ala Thr Phe Arg Val Ala Leu Ala Met Ser Ile Ile Gly
  1               5                  10                  15

Leu Val Ala Trp Ile Ile Cys Val Thr Val Leu Tyr Phe Gly Leu Asn
             20                  25                  30

Val Ala Gly Val Trp Gln Asn Phe Asn Asp Val Ile Gly Gly Val Gly
         35                  40                  45

Ala Glu Gln Thr Ile Thr Phe Gly Leu Val Leu Ser Ile Ser Ala Leu
     50                  55                  60

Leu Gly Ala Ile Gly Ala Ile Thr Val Ala Val Leu Ala Pro Leu Cys
 65                  70                  75                  80

Ala Ile Ile Tyr Asn Ser Ile Val Asp Leu Phe Gly Gly Leu Gln Ile
                 85                  90                  95

Gln Leu Gln Glu Glu Val Asp
            100
```

<210> 729
<211> 1023
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1000)
<223> RXN01694

<400> 729
cgacaccaat aatttattgg gtatccacca attaccgctg tgagcactgc aaattacgta 60

ttcgaaaagc catgtccacc acgtgttcta tcctggcggc atg caa aaa atc acc 115
Met Gln Lys Ile Thr
1 5

cca aac atc tgg tgc caa ggc acc gca gac gaa gca gcc gaa ttc tac 163
Pro Asn Ile Trp Cys Gln Gly Thr Ala Asp Glu Ala Ala Glu Phe Tyr
10 15 20

gtc aat gcg ttt tct gag ttt ccg ggt ggc gca gaa gta ctc acc aca 211
Val Asn Ala Phe Ser Glu Phe Pro Gly Gly Ala Glu Val Leu Thr Thr
25 30 35

gtt aag tat ccc gaa gct ggc ttg ctg gac ttc cag gag cct ttc gca 259
Val Lys Tyr Pro Glu Ala Gly Leu Leu Asp Phe Gln Glu Pro Phe Ala
40 45 50

gga aaa acc ttg acg gtg gaa ctc gct atc tca ggc ttt aag atc atc 307
Gly Lys Thr Leu Thr Val Glu Leu Ala Ile Ser Gly Phe Lys Ile Ile
55 60 65

ttg atc aat gct ggt gaa gag ttc act ccc aac cca tcg atc agc ttc 355
Leu Ile Asn Ala Gly Glu Glu Phe Thr Pro Asn Pro Ser Ile Ser Phe
70 75 80 85

atg gtg aat ttt gat gcg gtg cgt gat gaa aat gcc aaa gag cac ctt 403
Met Val Asn Phe Asp Ala Val Arg Asp Glu Asn Ala Lys Glu His Leu
90 95 100

gat gcg gtg tgg gaa aaa ctc cat gaa ggc ggc agc aca ctg atg cca 451
Asp Ala Val Trp Glu Lys Leu His Glu Gly Gly Ser Thr Leu Met Pro
105 110 115

gtc gat act tac cca ttt tcg gaa tac tac ggg tgg gta caa gac aaa 499
Val Asp Thr Tyr Pro Phe Ser Glu Tyr Tyr Gly Trp Val Gln Asp Lys
120 125 130

tat ggt gtg agc tgg caa ttg atg ctc agc cgc cca gaa gaa aag cca 547
Tyr Gly Val Ser Trp Gln Leu Met Leu Ser Arg Pro Glu Glu Lys Pro
135 140 145

ggt ccc gca gta atc cca acg ctc tta ttt ggt ggg gca gct caa aat 595
Gly Pro Ala Val Ile Pro Thr Leu Leu Phe Gly Gly Ala Ala Gln Asn
150 155 160 165

cag gca ggc cca gct caa gaa aac tac gtt gag gtg ttc ccg aac tcc 643
Gln Ala Gly Pro Ala Gln Glu Asn Tyr Val Glu Val Phe Pro Asn Ser
170 175 180

```
caa ctt ggt gat cgt gca cct tat gga cag caa aca ggt cct gcc act   691
Gln Leu Gly Asp Arg Ala Pro Tyr Gly Gln Gln Thr Gly Pro Ala Thr
            185                 190                 195

cct gag gcc ctc atg ttt tcc cag ttc caa ctc gac ggt cag tgg att   739
Pro Glu Ala Leu Met Phe Ser Gln Phe Gln Leu Asp Gly Gln Trp Ile
        200                 205                 210

ttc gcg atg gat tcc gga gtt gag caa gat ttc acc ttc agt gag ggt   787
Phe Ala Met Asp Ser Gly Val Glu Gln Asp Phe Thr Phe Ser Glu Gly
    215                 220                 225

gtc tca ttg atg tat gaa gct cat ggt caa gaa gaa ctc gat gcc atc   835
Val Ser Leu Met Tyr Glu Ala His Gly Gln Glu Glu Leu Asp Ala Ile
230                 235                 240                 245

tgg aat gca ctc tcg gca gtt cca gaa gct gag gct tgt ggt tgg ttg   883
Trp Asn Ala Leu Ser Ala Val Pro Glu Ala Glu Ala Cys Gly Trp Leu
                250                 255                 260

aag gac aag ttc ggc gtg agc tgg cag att gtt ccc gac aac atg gag   931
Lys Asp Lys Phe Gly Val Ser Trp Gln Ile Val Pro Asp Asn Met Glu
            265                 270                 275

gag ctc atg gct aaa ccc ggc gcg tat gaa aag ctt ctt gcg atg aag   979
Glu Leu Met Ala Lys Pro Gly Ala Tyr Glu Lys Leu Leu Ala Met Lys
        280                 285                 290

aag atc aat atc gcg gag ttc tagcagttct aagcgctcca cgc            1023
Lys Ile Asn Ile Ala Glu Phe
    295                 300
```

<210> 730
<211> 300
<212> PRT
<213> Corynebacterium glutamicum

<400> 730

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Met Gln Lys Ile Thr Pro Asn Ile Trp Cys Gln Gly Thr Ala Asp Glu
  1               5                  10                  15

Ala Ala Glu Phe Tyr Val Asn Ala Phe Ser Glu Phe Pro Gly Gly Ala
             20                  25                  30

Glu Val Leu Thr Thr Val Lys Tyr Pro Glu Ala Gly Leu Leu Asp Phe
         35                  40                  45

Gln Glu Pro Phe Ala Gly Lys Thr Leu Thr Val Glu Leu Ala Ile Ser
     50                  55                  60

Gly Phe Lys Ile Ile Leu Ile Asn Ala Gly Glu Glu Phe Thr Pro Asn
 65                  70                  75                  80

Pro Ser Ile Ser Phe Met Val Asn Phe Asp Ala Val Arg Asp Glu Asn
                 85                  90                  95

Ala Lys Glu His Leu Asp Ala Val Trp Glu Lys Leu His Glu Gly Gly
            100                 105                 110

Ser Thr Leu Met Pro Val Asp Thr Tyr Pro Phe Ser Glu Tyr Tyr Gly
```

```
        115                 120                 125

Trp Val Gln Asp Lys Tyr Gly Val Ser Trp Gln Leu Met Leu Ser Arg
    130                 135                 140

Pro Glu Glu Lys Pro Gly Pro Ala Val Ile Pro Thr Leu Leu Phe Gly
145                 150                 155                 160

Gly Ala Ala Gln Asn Gln Ala Gly Pro Ala Gln Glu Asn Tyr Val Glu
                165                 170                 175

Val Phe Pro Asn Ser Gln Leu Gly Asp Arg Ala Pro Tyr Gly Gln Gln
            180                 185                 190

Thr Gly Pro Ala Thr Pro Glu Ala Leu Met Phe Ser Gln Phe Gln Leu
        195                 200                 205

Asp Gly Gln Trp Ile Phe Ala Met Asp Ser Gly Val Glu Gln Asp Phe
    210                 215                 220

Thr Phe Ser Glu Gly Val Ser Leu Met Tyr Glu Ala His Gly Gln Glu
225                 230                 235                 240

Glu Leu Asp Ala Ile Trp Asn Ala Leu Ser Ala Val Pro Glu Ala Glu
                245                 250                 255

Ala Cys Gly Trp Leu Lys Asp Lys Phe Gly Val Ser Trp Gln Ile Val
            260                 265                 270

Pro Asp Asn Met Glu Glu Leu Met Ala Lys Pro Gly Ala Tyr Glu Lys
        275                 280                 285

Leu Leu Ala Met Lys Lys Ile Asn Ile Ala Glu Phe
    290                 295                 300


<210> 731
<211> 1023
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1000)
<223> FRXA01694

<400> 731
cgacaccaat aatttattgg gtatccacca attaccgctg tgagcactgc aaattacgta 60

ttcgaaaagc catgtccacc acgtgttcta tcctggcggc atg caa aaa atc acc   115
                                               Met Gln Lys Ile Thr
                                                 1               5

cca aac atc tgg tgc caa ggc acc gca gac gaa gca gcc gaa ttc tac   163
Pro Asn Ile Trp Cys Gln Gly Thr Ala Asp Glu Ala Ala Glu Phe Tyr
                10                  15                  20

gtc aat gcg ttt tct gag ttt ccg ggt ggc gca gaa gta ctc acc aca   211
Val Asn Ala Phe Ser Glu Phe Pro Gly Gly Ala Glu Val Leu Thr Thr
            25                  30                  35
```

```
gtt aag tat ccc gaa gct ggc ttg ctg gac ttc cag gag cct ttc gca   259
Val Lys Tyr Pro Glu Ala Gly Leu Leu Asp Phe Gln Glu Pro Phe Ala
         40                  45                  50

gga aaa acc ttg acg gtg gaa ctc gct atc tca ggc ttt aag atc atc   307
Gly Lys Thr Leu Thr Val Glu Leu Ala Ile Ser Gly Phe Lys Ile Ile
     55                  60                  65

ttg atc aat gct ggt gaa gag ttc act ccc aac cca tcg atc agc ttc   355
Leu Ile Asn Ala Gly Glu Glu Phe Thr Pro Asn Pro Ser Ile Ser Phe
 70                  75                  80                  85

atg gtg aat ttt gat gcg gtg cgt gat gaa aat gcc aaa gag cac ctt   403
Met Val Asn Phe Asp Ala Val Arg Asp Glu Asn Ala Lys Glu His Leu
                 90                  95                 100

gat gcg gtg tgg gaa aaa ctc cat gaa ggc ggc agc aca ctg atg cca   451
Asp Ala Val Trp Glu Lys Leu His Glu Gly Gly Ser Thr Leu Met Pro
            105                 110                 115

gtc gat act tac cca ttt tcg gaa tac tac ggg tgg gta caa gac aaa   499
Val Asp Thr Tyr Pro Phe Ser Glu Tyr Tyr Gly Trp Val Gln Asp Lys
        120                 125                 130

tat ggt gtg agc tgg caa ttg atg ctc agc cgc cca gaa gaa aag cca   547
Tyr Gly Val Ser Trp Gln Leu Met Leu Ser Arg Pro Glu Glu Lys Pro
    135                 140                 145

ggt ccc gca gta atc cca acg ctc tta ttt ggt ggg gca gct caa aat   595
Gly Pro Ala Val Ile Pro Thr Leu Leu Phe Gly Gly Ala Ala Gln Asn
150                 155                 160                 165

cag gca ggc cca gct caa gaa aac tac gtt gag gtg ttc ccg aac tcc   643
Gln Ala Gly Pro Ala Gln Glu Asn Tyr Val Glu Val Phe Pro Asn Ser
                170                 175                 180

caa ctt ggt gat cgt gca cct tat gga cag caa aca ggt cct gcc act   691
Gln Leu Gly Asp Arg Ala Pro Tyr Gly Gln Gln Thr Gly Pro Ala Thr
            185                 190                 195

cct gag gcc ctc atg ttt tcc cag ttc caa ctc gac ggt cag tgg att   739
Pro Glu Ala Leu Met Phe Ser Gln Phe Gln Leu Asp Gly Gln Trp Ile
        200                 205                 210

ttc gcg atg gat tcc gga gtt gag caa gat ttc acc ttc agt gag ggt   787
Phe Ala Met Asp Ser Gly Val Glu Gln Asp Phe Thr Phe Ser Glu Gly
    215                 220                 225

gtc tca ttg atg tat gaa gct cat ggt caa gaa gaa ctc gat gcc atc   835
Val Ser Leu Met Tyr Glu Ala His Gly Gln Glu Glu Leu Asp Ala Ile
230                 235                 240                 245

tgg aat gca ctc tcg gca gtt cca gaa gct gag gct tgt ggt tgg ttg   883
Trp Asn Ala Leu Ser Ala Val Pro Glu Ala Glu Ala Cys Gly Trp Leu
                250                 255                 260

aag gac aag ttc ggc gtg agc tgg cag att gtt ccc gac aac atg gag   931
Lys Asp Lys Phe Gly Val Ser Trp Gln Ile Val Pro Asp Asn Met Glu
            265                 270                 275

gag ctc atg gct aaa ccc ggc gcg tat gaa aag ctt ctt gcg atg aag   979
```

```
Glu Leu Met Ala Lys Pro Gly Ala Tyr Glu Lys Leu Leu Ala Met Lys
        280                 285                 290

aag atc aat atc gcg gag ttc tagcagttct aagcgctcca cgc            1023
Lys Ile Asn Ile Ala Glu Phe
    295                 300


<210> 732
<211> 300
<212> PRT
<213> Corynebacterium glutamicum

<400> 732
Met Gln Lys Ile Thr Pro Asn Ile Trp Cys Gln Gly Thr Ala Asp Glu
  1               5                  10                  15

Ala Ala Glu Phe Tyr Val Asn Ala Phe Ser Glu Phe Pro Gly Gly Ala
             20                  25                  30

Glu Val Leu Thr Thr Val Lys Tyr Pro Glu Ala Gly Leu Leu Asp Phe
         35                  40                  45

Gln Glu Pro Phe Ala Gly Lys Thr Leu Thr Val Glu Leu Ala Ile Ser
     50                  55                  60

Gly Phe Lys Ile Ile Leu Ile Asn Ala Gly Glu Glu Phe Thr Pro Asn
 65                  70                  75                  80

Pro Ser Ile Ser Phe Met Val Asn Phe Asp Ala Val Arg Asp Glu Asn
                 85                  90                  95

Ala Lys Glu His Leu Asp Ala Val Trp Glu Lys Leu His Glu Gly Gly
            100                 105                 110

Ser Thr Leu Met Pro Val Asp Thr Tyr Pro Phe Ser Glu Tyr Tyr Gly
        115                 120                 125

Trp Val Gln Asp Lys Tyr Gly Val Ser Trp Gln Leu Met Leu Ser Arg
    130                 135                 140

Pro Glu Glu Lys Pro Gly Pro Ala Val Ile Pro Thr Leu Leu Phe Gly
145                 150                 155                 160

Gly Ala Ala Gln Asn Gln Ala Gly Pro Ala Gln Glu Asn Tyr Val Glu
                165                 170                 175

Val Phe Pro Asn Ser Gln Leu Gly Asp Arg Ala Pro Tyr Gly Gln Gln
            180                 185                 190

Thr Gly Pro Ala Thr Pro Glu Ala Leu Met Phe Ser Gln Phe Gln Leu
        195                 200                 205

Asp Gly Gln Trp Ile Phe Ala Met Asp Ser Gly Val Glu Gln Asp Phe
    210                 215                 220

Thr Phe Ser Glu Gly Val Ser Leu Met Tyr Glu Ala His Gly Gln Glu
225                 230                 235                 240

Glu Leu Asp Ala Ile Trp Asn Ala Leu Ser Ala Val Pro Glu Ala Glu
                245                 250                 255
```

```
Ala Cys Gly Trp Leu Lys Asp Lys Phe Gly Val Ser Trp Gln Ile Val
            260                 265                 270

Pro Asp Asn Met Glu Glu Leu Met Ala Lys Pro Gly Ala Tyr Glu Lys
        275                 280                 285

Leu Leu Ala Met Lys Lys Ile Asn Ile Ala Glu Phe
    290                 295                 300


<210> 733
<211> 1302
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1279)
<223> RXN01696

<400> 733
aggtgacggt gatacaattt tgccataact gacttaaccc agaacgttgt ccggaagcac 60

acagaccttt gtgcggcttc cttttctagg agcatgtaac ttg tct acc cca atc   115
                                            Leu Ser Thr Pro Ile
                                              1               5

ggc ctt ggc ctt cct ccg acc cca cct cca gtg ttg gcg cca cgt cgt   163
Gly Leu Gly Leu Pro Pro Thr Pro Pro Pro Val Leu Ala Pro Arg Arg
                10                  15                  20

aaa aca cgc caa ctc atg gtc ggc aaa gtg ggc gtt ggt tcg gat cac   211
Lys Thr Arg Gln Leu Met Val Gly Lys Val Gly Val Gly Ser Asp His
            25                  30                  35

ccg att tcc gtc cag tcg atg acc acc acc aaa acc cac gac atc aac   259
Pro Ile Ser Val Gln Ser Met Thr Thr Thr Lys Thr His Asp Ile Asn
        40                  45                  50

ggc acc ctg caa cag atc gca cag ttg aca gcc acc ggt tgt gac atc   307
Gly Thr Leu Gln Gln Ile Ala Gln Leu Thr Ala Thr Gly Cys Asp Ile
    55                  60                  65

gtc cgc gtt gcc tgc cca aag act gtt gat gcg gaa gca ctg ccg atc   355
Val Arg Val Ala Cys Pro Lys Thr Val Asp Ala Glu Ala Leu Pro Ile
70                  75                  80                  85

atc gca aag aag tct ccg atc cca gtg atc gca gat atc cac ttc cag   403
Ile Ala Lys Lys Ser Pro Ile Pro Val Ile Ala Asp Ile His Phe Gln
                90                  95                  100

ccc aag tac atc ttc gcg gca atc gat gca ggt tgc gcc gcc gtt cgt   451
Pro Lys Tyr Ile Phe Ala Ala Ile Asp Ala Gly Cys Ala Ala Val Arg
            105                 110                 115

gtg aac cca ggc aac atc aag gaa ttc gat ggt cgc gtt aaa gaa gta   499
Val Asn Pro Gly Asn Ile Lys Glu Phe Asp Gly Arg Val Lys Glu Val
        120                 125                 130

gca aaa gct gca ggc gat gcc gga att cca att cgt att ggt gtc aac   547
```

```
Ala Lys Ala Ala Gly Asp Ala Gly Ile Pro Ile Arg Ile Gly Val Asn
    135                 140                 145

ggc gga tcc ctg gat aag cgc atc ctg gac aaa tac cac ggc aaa gcc   595
Gly Gly Ser Leu Asp Lys Arg Ile Leu Asp Lys Tyr His Gly Lys Ala
150                 155                 160                 165

acc cca gaa gct ctc gtg gaa tcc gca atg tgg gaa gcc ggc ctg ttt   643
Thr Pro Glu Ala Leu Val Glu Ser Ala Met Trp Glu Ala Gly Leu Phe
            170                 175                 180

gaa gag cac ggc ttc ggc gac atc gca atc tct gtg aag cac tcc gac   691
Glu Glu His Gly Phe Gly Asp Ile Ala Ile Ser Val Lys His Ser Asp
        185                 190                 195

cca gta ctc atg gtg gag gcc tac cgc cag ctc gct gaa caa agc gac   739
Pro Val Leu Met Val Glu Ala Tyr Arg Gln Leu Ala Glu Gln Ser Asp
    200                 205                 210

tac cca ctg cac ctc ggt gtt act gaa gct ggt ccc aag ttc atg gga   787
Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly Pro Lys Phe Met Gly
215                 220                 225

aca atc aag tct tcc gta gca ttc ggc gct ctg ctg tcc cag ggc atc   835
Thr Ile Lys Ser Ser Val Ala Phe Gly Ala Leu Leu Ser Gln Gly Ile
230                 235                 240                 245

ggc gac act atc cgt gtg tct ctt tct gct gac cca gtg gaa gaa atc   883
Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp Pro Val Glu Glu Ile
                250                 255                 260

aag gtt ggc gac cag att ctg cag tcc ctc aac ctg cgc cca cgc aag   931
Lys Val Gly Asp Gln Ile Leu Gln Ser Leu Asn Leu Arg Pro Arg Lys
            265                 270                 275

ctg gaa atc gtg tcc tgc cca tca tgt ggc cgc gca cag gtc gat gtg   979
Leu Glu Ile Val Ser Cys Pro Ser Cys Gly Arg Ala Gln Val Asp Val
        280                 285                 290

tac tca ctt gct gaa gaa gtc acc gaa gca ctc gac ggc atg gaa gtt   1027
Tyr Ser Leu Ala Glu Glu Val Thr Glu Ala Leu Asp Gly Met Glu Val
    295                 300                 305

cca ctg cgc gtc gct gtc atg ggt tgc gtt gtt aac ggc cca ggt gag   1075
Pro Leu Arg Val Ala Val Met Gly Cys Val Val Asn Gly Pro Gly Glu
310                 315                 320                 325

gct cgc gac gct gac ctc ggt gtt gca tcc ggt aac ggc aag ggc cag   1123
Ala Arg Asp Ala Asp Leu Gly Val Ala Ser Gly Asn Gly Lys Gly Gln
                330                 335                 340

atc ttt gtc aag ggc gaa gtc atc aag act gtc cca gaa tcc cag atc   1171
Ile Phe Val Lys Gly Glu Val Ile Lys Thr Val Pro Glu Ser Gln Ile
            345                 350                 355

gtg gaa acc ctc atc gaa gaa gca atg cgt atc gca gag gaa atg gac   1219
Val Glu Thr Leu Ile Glu Glu Ala Met Arg Ile Ala Glu Glu Met Asp
        360                 365                 370

cca gaa gtc ctc gct gca gca agt gct tcc ggt atg aag gct gaa gtg   1267
Pro Glu Val Leu Ala Ala Ala Ser Ala Ser Gly Met Lys Ala Glu Val
```

375 380 385

aag gta acc aag taagttttgg ttaattaagg cac 1302
Lys Val Thr Lys
390

<210> 734
<211> 393
<212> PRT
<213> Corynebacterium glutamicum

<400> 734
Leu Ser Thr Pro Ile Gly Leu Gly Leu Pro Pro Thr Pro Pro Pro Val
1 5 10 15

Leu Ala Pro Arg Arg Lys Thr Arg Gln Leu Met Val Gly Lys Val Gly
20 25 30

Val Gly Ser Asp His Pro Ile Ser Val Gln Ser Met Thr Thr Thr Lys
35 40 45

Thr His Asp Ile Asn Gly Thr Leu Gln Gln Ile Ala Gln Leu Thr Ala
50 55 60

Thr Gly Cys Asp Ile Val Arg Val Ala Cys Pro Lys Thr Val Asp Ala
65 70 75 80

Glu Ala Leu Pro Ile Ile Ala Lys Lys Ser Pro Ile Pro Val Ile Ala
85 90 95

Asp Ile His Phe Gln Pro Lys Tyr Ile Phe Ala Ala Ile Asp Ala Gly
100 105 110

Cys Ala Ala Val Arg Val Asn Pro Gly Asn Ile Lys Glu Phe Asp Gly
115 120 125

Arg Val Lys Glu Val Ala Lys Ala Ala Gly Asp Ala Gly Ile Pro Ile
130 135 140

Arg Ile Gly Val Asn Gly Gly Ser Leu Asp Lys Arg Ile Leu Asp Lys
145 150 155 160

Tyr His Gly Lys Ala Thr Pro Glu Ala Leu Val Glu Ser Ala Met Trp
165 170 175

Glu Ala Gly Leu Phe Glu Glu His Gly Phe Gly Asp Ile Ala Ile Ser
180 185 190

Val Lys His Ser Asp Pro Val Leu Met Val Glu Ala Tyr Arg Gln Leu
195 200 205

Ala Glu Gln Ser Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly
210 215 220

Pro Lys Phe Met Gly Thr Ile Lys Ser Ser Val Ala Phe Gly Ala Leu
225 230 235 240

Leu Ser Gln Gly Ile Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp
245 250 255

```
Pro Val Glu Glu Ile Lys Val Gly Asp Gln Ile Leu Gln Ser Leu Asn
            260                 265                 270

Leu Arg Pro Arg Lys Leu Glu Ile Val Ser Cys Pro Ser Cys Gly Arg
        275                 280                 285

Ala Gln Val Asp Val Tyr Ser Leu Ala Glu Glu Val Thr Glu Ala Leu
    290                 295                 300

Asp Gly Met Glu Val Pro Leu Arg Val Ala Val Met Gly Cys Val Val
305                 310                 315                 320

Asn Gly Pro Gly Glu Ala Arg Asp Ala Asp Leu Gly Val Ala Ser Gly
                325                 330                 335

Asn Gly Lys Gly Gln Ile Phe Val Lys Gly Glu Val Ile Lys Thr Val
            340                 345                 350

Pro Glu Ser Gln Ile Val Glu Thr Leu Ile Glu Glu Ala Met Arg Ile
        355                 360                 365

Ala Glu Glu Met Asp Pro Glu Val Leu Ala Ala Ala Ser Ala Ser Gly
    370                 375                 380

Met Lys Ala Glu Val Lys Val Thr Lys
385                 390


<210> 735
<211> 620
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(597)
<223> FRXA01696

<400> 735
cac tcc gac cca gta ctc atg gtg gag gcc tac cgc cag ctc gct gaa   48
His Ser Asp Pro Val Leu Met Val Glu Ala Tyr Arg Gln Leu Ala Glu
  1               5                  10                  15

caa agc gac tac cca ctg cac ctc ggt gtt act gaa gct ggt ccc aag   96
Gln Ser Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly Pro Lys
             20                  25                  30

ttc atg gga aca atc aag tct tcc gta gca ttc ggc gct ctg ctg tcc   144
Phe Met Gly Thr Ile Lys Ser Ser Val Ala Phe Gly Ala Leu Leu Ser
         35                  40                  45

cag ggc atc ggc gac act atc cgt gtg tct ctt tct gct gac cca gtg   192
Gln Gly Ile Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp Pro Val
     50                  55                  60

gaa gaa atc aag gtt ggc gac cag att ctg cag tcc ctc aac ctg cgc   240
Glu Glu Ile Lys Val Gly Asp Gln Ile Leu Gln Ser Leu Asn Leu Arg
 65                  70                  75                  80

cca cgc aag ctg gaa atc gtg tcc tgc cca tca tgt ggc cgc gca cag   288
Pro Arg Lys Leu Glu Ile Val Ser Cys Pro Ser Cys Gly Arg Ala Gln
```

```
                  85                  90                  95

gtc gat gtg tac tca ctt gct gaa gaa gtc acc gaa gca ctc gac ggc   336
Val Asp Val Tyr Ser Leu Ala Glu Glu Val Thr Glu Ala Leu Asp Gly
            100                 105                 110

atg gaa gtt cca ctg cgc gtc gct gtc atg ggt tgc gtt gtt aac ggc   384
Met Glu Val Pro Leu Arg Val Ala Val Met Gly Cys Val Val Asn Gly
        115                 120                 125

cca ggt gag gct cgc gac gct gac ctc ggt gtt gca tcc ggt aac ggc   432
Pro Gly Glu Ala Arg Asp Ala Asp Leu Gly Val Ala Ser Gly Asn Gly
    130                 135                 140

aag ggc cag atc ttt gtc aag ggc gaa gtc atc aag act gtc cca gaa   480
Lys Gly Gln Ile Phe Val Lys Gly Glu Val Ile Lys Thr Val Pro Glu
145                 150                 155                 160

tcc cag atc gtg gaa acc ctc atc gaa gaa gca atg cgt atc gca gag   528
Ser Gln Ile Val Glu Thr Leu Ile Glu Glu Ala Met Arg Ile Ala Glu
                165                 170                 175

gaa atg gac cca gaa gtc ctc gct gca gca agt gct tcc ggt atg aag   576
Glu Met Asp Pro Glu Val Leu Ala Ala Ala Ser Ala Ser Gly Met Lys
            180                 185                 190

gct gaa gtg aag gta acc aag taagttttgg ttaattaagg cac            620
Ala Glu Val Lys Val Thr Lys
        195
```

Sequence Listing

<210> 736
<211> 199
<212> PRT
<213> Corynebacterium glutamicum

<400> 736

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His Ser Asp Pro Val Leu Met Val Glu Ala Tyr Arg Gln Leu Ala Glu
  1               5                  10                  15

Gln Ser Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly Pro Lys
             20                  25                  30

Phe Met Gly Thr Ile Lys Ser Ser Val Ala Phe Gly Ala Leu Leu Ser
         35                  40                  45

Gln Gly Ile Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp Pro Val
     50                  55                  60

Glu Glu Ile Lys Val Gly Asp Gln Ile Leu Gln Ser Leu Asn Leu Arg
 65                  70                  75                  80

Pro Arg Lys Leu Glu Ile Val Ser Cys Pro Ser Cys Gly Arg Ala Gln
                 85                  90                  95

Val Asp Val Tyr Ser Leu Ala Glu Glu Val Thr Glu Ala Leu Asp Gly
            100                 105                 110

Met Glu Val Pro Leu Arg Val Ala Val Met Gly Cys Val Val Asn Gly
        115                 120                 125
```

```
Pro Gly Glu Ala Arg Asp Ala Asp Leu Gly Val Ala Ser Gly Asn Gly
    130                 135                 140

Lys Gly Gln Ile Phe Val Lys Gly Glu Val Ile Lys Thr Val Pro Glu
145                 150                 155                 160

Ser Gln Ile Val Glu Thr Leu Ile Glu Glu Ala Met Arg Ile Ala Glu
                165                 170                 175

Glu Met Asp Pro Glu Val Leu Ala Ala Ala Ser Ala Ser Gly Met Lys
            180                 185                 190

Ala Glu Val Lys Val Thr Lys
        195


<210> 737
<211> 1080
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1057)
<223> RXN01697

<400> 737
tagatcaact aagtatgaac gcgaatccga ctttggtcgt actgcaagaa tcgaccagag 60

cccgattaaa aaatgccccc gcgcaacgaa actagtaatc atg ttt caa gga cta   115
                                            Met Phe Gln Gly Leu
                                              1               5

aaa gaa ctc acc gca gca aaa ggc cgc acg ctg ctg atc acc gtc acc   163
Lys Glu Leu Thr Ala Ala Lys Gly Arg Thr Leu Leu Ile Thr Val Thr
                10                  15                  20

gtc ggg ctg atc gcc gtg ctg gtt act ttc ctc tct gcc ctc acc gcc   211
Val Gly Leu Ile Ala Val Leu Val Thr Phe Leu Ser Ala Leu Thr Ala
            25                  30                  35

ggg ctt ggc cac caa tca gta tcc gca ctg aaa tac cta gcg ggt gat   259
Gly Leu Gly His Gln Ser Val Ser Ala Leu Lys Tyr Leu Ala Gly Asp
        40                  45                  50

aat gaa ctt atc ctc gcc gat tcc gga tcc acc acg ctt tcc gcg tcc   307
Asn Glu Leu Ile Leu Ala Asp Ser Gly Ser Thr Thr Leu Ser Ala Ser
    55                  60                  65

acg ctt tct gat caa gca gtt gcc caa ctc gaa gac gaa ggc gca cag   355
Thr Leu Ser Asp Gln Ala Val Ala Gln Leu Glu Asp Glu Gly Ala Gln
70                  75                  80                  85

atg ctg tgg cag gtc cgc gac cga gta gca gac acc ccc acc atg ctc   403
Met Leu Trp Gln Val Arg Asp Arg Val Ala Asp Thr Pro Thr Met Leu
                90                  95                  100

ctc aac tcc cct gac ctt gcg cct ggt gaa gta tcc ctt cct gcc gaa   451
Leu Asn Ser Pro Asp Leu Ala Pro Gly Glu Val Ser Leu Pro Ala Glu
            105                 110                 115
```

```
ctc gct gat tcg gaa ctc gct act gcg cat gat gta gtg gat tct tcc   499
Leu Ala Asp Ser Glu Leu Ala Thr Ala His Asp Val Val Asp Ser Ser
        120                 125                 130

aac gat ctg tac ctc gat cac ctg ccc gtg gta ttg atg aac acc tcc   547
Asn Asp Leu Tyr Leu Asp His Leu Pro Val Val Leu Met Asn Thr Ser
    135                 140                 145

gat tta gcc tca ctc gcg caa gtc cga ggc gtg aca gga cca gca ggc   595
Asp Leu Ala Ser Leu Ala Gln Val Arg Gly Val Thr Gly Pro Ala Gly
150                 155                 160                 165

gca ttc gcc tct gac gtt gcg ctc ccc tcc gac acc gtt gcg ctc tct   643
Ala Phe Ala Ser Asp Val Ala Leu Pro Ser Asp Thr Val Ala Leu Ser
                170                 175                 180

gga tcc gaa cgg tgg aac gca tcc gcc tcc tac cag ggc gaa cag atg   691
Gly Ser Glu Arg Trp Asn Ala Ser Ala Ser Tyr Gln Gly Glu Gln Met
            185                 190                 195

tca ctc aac ctc atg atc gtc atg ctg tat gtt atc tcc gca ctc gtg   739
Ser Leu Asn Leu Met Ile Val Met Leu Tyr Val Ile Ser Ala Leu Val
        200                 205                 210

ctc ggc gca ttc ttc acc gtc tgg acc atc caa cgc ctc cgc ggc atc   787
Leu Gly Ala Phe Phe Thr Val Trp Thr Ile Gln Arg Leu Arg Gly Ile
    215                 220                 225

gcc atc tct agt gct ttg gga gca gcc cgc cga gta ctt atc gcc gac   835
Ala Ile Ser Ser Ala Leu Gly Ala Ala Arg Arg Val Leu Ile Ala Asp
230                 235                 240                 245

gct ctc ggc caa gcc atc atc gtc tta gga atc ggc atc acc gca ggc   883
Ala Leu Gly Gln Ala Ile Ile Val Leu Gly Ile Gly Ile Thr Ala Gly
                250                 255                 260

aca ttg atc aca gtc atc tcc gca ttc ggc atg gga gac gca atg ccc   931
Thr Leu Ile Thr Val Ile Ser Ala Phe Gly Met Gly Asp Ala Met Pro
            265                 270                 275

gtg gtc atc tcc tcc tcc acc acg ctc ttc ccc gca ctt atc ctc gcc   979
Val Val Ile Ser Ser Ser Thr Thr Leu Phe Pro Ala Leu Ile Leu Ala
        280                 285                 290

gca gca gga ctc atc ggt gcc gcc att tca ctc ggc ccc atc ctt cgc   1027
Ala Ala Gly Leu Ile Gly Ala Ala Ile Ser Leu Gly Pro Ile Leu Arg
    295                 300                 305

gtc gaa cca cgc tcc gca ctc atg aac gca taagaaaagg aacctcacat     1077
Val Glu Pro Arg Ser Ala Leu Met Asn Ala
310                 315

gac                                                               1080
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<210> 738
<211> 319
<212> PRT
<213> Corynebacterium glutamicum

<400> 738

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Met Phe Gln Gly Leu Lys Glu Leu Thr Ala Ala Lys Gly Arg Thr Leu
 1               5                  10                  15

Leu Ile Thr Val Thr Val Gly Leu Ile Ala Val Leu Val Thr Phe Leu
            20                  25                  30

Ser Ala Leu Thr Ala Gly Leu Gly His Gln Ser Val Ser Ala Leu Lys
        35                  40                  45

Tyr Leu Ala Gly Asp Asn Glu Leu Ile Leu Ala Asp Ser Gly Ser Thr
    50                  55                  60

Thr Leu Ser Ala Ser Thr Leu Ser Asp Gln Ala Val Ala Gln Leu Glu
65                  70                  75                  80

Asp Glu Gly Ala Gln Met Leu Trp Gln Val Arg Asp Arg Val Ala Asp
                85                  90                  95

Thr Pro Thr Met Leu Leu Asn Ser Pro Asp Leu Ala Pro Gly Glu Val
            100                 105                 110

Ser Leu Pro Ala Glu Leu Ala Asp Ser Glu Leu Ala Thr Ala His Asp
        115                 120                 125

Val Val Asp Ser Ser Asn Asp Leu Tyr Leu Asp His Leu Pro Val Val
    130                 135                 140

Leu Met Asn Thr Ser Asp Leu Ala Ser Leu Ala Gln Val Arg Gly Val
145                 150                 155                 160

Thr Gly Pro Ala Gly Ala Phe Ala Ser Asp Val Ala Leu Pro Ser Asp
                165                 170                 175

Thr Val Ala Leu Ser Gly Ser Glu Arg Trp Asn Ala Ser Ala Ser Tyr
            180                 185                 190

Gln Gly Glu Gln Met Ser Leu Asn Leu Met Ile Val Met Leu Tyr Val
        195                 200                 205

Ile Ser Ala Leu Val Leu Gly Ala Phe Phe Thr Val Trp Thr Ile Gln
    210                 215                 220

Arg Leu Arg Gly Ile Ala Ile Ser Ser Ala Leu Gly Ala Ala Arg Arg
225                 230                 235                 240

Val Leu Ile Ala Asp Ala Leu Gly Gln Ala Ile Ile Val Leu Gly Ile
                245                 250                 255

Gly Ile Thr Ala Gly Thr Leu Ile Thr Val Ile Ser Ala Phe Gly Met
            260                 265                 270

Gly Asp Ala Met Pro Val Val Ile Ser Ser Ser Thr Thr Leu Phe Pro
        275                 280                 285

Ala Leu Ile Leu Ala Ala Ala Gly Leu Ile Gly Ala Ala Ile Ser Leu
    290                 295                 300

Gly Pro Ile Leu Arg Val Glu Pro Arg Ser Ala Leu Met Asn Ala
305                 310                 315
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<210> 739
<211> 826
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(826)
<223> FRXA01697

<400> 739
tagatcaact aagtatgaac gcgaatccga ctttggtcgt actgcaagaa tcgaccagag 60

cccgattaaa aaatgccccc gcgcaacgaa actagtaatc atg ttt caa gga cta 115
Met Phe Gln Gly Leu
1 5

aaa gaa ctc acc gca gca aaa ggc cgc acg ctg ctg atc acc gtc acc 163
Lys Glu Leu Thr Ala Ala Lys Gly Arg Thr Leu Leu Ile Thr Val Thr
10 15 20

gtc ggg ctg atc gcc gtg ctg gtt act ttc ctc tct gcc ctc acc gcc 211
Val Gly Leu Ile Ala Val Leu Val Thr Phe Leu Ser Ala Leu Thr Ala
25 30 35

ggg ctt ggc cac caa tca gta tcc gca ctg aaa tac cta gcg ggt gat 259
Gly Leu Gly His Gln Ser Val Ser Ala Leu Lys Tyr Leu Ala Gly Asp
40 45 50

aat gaa ctt atc ctc gcc gat tcc gga tcc acc acg ctt tcc gcg tcc 307
Asn Glu Leu Ile Leu Ala Asp Ser Gly Ser Thr Thr Leu Ser Ala Ser
55 60 65

acg ctt tct gat caa gca gtt gcc caa ctc gaa gac gaa ggc gca cag 355
Thr Leu Ser Asp Gln Ala Val Ala Gln Leu Glu Asp Glu Gly Ala Gln
70 75 80 85

atg ctg tgg cag gtc cgc gac cga gta gca gac acc ccc acc atg ctc 403
Met Leu Trp Gln Val Arg Asp Arg Val Ala Asp Thr Pro Thr Met Leu
90 95 100

ctc aac tcc cct gac ctt gcg cct ggt gaa gta tcc ctt cct gcc gaa 451
Leu Asn Ser Pro Asp Leu Ala Pro Gly Glu Val Ser Leu Pro Ala Glu
105 110 115

ctc gct gat tcg gaa ctc gct act gcg cat gat gta gtg gat tct tcc 499
Leu Ala Asp Ser Glu Leu Ala Thr Ala His Asp Val Val Asp Ser Ser
120 125 130

aac gat ctg tac ctc gat cac ctg ccc gtg gta ttg atg aac acc tcc 547
Asn Asp Leu Tyr Leu Asp His Leu Pro Val Val Leu Met Asn Thr Ser
135 140 145

gat tta gcc tca ctc gcg caa gtc cga ggc gtg aca gga cca gca ggc 595
Asp Leu Ala Ser Leu Ala Gln Val Arg Gly Val Thr Gly Pro Ala Gly
150 155 160 165

gca ttc gcc tct gac gtt gcg ctc ccc tcc gac acc gtt gcg ctc tct 643
Ala Phe Ala Ser Asp Val Ala Leu Pro Ser Asp Thr Val Ala Leu Ser
170 175 180

```
gga tcc gaa cgg tgg aac gca tcc gcc tcc tac cag ggc gaa cag atg   691
Gly Ser Glu Arg Trp Asn Ala Ser Ala Ser Tyr Gln Gly Glu Gln Met
            185                 190                 195

tca ctc aac ctc atg atc gtc atg ctg tat gtc atc tcc gca ctc gtg   739
Ser Leu Asn Leu Met Ile Val Met Leu Tyr Val Ile Ser Ala Leu Val
        200                 205                 210

ctc ggc gca ttc ttc acc gtc tgg acc atc caa cgc ctc cgc ggc atc   787
Leu Gly Ala Phe Phe Thr Val Trp Thr Ile Gln Arg Leu Arg Gly Ile
    215                 220                 225

gcc atc tct agt gct ttg gga gca gcc cgc cga gta ctt               826
Ala Ile Ser Ser Ala Leu Gly Ala Ala Arg Arg Val Leu
230                 235                 240
```

<210> 740
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

<400> 740

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Met Phe Gln Gly Leu Lys Glu Leu Thr Ala Ala Lys Gly Arg Thr Leu
  1               5                  10                  15

Leu Ile Thr Val Thr Val Gly Leu Ile Ala Val Leu Val Thr Phe Leu
             20                  25                  30

Ser Ala Leu Thr Ala Gly Leu Gly His Gln Ser Val Ser Ala Leu Lys
         35                  40                  45

Tyr Leu Ala Gly Asp Asn Glu Leu Ile Leu Ala Asp Ser Gly Ser Thr
     50                  55                  60

Thr Leu Ser Ala Ser Thr Leu Ser Asp Gln Ala Val Ala Gln Leu Glu
 65                  70                  75                  80

Asp Glu Gly Ala Gln Met Leu Trp Gln Val Arg Asp Arg Val Ala Asp
                 85                  90                  95

Thr Pro Thr Met Leu Leu Asn Ser Pro Asp Leu Ala Pro Gly Glu Val
            100                 105                 110

Ser Leu Pro Ala Glu Leu Ala Asp Ser Glu Leu Ala Thr Ala His Asp
        115                 120                 125

Val Val Asp Ser Ser Asn Asp Leu Tyr Leu Asp His Leu Pro Val Val
    130                 135                 140

Leu Met Asn Thr Ser Asp Leu Ala Ser Leu Ala Gln Val Arg Gly Val
145                 150                 155                 160

Thr Gly Pro Ala Gly Ala Phe Ala Ser Asp Val Ala Leu Pro Ser Asp
                165                 170                 175

Thr Val Ala Leu Ser Gly Ser Glu Arg Trp Asn Ala Ser Ala Ser Tyr
            180                 185                 190

Gln Gly Glu Gln Met Ser Leu Asn Leu Met Ile Val Met Leu Tyr Val
        195                 200                 205
```

```
Ile Ser Ala Leu Val Leu Gly Ala Phe Phe Thr Val Trp Thr Ile Gln
    210                 215                 220

Arg Leu Arg Gly Ile Ala Ile Ser Ser Ala Leu Gly Ala Ala Arg Arg
225                 230                 235                 240

Val Leu
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<210> 741
<211> 472
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(472)
<223> RXN01701

<400> 741

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gccgatcaaa ttcattgatt gttaatcgga agtttttga acaggtaaag ctaggggacc 60

tgttcagtgc ctgttggcgg atgtattaag gagaatgccc atg ctg agc cac gaa   115
                                          Met Leu Ser His Glu
                                            1               5

gaa att gtt gcg atc gca gaa gat ttg ctg tct aaa cgc tac ggc ggt   163
Glu Ile Val Ala Ile Ala Glu Asp Leu Leu Ser Lys Arg Tyr Gly Gly
                10                  15                  20

gta caa act ctt tct gac gtg gag cag ctc aac ggt tcc ggc acc tcc   211
Val Gln Thr Leu Ser Asp Val Glu Gln Leu Asn Gly Ser Gly Thr Ser
            25                  30                  35

gcg gtg ctg cgt gcc agg gtg gct aac tcc cca ttc ctc caa cag cgc   259
Ala Val Leu Arg Ala Arg Val Ala Asn Ser Pro Phe Leu Gln Gln Arg
        40                  45                  50

tcc gtg gtg ctg aag tac gtg ccc agc acc gga gac gtc ttt gat gat   307
Ser Val Val Leu Lys Tyr Val Pro Ser Thr Gly Asp Val Phe Asp Asp
    55                  60                  65

tct gcg ctg gtg cgt gaa atc gtc tcc tac cag ttc acc acc tcc ttg   355
Ser Ala Leu Val Arg Glu Ile Val Ser Tyr Gln Phe Thr Thr Ser Leu
70                  75                  80                  85

tcg gaa gat gtc cgc cca ggg cca gtc att ttg gcc tat gac att gac   403
Ser Glu Asp Val Arg Pro Gly Pro Val Ile Leu Ala Tyr Asp Ile Asp
                90                  95                  100

aag cgc atc ctg gtc att tca gat tcc ggc aac ggc gac acc ttt gcg   451
Lys Arg Ile Leu Val Ile Ser Asp Ser Gly Asn Gly Asp Thr Phe Ala
            105                 110                 115

gat ctg atc gat cag cgt ccg                                      472
Asp Leu Ile Asp Gln Arg Pro
        120
```

<210> 742
<211> 124
<212> PRT
<213> Corynebacterium glutamicum

<400> 742
Met Leu Ser His Glu Glu Ile Val Ala Ile Ala Glu Asp Leu Leu Ser
1 5 10 15

Lys Arg Tyr Gly Gly Val Gln Thr Leu Ser Asp Val Glu Gln Leu Asn
20 25 30

Gly Ser Gly Thr Ser Ala Val Leu Arg Ala Arg Val Ala Asn Ser Pro
35 40 45

Phe Leu Gln Gln Arg Ser Val Val Leu Lys Tyr Val Pro Ser Thr Gly
50 55 60

Asp Val Phe Asp Asp Ser Ala Leu Val Arg Glu Ile Val Ser Tyr Gln
65 70 75 80

Phe Thr Thr Ser Leu Ser Glu Asp Val Arg Pro Gly Pro Val Ile Leu
85 90 95

Ala Tyr Asp Ile Asp Lys Arg Ile Leu Val Ile Ser Asp Ser Gly Asn
100 105 110

Gly Asp Thr Phe Ala Asp Leu Ile Asp Gln Arg Pro
115 120

<210> 743
<211> 433
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(433)
<223> FRXA01701

<400> 743
gccgatcaaa ttcattgatt gttaatcgga agtttttga acaggtaaag ctaggggacc 60

tgttcagtgc ctgttggcgg atgtattaag gagaatgccc atg ctg agc cac gaa 115
Met Leu Ser His Glu
1 5

gaa att gtt gcg atc gca gaa gat ttg ctg tct aaa cgc tac ggc ggt 163
Glu Ile Val Ala Ile Ala Glu Asp Leu Leu Ser Lys Arg Tyr Gly Gly
10 15 20

gta caa act ctt tct gac gtg gag cag ctc aac ggt tcc ggc acc tcc 211
Val Gln Thr Leu Ser Asp Val Glu Gln Leu Asn Gly Ser Gly Thr Ser
25 30 35

gcg gtg ctg cgt gcc agg gtg gct aac tcc cca ttc ctc caa cag cgc 259
Ala Val Leu Arg Ala Arg Val Ala Asn Ser Pro Phe Leu Gln Gln Arg
40 45 50

tcc gtg gtg ctg aag tac gtg ccc agc acc gga gac gtc ttt gat gat 307

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Ser Val Val Leu Lys Tyr Val Pro Ser Thr Gly Asp Val Phe Asp Asp
     55                  60                  65

tct gcg ctg gtg cgt gaa atc gtc tcc tac cag ttc acc acc tcc ttg   355
Ser Ala Leu Val Arg Glu Ile Val Ser Tyr Gln Phe Thr Thr Ser Leu
 70                  75                  80                  85

tcg gaa gat gtc cgc cca ggg cca gtc att ttg gcc tat gac att gac   403
Ser Glu Asp Val Arg Pro Gly Pro Val Ile Leu Ala Tyr Asp Ile Asp
                 90                  95                 100

aag cgc atc ctg gtc att tca gat tcc ggc                          433
Lys Arg Ile Leu Val Ile Ser Asp Ser Gly
            105                 110


<210> 744
<211> 111
<212> PRT
<213> Corynebacterium glutamicum

<400> 744
Met Leu Ser His Glu Glu Ile Val Ala Ile Ala Glu Asp Leu Leu Ser
  1               5                  10                  15

Lys Arg Tyr Gly Gly Val Gln Thr Leu Ser Asp Val Glu Gln Leu Asn
             20                  25                  30

Gly Ser Gly Thr Ser Ala Val Leu Arg Ala Arg Val Ala Asn Ser Pro
         35                  40                  45

Phe Leu Gln Gln Arg Ser Val Val Leu Lys Tyr Val Pro Ser Thr Gly
     50                  55                  60

Asp Val Phe Asp Asp Ser Ala Leu Val Arg Glu Ile Val Ser Tyr Gln
 65                  70                  75                  80

Phe Thr Thr Ser Leu Ser Glu Asp Val Arg Pro Gly Pro Val Ile Leu
                 85                  90                  95

Ala Tyr Asp Ile Asp Lys Arg Ile Leu Val Ile Ser Asp Ser Gly
            100                 105                 110


<210> 745
<211> 1236
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1213)
<223> RXN01703

<400> 745
gttagacaaa tgggtaaaca gagctgacct agcggaatcc gccatcaacg aaaggcattc 60

cgcgagggtt tggggtctgc ctcgaacaaa tcttgggttt gtg gca tgg cca tcc   115
                                              Val Ala Trp Pro Ser
                                                1               5
```

```
aac gcc aaa gaa aaa ctg ttt atc cac tgg cac tac tgg tgg caa gcg   163
Asn Ala Lys Glu Lys Leu Phe Ile His Trp His Tyr Trp Trp Gln Ala
                 10                  15                  20

cat tat cta gac tgc ctg gtg gat gct gct cgt cga cgc acc aca aag   211
His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg Arg Arg Thr Thr Lys
             25                  30                  35

gcc cgt cgc gac cgc atc agg gac acc atc cgc ggc att tcg gtg cgc   259
Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg Gly Ile Ser Val Arg
         40                  45                  50

aat gtg ggc aag ctg acc tcg aat cgt tat tac gac gac aaa gct tgg   307
Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr Asp Asp Lys Ala Trp
     55                  60                  65

ctg gcc ctt gct ctt ggg cgt gcc gga aaa gtg cga aag gtg cgc aca   355
Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val Arg Lys Val Arg Thr
 70                  75                  80                  85

cca aaa tca ttg ccc tcg ttg gaa caa aac atc gtc gat ggc att gat   403
Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile Val Asp Gly Ile Asp
                 90                  95                 100

tcc ctt act ggt gtg ctg ccg tgg cgt tcc ggc gaa acc ttc tac aac   451
Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly Glu Thr Phe Tyr Asn
             105                 110                 115

gtt ccc tcc aac ggt cct gct gcg atc atg atg gcc cgc acc gac cgt   499
Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met Ala Arg Thr Asp Arg
         120                 125                 130

ttg gac gag gct atg aaa atc acc gat tgg att ttt gac aac ctg atc   547
Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile Phe Asp Asn Leu Ile
     135                 140                 145

gat ggc gac ggc ctt gtg atg gac gga ttg cgc atg cgc atg cac gga   595
Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg Met Arg Met His Gly
150                 155                 160                 165

cct gag ctt gtc cgt tcc atc cac ccg tat tgc caa ggt gtc gcc att   643
Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys Gln Gly Val Ala Ile
                 170                 175                 180

ggt gcg tgt ttg gaa att gct ctc aaa ctg cgt gag cgc gca ggc ttg   691
Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg Glu Arg Ala Gly Leu
             185                 190                 195

acc act act gtg gtg gat cac tgg tcg gat gcc gat aag gca gaa gac   739
Thr Thr Thr Val Val Asp His Trp Ser Asp Ala Asp Lys Ala Glu Asp
         200                 205                 210

tcc ctc aaa tac ttt gca cac atc cac gct gtg gtt cag gct gtg tcg   787
Ser Leu Lys Tyr Phe Ala His Ile His Ala Val Val Gln Ala Val Ser
     215                 220                 225

cgg aag atg acc aac ttc cac ggc gtt att gat tgg gac acc ggt gac   835
Arg Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp
230                 235                 240                 245

ggc gac ggc ggt ttg ttc aag ggc att ttg gtc cgc tat tta gct gat   883
```

```
Gly Asp Gly Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp
                250                 255                 260

gtg gcc atc cgc ctg cct gac gat tca cca acc aac cgg gaa acc aaa   931
Val Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr Asn Arg Glu Thr Lys
            265                 270                 275

aag att gca gca cgc ctg gta ctg gaa tcg gcg gaa agc gta tgg aac   979
Lys Ile Ala Ala Arg Leu Val Leu Glu Ser Ala Glu Ser Val Trp Asn
        280                 285                 290

cac cga ttg gaa gtt gat ggc ctt ccg gta ttc gcc aca gac tgg aca   1027
His Arg Leu Glu Val Asp Gly Leu Pro Val Phe Ala Thr Asp Trp Thr
    295                 300                 305

acg gat gca cgc ctg cca caa aac ttt ggt ttg agt tcc tct agt ttg   1075
Thr Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu Ser Ser Ser Ser Leu
310                 315                 320                 325

agc gat ctg gtg agt gtt gtg cgc gtg gat gaa cgt gat ctg tcc gtg   1123
Ser Asp Leu Val Ser Val Val Arg Val Asp Glu Arg Asp Leu Ser Val
                330                 335                 340

caa ttg tcc ggt tgg atg ctc atg gaa gca gca gcg aaa gtg gcc gaa   1171
Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu
            345                 350                 355

gaa ctg gaa aac aac ggc aat agt tac acc ggt cgc tcc cga           1213
Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg
        360                 365                 370

tagccccgat agtgtatgtg ctg                                        1236


<210> 746
<211> 371
<212> PRT
<213> Corynebacterium glutamicum

<400> 746
Val Ala Trp Pro Ser Asn Ala Lys Glu Lys Leu Phe Ile His Trp His
  1               5                  10                  15

Tyr Trp Trp Gln Ala His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg
             20                  25                  30

Arg Arg Thr Thr Lys Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg
         35                  40                  45

Gly Ile Ser Val Arg Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr
     50                  55                  60

Asp Asp Lys Ala Trp Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val
 65                  70                  75                  80

Arg Lys Val Arg Thr Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile
                 85                  90                  95

Val Asp Gly Ile Asp Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly
            100                 105                 110
```

```
Glu Thr Phe Tyr Asn Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met
        115                 120                 125

Ala Arg Thr Asp Arg Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile
    130                 135                 140

Phe Asp Asn Leu Ile Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg
145                 150                 155                 160

Met Arg Met His Gly Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys
                165                 170                 175

Gln Gly Val Ala Ile Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg
            180                 185                 190

Glu Arg Ala Gly Leu Thr Thr Thr Val Val Asp His Trp Ser Asp Ala
        195                 200                 205

Asp Lys Ala Glu Asp Ser Leu Lys Tyr Phe Ala His Ile His Ala Val
    210                 215                 220

Val Gln Ala Val Ser Arg Lys Met Thr Asn Phe His Gly Val Ile Asp
225                 230                 235                 240

Trp Asp Thr Gly Asp Gly Asp Gly Gly Leu Phe Lys Gly Ile Leu Val
                245                 250                 255

Arg Tyr Leu Ala Asp Val Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr
            260                 265                 270

Asn Arg Glu Thr Lys Lys Ile Ala Ala Arg Leu Val Leu Glu Ser Ala
        275                 280                 285

Glu Ser Val Trp Asn His Arg Leu Glu Val Asp Gly Leu Pro Val Phe
    290                 295                 300

Ala Thr Asp Trp Thr Thr Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu
305                 310                 315                 320

Ser Ser Ser Ser Leu Ser Asp Leu Val Ser Val Val Arg Val Asp Glu
                325                 330                 335

Arg Asp Leu Ser Val Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala
            340                 345                 350

Ala Lys Val Ala Glu Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly
        355                 360                 365

Arg Ser Arg
    370
```

<210> 747
<211> 494
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(471)
<223> FRXA01703

<400> 747
ctc aaa tac ttt gca cac atc cac gct gtg gtt cag gct gtg tcg cgg 48
Leu Lys Tyr Phe Ala His Ile His Ala Val Val Gln Ala Val Ser Arg
1 5 10 15

aag atg acc aac ttc cac ggc gtt att gat tgg gac acc ggt gac ggc 96
Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp Gly
20 25 30

gac ggc ggt ttg ttc aag ggc att ttg gtc cgc tat tta gct gat gtg 144
Asp Gly Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp Val
35 40 45

gcc atc cgc ctg cct gac gat tca cca acc aac cgg gaa acc aaa aag 192
Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr Asn Arg Glu Thr Lys Lys
50 55 60

att gca gca cgc ctg gta ctg gaa tcg gcg gaa agc gta tgg aac cac 240
Ile Ala Ala Arg Leu Val Leu Glu Ser Ala Glu Ser Val Trp Asn His
65 70 75 80

cga ttg gaa gtt gat ggc ctt ccg gta ttc gcc aca gac tgg aca acg 288
Arg Leu Glu Val Asp Gly Leu Pro Val Phe Ala Thr Asp Trp Thr Thr
85 90 95

gat gca cgc ctg cca caa aac ttt ggt ttg agt tcc tct agt ttg agc 336
Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu Ser Ser Ser Ser Leu Ser
100 105 110

gat ctg gtg agt gtt gtg cgc gtg gat gaa cgt gat ctg tcc gtg caa 384
Asp Leu Val Ser Val Val Arg Val Asp Glu Arg Asp Leu Ser Val Gln
115 120 125

ttg tcc ggt tgg atg ctc atg gaa gca gca gcg aaa gtg gcc gaa gaa 432
Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu Glu
130 135 140

ctg gaa aac aac ggc aat agt tac acc ggt cgc tcc cga tagccccgat 481
Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg
145 150 155

agtgtatgtg ctg 494

<210> 748
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 748
Leu Lys Tyr Phe Ala His Ile His Ala Val Val Gln Ala Val Ser Arg
1 5 10 15

Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp Gly
20 25 30

Asp Gly Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp Val
35 40 45

Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr Asn Arg Glu Thr Lys Lys

```
     50                  55                  60

Ile Ala Ala Arg Leu Val Leu Glu Ser Ala Glu Ser Val Trp Asn His
 65                  70                  75                  80

Arg Leu Glu Val Asp Gly Leu Pro Val Phe Ala Thr Asp Trp Thr Thr
                 85                  90                  95

Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu Ser Ser Ser Ser Leu Ser
            100                 105                 110

Asp Leu Val Ser Val Val Arg Val Asp Glu Arg Asp Leu Ser Val Gln
        115                 120                 125

Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu Glu
    130                 135                 140

Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg
145                 150                 155


<210> 749
<211> 555
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(532)
<223> RXN01709

<400> 749
gcaagtggaa ccacgatggg aacggtaact gctgccgctg cggtattact cgtagtttca 60

gaaattaggt gtcgatgcag caatacggaa ctttgccaat gtg ttt gaa caa gct   115
                                            Val Phe Glu Gln Ala
                                              1               5

ctc ggg ctc acc acc ctt gca caa aca gct gga gcg ggc gca gcg ggg   163
Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly Ala Gly Ala Ala Gly
                 10                  15                  20

ggc ttg ggt ttc atg gca atg gcg ttg ttg tct gca ggg atg cgc tcc   211
Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser Ala Gly Met Arg Ser
             25                  30                  35

ggc gtg gac atg att ctt aat gaa acc ggg ggt gaa aag atg ctt gca   259
Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly Glu Lys Met Leu Ala
         40                  45                  50

cag gca gat tta gtc atc act gga gaa gga cgc att gat gca cag acc   307
Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg Ile Asp Ala Gln Thr
     55                  60                  65

ctc agc ggg aaa gct cct act gga atc gcc aaa cgg gca cgt gcg aaa   355
Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys Arg Ala Arg Ala Lys
 70                  75                  80                  85

gga att cca gta ctg gcg gtt tgt ggg cag agc cta ttg ggt cca gca   403
Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser Leu Leu Gly Pro Ala
                 90                  95                 100
```

```
atc tca aat gag cta ttt gaa gac atc tac agc ttt acc gat ttc gaa   451
Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser Phe Thr Asp Phe Glu
            105                 110                 115

tct gac atc aat gaa tgc att cga aac ccg ctc cca att ttg gaa ggt   499
Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu Pro Ile Leu Glu Gly
        120                 125                 130

atc ggt ttt aac atc gcc aaa cat cat ctg agt tagcgatatt tcagcaaacc 552
Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
    135                 140

gat                                                               555
```

<210> 750
<211> 144
<212> PRT
<213> Corynebacterium glutamicum

<400> 750

```
Val Phe Glu Gln Ala Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly
  1               5                  10                  15

Ala Gly Ala Ala Gly Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser
             20                  25                  30

Ala Gly Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly
         35                  40                  45

Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg
     50                  55                  60

Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys
 65                  70                  75                  80

Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser
                 85                  90                  95

Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser
            100                 105                 110

Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu
        115                 120                 125

Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
    130                 135                 140
```

<210> 751
<211> 368
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (16)..(345)

<223> FRXA01709

<400> 751

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ttgttgtctg cagggatg cgc tcc ggc gtg gac atg att ctt aat gaa acc   51
                Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr
                  1               5                  10

ggg ggt gaa aag atg ctt gca cag gca gat tta gtc atc act gga gaa   99
Gly Gly Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu
         15                  20                  25

gga cgc att gat gca cag acc ctc agc ggg aaa gct cct act gga atc   147
Gly Arg Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile
     30                  35                  40

gcc aaa cgg gca cgt gcg aaa gga att cca gta ctg gcg gtt tgt ggg   195
Ala Lys Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly
 45                  50                  55                  60

cag agc cta ttg ggt cca gca atc tca aat gag cta ttt gaa gac atc   243
Gln Ser Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile
                 65                  70                  75

tac agc ttt acc gat ttc gaa tct gac atc aat gaa tgc att cga aac   291
Tyr Ser Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn
             80                  85                  90

ccg ctc cca att ttg gaa ggt atc ggt ttt aac atc gcc aaa cat cat   339
Pro Leu Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His
         95                  100                 105

ctg agt tagcgatatt tcagcaaacc gat                                 368
Leu Ser
    110
```

<210> 752
<211> 110
<212> PRT
<213> Corynebacterium glutamicum

<400> 752

```
Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly Glu Lys
  1               5                  10                  15

Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg Ile Asp
             20                  25                  30

Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys Arg Ala
         35                  40                  45

Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser Leu Leu
     50                  55                  60

Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser Phe Thr
 65                  70                  75                  80

Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu Pro Ile
                 85                  90                  95

Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
```

100 105 110

<210> 753
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1258)
<223> RXN01711

<400> 753
tctcgtgagt ttctccccgg tagcaccttc tatatcagcc cccacgccgc gtcggagcag 60

gtgggatagc atcggcaacg cggttgcatg gccgttggcc atg ttg ttg atg gcg 115
Met Leu Leu Met Ala
1 5

cat cgc ttc ttc gtg ctt gcg att aac ggc gca gtc acc gac gat ttc 163
His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala Val Thr Asp Asp Phe
10 15 20

acg acg gtt tat agt gct tta cga cgt ttc gtt gaa ggt att ccg gtc 211
Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val Glu Gly Ile Pro Val
25 30 35

tac aac gag gtc tac cac ttc gtc gat ccg cac tac ctc tat aac ccg 259
Tyr Asn Glu Val Tyr His Phe Val Asp Pro His Tyr Leu Tyr Asn Pro
40 45 50

ggc gcc acc ctc cta ttg gca cca ttg gga tat atc acc cat ttc acg 307
Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr Ile Thr His Phe Thr
55 60 65

ttg gct cgg tgg atg ttc atc gcg gtg aac ctc ctt gcc att gtt tta 355
Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu Leu Ala Ile Val Leu
70 75 80 85

gcg ttc ggg ctg ctg acc aga ctc tcc ggt tgg gcg ctg cgc agc atg 403
Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp Ala Leu Arg Ser Met
90 95 100

gtg tgg ccg att gcg atc gcc ttg gcg atg ctg aca gaa acc gtg caa 451
Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu Thr Glu Thr Val Gln
105 110 115

aac acc ctc att ttc tcc aac atc aac ggc atc ctg ctg ctc atg ttg 499
Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile Leu Leu Leu Met Leu
120 125 130

gcg att ttc ctg tgg tgc gtg gtg cac aaa aaa tcc tgg ttg ggc gga 547
Ala Ile Phe Leu Trp Cys Val Val His Lys Lys Ser Trp Leu Gly Gly
135 140 145

cta gtc att ggt ttg gcc att ttg atc aaa ccc atg ttc ctg cca ctt 595
Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro Met Phe Leu Pro Leu
150 155 160 165

ctc ttc cta cct ttg gtg aaa aag caa tgg gga tcg ctc atc ctc ggc 643

```
Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly Ser Leu Ile Leu Gly
                170                 175                 180

att tta acc cca gtg att ttc aat gca gtg gcc tgg ttc tta gtt ccg   691
Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala Trp Phe Leu Val Pro
            185                 190                 195

gga gca tct gaa tac gtc acc cgc acg atg ccc tac ctt ggt gaa act   739
Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro Tyr Leu Gly Glu Thr
        200                 205                 210

cga gat ttt gcc aac agc tca ctc cca ggc ttg gcc atc tat ttc gga   787
Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu Ala Ile Tyr Phe Gly
    215                 220                 225

atg ccc acc tgg atg gaa atc acc tgg ttc ctc atc ttc ggc gca atg   835
Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu Ile Phe Gly Ala Met
230                 235                 240                 245

gtc ggc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca   883
Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro
                250                 255                 260

tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act ggc gta ttc   931
Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe
            265                 270                 275

ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct   979
Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro
        280                 285                 290

atg atc ttc acc ctg ctc gga agc cga tcc gta ttc cac aac tgg gtt   1027
Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val
    295                 300                 305

gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc   1075
Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser
310                 315                 320                 325

cag cga cta ccc gat gta gcc cgc tgg atg gaa ttt ttc agc gcg acc   1123
Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr
                330                 335                 340

gtt ggt tgg gga cta ttg ata gtg gtt aca ttt gtc tcg gcg cta atc   1171
Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile
            345                 350                 355

tgg ttt att ggt gat atc cga gcc aag gga act ccg agc tca ccc att   1219
Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile
        360                 365                 370

acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt    1268
Thr Thr Asp Pro Thr His Asp His Leu Glu Arg Thr Ala
    375                 380                 385

caaactcatc agc                                                   1281

<210> 754
<211> 386
<212> PRT
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<213> Corynebacterium glutamicum

<400> 754

```
Met Leu Leu Met Ala His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala
  1               5                  10                  15

Val Thr Asp Asp Phe Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val
             20                  25                  30

Glu Gly Ile Pro Val Tyr Asn Glu Val Tyr His Phe Val Asp Pro His
         35                  40                  45

Tyr Leu Tyr Asn Pro Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr
     50                  55                  60

Ile Thr His Phe Thr Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu
 65                  70                  75                  80

Leu Ala Ile Val Leu Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp
                 85                  90                  95

Ala Leu Arg Ser Met Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu
            100                 105                 110

Thr Glu Thr Val Gln Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile
        115                 120                 125

Leu Leu Leu Met Leu Ala Ile Phe Leu Trp Cys Val Val His Lys Lys
    130                 135                 140

Ser Trp Leu Gly Gly Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro
145                 150                 155                 160

Met Phe Leu Pro Leu Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly
                165                 170                 175

Ser Leu Ile Leu Gly Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala
            180                 185                 190

Trp Phe Leu Val Pro Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro
        195                 200                 205

Tyr Leu Gly Glu Thr Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu
    210                 215                 220

Ala Ile Tyr Phe Gly Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu
225                 230                 235                 240

Ile Phe Gly Ala Met Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe
                245                 250                 255

Arg Asn Thr Glu Pro Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu
            260                 265                 270

Leu Thr Gly Val Phe Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser
        275                 280                 285

Met Met Ile Phe Pro Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val
    290                 295                 300

Phe His Asn Trp Val Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro
```

```
305                 310                 315                 320

Asp Thr Phe Thr Ser Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu
                325                 330                 335

Phe Phe Ser Ala Thr Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe
            340                 345                 350

Val Ser Ala Leu Ile Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr
        355                 360                 365

Pro Ser Ser Pro Ile Thr Thr Asp Pro Thr His Asp His Leu Glu Arg
    370                 375                 380

Thr Ala
385
```

<210> 755
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1258)
<223> FRXA01711

<400> 755

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tctcgtgagt ttctccccgg tagcaccttc tatatcagcc cccacgccgc gtcggagcag 60

gtgggatagc atcggcaacg cggttgcatg gccgttggcc atg ttg ttg atg gcg   115
                                            Met Leu Leu Met Ala
                                              1               5

cat cgc ttc ttc gtg ctt gcg att aac ggc gca gtc acc gac gat ttc   163
His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala Val Thr Asp Asp Phe
                10                  15                  20

acg acg gtt tat agt gct tta cga cgt ttc gtt gaa ggt att ccg gtc   211
Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val Glu Gly Ile Pro Val
            25                  30                  35

tac aac gag gtc tac cac ttc gtc gat ccg cac tac ctc tat aac ccg   259
Tyr Asn Glu Val Tyr His Phe Val Asp Pro His Tyr Leu Tyr Asn Pro
        40                  45                  50

ggc gcc acc ctc cta ttg gca cca ttg gga tat atc acc cat ttc acg   307
Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr Ile Thr His Phe Thr
    55                  60                  65

ttg gct cgg tgg atg ttc atc gcg gtg aac ctc ctt gcc att gtt tta   355
Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu Leu Ala Ile Val Leu
70                  75                  80                  85

gcg ttc ggg ctg ctg acc aga ctc tcc ggt tgg gcg ctg cgc agc atg   403
Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp Ala Leu Arg Ser Met
                90                  95                  100

gtg tgg ccg att gcg atc gcc ttg gcg atg ctg aca gaa acc gtg caa   451
Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu Thr Glu Thr Val Gln
```

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                105                 110                 115

aac acc ctc att ttc tcc aac atc aac ggc atc ctg ctg ctc atg ttg   499
Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile Leu Leu Leu Met Leu
        120                 125                 130

gcg att ttc ctg tgg tgc gtg gtg cac aaa aaa tcc tgg ttg ggc gga   547
Ala Ile Phe Leu Trp Cys Val Val His Lys Lys Ser Trp Leu Gly Gly
    135                 140                 145

cta gtc att ggt ttg gcc att ttg atc aaa ccc atg ttc ctg cca ctt   595
Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro Met Phe Leu Pro Leu
150                 155                 160                 165

ctc ttc cta cct ttg gtg aaa aag caa tgg gga tcg ctc atc ctc ggc   643
Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly Ser Leu Ile Leu Gly
                170                 175                 180

att tta acc cca gtg att ttc aat gca gtg gcc tgg ttc tta gtt ccg   691
Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala Trp Phe Leu Val Pro
            185                 190                 195

gga gca tct gaa tac gtc acc cgc acg atg ccc tac ctt ggt gaa act   739
Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro Tyr Leu Gly Glu Thr
        200                 205                 210

cga gat ttt gcc aac agc tca ctc cca ggc ttg gcc atc tat ttc gga   787
Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu Ala Ile Tyr Phe Gly
    215                 220                 225

atg ccc acc tgg atg gaa atc acc tgg ttc ctc atc ttc ggc gca atg   835
Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu Ile Phe Gly Ala Met
230                 235                 240                 245

gtc ggc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca   883
Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro
                250                 255                 260

tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act ggc gta ttc   931
Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe
            265                 270                 275

ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct   979
Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro
        280                 285                 290

atg atc ttc acc ctg ctc gga agc cga tcc gta ttc cac aac tgg gtt   1027
Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val
    295                 300                 305

gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc   1075
Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser
310                 315                 320                 325

cag cga cta ccc gat gta gcc cgc tgg atg gaa ttt ttc agc gcg acc   1123
Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr
                330                 335                 340

gtt ggt tgg gga cta ttg ata gtg gtt aca ttt gtc tcg gcg cta atc   1171
Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile
            345                 350                 355
```

```
tgg ttt att ggt gat atc cga gcc aag gga act ccg agc tca ccc att   1219
Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile
        360                 365                 370

acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt   1268
Thr Thr Asp Pro Thr His Asp His Leu Glu Arg Thr Ala
    375                 380                 385

caaactcatc agc                                                   1281
```

<210> 756
<211> 386
<212> PRT
<213> Corynebacterium glutamicum

<400> 756

```
Met Leu Leu Met Ala His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala
  1               5                  10                  15

Val Thr Asp Asp Phe Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val
             20                  25                  30

Glu Gly Ile Pro Val Tyr Asn Glu Val Tyr His Phe Val Asp Pro His
         35                  40                  45

Tyr Leu Tyr Asn Pro Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr
     50                  55                  60

Ile Thr His Phe Thr Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu
 65                  70                  75                  80

Leu Ala Ile Val Leu Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp
                 85                  90                  95

Ala Leu Arg Ser Met Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu
            100                 105                 110

Thr Glu Thr Val Gln Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile
        115                 120                 125

Leu Leu Leu Met Leu Ala Ile Phe Leu Trp Cys Val Val His Lys Lys
    130                 135                 140

Ser Trp Leu Gly Gly Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro
145                 150                 155                 160

Met Phe Leu Pro Leu Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly
                165                 170                 175

Ser Leu Ile Leu Gly Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala
            180                 185                 190

Trp Phe Leu Val Pro Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro
        195                 200                 205

Tyr Leu Gly Glu Thr Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu
    210                 215                 220

Ala Ile Tyr Phe Gly Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu
```

```
225                 230                 235                 240

Ile Phe Gly Ala Met Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe
                245                 250                 255

Arg Asn Thr Glu Pro Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu
            260                 265                 270

Leu Thr Gly Val Phe Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser
        275                 280                 285

Met Met Ile Phe Pro Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val
    290                 295                 300

Phe His Asn Trp Val Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro
305                 310                 315                 320

Asp Thr Phe Thr Ser Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu
                325                 330                 335

Phe Phe Ser Ala Thr Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe
            340                 345                 350

Val Ser Ala Leu Ile Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr
        355                 360                 365

Pro Ser Ser Pro Ile Thr Thr Asp Pro Thr His Asp His Leu Glu Arg
    370                 375                 380

Thr Ala
385


<210> 757
<211> 1123
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1123)
<223> RXN01721

<400> 757
ttcgccaacg ccgccccgaa atgatcggga gggggcgtcg aaaagcactt ctgcgagcat 60

caaacatgat gcgtacctgc cacccgcaga cggcaatcgc gtg ctt gtg gac aga   115
                                            Val Leu Val Asp Arg
                                              1               5

ttc gga cgc atc gcg cgt gac ctg cgg gtg tca ctg acc gac cga tgc   163
Phe Gly Arg Ile Ala Arg Asp Leu Arg Val Ser Leu Thr Asp Arg Cys
                 10                  15                  20

aac ctc cgc tgc acc tat tgc atg ccc gcg gag ggt tta gag tgg ctg   211
Asn Leu Arg Cys Thr Tyr Cys Met Pro Ala Glu Gly Leu Glu Trp Leu
             25                  30                  35

ccc acc gag cag acg ctt aac gac gcc gag gtg ctg cga ctc atc cgc   259
Pro Thr Glu Gln Thr Leu Asn Asp Ala Glu Val Leu Arg Leu Ile Arg
         40                  45                  50
```

```
att gcg gtg gtt aag ctg ggc att cgt caa att cga ttc acc ggc ggc   307
Ile Ala Val Val Lys Leu Gly Ile Arg Gln Ile Arg Phe Thr Gly Gly
     55                  60                  65

gag cct tta ctg cgg aaa aat ttg gaa gac atc atc gcc ggc acc gca   355
Glu Pro Leu Leu Arg Lys Asn Leu Glu Asp Ile Ile Ala Gly Thr Ala
 70                  75                  80                  85

gcc ctg cgc acc gac gaa ggc gaa aaa gtt cac atc gct ctc acc acc   403
Ala Leu Arg Thr Asp Glu Gly Glu Lys Val His Ile Ala Leu Thr Thr
                 90                  95                 100

aac ggc ctt ggc cta gac aaa cgc atc gca gga ctg aaa gaa gct ggt   451
Asn Gly Leu Gly Leu Asp Lys Arg Ile Ala Gly Leu Lys Glu Ala Gly
            105                 110                 115

ctt gac cgg gtc aat att tca ctc gac acc atc gac gcc gaa cgc tac   499
Leu Asp Arg Val Asn Ile Ser Leu Asp Thr Ile Asp Ala Glu Arg Tyr
        120                 125                 130

gtc tcg cta acc aag cgt gat cga ttg tcc ggt gtg ttg gcg tcc atc   547
Val Ser Leu Thr Lys Arg Asp Arg Leu Ser Gly Val Leu Ala Ser Ile
    135                 140                 145

gat gcc gct gtt gcc gct ggc ctt cac cca gtg aag atc aac gcc gtg   595
Asp Ala Ala Val Ala Ala Gly Leu His Pro Val Lys Ile Asn Ala Val
150                 155                 160                 165

gtc atg cct ggg gtc aat gaa gta gat atc gtc ccc ctt gcg gaa tac   643
Val Met Pro Gly Val Asn Glu Val Asp Ile Val Pro Leu Ala Glu Tyr
                170                 175                 180

tgc att tcc aaa ggc tcc caa ctg cga ttc atc gaa caa atg cca ctt   691
Cys Ile Ser Lys Gly Ser Gln Leu Arg Phe Ile Glu Gln Met Pro Leu
            185                 190                 195

ggc ccg cgc gag cag tgg aaa cgc ggc gat atg gtc aca gcc gaa gaa   739
Gly Pro Arg Glu Gln Trp Lys Arg Gly Asp Met Val Thr Ala Glu Glu
        200                 205                 210

atc ctg gcg cgc ctg gaa gaa aaa ttc acc tta tcc ccc gcc aag gaa   787
Ile Leu Ala Arg Leu Glu Glu Lys Phe Thr Leu Ser Pro Ala Lys Glu
    215                 220                 225

ccc cga gga gct gca cct gct gcg ctg tgg aat gtg gta gat aaa tcc   835
Pro Arg Gly Ala Ala Pro Ala Ala Leu Trp Asn Val Val Asp Lys Ser
230                 235                 240                 245

aac cct gat atc act gga caa atc ggc atc atc gcc tcg gtg acg cac   883
Asn Pro Asp Ile Thr Gly Gln Ile Gly Ile Ile Ala Ser Val Thr His
                250                 255                 260

cca ttt tgc gga gat tgc gat cgc tcc cgc ctc acc acc gac ggc acc   931
Pro Phe Cys Gly Asp Cys Asp Arg Ser Arg Leu Thr Thr Asp Gly Thr
            265                 270                 275

atc cga aac tgc ctt ttc tcc cgc act gaa act ccc cta cgt gac gcg   979
Ile Arg Asn Cys Leu Phe Ser Arg Thr Glu Thr Pro Leu Arg Asp Ala
        280                 285                 290
```

```
ctt cgc gac ggc gcc tcc gac gat gag ctc gcg caa ctg tgg gca ggc   1027
Leu Arg Asp Gly Ala Ser Asp Asp Glu Leu Ala Gln Leu Trp Ala Gly
    295                 300                 305

gcc atg tgg gag aag aaa ccc ggc cat ggc atc gac gat gaa ggc ttc   1075
Ala Met Trp Glu Lys Lys Pro Gly His Gly Ile Asp Asp Glu Gly Phe
310                 315                 320                 325

ctc caa cca gat cgc ccc atg tct gcc atc ggg gct agc cca tac cag   1123
Leu Gln Pro Asp Arg Pro Met Ser Ala Ile Gly Ala Ser Pro Tyr Gln
                330                 335                 340
```

<210> 758
<211> 341
<212> PRT
<213> Corynebacterium glutamicum

<400> 758

```
Val Leu Val Asp Arg Phe Gly Arg Ile Ala Arg Asp Leu Arg Val Ser
  1               5                  10                  15

Leu Thr Asp Arg Cys Asn Leu Arg Cys Thr Tyr Cys Met Pro Ala Glu
             20                  25                  30

Gly Leu Glu Trp Leu Pro Thr Glu Gln Thr Leu Asn Asp Ala Glu Val
         35                  40                  45

Leu Arg Leu Ile Arg Ile Ala Val Val Lys Leu Gly Ile Arg Gln Ile
     50                  55                  60

Arg Phe Thr Gly Gly Glu Pro Leu Leu Arg Lys Asn Leu Glu Asp Ile
 65                  70                  75                  80

Ile Ala Gly Thr Ala Ala Leu Arg Thr Asp Glu Gly Glu Lys Val His
                 85                  90                  95

Ile Ala Leu Thr Thr Asn Gly Leu Gly Leu Asp Lys Arg Ile Ala Gly
            100                 105                 110

Leu Lys Glu Ala Gly Leu Asp Arg Val Asn Ile Ser Leu Asp Thr Ile
        115                 120                 125

Asp Ala Glu Arg Tyr Val Ser Leu Thr Lys Arg Asp Arg Leu Ser Gly
    130                 135                 140

Val Leu Ala Ser Ile Asp Ala Ala Val Ala Ala Gly Leu His Pro Val
145                 150                 155                 160

Lys Ile Asn Ala Val Val Met Pro Gly Val Asn Glu Val Asp Ile Val
                165                 170                 175

Pro Leu Ala Glu Tyr Cys Ile Ser Lys Gly Ser Gln Leu Arg Phe Ile
            180                 185                 190

Glu Gln Met Pro Leu Gly Pro Arg Glu Gln Trp Lys Arg Gly Asp Met
        195                 200                 205

Val Thr Ala Glu Glu Ile Leu Ala Arg Leu Glu Glu Lys Phe Thr Leu
    210                 215                 220
```

```
Ser Pro Ala Lys Glu Pro Arg Gly Ala Ala Pro Ala Ala Leu Trp Asn
225                 230                 235                 240

Val Val Asp Lys Ser Asn Pro Asp Ile Thr Gly Gln Ile Gly Ile Ile
                245                 250                 255

Ala Ser Val Thr His Pro Phe Cys Gly Asp Cys Asp Arg Ser Arg Leu
            260                 265                 270

Thr Thr Asp Gly Thr Ile Arg Asn Cys Leu Phe Ser Arg Thr Glu Thr
        275                 280                 285

Pro Leu Arg Asp Ala Leu Arg Asp Gly Ala Ser Asp Asp Glu Leu Ala
    290                 295                 300

Gln Leu Trp Ala Gly Ala Met Trp Glu Lys Lys Pro Gly His Gly Ile
305                 310                 315                 320

Asp Asp Glu Gly Phe Leu Gln Pro Asp Arg Pro Met Ser Ala Ile Gly
                325                 330                 335

Ala Ser Pro Tyr Gln
            340
```

<210> 759
<211> 657
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(634)
<223> RXN01734

<400> 759

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acgatctgcc ggagaatctc aagaaagtgc tcactgcgca gcacaccgtc accgtccaag 60

acaccggcac cgggcggatt tcactcctgg atgtgcaacc atg aca gat cca att   115
                                            Met Thr Asp Pro Ile
                                              1               5

gag cag gca ttt gaa cgc atc cgc gcc gaa gcc atg cgc aga aat gga   163
Glu Gln Ala Phe Glu Arg Ile Arg Ala Glu Ala Met Arg Arg Asn Gly
                 10                  15                  20

tcc gtt ccc gac ctc aat aaa aac gat gct ttt cga cgc cca cct gcg   211
Ser Val Pro Asp Leu Asn Lys Asn Asp Ala Phe Arg Arg Pro Pro Ala
             25                  30                  35

ccg aaa ggg ggc gtc gaa aag cgc aaa aaa ggc cgt gca agc ggc cta   259
Pro Lys Gly Gly Val Glu Lys Arg Lys Lys Gly Arg Ala Ser Gly Leu
         40                  45                  50

gac ggc cgc cag aaa cga tat gtg cgc ggc gcg gag tcg ctg gga tcg   307
Asp Gly Arg Gln Lys Arg Tyr Val Arg Gly Ala Glu Ser Leu Gly Ser
     55                  60                  65

gtg ctg aac aag gaa att cag cgt cgt ggc tgg ggc aaa gac att gcc   355
Val Leu Asn Lys Glu Ile Gln Arg Arg Gly Trp Gly Lys Asp Ile Ala
 70                  75                  80                  85
```

```
ggc ggt tgg gtg acg tcc aac tgg gaa gag ctt gtt ggc gcg aag att   403
Gly Gly Trp Val Thr Ser Asn Trp Glu Glu Leu Val Gly Ala Lys Ile
                 90                  95                 100

gcg cag cat acg cgc gtg gaa atg atc aaa gat aag aag ctt ttt atc   451
Ala Gln His Thr Arg Val Glu Met Ile Lys Asp Lys Lys Leu Phe Ile
            105                 110                 115

act tgt gat tcc aca gcg tgg gcc acc aat ctg cgc atg atg cag cgg   499
Thr Cys Asp Ser Thr Ala Trp Ala Thr Asn Leu Arg Met Met Gln Arg
        120                 125                 130

caa atc ctg cag gta atc gct gaa aaa gtg ggt cca aat att att aca   547
Gln Ile Leu Gln Val Ile Ala Glu Lys Val Gly Pro Asn Ile Ile Thr
    135                 140                 145

gag ctg cgt att ttt ggg cct cag gcc cca agc tgg cgc aag ggg ccg   595
Glu Leu Arg Ile Phe Gly Pro Gln Ala Pro Ser Trp Arg Lys Gly Pro
150                 155                 160                 165

ttg cac gta aaa gga cgc ggt ccg aga gac aca tac gga tagtttggtg    644
Leu His Val Lys Gly Arg Gly Pro Arg Asp Thr Tyr Gly
                170                 175

ataaaaaccg tcg                                                   657


<210> 760
<211> 178
<212> PRT
<213> Corynebacterium glutamicum

<400> 760
Met Thr Asp Pro Ile Glu Gln Ala Phe Glu Arg Ile Arg Ala Glu Ala
  1               5                  10                  15

Met Arg Arg Asn Gly Ser Val Pro Asp Leu Asn Lys Asn Asp Ala Phe
             20                  25                  30

Arg Arg Pro Pro Ala Pro Lys Gly Gly Val Glu Lys Arg Lys Lys Gly
         35                  40                  45

Arg Ala Ser Gly Leu Asp Gly Arg Gln Lys Arg Tyr Val Arg Gly Ala
     50                  55                  60

Glu Ser Leu Gly Ser Val Leu Asn Lys Glu Ile Gln Arg Arg Gly Trp
 65                  70                  75                  80

Gly Lys Asp Ile Ala Gly Gly Trp Val Thr Ser Asn Trp Glu Glu Leu
                 85                  90                  95

Val Gly Ala Lys Ile Ala Gln His Thr Arg Val Glu Met Ile Lys Asp
            100                 105                 110

Lys Lys Leu Phe Ile Thr Cys Asp Ser Thr Ala Trp Ala Thr Asn Leu
        115                 120                 125

Arg Met Met Gln Arg Gln Ile Leu Gln Val Ile Ala Glu Lys Val Gly
    130                 135                 140
```

```
Pro Asn Ile Ile Thr Glu Leu Arg Ile Phe Gly Pro Gln Ala Pro Ser
145                 150                 155                 160

Trp Arg Lys Gly Pro Leu His Val Lys Gly Arg Gly Pro Arg Asp Thr
                165                 170                 175

Tyr Gly
```

<210> 761
<211> 657
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(634)
<223> FRXA01734

<400> 761

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acgatctgcc ggagaatctc aagaaagtgc tcactgcgca gcacaccgtc accgtccaag 60

acaccggcac cgggcggatt tcactcctgg atgtgcaacc atg aca gat cca att   115
                                              Met Thr Asp Pro Ile
                                                1               5

gag cag gca ttt gaa cgc atc cgc gcc gaa gcc atg cgc aga aat gga   163
Glu Gln Ala Phe Glu Arg Ile Arg Ala Glu Ala Met Arg Arg Asn Gly
                10                  15                  20

tcc gtt ccc gac ctc aat aaa aac gat gct ttt cga cgc cca cct gcg   211
Ser Val Pro Asp Leu Asn Lys Asn Asp Ala Phe Arg Arg Pro Pro Ala
            25                  30                  35

ccg aaa ggg ggc gtc gaa aag cgc aaa aaa ggc cgt gca agc ggc cta   259
Pro Lys Gly Gly Val Glu Lys Arg Lys Lys Gly Arg Ala Ser Gly Leu
        40                  45                  50

gac ggc cgc cag aaa cga tat gtg cgc ggc gcg gag tcg ctg gga tcg   307
Asp Gly Arg Gln Lys Arg Tyr Val Arg Gly Ala Glu Ser Leu Gly Ser
    55                  60                  65

gtg ctg aac aag gaa att cag cgt cgt ggc tgg ggc aaa gac att gcc   355
Val Leu Asn Lys Glu Ile Gln Arg Arg Gly Trp Gly Lys Asp Ile Ala
70                  75                  80                  85

ggc ggt tgg gtg acg tcc aac tgg gaa gag ctt gtt ggc gcg aag att   403
Gly Gly Trp Val Thr Ser Asn Trp Glu Glu Leu Val Gly Ala Lys Ile
                90                  95                  100

gcg cag cat acg cgc gtg gaa atg atc aaa gat aag aag ctt ttt atc   451
Ala Gln His Thr Arg Val Glu Met Ile Lys Asp Lys Lys Leu Phe Ile
            105                 110                 115

act tgt gat tcc aca gcg tgg gcc acc aat ctg cgc atg atg cag cgg   499
Thr Cys Asp Ser Thr Ala Trp Ala Thr Asn Leu Arg Met Met Gln Arg
        120                 125                 130

caa atc ctg cag gta atc gct gaa aaa gtg ggt cca aat att att aca   547
Gln Ile Leu Gln Val Ile Ala Glu Lys Val Gly Pro Asn Ile Ile Thr
```

```
    135                 140                 145

gag ctg cgt att ttt ggg cct cag gcc cca agc tgg cgc aag ggg ccg   595
Glu Leu Arg Ile Phe Gly Pro Gln Ala Pro Ser Trp Arg Lys Gly Pro
150                 155                 160                 165

ttg cac gta aaa gga cgc ggt ccg aga gac aca tac gga tagtttggtg   644
Leu His Val Lys Gly Arg Gly Pro Arg Asp Thr Tyr Gly
                170                 175

ataaaaaccg tcg                                                  657


<210> 762
<211> 178
<212> PRT
<213> Corynebacterium glutamicum

<400> 762
Met Thr Asp Pro Ile Glu Gln Ala Phe Glu Arg Ile Arg Ala Glu Ala
  1               5                  10                  15

Met Arg Arg Asn Gly Ser Val Pro Asp Leu Asn Lys Asn Asp Ala Phe
             20                  25                  30

Arg Arg Pro Pro Ala Pro Lys Gly Gly Val Glu Lys Arg Lys Lys Gly
         35                  40                  45

Arg Ala Ser Gly Leu Asp Gly Arg Gln Lys Arg Tyr Val Arg Gly Ala
     50                  55                  60

Glu Ser Leu Gly Ser Val Leu Asn Lys Glu Ile Gln Arg Arg Gly Trp
 65                  70                  75                  80

Gly Lys Asp Ile Ala Gly Gly Trp Val Thr Ser Asn Trp Glu Glu Leu
                 85                  90                  95

Val Gly Ala Lys Ile Ala Gln His Thr Arg Val Glu Met Ile Lys Asp
            100                 105                 110

Lys Lys Leu Phe Ile Thr Cys Asp Ser Thr Ala Trp Ala Thr Asn Leu
        115                 120                 125

Arg Met Met Gln Arg Gln Ile Leu Gln Val Ile Ala Glu Lys Val Gly
    130                 135                 140

Pro Asn Ile Ile Thr Glu Leu Arg Ile Phe Gly Pro Gln Ala Pro Ser
145                 150                 155                 160

Trp Arg Lys Gly Pro Leu His Val Lys Gly Arg Gly Pro Arg Asp Thr
                165                 170                 175

Tyr Gly


<210> 763
<211> 627
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(604)
<223> RXN01742

<400> 763
tggctaaagc gatgtgtgtc atctgaaaaa tttcccccaa aacttaatcg acacagttac 60

ttcatctggc cttatttcat cacagttaca atcatctgtc atg cag gaa aag cca 115
Met Gln Glu Lys Pro
1 5

gag atg cca gcg att gag gtc atc cgt tca gcg aaa cgc acc aaa act 163
Glu Met Pro Ala Ile Glu Val Ile Arg Ser Ala Lys Arg Thr Lys Thr
10 15 20

gtt caa gct cga att gtg gac ggg caa atc cag gtg cgc atc cct gcg 211
Val Gln Ala Arg Ile Val Asp Gly Gln Ile Gln Val Arg Ile Pro Ala
25 30 35

agg atg tct aaa gcg gag gaa gaa aaa gcg gtg ggg gag atc gtc gca 259
Arg Met Ser Lys Ala Glu Glu Glu Lys Ala Val Gly Glu Ile Val Ala
40 45 50

aag cta aag cga cgc acc caa tcg gcc gtc tca agc gac gct gac ctg 307
Lys Leu Lys Arg Arg Thr Gln Ser Ala Val Ser Ser Asp Ala Asp Leu
55 60 65

att gag cgc gcc cat aag ttg aac aag act gtg ttg gag ggg cgg gcg 355
Ile Glu Arg Ala His Lys Leu Asn Lys Thr Val Leu Glu Gly Arg Ala
70 75 80 85

cgg gtg gaa agt att cgg tgg gtg agt aat cag aag ggg cgg tgg ggg 403
Arg Val Glu Ser Ile Arg Trp Val Ser Asn Gln Lys Gly Arg Trp Gly
90 95 100

tcg tgc acg gtg gcg act gcg gag att cgg att tcg gat cgt tta aag 451
Ser Cys Thr Val Ala Thr Ala Glu Ile Arg Ile Ser Asp Arg Leu Lys
105 110 115

cac gtg ccg gat tat gtg ttg gat gcg gtg ttg gtg cat gag ctg acg 499
His Val Pro Asp Tyr Val Leu Asp Ala Val Leu Val His Glu Leu Thr
120 125 130

cat acg ttt att gcg ggg cat tcg gcg gag ttt tgg gag tgg gca gac 547
His Thr Phe Ile Ala Gly His Ser Ala Glu Phe Trp Glu Trp Ala Asp
135 140 145

aaa acg ccc ctg gca gag agg gcc aag ggc tat ttg gag gcg tat cag 595
Lys Thr Pro Leu Ala Glu Arg Ala Lys Gly Tyr Leu Glu Ala Tyr Gln
150 155 160 165

cgg tgg ggc tgaaggttta gttcttgtcg gag 627
Arg Trp Gly

<210> 764
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 764
Met Gln Glu Lys Pro Glu Met Pro Ala Ile Glu Val Ile Arg Ser Ala
1 5 10 15

Lys Arg Thr Lys Thr Val Gln Ala Arg Ile Val Asp Gly Gln Ile Gln
20 25 30

Val Arg Ile Pro Ala Arg Met Ser Lys Ala Glu Glu Glu Lys Ala Val
35 40 45

Gly Glu Ile Val Ala Lys Leu Lys Arg Arg Thr Gln Ser Ala Val Ser
50 55 60

Ser Asp Ala Asp Leu Ile Glu Arg Ala His Lys Leu Asn Lys Thr Val
65 70 75 80

Leu Glu Gly Arg Ala Arg Val Glu Ser Ile Arg Trp Val Ser Asn Gln
85 90 95

Lys Gly Arg Trp Gly Ser Cys Thr Val Ala Thr Ala Glu Ile Arg Ile
100 105 110

Ser Asp Arg Leu Lys His Val Pro Asp Tyr Val Leu Asp Ala Val Leu
115 120 125

Val His Glu Leu Thr His Thr Phe Ile Ala Gly His Ser Ala Glu Phe
130 135 140

Trp Glu Trp Ala Asp Lys Thr Pro Leu Ala Glu Arg Ala Lys Gly Tyr
145 150 155 160

Leu Glu Ala Tyr Gln Arg Trp Gly
165

<210> 765
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> FRXA01742

<400> 765
tggctaaagc gatgtgtgtc atctgaaaaa tttcccccaa aacttaatcg acacagttac 60

ttcatctggc cttatttcat cacagttaca atcatctgtc atg cag gaa aag cca 115
Met Gln Glu Lys Pro
1 5

gag atg cca gcg att gag gtc atc cgt tca gcg aaa cgc acc aaa act 163
Glu Met Pro Ala Ile Glu Val Ile Arg Ser Ala Lys Arg Thr Lys Thr
10 15 20

gtt caa gct cga att gtg gac ggg caa atc cag gtg cgc atc cct gcg 211
Val Gln Ala Arg Ile Val Asp Gly Gln Ile Gln Val Arg Ile Pro Ala
25 30 35

```
agg atg tct aaa gcg gag gaa gaa aaa gcg gtg ggg gag atc gtc gca   259
Arg Met Ser Lys Ala Glu Glu Lys Ala Val Gly Glu Ile Val Ala
         40                  45                  50

aag cta aag cga cgc acc caa tcg gcc gtc tca agc gac gct gac ctg   307
Lys Leu Lys Arg Arg Thr Gln Ser Ala Val Ser Ser Asp Ala Asp Leu
     55                  60                  65

att gag cgc gcc cat aag ttg aac aag act gtg ttg gag ggg cgg gcg   355
Ile Glu Arg Ala His Lys Leu Asn Lys Thr Val Leu Glu Gly Arg Ala
 70                  75                  80                  85

cgg gtg gaa agt att cgg tgg gtg agt aat cag aag ggg cgg tgg ggg   403
Arg Val Glu Ser Ile Arg Trp Val Ser Asn Gln Lys Gly Arg Trp Gly
                 90                  95                 100

tcg tgc acg gtg gcg act gcg gag att cgg att tcg gat cgt tta aag   451
Ser Cys Thr Val Ala Thr Ala Glu Ile Arg Ile Ser Asp Arg Leu Lys
            105                 110                 115

cac gtg ccg gat tat gtg ttg gat gcg gtg ttg gtg cat gag ctg acg   499
His Val Pro Asp Tyr Val Leu Asp Ala Val Leu Val His Glu Leu Thr
        120                 125                 130

cat acg ttt att gcg ggg cat tcg gcg gag ttt tgg gag tgg gca gac   547
His Thr Phe Ile Ala Gly His Ser Ala Glu Phe Trp Glu Trp Ala Asp
    135                 140                 145

aaa acg ccc ctg gca gag agg gcc aag ggc tat ttg gag gcg tat cag   595
Lys Thr Pro Leu Ala Glu Arg Ala Lys Gly Tyr Leu Glu Ala Tyr Gln
150                 155                 160                 165

cgg tgg ggc tgaaggttta gttcttgtcg gag                            627
Arg Trp Gly
```

<210> 766
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 766

```
Met Gln Glu Lys Pro Glu Met Pro Ala Ile Glu Val Ile Arg Ser Ala
  1               5                  10                  15

Lys Arg Thr Lys Thr Val Gln Ala Arg Ile Val Asp Gly Gln Ile Gln
             20                  25                  30

Val Arg Ile Pro Ala Arg Met Ser Lys Ala Glu Glu Glu Lys Ala Val
         35                  40                  45

Gly Glu Ile Val Ala Lys Leu Lys Arg Arg Thr Gln Ser Ala Val Ser
     50                  55                  60

Ser Asp Ala Asp Leu Ile Glu Arg Ala His Lys Leu Asn Lys Thr Val
 65                  70                  75                  80

Leu Glu Gly Arg Ala Arg Val Glu Ser Ile Arg Trp Val Ser Asn Gln
                 85                  90                  95
```

```
Lys Gly Arg Trp Gly Ser Cys Thr Val Ala Thr Ala Glu Ile Arg Ile
            100                 105                 110

Ser Asp Arg Leu Lys His Val Pro Asp Tyr Val Leu Asp Ala Val Leu
        115                 120                 125

Val His Glu Leu Thr His Thr Phe Ile Ala Gly His Ser Ala Glu Phe
    130                 135                 140

Trp Glu Trp Ala Asp Lys Thr Pro Leu Ala Glu Arg Ala Lys Gly Tyr
145                 150                 155                 160

Leu Glu Ala Tyr Gln Arg Trp Gly
                165


<210> 767
<211> 2064
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2041)
<223> RXN01754

<400> 767
tgtggctgaa gacaagaatg aatagcattc atctcgtcga atttcatgta gaaatttgtc 60

ccccttttttt ttgatgtgaa agttgaatcg gtaagctcct gtg aaa att aaa tcc   115
                                              Val Lys Ile Lys Ser
                                                1               5

gta ttt ttg agc acc gct tta agc gct tcc tta ctg ctc gga atc acc   163
Val Phe Leu Ser Thr Ala Leu Ser Ala Ser Leu Leu Leu Gly Ile Thr
                10                  15                  20

cca ccc gtg ctg gga gca acg atc aac ccc agt ttg cct ctt tct gcg   211
Pro Pro Val Leu Gly Ala Thr Ile Asn Pro Ser Leu Pro Leu Ser Ala
            25                  30                  35

ttg agc tcc tcg gac gat atc gcc gta ccc aac ttc gcc aaa gaa tta   259
Leu Ser Ser Ser Asp Asp Ile Ala Val Pro Asn Phe Ala Lys Glu Leu
        40                  45                  50

ccg tta gct ttt gat gta cca gca ggc act gtt ccc caa agc ttg agt   307
Pro Leu Ala Phe Asp Val Pro Ala Gly Thr Val Pro Gln Ser Leu Ser
    55                  60                  65

gga acg ctg cag att cct gcc gag ttt tct ggc ggc gtc gtg gag ttt   355
Gly Thr Leu Gln Ile Pro Ala Glu Phe Ser Gly Gly Val Val Glu Phe
70                  75                  80                  85

tat gac ggt gac cgg ctc ttt cac acc ctg cgc cta gaa gtt aat gat   403
Tyr Asp Gly Asp Arg Leu Phe His Thr Leu Arg Leu Glu Val Asn Asp
                90                  95                  100

tcc cga gca cac att gag gtt ccg ctg caa agc gtt cct gtc gaa gac   451
Ser Arg Ala His Ile Glu Val Pro Leu Gln Ser Val Pro Val Glu Asp
            105                 110                 115
```

```
ggc cgc gcc acc ttt tgg ttg cgc gcc atg ttg gat cct gta aac aac   499
Gly Arg Ala Thr Phe Trp Leu Arg Ala Met Leu Asp Pro Val Asn Asn
        120                 125                 130

cag tgg tgc tac gag gag cag gaa gtc cgc ttc tta gac gga aac gtc   547
Gln Trp Cys Tyr Glu Glu Gln Glu Val Arg Phe Leu Asp Gly Asn Val
    135                 140                 145

acc ttt gaa ggg gcg acg att aac cca gct gtg gtg gct gat tac ttc   595
Thr Phe Glu Gly Ala Thr Ile Asn Pro Ala Val Val Ala Asp Tyr Phe
150                 155                 160                 165

ccg tca gtg ctg cgc gcg ttg aca att tac gtc ccg gaa aac ccc tct   643
Pro Ser Val Leu Arg Ala Leu Thr Ile Tyr Val Pro Glu Asn Pro Ser
                170                 175                 180

gag gca gta caa gaa gcc acg tta gag gtt gcg acc tcc ctg gat tcg   691
Glu Ala Val Gln Glu Ala Thr Leu Glu Val Ala Thr Ser Leu Asp Ser
            185                 190                 195

gtg tac cga aga tca ggt ctg gat gtc aac gta gaa acg ctt cca acc   739
Val Tyr Arg Arg Ser Gly Leu Asp Val Asn Val Glu Thr Leu Pro Thr
        200                 205                 210

ggc acc gat gct cct cct aca cgt cct caa gat ttt gaa cgc cag att   787
Gly Thr Asp Ala Pro Pro Thr Arg Pro Gln Asp Phe Glu Arg Gln Ile
    215                 220                 225

gtg ctg gtt gac gag gca aca gaa agt aac acg caa aaa acc gaa ttg   835
Val Leu Val Asp Glu Ala Thr Glu Ser Asn Thr Gln Lys Thr Glu Leu
230                 235                 240                 245

gtc aat ccc ggc caa gac aat gca ttc ttg cgc ctg aac ggc aac gcc   883
Val Asn Pro Gly Gln Asp Asn Ala Phe Leu Arg Leu Asn Gly Asn Ala
                250                 255                 260

gac gag ctt tac gat caa gcg cgc ttg ctt acc gac gca acc ctg cca   931
Asp Glu Leu Tyr Asp Gln Ala Arg Leu Leu Thr Asp Ala Thr Leu Pro
            265                 270                 275

ctt gcc gta gac acc gaa gta acg gcc tca ggt ttt ggt gat gtg ccc   979
Leu Ala Val Asp Thr Glu Val Thr Ala Ser Gly Phe Gly Asp Val Pro
        280                 285                 290

aac ctt tct aca gat gtg gcc acc ctc caa gaa ctg ggt atc acg cag  1027
Asn Leu Ser Thr Asp Val Ala Thr Leu Gln Glu Leu Gly Ile Thr Gln
    295                 300                 305

ctc acc tct gaa tca gtt gcg cgc aca agc gtc acc ttg ggc att gaa  1075
Leu Thr Ser Glu Ser Val Ala Arg Thr Ser Val Thr Leu Gly Ile Glu
310                 315                 320                 325

cgc tcc cgc ctg cgg acc tac tcg cag tcc atg gac ctg cac ata acg  1123
Arg Ser Arg Leu Arg Thr Tyr Ser Gln Ser Met Asp Leu His Ile Thr
                330                 335                 340

gga acc tac acc cca ttg cca ccc caa aat gca gga cag atc acg ttc  1171
Gly Thr Tyr Thr Pro Leu Pro Pro Gln Asn Ala Gly Gln Ile Thr Phe
            345                 350                 355

tcc att ggt gac acc gtg ttg gac tcc ttg acc acc gat gac act ggc  1219
```

```
Ser Ile Gly Asp Thr Val Leu Asp Ser Leu Thr Thr Asp Asp Thr Gly
        360                 365                 370

atc att gac cgt gag ttc aac gtt cct gga gac ttg gtc aac cgc tac   1267
Ile Ile Asp Arg Glu Phe Asn Val Pro Gly Asp Leu Val Asn Arg Tyr
    375                 380                 385

acg gcg atc gtc gtg gaa ttc acc agc acc ggc gac gtt aat tgt ggg   1315
Thr Ala Ile Val Val Glu Phe Thr Ser Thr Gly Asp Val Asn Cys Gly
390                 395                 400                 405

gtc acc cag ccc gta ggc ctc aac att gat tcc gac agc ctt gtc acc   1363
Val Thr Gln Pro Val Gly Leu Asn Ile Asp Ser Asp Ser Leu Val Thr
                410                 415                 420

tcc caa cat tca gat gtt cct gta ctc aac ggc ttc cgg tcc cta ccg   1411
Ser Gln His Ser Asp Val Pro Val Leu Asn Gly Phe Arg Ser Leu Pro
            425                 430                 435

cag tcc ttc caa cct cgt gtg gac gtg gcg ttt gct gat ccc agc gtg   1459
Gln Ser Phe Gln Pro Arg Val Asp Val Ala Phe Ala Asp Pro Ser Val
        440                 445                 450

cag gaa ctc tcc cgc gct gtc agc gta gtg ttg gga att caa tct atg   1507
Gln Glu Leu Ser Arg Ala Val Ser Val Val Leu Gly Ile Gln Ser Met
    455                 460                 465

agc tcc cag cgc atc cgc cca cac ctg gtt aac tgg gat gaa gcc gta   1555
Ser Ser Gln Arg Ile Arg Pro His Leu Val Asn Trp Asp Glu Ala Val
470                 475                 480                 485

gcc agc gag cgc cca aca att ttc att gat gct gcg ggc gca aag act   1603
Ala Ser Glu Arg Pro Thr Ile Phe Ile Asp Ala Ala Gly Ala Lys Thr
                490                 495                 500

gat caa gtg cca agc tac ctc gcc caa caa ggc caa acc cta gag atc   1651
Asp Gln Val Pro Ser Tyr Leu Ala Gln Gln Gly Gln Thr Leu Glu Ile
            505                 510                 515

acc agc aag aac gac caa aat gcg gac ggc gaa caa ctc acc cga tcc   1699
Thr Ser Lys Asn Asp Gln Asn Ala Asp Gly Glu Gln Leu Thr Arg Ser
        520                 525                 530

ctg caa acc aac gct gcg ctt gtt gtc ggt tcc att cag gcc gtg tgg   1747
Leu Gln Thr Asn Ala Ala Leu Val Val Gly Ser Ile Gln Ala Val Trp
    535                 540                 545

gat gcc gat aag aag cgc acg gtg att gtg gca agt tcc cag gac aac   1795
Asp Ala Asp Lys Lys Arg Thr Val Ile Val Ala Ser Ser Gln Asp Asn
550                 555                 560                 565

ccc ccc gat ttg gat gcc ttg att tcg tgg atg gga gaa gac cgc gaa   1843
Pro Pro Asp Leu Asp Ala Leu Ile Ser Trp Met Gly Glu Asp Arg Glu
                570                 575                 580

cgc tgg agt gat ctc aac ggc gac ctg att gtc aaa gtc cga gac cgc   1891
Arg Trp Ser Asp Leu Asn Gly Asp Leu Ile Val Lys Val Arg Asp Arg
            585                 590                 595

gaa cct gtg caa ttg acc acc gtg gaa gcc cca gat cag cct ggt cga   1939
Glu Pro Val Gln Leu Thr Thr Val Glu Ala Pro Asp Gln Pro Gly Arg
```

```
        600                 605                 610

tcg gcc aca gcc ttt att gcg atc ggc gtc agc ctt gtg gtc att gcc   1987
Ser Ala Thr Ala Phe Ile Ala Ile Gly Val Ser Leu Val Val Ile Ala
    615                 620                 625

ctg att gtc gca gcc gtg gtg tca gtg tcc agg cgt tcg caa aaa gga   2035
Leu Ile Val Ala Ala Val Val Ser Val Ser Arg Arg Ser Gln Lys Gly
630                 635                 640                 645

tac aaa tgatttcttc tttacccagt aga                                 2064
Tyr Lys
```

<210> 768
<211> 647
<212> PRT
<213> Corynebacterium glutamicum

<400> 768

```
Val Lys Ile Lys Ser Val Phe Leu Ser Thr Ala Leu Ser Ala Ser Leu
  1               5                  10                  15

Leu Leu Gly Ile Thr Pro Pro Val Leu Gly Ala Thr Ile Asn Pro Ser
             20                  25                  30

Leu Pro Leu Ser Ala Leu Ser Ser Ser Asp Asp Ile Ala Val Pro Asn
         35                  40                  45

Phe Ala Lys Glu Leu Pro Leu Ala Phe Asp Val Pro Ala Gly Thr Val
     50                  55                  60

Pro Gln Ser Leu Ser Gly Thr Leu Gln Ile Pro Ala Glu Phe Ser Gly
 65                  70                  75                  80

Gly Val Val Glu Phe Tyr Asp Gly Asp Arg Leu Phe His Thr Leu Arg
                 85                  90                  95

Leu Glu Val Asn Asp Ser Arg Ala His Ile Glu Val Pro Leu Gln Ser
            100                 105                 110

Val Pro Val Glu Asp Gly Arg Ala Thr Phe Trp Leu Arg Ala Met Leu
        115                 120                 125

Asp Pro Val Asn Asn Gln Trp Cys Tyr Glu Glu Gln Glu Val Arg Phe
    130                 135                 140

Leu Asp Gly Asn Val Thr Phe Glu Gly Ala Thr Ile Asn Pro Ala Val
145                 150                 155                 160

Val Ala Asp Tyr Phe Pro Ser Val Leu Arg Ala Leu Thr Ile Tyr Val
                165                 170                 175

Pro Glu Asn Pro Ser Glu Ala Val Gln Glu Ala Thr Leu Glu Val Ala
            180                 185                 190

Thr Ser Leu Asp Ser Val Tyr Arg Arg Ser Gly Leu Asp Val Asn Val
        195                 200                 205

Glu Thr Leu Pro Thr Gly Thr Asp Ala Pro Pro Thr Arg Pro Gln Asp
```

```
    210                 215                 220

Phe Glu Arg Gln Ile Val Leu Val Asp Glu Ala Thr Glu Ser Asn Thr
225                 230                 235                 240

Gln Lys Thr Glu Leu Val Asn Pro Gly Gln Asp Asn Ala Phe Leu Arg
                245                 250                 255

Leu Asn Gly Asn Ala Asp Glu Leu Tyr Asp Gln Ala Arg Leu Leu Thr
            260                 265                 270

Asp Ala Thr Leu Pro Leu Ala Val Asp Thr Glu Val Thr Ala Ser Gly
        275                 280                 285

Phe Gly Asp Val Pro Asn Leu Ser Thr Asp Val Ala Thr Leu Gln Glu
    290                 295                 300

Leu Gly Ile Thr Gln Leu Thr Ser Glu Ser Val Ala Arg Thr Ser Val
305                 310                 315                 320

Thr Leu Gly Ile Glu Arg Ser Arg Leu Arg Thr Tyr Ser Gln Ser Met
                325                 330                 335

Asp Leu His Ile Thr Gly Thr Tyr Thr Pro Leu Pro Pro Gln Asn Ala
            340                 345                 350

Gly Gln Ile Thr Phe Ser Ile Gly Asp Thr Val Leu Asp Ser Leu Thr
        355                 360                 365

Thr Asp Asp Thr Gly Ile Ile Asp Arg Glu Phe Asn Val Pro Gly Asp
    370                 375                 380

Leu Val Asn Arg Tyr Thr Ala Ile Val Val Glu Phe Thr Ser Thr Gly
385                 390                 395                 400

Asp Val Asn Cys Gly Val Thr Gln Pro Val Gly Leu Asn Ile Asp Ser
                405                 410                 415

Asp Ser Leu Val Thr Ser Gln His Ser Asp Val Pro Val Leu Asn Gly
            420                 425                 430

Phe Arg Ser Leu Pro Gln Ser Phe Gln Pro Arg Val Asp Val Ala Phe
        435                 440                 445

Ala Asp Pro Ser Val Gln Glu Leu Ser Arg Ala Val Ser Val Val Leu
    450                 455                 460

Gly Ile Gln Ser Met Ser Ser Gln Arg Ile Arg Pro His Leu Val Asn
465                 470                 475                 480

Trp Asp Glu Ala Val Ala Ser Glu Arg Pro Thr Ile Phe Ile Asp Ala
                485                 490                 495

Ala Gly Ala Lys Thr Asp Gln Val Pro Ser Tyr Leu Ala Gln Gln Gly
            500                 505                 510

Gln Thr Leu Glu Ile Thr Ser Lys Asn Asp Gln Asn Ala Asp Gly Glu
        515                 520                 525

Gln Leu Thr Arg Ser Leu Gln Thr Asn Ala Ala Leu Val Val Gly Ser
    530                 535                 540
```

```
Ile Gln Ala Val Trp Asp Ala Asp Lys Lys Arg Thr Val Ile Val Ala
545                 550                 555                 560

Ser Ser Gln Asp Asn Pro Pro Asp Leu Asp Ala Leu Ile Ser Trp Met
                565                 570                 575

Gly Glu Asp Arg Glu Arg Trp Ser Asp Leu Asn Gly Asp Leu Ile Val
            580                 585                 590

Lys Val Arg Asp Arg Glu Pro Val Gln Leu Thr Thr Val Glu Ala Pro
        595                 600                 605

Asp Gln Pro Gly Arg Ser Ala Thr Ala Phe Ile Ala Ile Gly Val Ser
    610                 615                 620

Leu Val Val Ile Ala Leu Ile Val Ala Ala Val Val Ser Val Ser Arg
625                 630                 635                 640

Arg Ser Gln Lys Gly Tyr Lys
                645
```

<210> 769
<211> 2064
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2041)
<223> FRXA01754

<400> 769

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tgtggctgaa gacaagaatg aatagcattc atctcgtcga atttcatgta gaaatttgtc 60

ccccttttt ttgatgtgaa agttgaatcg gtaagctcct gtg aaa att aaa tcc   115
                                            Val Lys Ile Lys Ser
                                              1               5

gta ttt ttg agc acc gct tta agc gct tcc tta ctg ctc gga atc acc   163
Val Phe Leu Ser Thr Ala Leu Ser Ala Ser Leu Leu Leu Gly Ile Thr
                 10                  15                  20

cca ccc gtg ctg gga gca acg atc aac ccc agt ttg cct ctt tct gcg   211
Pro Pro Val Leu Gly Ala Thr Ile Asn Pro Ser Leu Pro Leu Ser Ala
             25                  30                  35

ttg agc tcc tcg gac gat atc gcc gta ccc aac ttc gcc aaa gaa tta   259
Leu Ser Ser Ser Asp Asp Ile Ala Val Pro Asn Phe Ala Lys Glu Leu
         40                  45                  50

ccg tta gct ttt gat gta cca gca ggc act gtt ccc caa agc ttg agt   307
Pro Leu Ala Phe Asp Val Pro Ala Gly Thr Val Pro Gln Ser Leu Ser
     55                  60                  65

gga acg ctg cag att cct gcc gag ttt tct ggc ggc gtc gtg gag ttt   355
Gly Thr Leu Gln Ile Pro Ala Glu Phe Ser Gly Gly Val Val Glu Phe
 70                  75                  80                  85

tat gac ggt gac cgg ctc ttt cac acc ctg cgc cta gaa gtt aat gat   403
```

```
Tyr Asp Gly Asp Arg Leu Phe His Thr Leu Arg Leu Glu Val Asn Asp
                 90                  95                 100

tcc cga gca cac att gag gtt ccg ctg caa agc gtt cct gtc gaa gac   451
Ser Arg Ala His Ile Glu Val Pro Leu Gln Ser Val Pro Val Glu Asp
            105                 110                 115

ggc cgc gcc acc ttt tgg ttg cgc gcc atg ttg gat cct gta aac aac   499
Gly Arg Ala Thr Phe Trp Leu Arg Ala Met Leu Asp Pro Val Asn Asn
        120                 125                 130

cag tgg tgc tac gag gag cag gaa gtc cgc ttc tta gac gga aac gtc   547
Gln Trp Cys Tyr Glu Glu Gln Glu Val Arg Phe Leu Asp Gly Asn Val
    135                 140                 145

acc ttt gaa ggg gcg acg att aac cca gct gtg gtg gct gat tac ttc   595
Thr Phe Glu Gly Ala Thr Ile Asn Pro Ala Val Val Ala Asp Tyr Phe
150                 155                 160                 165

ccg tca gtg ctg cgc gcg ttg aca att tac gtc ccg gaa aac ccc tct   643
Pro Ser Val Leu Arg Ala Leu Thr Ile Tyr Val Pro Glu Asn Pro Ser
                170                 175                 180

gag gca gta caa gaa gcc acg tta gag gtt gcg acc tcc ctg gat tcg   691
Glu Ala Val Gln Glu Ala Thr Leu Glu Val Ala Thr Ser Leu Asp Ser
            185                 190                 195

gtg tac cga aga tca ggt ctg gat gtc aac gta gaa acg ctt cca acc   739
Val Tyr Arg Arg Ser Gly Leu Asp Val Asn Val Glu Thr Leu Pro Thr
        200                 205                 210

ggc acc gat gct cct cct aca cgt cct caa gat ttt gaa cgc cag att   787
Gly Thr Asp Ala Pro Pro Thr Arg Pro Gln Asp Phe Glu Arg Gln Ile
    215                 220                 225

gtg ctg gtt gac gag gca aca gaa agt aac acg caa aaa acc gaa ttg   835
Val Leu Val Asp Glu Ala Thr Glu Ser Asn Thr Gln Lys Thr Glu Leu
230                 235                 240                 245

gtc aat ccc ggc caa gac aat gca ttc ttg cgc ctg aac ggc aac gcc   883
Val Asn Pro Gly Gln Asp Asn Ala Phe Leu Arg Leu Asn Gly Asn Ala
                250                 255                 260

gac gag ctt tac gat caa gcg cgc ttg ctt acc gac gca acc ctg cca   931
Asp Glu Leu Tyr Asp Gln Ala Arg Leu Leu Thr Asp Ala Thr Leu Pro
            265                 270                 275

ctt gcc gta gac acc gaa gta acg gcc tca ggt ttt ggt gat gtg ccc   979
Leu Ala Val Asp Thr Glu Val Thr Ala Ser Gly Phe Gly Asp Val Pro
        280                 285                 290

aac ctt tct aca gat gtg gcc acc ctc caa gaa ctg ggt atc acg cag   1027
Asn Leu Ser Thr Asp Val Ala Thr Leu Gln Glu Leu Gly Ile Thr Gln
    295                 300                 305

ctc acc tct gaa tca gtt gcg cgc aca agc gtc acc ttg ggc att gaa   1075
Leu Thr Ser Glu Ser Val Ala Arg Thr Ser Val Thr Leu Gly Ile Glu
310                 315                 320                 325

cgc tcc cgc ctg cgg acc tac tcg cag tcc atg gac ctg cac ata acg   1123
Arg Ser Arg Leu Arg Thr Tyr Ser Gln Ser Met Asp Leu His Ile Thr
```

```
                  330                 335                 340

gga acc tac acc cca ttg cca ccc caa aat gca gga cag atc acg ttc   1171
Gly Thr Tyr Thr Pro Leu Pro Pro Gln Asn Ala Gly Gln Ile Thr Phe
            345                 350                 355

tcc att ggt gac acc gtg ttg gac tcc ttg acc acc gat gac act ggc   1219
Ser Ile Gly Asp Thr Val Leu Asp Ser Leu Thr Thr Asp Asp Thr Gly
        360                 365                 370

atc att gac cgt gag ttc aac gtt cct gga gac ttg gtc aac cgc tac   1267
Ile Ile Asp Arg Glu Phe Asn Val Pro Gly Asp Leu Val Asn Arg Tyr
    375                 380                 385

acg gcg atc gtc gtg gaa ttc acc agc acc ggc gac gtt aat tgt ggg   1315
Thr Ala Ile Val Val Glu Phe Thr Ser Thr Gly Asp Val Asn Cys Gly
390                 395                 400                 405

gtc acc cag ccc gta ggc ctc aac att gat tcc gac agc ctt gtc acc   1363
Val Thr Gln Pro Val Gly Leu Asn Ile Asp Ser Asp Ser Leu Val Thr
                410                 415                 420

tcc caa cat tca gat gtt cct gta ctc aac ggc ttc cgg tcc cta ccg   1411
Ser Gln His Ser Asp Val Pro Val Leu Asn Gly Phe Arg Ser Leu Pro
            425                 430                 435

cag tcc ttc caa cct cgt gtg gac gtg gcg ttt gct gat ccc agc gtg   1459
Gln Ser Phe Gln Pro Arg Val Asp Val Ala Phe Ala Asp Pro Ser Val
        440                 445                 450

cag gaa ctc tcc cgc gct gtc agc gta gtg ttg gga att caa tct atg   1507
Gln Glu Leu Ser Arg Ala Val Ser Val Val Leu Gly Ile Gln Ser Met
    455                 460                 465

agc tcc cag cgc atc cgc cca cac ctg gtt aac tgg gat gaa gcc gta   1555
Ser Ser Gln Arg Ile Arg Pro His Leu Val Asn Trp Asp Glu Ala Val
470                 475                 480                 485

gcc agc gag cgc cca aca att ttc att gat gct gcg ggc gca aag act   1603
Ala Ser Glu Arg Pro Thr Ile Phe Ile Asp Ala Ala Gly Ala Lys Thr
                490                 495                 500

gat caa gtg cca agc tac ctc gcc caa caa ggc caa acc cta gag atc   1651
Asp Gln Val Pro Ser Tyr Leu Ala Gln Gln Gly Gln Thr Leu Glu Ile
            505                 510                 515

acc agc aag aac gac caa aat gcg gac ggc gaa caa ctc acc cga tcc   1699
Thr Ser Lys Asn Asp Gln Asn Ala Asp Gly Glu Gln Leu Thr Arg Ser
        520                 525                 530

ctg caa acc aac gct gcg ctt gtt gtc ggt tcc att cag gcc gtg tgg   1747
Leu Gln Thr Asn Ala Ala Leu Val Val Gly Ser Ile Gln Ala Val Trp
    535                 540                 545

gat gcc gat aag aag cgc acg gtg att gtg gca agt tcc cag gac aac   1795
Asp Ala Asp Lys Lys Arg Thr Val Ile Val Ala Ser Ser Gln Asp Asn
550                 555                 560                 565

ccc ccc gat ttg gat gcc ttg att tcg tgg atg gga gaa gac cgc gaa   1843
Pro Pro Asp Leu Asp Ala Leu Ile Ser Trp Met Gly Glu Asp Arg Glu
                570                 575                 580
```

```
cgc tgg agt gat ctc aac ggc gac ctg att gtc aaa gtc cga gac cgc   1891
Arg Trp Ser Asp Leu Asn Gly Asp Leu Ile Val Lys Val Arg Asp Arg
            585                 590                 595

gaa cct gtg caa ttg acc acc gtg gaa gcc cca gat cag cct ggt cga   1939
Glu Pro Val Gln Leu Thr Thr Val Glu Ala Pro Asp Gln Pro Gly Arg
        600                 605                 610

tcg gcc aca gcc ttt att gcg atc ggc gtc agc ctt gtg gtc att gcc   1987
Ser Ala Thr Ala Phe Ile Ala Ile Gly Val Ser Leu Val Val Ile Ala
    615                 620                 625

ctg att gtc gca gcc gtg gtg tca gtg tcc agg cgt tcg caa aaa gga   2035
Leu Ile Val Ala Ala Val Val Ser Val Ser Arg Arg Ser Gln Lys Gly
630                 635                 640                 645

tac aaa tgatttcttc tttacccagt aga                                 2064
Tyr Lys
```

<210> 770
<211> 647
<212> PRT
<213> Corynebacterium glutamicum

<400> 770

```
Val Lys Ile Lys Ser Val Phe Leu Ser Thr Ala Leu Ser Ala Ser Leu
  1               5                  10                  15

Leu Leu Gly Ile Thr Pro Pro Val Leu Gly Ala Thr Ile Asn Pro Ser
            20                  25                  30

Leu Pro Leu Ser Ala Leu Ser Ser Ser Asp Asp Ile Ala Val Pro Asn
        35                  40                  45

Phe Ala Lys Glu Leu Pro Leu Ala Phe Asp Val Pro Ala Gly Thr Val
    50                  55                  60

Pro Gln Ser Leu Ser Gly Thr Leu Gln Ile Pro Ala Glu Phe Ser Gly
65                  70                  75                  80

Gly Val Val Glu Phe Tyr Asp Gly Asp Arg Leu Phe His Thr Leu Arg
                85                  90                  95

Leu Glu Val Asn Asp Ser Arg Ala His Ile Glu Val Pro Leu Gln Ser
            100                 105                 110

Val Pro Val Glu Asp Gly Arg Ala Thr Phe Trp Leu Arg Ala Met Leu
        115                 120                 125

Asp Pro Val Asn Asn Gln Trp Cys Tyr Glu Glu Gln Glu Val Arg Phe
    130                 135                 140

Leu Asp Gly Asn Val Thr Phe Glu Gly Ala Thr Ile Asn Pro Ala Val
145                 150                 155                 160

Val Ala Asp Tyr Phe Pro Ser Val Leu Arg Ala Leu Thr Ile Tyr Val
                165                 170                 175
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Pro Glu Asn Pro Ser Glu Ala Val Gln Glu Ala Thr Leu Glu Val Ala
            180                 185                 190

Thr Ser Leu Asp Ser Val Tyr Arg Arg Ser Gly Leu Asp Val Asn Val
        195                 200                 205

Glu Thr Leu Pro Thr Gly Thr Asp Ala Pro Pro Thr Arg Pro Gln Asp
    210                 215                 220

Phe Glu Arg Gln Ile Val Leu Val Asp Glu Ala Thr Glu Ser Asn Thr
225                 230                 235                 240

Gln Lys Thr Glu Leu Val Asn Pro Gly Gln Asp Asn Ala Phe Leu Arg
                245                 250                 255

Leu Asn Gly Asn Ala Asp Glu Leu Tyr Asp Gln Ala Arg Leu Leu Thr
            260                 265                 270

Asp Ala Thr Leu Pro Leu Ala Val Asp Thr Glu Val Thr Ala Ser Gly
        275                 280                 285

Phe Gly Asp Val Pro Asn Leu Ser Thr Asp Val Ala Thr Leu Gln Glu
    290                 295                 300

Leu Gly Ile Thr Gln Leu Thr Ser Glu Ser Val Ala Arg Thr Ser Val
305                 310                 315                 320

Thr Leu Gly Ile Glu Arg Ser Arg Leu Arg Thr Tyr Ser Gln Ser Met
                325                 330                 335

Asp Leu His Ile Thr Gly Thr Tyr Thr Pro Leu Pro Pro Gln Asn Ala
            340                 345                 350

Gly Gln Ile Thr Phe Ser Ile Gly Asp Thr Val Leu Asp Ser Leu Thr
        355                 360                 365

Thr Asp Asp Thr Gly Ile Ile Asp Arg Glu Phe Asn Val Pro Gly Asp
    370                 375                 380

Leu Val Asn Arg Tyr Thr Ala Ile Val Val Glu Phe Thr Ser Thr Gly
385                 390                 395                 400

Asp Val Asn Cys Gly Val Thr Gln Pro Val Gly Leu Asn Ile Asp Ser
                405                 410                 415

Asp Ser Leu Val Thr Ser Gln His Ser Asp Val Pro Val Leu Asn Gly
            420                 425                 430

Phe Arg Ser Leu Pro Gln Ser Phe Gln Pro Arg Val Asp Val Ala Phe
        435                 440                 445

Ala Asp Pro Ser Val Gln Glu Leu Ser Arg Ala Val Ser Val Val Leu
    450                 455                 460

Gly Ile Gln Ser Met Ser Ser Gln Arg Ile Arg Pro His Leu Val Asn
465                 470                 475                 480

Trp Asp Glu Ala Val Ala Ser Glu Arg Pro Thr Ile Phe Ile Asp Ala
                485                 490                 495

Ala Gly Ala Lys Thr Asp Gln Val Pro Ser Tyr Leu Ala Gln Gln Gly
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            500                 505                 510

Gln Thr Leu Glu Ile Thr Ser Lys Asn Asp Gln Asn Ala Asp Gly Glu
        515                 520                 525

Gln Leu Thr Arg Ser Leu Gln Thr Asn Ala Ala Leu Val Val Gly Ser
    530                 535                 540

Ile Gln Ala Val Trp Asp Ala Asp Lys Lys Arg Thr Val Ile Val Ala
545                 550                 555                 560

Ser Ser Gln Asp Asn Pro Pro Asp Leu Asp Ala Leu Ile Ser Trp Met
                565                 570                 575

Gly Glu Asp Arg Glu Arg Trp Ser Asp Leu Asn Gly Asp Leu Ile Val
            580                 585                 590

Lys Val Arg Asp Arg Glu Pro Val Gln Leu Thr Thr Val Glu Ala Pro
        595                 600                 605

Asp Gln Pro Gly Arg Ser Ala Thr Ala Phe Ile Ala Ile Gly Val Ser
    610                 615                 620

Leu Val Val Ile Ala Leu Ile Val Ala Ala Val Val Ser Val Ser Arg
625                 630                 635                 640

Arg Ser Gln Lys Gly Tyr Lys
                645
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<210> 771
<211> 4587
<212> DNA
<213> Corynebacterium glutamicum

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<221> CDS
<222> (101)..(4564)
<223> RXN01761

<400> 771

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agcaattgtt taaaacgaat attgaggggg tggcgggcaa gtg act gcg aca gtt   115
                                            Val Thr Ala Thr Val
                                              1               5

tta gaa ccg caa cct gta cag ctt agt gag cag gac gta gat gct gag   163
Leu Glu Pro Gln Pro Val Gln Leu Ser Glu Gln Asp Val Asp Ala Glu
                 10                  15                  20

att gcg cgc atg gag ctt aaa cac aac cga cac aag acg tgg cga cgc   211
Ile Ala Arg Met Glu Leu Lys His Asn Arg His Lys Thr Trp Arg Arg
             25                  30                  35

cga acg atg gct gtt gtc atg acg ctc ttg atc tca gtg ggt ttg agc   259
Arg Thr Met Ala Val Val Met Thr Leu Leu Ile Ser Val Gly Leu Ser
         40                  45                  50

ttt ggt gcg ttt ggt aac aag gaa cgt gaa gct aat gct ttc gcc agc   307
Phe Gly Ala Phe Gly Asn Lys Glu Arg Glu Ala Asn Ala Phe Ala Ser
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     55                  60                  65

gct att att gcc cag gtt gtc ggt gct atg ggc gag gtt gcc ttt gaa   355
Ala Ile Ile Ala Gln Val Val Gly Ala Met Gly Glu Val Ala Phe Glu
 70                  75                  80                  85

gcg att tgt ccc agt gat ggt gac acc gag atg ctt ctt aag tgc atc   403
Ala Ile Cys Pro Ser Asp Gly Asp Thr Glu Met Leu Leu Lys Cys Ile
                 90                  95                 100

acc gag aac tta ggt gaa atg cac att atc gag aag tgt ctc gaa gca   451
Thr Glu Asn Leu Gly Glu Met His Ile Ile Glu Lys Cys Leu Glu Ala
            105                 110                 115

gaa gat gtc ttg aag tgc ttc tac gat gcg aaa aac gaa gag caa cgt   499
Glu Asp Val Leu Lys Cys Phe Tyr Asp Ala Lys Asn Glu Glu Gln Arg
        120                 125                 130

aaa gaa cag aac ctt gat aaa gcc cct gat tac tcc atg tac cgt atg   547
Lys Glu Gln Asn Leu Asp Lys Ala Pro Asp Tyr Ser Met Tyr Arg Met
    135                 140                 145

gcc tct gcg atg gca tcg ttc tat ggc aat ggt cgg gca gct act gcc   595
Ala Ser Ala Met Ala Ser Phe Tyr Gly Asn Gly Arg Ala Ala Thr Ala
150                 155                 160                 165

ggt gta gag gaa ggc gga ccg aac gag ttc ctc gat tct gag gac gcc   643
Gly Val Glu Glu Gly Gly Pro Asn Glu Phe Leu Asp Ser Glu Asp Ala
                170                 175                 180

ggt ctt aag gtg tgg gag ggc att ctc agt aag gcc gcc aac gga ggc   691
Gly Leu Lys Val Trp Glu Gly Ile Leu Ser Lys Ala Ala Asn Gly Gly
            185                 190                 195

aat gtc ctt ggt tat gct gac gcg aaa cac aac gag gac tct ggt tgg   739
Asn Val Leu Gly Tyr Ala Asp Ala Lys His Asn Glu Asp Ser Gly Trp
        200                 205                 210

ttc ttt ggt aat ggt gtt gcc aac aac gag aaa acg tac tcc tat gat   787
Phe Phe Gly Asn Gly Val Ala Asn Asn Glu Lys Thr Tyr Ser Tyr Asp
    215                 220                 225

tct cta gct gat cat gcc ttt caa ggg cct tat cac ttt gca tta ttt   835
Ser Leu Ala Asp His Ala Phe Gln Gly Pro Tyr His Phe Ala Leu Phe
230                 235                 240                 245

ggc gcg aca ctg agt ggc tta ggc ttt gat agc tca aag gcg gag gat   883
Gly Ala Thr Leu Ser Gly Leu Gly Phe Asp Ser Ser Lys Ala Glu Asp
                250                 255                 260

tcg cag act gat ttt gct cag cgt aag ggc atg ggg tac gcg atg atg   931
Ser Gln Thr Asp Phe Ala Gln Arg Lys Gly Met Gly Tyr Ala Met Met
            265                 270                 275

atc gcg tac atc atc tcc gga ggc att gat ctg gtt ttt aac act gtg   979
Ile Ala Tyr Ile Ile Ser Gly Gly Ile Asp Leu Val Phe Asn Thr Val
        280                 285                 290

ctg aat atc ttg agc acc ata aac cca ttt aga ctg ctc gtt gga cca   1027
Leu Asn Ile Leu Ser Thr Ile Asn Pro Phe Arg Leu Leu Val Gly Pro
    295                 300                 305
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gta tct cag aat act aac aag aca ttc act gag aat atg gct ggt ggg   1075
Val Ser Gln Asn Thr Asn Lys Thr Phe Thr Glu Asn Met Ala Gly Gly
310                 315                 320                 325

cag acc aca gaa gga aca ccg ttt gaa gga atg act gat ttc ttc ggg   1123
Gln Thr Thr Glu Gly Thr Pro Phe Glu Gly Met Thr Asp Phe Phe Gly
                330                 335                 340

ttg atc tat aac tgg tca gtg act gtg ggc tgg ctc atc ggt att cct   1171
Leu Ile Tyr Asn Trp Ser Val Thr Val Gly Trp Leu Ile Gly Ile Pro
            345                 350                 355

gtc tcc att ggt ctg ttt atg atg ggt gcg ttg atg ttt cga cgc atg   1219
Val Ser Ile Gly Leu Phe Met Met Gly Ala Leu Met Phe Arg Arg Met
        360                 365                 370

gac aag gga tca gcg ttt aaa aag gtt gtt atc cgc gtc gtg tac ggt   1267
Asp Lys Gly Ser Ala Phe Lys Lys Val Val Ile Arg Val Val Tyr Gly
    375                 380                 385

gtc gtt ggc ctg cca ctg ctt ggt gtc tct tat acc ggt gcg ctg gat   1315
Val Val Gly Leu Pro Leu Leu Gly Val Ser Tyr Thr Gly Ala Leu Asp
390                 395                 400                 405

tcc ttc ctc gac agc ggt agt tcc aca agt gct gga tca aat gcg aca   1363
Ser Phe Leu Asp Ser Gly Ser Ser Thr Ser Ala Gly Ser Asn Ala Thr
                410                 415                 420

aag att gtg ttg tcc acc tac gtg gat ttc caa tca tgg gca gaa aac   1411
Lys Ile Val Leu Ser Thr Tyr Val Asp Phe Gln Ser Trp Ala Glu Asn
            425                 430                 435

acc cgt atg cgt gtt cct gac aaa gta aca ctg gcg tgg agt ctg gag   1459
Thr Arg Met Arg Val Pro Asp Lys Val Thr Leu Ala Trp Ser Leu Glu
        440                 445                 450

gat cag gcg cca aca ggg cag tcc atg cgg atg gta cgc aat tcg gcg   1507
Asp Gln Ala Pro Thr Gly Gln Ser Met Arg Met Val Arg Asn Ser Ala
    455                 460                 465

ttg gaa att aat gct caa tca aat gag agt ttt act act ttt aag aat   1555
Leu Glu Ile Asn Ala Gln Ser Asn Glu Ser Phe Thr Thr Phe Lys Asn
470                 475                 480                 485

cca ggt tcc atg gat cta ggc tat agc atg gac tgg atg gaa aag atg   1603
Pro Gly Ser Met Asp Leu Gly Tyr Ser Met Asp Trp Met Glu Lys Met
                490                 495                 500

gcg gat cca gcc aat tct ggc acc gat ggg acc tca tca agt tcg gcg   1651
Ala Asp Pro Ala Asn Ser Gly Thr Asp Gly Thr Ser Ser Ser Ser Ala
            505                 510                 515

acg act att ttc cag gga acc atc gcg cta ctg agt cgt tat atc gac   1699
Thr Thr Ile Phe Gln Gly Thr Ile Ala Leu Leu Ser Arg Tyr Ile Asp
        520                 525                 530

aac gac agt atc tcc tct ggc agt ttc gaa acc tct att cga agt gcg   1747
Asn Asp Ser Ile Ser Ser Gly Ser Phe Glu Thr Ser Ile Arg Ser Ala
    535                 540                 545
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atg gaa tct ttg acc tcg aaa gag gga agt ggc gaa gct gtt gcc ggt   1795
Met Glu Ser Leu Thr Ser Lys Glu Gly Ser Gly Glu Ala Val Ala Gly
550                 555                 560                 565

ggt gat gta atg gcc tgg gtt act ggt tac aac aca gcc tct ggt ctt   1843
Gly Asp Val Met Ala Trp Val Thr Gly Tyr Asn Thr Ala Ser Gly Leu
                570                 575                 580

aat gag atc act gct gct gaa tta gct gat gcg aac aat cca ttg ctt   1891
Asn Glu Ile Thr Ala Ala Glu Leu Ala Asp Ala Asn Asn Pro Leu Leu
            585                 590                 595

gag gtc agc gac tca gct ggt ctg cag gga cga cct att gac cgc aat   1939
Glu Val Ser Asp Ser Ala Gly Leu Gln Gly Arg Pro Ile Asp Arg Asn
        600                 605                 610

gcg gtg tca ttt aaa tct ggt gat gcg aca gcg tca tgc aac aac tca   1987
Ala Val Ser Phe Lys Ser Gly Asp Ala Thr Ala Ser Cys Asn Asn Ser
    615                 620                 625

gtc gtg aca ggt tct cgt gct gtg gtc ggg gac tac cga agt gac tgc   2035
Val Val Thr Gly Ser Arg Ala Val Val Gly Asp Tyr Arg Ser Asp Cys
630                 635                 640                 645

aat atg tcg ccc ttg acg atg tac aac ttc ctc aac acc tca ttc cat   2083
Asn Met Ser Pro Leu Thr Met Tyr Asn Phe Leu Asn Thr Ser Phe His
                650                 655                 660

cca gct gat gca agt gtc ttt tct acg tcc act tct gcg tca agc tac   2131
Pro Ala Asp Ala Ser Val Phe Ser Thr Ser Thr Ser Ala Ser Ser Tyr
            665                 670                 675

acc cgt gca tcg cat agc gca gtg agt ctt atc ggt tct ggt gcc atg   2179
Thr Arg Ala Ser His Ser Ala Val Ser Leu Ile Gly Ser Gly Ala Met
        680                 685                 690

aac ttt gtg tac tgg ttc tct gca atg tcc ctg atg ggt agc ttc atc   2227
Asn Phe Val Tyr Trp Phe Ser Ala Met Ser Leu Met Gly Ser Phe Ile
    695                 700                 705

gtg atc ggt atc ggt tac gcc ggt gcc atg ctg ttt aat acg att cga   2275
Val Ile Gly Ile Gly Tyr Ala Gly Ala Met Leu Phe Asn Thr Ile Arg
710                 715                 720                 725

cgc acg ctg tcg ctc att ggt gcc gtt cct ttt gct gcg atg ggc ttt   2323
Arg Thr Leu Ser Leu Ile Gly Ala Val Pro Phe Ala Ala Met Gly Phe
                730                 735                 740

att gct ggt gtt gcc aag gtc att gtg tac acc atc gct atg ctc gta   2371
Ile Ala Gly Val Ala Lys Val Ile Val Tyr Thr Ile Ala Met Leu Val
            745                 750                 755

gag gtt atc gga acg atc att ttg tac cag ctc att acc cgg ttc ttg   2419
Glu Val Ile Gly Thr Ile Ile Leu Tyr Gln Leu Ile Thr Arg Phe Leu
        760                 765                 770

atg gct gta cca gca ctc ttt gaa caa cct ttg gct gat tcc tta agt   2467
Met Ala Val Pro Ala Leu Phe Glu Gln Pro Leu Ala Asp Ser Leu Ser
    775                 780                 785

agt aac gag agt gct gag ctg gtt gcc ggt gct ggt atg ggg cta gtc   2515
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Ser Asn Glu Ser Ala Glu Leu Val Ala Gly Ala Gly Met Gly Leu Val
790                 795                 800                 805

ggt atg gca cta gct acc tca ggc aac tgg gcg att gcc ggc atg gtg   2563
Gly Met Ala Leu Ala Thr Ser Gly Asn Trp Ala Ile Ala Gly Met Val
                810                 815                 820

atc aca gtg gcc tca tcc atg ggg gtc atc atc ttc acg att att gcg   2611
Ile Thr Val Ala Ser Ser Met Gly Val Ile Ile Phe Thr Ile Ile Ala
            825                 830                 835

atg aag gtg cgc gga tct ttg gta tca ggt gtc gat gaa acc gtg acc   2659
Met Lys Val Arg Gly Ser Leu Val Ser Gly Val Asp Glu Thr Val Thr
        840                 845                 850

agt gtt att aac cgc ttc ttg gat aca cag gtc tct tct gca ggt gct   2707
Ser Val Ile Asn Arg Phe Leu Asp Thr Gln Val Ser Ser Ala Gly Ala
    855                 860                 865

acc tct ggt gac ggc atg atg cgt cgt gca gcc gca acg ggt ctt ggt   2755
Thr Ser Gly Asp Gly Met Met Arg Arg Ala Ala Ala Thr Gly Leu Gly
870                 875                 880                 885

att ggt gcg aca cat atg gta ctc aac cgt gat ggt gac ggt ggt gga   2803
Ile Gly Ala Thr His Met Val Leu Asn Arg Asp Gly Asp Gly Gly Gly
                890                 895                 900

tct gat tca ggc tct ggt gga tca ggt ggc ggt agc gat tca ggc ttg   2851
Ser Asp Ser Gly Ser Gly Gly Ser Gly Gly Gly Ser Asp Ser Gly Leu
            905                 910                 915

ggt gag aag gct gct ggt ctg gcg aag gtt gtc aca act gtg gct ggt   2899
Gly Glu Lys Ala Ala Gly Leu Ala Lys Val Val Thr Thr Val Ala Gly
        920                 925                 930

gcc gga tta gtc ggt aag tat gct acg gat gcg ctc gat aat tat gca   2947
Ala Gly Leu Val Gly Lys Tyr Ala Thr Asp Ala Leu Asp Asn Tyr Ala
    935                 940                 945

gat ggc gtt atc aac ggc gac ggt gat ggt gcg ttc gca gca ggt ggt   2995
Asp Gly Val Ile Asn Gly Asp Gly Asp Gly Ala Phe Ala Ala Gly Gly
950                 955                 960                 965

gac gct acc gtt gat ggc gac tat gta gca gat gga gat gca att gct   3043
Asp Ala Thr Val Asp Gly Asp Tyr Val Ala Asp Gly Asp Ala Ile Ala
                970                 975                 980

tct gct gat gct aac gct gat ttt gta gac ggt gtt gtt gat ggt gct   3091
Ser Ala Asp Ala Asn Ala Asp Phe Val Asp Gly Val Val Asp Gly Ala
            985                 990                 995

ggt cgc gcg tca ttt agc aat gct gcg tat agc tcc gat gga acc act   3139
Gly Arg Ala Ser Phe Ser Asn Ala Ala Tyr Ser Ser Asp Gly Thr Thr
        1000                1005                1010

ctc gac ggt gag ggt gcg agc gtt gat gca cag ggt aac ccg ctt cat   3187
Leu Asp Gly Glu Gly Ala Ser Val Asp Ala Gln Gly Asn Pro Leu His
    1015                1020                1025

gct gat ggc aca cca atg agt gct gct gaa gct gaa atg aag atg gct   3235
Ala Asp Gly Thr Pro Met Ser Ala Ala Glu Ala Glu Met Lys Met Ala
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1030                1035                1040                1045

ggt ctg agc tcg tca gga acc atg atg gag aaa tct ggt gtg aaa tcg   3283
Gly Leu Ser Ser Ser Gly Thr Met Met Glu Lys Ser Gly Val Lys Ser
                1050                1055                1060

agt ggc att acc act gca gcg gat gtc atg gac gat cag tct ctg gca   3331
Ser Gly Ile Thr Thr Ala Ala Asp Val Met Asp Asp Gln Ser Leu Ala
            1065                1070                1075

agc agt gtc act gag tct ggt ctg tcc aag att cca gac acc tat ggt   3379
Ser Ser Val Thr Glu Ser Gly Leu Ser Lys Ile Pro Asp Thr Tyr Gly
        1080                1085                1090

gca gat gtc tcg ggt gct gcg ggc aca gtc gga act acc ggt gct gat   3427
Ala Asp Val Ser Gly Ala Ala Gly Thr Val Gly Thr Thr Gly Ala Asp
    1095                1100                1105

tac agt gcg acc gat tca agc gca ggt ctg aac atg agc gag gct gca   3475
Tyr Ser Ala Thr Asp Ser Ser Ala Gly Leu Asn Met Ser Glu Ala Ala
1110                1115                1120                1125

ttg cag agt ggc acc cca atg ggc gct ctc gct ggt gga tct gtg tcg   3523
Leu Gln Ser Gly Thr Pro Met Gly Ala Leu Ala Gly Gly Ser Val Ser
                1130                1135                1140

agt tcc gat cag gcc atg aat gac gca gct ctt cag att gca gcg tct   3571
Ser Ser Asp Gln Ala Met Asn Asp Ala Ala Leu Gln Ile Ala Ala Ser
            1145                1150                1155

cag ggt ctt gca cca gca ggt tcc ata gct ggt atg gag caa ctt agt   3619
Gln Gly Leu Ala Pro Ala Gly Ser Ile Ala Gly Met Glu Gln Leu Ser
        1160                1165                1170

gct caa gcc act gaa gca cct gct gga aag gcc ggc aag cag ctt ggc   3667
Ala Gln Ala Thr Glu Ala Pro Ala Gly Lys Ala Gly Lys Gln Leu Gly
    1175                1180                1185

gat ctt tct ggc tca gcg ctc aat act cag ctg gcg tcc atg gga cag   3715
Asp Leu Ser Gly Ser Ala Leu Asn Thr Gln Leu Ala Ser Met Gly Gln
1190                1195                1200                1205

cag gta ggt gac agt gtg aac agc gct tat gct gca ggc ggt atg ggt   3763
Gln Val Gly Asp Ser Val Asn Ser Ala Tyr Ala Ala Gly Gly Met Gly
                1210                1215                1220

ggt gtt gat gtg gct ggc aag gtc acc gag gca gca cag cac ttg tct   3811
Gly Val Asp Val Ala Gly Lys Val Thr Glu Ala Ala Gln His Leu Ser
            1225                1230                1235

cag gtt cca ggt cag att cag aat gct gtg acc aat gcg gat gct ggt   3859
Gln Val Pro Gly Gln Ile Gln Asn Ala Val Thr Asn Ala Asp Ala Gly
        1240                1245                1250

tcc tct ggc gca agc ttt ggt cag atg gca cag ggg gca gct ggt att   3907
Ser Ser Gly Ala Ser Phe Gly Gln Met Ala Gln Gly Ala Ala Gly Ile
    1255                1260                1265

gcc ggt gtc gca ggt gtg atc ggt gca gcg ggc gca gca agc tct gca   3955
Ala Gly Val Ala Gly Val Ile Gly Ala Ala Gly Ala Ala Ser Ser Ala
1270                1275                1280                1285
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gca caa ggc gca ggt act gtc cag ggt gcg atg ggt aat gct gca gct   4003
Ala Gln Gly Ala Gly Thr Val Gln Gly Ala Met Gly Asn Ala Ala Ala
                1290                1295                1300

ggt gcg gga atg atc aac aac gct gtt tcc ggt gga gct act ggc tca   4051
Gly Ala Gly Met Ile Asn Asn Ala Val Ser Gly Gly Ala Thr Gly Ser
            1305                1310                1315

aca ggt gcc gca cat gtg gtc aat gca tca cat gga cca gtg gcg cct   4099
Thr Gly Ala Ala His Val Val Asn Ala Ser His Gly Pro Val Ala Pro
        1320                1325                1330

ggt cag gct cac tac caa gag tct ggt cat gca caa gca ttt gtg cag   4147
Gly Gln Ala His Tyr Gln Glu Ser Gly His Ala Gln Ala Phe Val Gln
    1335                1340                1345

aac aac cag gcc aac acc gcg cac aca gca aac acg cgt gca ccg tca   4195
Asn Asn Gln Ala Asn Thr Ala His Thr Ala Asn Thr Arg Ala Pro Ser
1350                1355                1360                1365

tca gct caa att atg ggc gcg aac gtt gct ggc tca ctg gca tca cag   4243
Ser Ala Gln Ile Met Gly Ala Asn Val Ala Gly Ser Leu Ala Ser Gln
                1370                1375                1380

gct gta cga gga atc ggt cag cct ggt cag atg ggt gct aat gtt cgc   4291
Ala Val Arg Gly Ile Gly Gln Pro Gly Gln Met Gly Ala Asn Val Arg
            1385                1390                1395

gac gcg atg ggt ggc agc gga cgc tct ggt ggc cgt ggt gga gca act   4339
Asp Ala Met Gly Gly Ser Gly Arg Ser Gly Gly Arg Gly Gly Ala Thr
        1400                1405                1410

caa ggc ggt cga ggc gca cag cgc agc ggt gtc agt gct aag aac ggt   4387
Gln Gly Gly Arg Gly Ala Gln Arg Ser Gly Val Ser Ala Lys Asn Gly
    1415                1420                1425

atc cgt gca cag cga ggt cag aag cct tct gtg acc ggc cag gcg atg   4435
Ile Arg Ala Gln Arg Gly Gln Lys Pro Ser Val Thr Gly Gln Ala Met
1430                1435                1440                1445

aat gca gca atg cgt tca gca gcg gta agc ggt cgc atg gca aac atg   4483
Asn Ala Ala Met Arg Ser Ala Ala Val Ser Gly Arg Met Ala Asn Met
                1450                1455                1460

gac ggc aac agt gta ggt ggc act gaa gca gat cca cag cag ggg agt   4531
Asp Gly Asn Ser Val Gly Gly Thr Glu Ala Asp Pro Gln Gln Gly Ser
            1465                1470                1475

ggc gta acc gag aag ggt gat aaa ggc gtt aaa tagcgtgtaa aacacaatga 4584
Gly Val Thr Glu Lys Gly Asp Lys Gly Val Lys
        1480                1485

ccg                                                               4587
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<210> 772
<211> 1488
<212> PRT
<213> Corynebacterium glutamicum

<400> 772

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Val Thr Ala Thr Val Leu Glu Pro Gln Pro Val Gln Leu Ser Glu Gln
  1               5                  10                  15

Asp Val Asp Ala Glu Ile Ala Arg Met Glu Leu Lys His Asn Arg His
             20                  25                  30

Lys Thr Trp Arg Arg Arg Thr Met Ala Val Val Met Thr Leu Leu Ile
         35                  40                  45

Ser Val Gly Leu Ser Phe Gly Ala Phe Gly Asn Lys Glu Arg Glu Ala
     50                  55                  60

Asn Ala Phe Ala Ser Ala Ile Ile Ala Gln Val Val Gly Ala Met Gly
 65                  70                  75                  80

Glu Val Ala Phe Glu Ala Ile Cys Pro Ser Asp Gly Asp Thr Glu Met
                 85                  90                  95

Leu Leu Lys Cys Ile Thr Glu Asn Leu Gly Glu Met His Ile Ile Glu
            100                 105                 110

Lys Cys Leu Glu Ala Glu Asp Val Leu Lys Cys Phe Tyr Asp Ala Lys
        115                 120                 125

Asn Glu Glu Gln Arg Lys Glu Gln Asn Leu Asp Lys Ala Pro Asp Tyr
    130                 135                 140

Ser Met Tyr Arg Met Ala Ser Ala Met Ala Ser Phe Tyr Gly Asn Gly
145                 150                 155                 160

Arg Ala Ala Thr Ala Gly Val Glu Glu Gly Gly Pro Asn Glu Phe Leu
                165                 170                 175

Asp Ser Glu Asp Ala Gly Leu Lys Val Trp Glu Gly Ile Leu Ser Lys
            180                 185                 190

Ala Ala Asn Gly Gly Asn Val Leu Gly Tyr Ala Asp Ala Lys His Asn
        195                 200                 205

Glu Asp Ser Gly Trp Phe Phe Gly Asn Gly Val Ala Asn Asn Glu Lys
    210                 215                 220

Thr Tyr Ser Tyr Asp Ser Leu Ala Asp His Ala Phe Gln Gly Pro Tyr
225                 230                 235                 240

His Phe Ala Leu Phe Gly Ala Thr Leu Ser Gly Leu Gly Phe Asp Ser
                245                 250                 255

Ser Lys Ala Glu Asp Ser Gln Thr Asp Phe Ala Gln Arg Lys Gly Met
            260                 265                 270

Gly Tyr Ala Met Met Ile Ala Tyr Ile Ile Ser Gly Gly Ile Asp Leu
        275                 280                 285

Val Phe Asn Thr Val Leu Asn Ile Leu Ser Thr Ile Asn Pro Phe Arg
    290                 295                 300

Leu Leu Val Gly Pro Val Ser Gln Asn Thr Asn Lys Thr Phe Thr Glu
305                 310                 315                 320
```

```
Asn Met Ala Gly Gly Gln Thr Thr Glu Gly Thr Pro Phe Glu Gly Met
                325                 330                 335

Thr Asp Phe Phe Gly Leu Ile Tyr Asn Trp Ser Val Thr Val Gly Trp
            340                 345                 350

Leu Ile Gly Ile Pro Val Ser Ile Gly Leu Phe Met Met Gly Ala Leu
        355                 360                 365

Met Phe Arg Arg Met Asp Lys Gly Ser Ala Phe Lys Lys Val Val Ile
    370                 375                 380

Arg Val Val Tyr Gly Val Val Gly Leu Pro Leu Leu Gly Val Ser Tyr
385                 390                 395                 400

Thr Gly Ala Leu Asp Ser Phe Leu Asp Ser Gly Ser Ser Thr Ser Ala
                405                 410                 415

Gly Ser Asn Ala Thr Lys Ile Val Leu Ser Thr Tyr Val Asp Phe Gln
            420                 425                 430

Ser Trp Ala Glu Asn Thr Arg Met Arg Val Pro Asp Lys Val Thr Leu
        435                 440                 445

Ala Trp Ser Leu Glu Asp Gln Ala Pro Thr Gly Gln Ser Met Arg Met
    450                 455                 460

Val Arg Asn Ser Ala Leu Glu Ile Asn Ala Gln Ser Asn Glu Ser Phe
465                 470                 475                 480

Thr Thr Phe Lys Asn Pro Gly Ser Met Asp Leu Gly Tyr Ser Met Asp
                485                 490                 495

Trp Met Glu Lys Met Ala Asp Pro Ala Asn Ser Gly Thr Asp Gly Thr
            500                 505                 510

Ser Ser Ser Ser Ala Thr Thr Ile Phe Gln Gly Thr Ile Ala Leu Leu
        515                 520                 525

Ser Arg Tyr Ile Asp Asn Asp Ser Ile Ser Ser Gly Ser Phe Glu Thr
    530                 535                 540

Ser Ile Arg Ser Ala Met Glu Ser Leu Thr Ser Lys Glu Gly Ser Gly
545                 550                 555                 560

Glu Ala Val Ala Gly Gly Asp Val Met Ala Trp Val Thr Gly Tyr Asn
                565                 570                 575

Thr Ala Ser Gly Leu Asn Glu Ile Thr Ala Ala Glu Leu Ala Asp Ala
            580                 585                 590

Asn Asn Pro Leu Leu Glu Val Ser Asp Ser Ala Gly Leu Gln Gly Arg
        595                 600                 605

Pro Ile Asp Arg Asn Ala Val Ser Phe Lys Ser Gly Asp Ala Thr Ala
    610                 615                 620

Ser Cys Asn Asn Ser Val Val Thr Gly Ser Arg Ala Val Val Gly Asp
625                 630                 635                 640

Tyr Arg Ser Asp Cys Asn Met Ser Pro Leu Thr Met Tyr Asn Phe Leu
```

645 650 655

Asn Thr Ser Phe His Pro Ala Asp Ala Ser Val Phe Ser Thr Ser Thr
660 665 670

Ser Ala Ser Ser Tyr Thr Arg Ala Ser His Ser Ala Val Ser Leu Ile
675 680 685

Gly Ser Gly Ala Met Asn Phe Val Tyr Trp Phe Ser Ala Met Ser Leu
690 695 700

Met Gly Ser Phe Ile Val Ile Gly Ile Gly Tyr Ala Gly Ala Met Leu
705 710 715 720

Phe Asn Thr Ile Arg Arg Thr Leu Ser Leu Ile Gly Ala Val Pro Phe
725 730 735

Ala Ala Met Gly Phe Ile Ala Gly Val Ala Lys Val Ile Val Tyr Thr
740 745 750

Ile Ala Met Leu Val Glu Val Ile Gly Thr Ile Ile Leu Tyr Gln Leu
755 760 765

Ile Thr Arg Phe Leu Met Ala Val Pro Ala Leu Phe Glu Gln Pro Leu
770 775 780

Ala Asp Ser Leu Ser Ser Asn Glu Ser Ala Glu Leu Val Ala Gly Ala
785 790 795 800

Gly Met Gly Leu Val Gly Met Ala Leu Ala Thr Ser Gly Asn Trp Ala
805 810 815

Ile Ala Gly Met Val Ile Thr Val Ala Ser Ser Met Gly Val Ile Ile
820 825 830

Phe Thr Ile Ile Ala Met Lys Val Arg Gly Ser Leu Val Ser Gly Val
835 840 845

Asp Glu Thr Val Thr Ser Val Ile Asn Arg Phe Leu Asp Thr Gln Val
850 855 860

Ser Ser Ala Gly Ala Thr Ser Gly Asp Gly Met Met Arg Arg Ala Ala
865 870 875 880

Ala Thr Gly Leu Gly Ile Gly Ala Thr His Met Val Leu Asn Arg Asp
885 890 895

Gly Asp Gly Gly Gly Ser Asp Ser Gly Ser Gly Gly Ser Gly Gly Gly
900 905 910

Ser Asp Ser Gly Leu Gly Glu Lys Ala Ala Gly Leu Ala Lys Val Val
915 920 925

Thr Thr Val Ala Gly Ala Gly Leu Val Gly Lys Tyr Ala Thr Asp Ala
930 935 940

Leu Asp Asn Tyr Ala Asp Gly Val Ile Asn Gly Asp Gly Asp Gly Ala
945 950 955 960

Phe Ala Ala Gly Gly Asp Ala Thr Val Asp Gly Asp Tyr Val Ala Asp
965 970 975

```
Gly Asp Ala Ile Ala Ser Ala Asp Ala Asn Ala Asp Phe Val Asp Gly
            980                 985                 990

Val Val Asp Gly Ala Gly Arg Ala Ser Phe Ser Asn Ala Ala Tyr Ser
        995                 1000                1005

Ser Asp Gly Thr Thr Leu Asp Gly Glu Gly Ala Ser Val Asp Ala Gln
    1010                1015                1020

Gly Asn Pro Leu His Ala Asp Gly Thr Pro Met Ser Ala Ala Glu Ala
1025                1030                1035                1040

Glu Met Lys Met Ala Gly Leu Ser Ser Ser Gly Thr Met Met Glu Lys
                1045                1050                1055

Ser Gly Val Lys Ser Ser Gly Ile Thr Thr Ala Ala Asp Val Met Asp
            1060                1065                1070

Asp Gln Ser Leu Ala Ser Ser Val Thr Glu Ser Gly Leu Ser Lys Ile
        1075                1080                1085

Pro Asp Thr Tyr Gly Ala Asp Val Ser Gly Ala Ala Gly Thr Val Gly
    1090                1095                1100

Thr Thr Gly Ala Asp Tyr Ser Ala Thr Asp Ser Ser Ala Gly Leu Asn
1105                1110                1115                1120

Met Ser Glu Ala Ala Leu Gln Ser Gly Thr Pro Met Gly Ala Leu Ala
                1125                1130                1135

Gly Gly Ser Val Ser Ser Ser Asp Gln Ala Met Asn Asp Ala Ala Leu
            1140                1145                1150

Gln Ile Ala Ala Ser Gln Gly Leu Ala Pro Ala Gly Ser Ile Ala Gly
        1155                1160                1165

Met Glu Gln Leu Ser Ala Gln Ala Thr Glu Ala Pro Ala Gly Lys Ala
    1170                1175                1180

Gly Lys Gln Leu Gly Asp Leu Ser Gly Ser Ala Leu Asn Thr Gln Leu
1185                1190                1195                1200

Ala Ser Met Gly Gln Gln Val Gly Asp Ser Val Asn Ser Ala Tyr Ala
                1205                1210                1215

Ala Gly Gly Met Gly Gly Val Asp Val Ala Gly Lys Val Thr Glu Ala
            1220                1225                1230

Ala Gln His Leu Ser Gln Val Pro Gly Gln Ile Gln Asn Ala Val Thr
        1235                1240                1245

Asn Ala Asp Ala Gly Ser Ser Gly Ala Ser Phe Gly Gln Met Ala Gln
    1250                1255                1260

Gly Ala Ala Gly Ile Ala Gly Val Ala Gly Val Ile Gly Ala Ala Gly
1265                1270                1275                1280

Ala Ala Ser Ser Ala Ala Gln Gly Ala Gly Thr Val Gln Gly Ala Met
                1285                1290                1295
```

```
Gly Asn Ala Ala Ala Gly Ala Gly Met Ile Asn Asn Ala Val Ser Gly
            1300                1305                1310

Gly Ala Thr Gly Ser Thr Gly Ala Ala His Val Val Asn Ala Ser His
        1315                1320                1325

Gly Pro Val Ala Pro Gly Gln Ala His Tyr Gln Glu Ser Gly His Ala
    1330                1335                1340

Gln Ala Phe Val Gln Asn Asn Gln Ala Asn Thr Ala His Thr Ala Asn
1345                1350                1355                1360

Thr Arg Ala Pro Ser Ser Ala Gln Ile Met Gly Ala Asn Val Ala Gly
                1365                1370                1375

Ser Leu Ala Ser Gln Ala Val Arg Gly Ile Gly Gln Pro Gly Gln Met
            1380                1385                1390

Gly Ala Asn Val Arg Asp Ala Met Gly Gly Ser Gly Arg Ser Gly Gly
        1395                1400                1405

Arg Gly Gly Ala Thr Gln Gly Gly Arg Gly Ala Gln Arg Ser Gly Val
    1410                1415                1420

Ser Ala Lys Asn Gly Ile Arg Ala Gln Arg Gly Gln Lys Pro Ser Val
1425                1430                1435                1440

Thr Gly Gln Ala Met Asn Ala Ala Met Arg Ser Ala Ala Val Ser Gly
                1445                1450                1455

Arg Met Ala Asn Met Asp Gly Asn Ser Val Gly Gly Thr Glu Ala Asp
            1460                1465                1470

Pro Gln Gln Gly Ser Gly Val Thr Glu Lys Gly Asp Lys Gly Val Lys
        1475                1480                1485
```

<210> 773
<211> 916
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(916)
<223> FRXA00739

<400> 773

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ttaaagtttc tatattccat tctaaaataa ctttgaattg gggattaatg aaacttttta 60

agcaattgtt taaaacgaat attgaggggg tggcgggcaa gtg act gcg aca gtt   115
                                        Val Thr Ala Thr Val
                                          1               5

tta gaa ccg caa cct gta cag ctt agt gag cag gac gta gat gct gag   163
Leu Glu Pro Gln Pro Val Gln Leu Ser Glu Gln Asp Val Asp Ala Glu
                10                  15                  20
```

```
att gcg cgc atg gag ctt aaa cac aac cga cac aag acg tgg cga cgc   211
Ile Ala Arg Met Glu Leu Lys His Asn Arg His Lys Thr Trp Arg Arg
            25                  30                  35

cga acg atg gct gtt gtc atg acg ctc ttg atc tca gtg ggt ttg agc   259
Arg Thr Met Ala Val Val Met Thr Leu Leu Ile Ser Val Gly Leu Ser
        40                  45                  50

ttt ggt gcg ttt ggt aac aag gaa cgt gaa gct aat gct ttc gcc agc   307
Phe Gly Ala Phe Gly Asn Lys Glu Arg Glu Ala Asn Ala Phe Ala Ser
    55                  60                  65

gct att att gcc cag gtt gtc ggt gct atg ggc gag gtt gcc ttt gaa   355
Ala Ile Ile Ala Gln Val Val Gly Ala Met Gly Glu Val Ala Phe Glu
70                  75                  80                  85

gcg att tgt ccc agt gat ggt gac acc gag atg ctt ctt aag tgc atc   403
Ala Ile Cys Pro Ser Asp Gly Asp Thr Glu Met Leu Leu Lys Cys Ile
                90                  95                  100

acc gag aac tta ggt gaa atg cac att atc gag aag tgt ctc gaa gca   451
Thr Glu Asn Leu Gly Glu Met His Ile Ile Glu Lys Cys Leu Glu Ala
            105                 110                 115

gaa gat gtc ttg aag tgc ttc tac gat gcg aaa aac gaa gag caa cgt   499
Glu Asp Val Leu Lys Cys Phe Tyr Asp Ala Lys Asn Glu Glu Gln Arg
        120                 125                 130

aaa gaa cag aac ctt gat aaa gcc cct gat tac tcc atg tac cgt atg   547
Lys Glu Gln Asn Leu Asp Lys Ala Pro Asp Tyr Ser Met Tyr Arg Met
    135                 140                 145

gcc tct gcg atg gca tcg ttc tat ggc aat ggt cgg gca gct act gcc   595
Ala Ser Ala Met Ala Ser Phe Tyr Gly Asn Gly Arg Ala Ala Thr Ala
150                 155                 160                 165

ggt gta gag gaa ggc gga ccg aac gag ttc ctc gat tct gag gac gcc   643
Gly Val Glu Glu Gly Gly Pro Asn Glu Phe Leu Asp Ser Glu Asp Ala
                170                 175                 180

ggt ctt aag gtg tgg gag ggc att ctc agt aag gcc gcc aac gga ggc   691
Gly Leu Lys Val Trp Glu Gly Ile Leu Ser Lys Ala Ala Asn Gly Gly
            185                 190                 195

aat gtc ctt ggt tat gct gac gcg aaa cac aac gag gac tct ggt tgg   739
Asn Val Leu Gly Tyr Ala Asp Ala Lys His Asn Glu Asp Ser Gly Trp
        200                 205                 210

ttc ttt ggt aat ggt gtt gcc aac aac gag aaa acg tac tcc tat gat   787
Phe Phe Gly Asn Gly Val Ala Asn Asn Glu Lys Thr Tyr Ser Tyr Asp
    215                 220                 225

tct cta gct gat cat gcc ttt caa ggg cct tat cac ttt gca tta ttt   835
Ser Leu Ala Asp His Ala Phe Gln Gly Pro Tyr His Phe Ala Leu Phe
230                 235                 240                 245

ggc gcg aca ctg agt ggc tta ggc ttt gat agc tca aag gcg gag gat   883
Gly Ala Thr Leu Ser Gly Leu Gly Phe Asp Ser Ser Lys Ala Glu Asp
                250                 255                 260

tcg cag act gat ttt gct cag cgt aag ggc atg                      916
```

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Ser Gln Thr Asp Phe Ala Gln Arg Lys Gly Met
            265                 270


<210> 774
<211> 272
<212> PRT
<213> Corynebacterium glutamicum

<400> 774
Val Thr Ala Thr Val Leu Glu Pro Gln Pro Val Gln Leu Ser Glu Gln
  1               5                  10                  15

Asp Val Asp Ala Glu Ile Ala Arg Met Glu Leu Lys His Asn Arg His
             20                  25                  30

Lys Thr Trp Arg Arg Arg Thr Met Ala Val Val Met Thr Leu Leu Ile
         35                  40                  45

Ser Val Gly Leu Ser Phe Gly Ala Phe Gly Asn Lys Glu Arg Glu Ala
     50                  55                  60

Asn Ala Phe Ala Ser Ala Ile Ile Ala Gln Val Val Gly Ala Met Gly
 65                  70                  75                  80

Glu Val Ala Phe Glu Ala Ile Cys Pro Ser Asp Gly Asp Thr Glu Met
                 85                  90                  95

Leu Leu Lys Cys Ile Thr Glu Asn Leu Gly Glu Met His Ile Ile Glu
            100                 105                 110

Lys Cys Leu Glu Ala Glu Asp Val Leu Lys Cys Phe Tyr Asp Ala Lys
        115                 120                 125

Asn Glu Glu Gln Arg Lys Glu Gln Asn Leu Asp Lys Ala Pro Asp Tyr
    130                 135                 140

Ser Met Tyr Arg Met Ala Ser Ala Met Ala Ser Phe Tyr Gly Asn Gly
145                 150                 155                 160

Arg Ala Ala Thr Ala Gly Val Glu Glu Gly Gly Pro Asn Glu Phe Leu
                165                 170                 175

Asp Ser Glu Asp Ala Gly Leu Lys Val Trp Glu Gly Ile Leu Ser Lys
            180                 185                 190

Ala Ala Asn Gly Gly Asn Val Leu Gly Tyr Ala Asp Ala Lys His Asn
        195                 200                 205

Glu Asp Ser Gly Trp Phe Phe Gly Asn Gly Val Ala Asn Asn Glu Lys
    210                 215                 220

Thr Tyr Ser Tyr Asp Ser Leu Ala Asp His Ala Phe Gln Gly Pro Tyr
225                 230                 235                 240

His Phe Ala Leu Phe Gly Ala Thr Leu Ser Gly Leu Gly Phe Asp Ser
                245                 250                 255

Ser Lys Ala Glu Asp Ser Gln Thr Asp Phe Ala Gln Arg Lys Gly Met
            260                 265                 270
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<210> 775
<211> 2083
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2083)
<223> FRXA01587

<400> 775
catttagact ggtcggtgga cccgttctta gaatactaac aagacattca ctgagaatat 60

ggctggtggg cagaccacag aaggaacacc gcttggagga atg act gat ttc ttc 115
Met Thr Asp Phe Phe
1 5

ggg ttg atc tat aac tgg tca gtg act gtg ggc tgg ctc atc ggt att 163
Gly Leu Ile Tyr Asn Trp Ser Val Thr Val Gly Trp Leu Ile Gly Ile
10 15 20

cct gtc tcc att ggt ctg ttt atg atg ggt gcg ttg atg ttt cga cgc 211
Pro Val Ser Ile Gly Leu Phe Met Met Gly Ala Leu Met Phe Arg Arg
25 30 35

atg gac aag gga tca gcg ttt aaa aag gtt gtt atc cgc gtc gtg tac 259
Met Asp Lys Gly Ser Ala Phe Lys Lys Val Val Ile Arg Val Val Tyr
40 45 50

ggt gtc gtt ggc ctg cca ctg ctt ggt gtc tct tat acc ggt gcg ctg 307
Gly Val Val Gly Leu Pro Leu Leu Gly Val Ser Tyr Thr Gly Ala Leu
55 60 65

gat tcc ttc ctc gac agc ggt agt tcc aca agt gct gga tca aat gcg 355
Asp Ser Phe Leu Asp Ser Gly Ser Ser Thr Ser Ala Gly Ser Asn Ala
70 75 80 85

aca aag att gtg ttg tcc acc tac gtg gat ttc caa tca tgg gca gaa 403
Thr Lys Ile Val Leu Ser Thr Tyr Val Asp Phe Gln Ser Trp Ala Glu
90 95 100

aac acc cgt atg cgt gtt cct gac aaa gta aca ctg gcg tgg agt ctg 451
Asn Thr Arg Met Arg Val Pro Asp Lys Val Thr Leu Ala Trp Ser Leu
105 110 115

gag gat cag gcg cca aca ggg cag tcc atg cgg atg gta cgc aat tcg 499
Glu Asp Gln Ala Pro Thr Gly Gln Ser Met Arg Met Val Arg Asn Ser
120 125 130

gcg ttg gaa att aat gct caa tca aat gag agt ttt act act ttt aag 547
Ala Leu Glu Ile Asn Ala Gln Ser Asn Glu Ser Phe Thr Thr Phe Lys
135 140 145

aat cca ggt tcc atg gat cta ggc tat agc atg gac tgg atg gaa aag 595
Asn Pro Gly Ser Met Asp Leu Gly Tyr Ser Met Asp Trp Met Glu Lys
150 155 160 165

```
atg gcg gat cca gcc aat tct ggc acc gat ggg acc tca tca agt tcg   643
Met Ala Asp Pro Ala Asn Ser Gly Thr Asp Gly Thr Ser Ser Ser Ser
                170                 175                 180

gcg acg act att ttc cag gga acc atc gcg cta ctg agt cgt tat atc   691
Ala Thr Thr Ile Phe Gln Gly Thr Ile Ala Leu Leu Ser Arg Tyr Ile
            185                 190                 195

gac aac gac agt atc tcc tct ggc agt ttc gaa acc tct att cga agt   739
Asp Asn Asp Ser Ile Ser Ser Gly Ser Phe Glu Thr Ser Ile Arg Ser
        200                 205                 210

gcg atg gaa tct ttg acc tcg aaa gag gga agt ggc gaa gct gtt gcc   787
Ala Met Glu Ser Leu Thr Ser Lys Glu Gly Ser Gly Glu Ala Val Ala
    215                 220                 225

ggt ggt gat gta atg gcc tgg gtt act ggt tac aac aca gcc tct ggt   835
Gly Gly Asp Val Met Ala Trp Val Thr Gly Tyr Asn Thr Ala Ser Gly
230                 235                 240                 245

ctt aat gag atc act gct gct gaa tta gct gat gcg aac aat cca ttg   883
Leu Asn Glu Ile Thr Ala Ala Glu Leu Ala Asp Ala Asn Asn Pro Leu
                250                 255                 260

ctt gag gtc agc gac tca gct ggt ctg cag gga cga cct att gac cgc   931
Leu Glu Val Ser Asp Ser Ala Gly Leu Gln Gly Arg Pro Ile Asp Arg
            265                 270                 275

aat gcg gtg tca ttt aaa tct ggt gat gcg aca gcg tca tgc aac aac   979
Asn Ala Val Ser Phe Lys Ser Gly Asp Ala Thr Ala Ser Cys Asn Asn
        280                 285                 290

tca gtc gtg aca ggt tct cgt gct gtg gtc ggg gac tac cga agt gac  1027
Ser Val Val Thr Gly Ser Arg Ala Val Val Gly Asp Tyr Arg Ser Asp
    295                 300                 305

tgc aat atg tcg ccc ttg acg atg tac aac ttc ctc aac acc tca ttc  1075
Cys Asn Met Ser Pro Leu Thr Met Tyr Asn Phe Leu Asn Thr Ser Phe
310                 315                 320                 325

cat cca gct gat gca agt gtc ttt tct acg tcc act tct gcg tca agc  1123
His Pro Ala Asp Ala Ser Val Phe Ser Thr Ser Thr Ser Ala Ser Ser
                330                 335                 340

tac acc cgt gca tcg cat agc gca gtg agt ctt atc ggt tct ggt gcc  1171
Tyr Thr Arg Ala Ser His Ser Ala Val Ser Leu Ile Gly Ser Gly Ala
            345                 350                 355

atg aac ttt gtg tac tgg ttc tct gca atg tcc ctg atg ggt agc ttc  1219
Met Asn Phe Val Tyr Trp Phe Ser Ala Met Ser Leu Met Gly Ser Phe
        360                 365                 370

atc gtg atc ggt atc ggt tac gcc ggt gcc atg ctg ttt aat acg att  1267
Ile Val Ile Gly Ile Gly Tyr Ala Gly Ala Met Leu Phe Asn Thr Ile
    375                 380                 385

cga cgc acg ctg tcg ctc att ggt gcc gtt cct ttt gct gcg atg ggc  1315
Arg Arg Thr Leu Ser Leu Ile Gly Ala Val Pro Phe Ala Ala Met Gly
390                 395                 400                 405

ttt att gct ggt gtt gcc aag gtc att gtg tac acc atc gct atg ctc  1363
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```
Phe Ile Ala Gly Val Ala Lys Val Ile Val Tyr Thr Ile Ala Met Leu
                410                 415                 420

gta gag gtt atc gga acg atc att ttg tac cag ctc att acc cgg ttc   1411
Val Glu Val Ile Gly Thr Ile Ile Leu Tyr Gln Leu Ile Thr Arg Phe
            425                 430                 435

ttg atg gct gta cca gca ctc ttt gaa caa cct ttg gct gat tcc tta   1459
Leu Met Ala Val Pro Ala Leu Phe Glu Gln Pro Leu Ala Asp Ser Leu
        440                 445                 450

agt agt aac gag agt gct gag ctg gtt gcc ggt gct ggt atg ggg cta   1507
Ser Ser Asn Glu Ser Ala Glu Leu Val Ala Gly Ala Gly Met Gly Leu
    455                 460                 465

gtc ggt atg gca cta gct acc tca ggc aac tgg gcg att gcc ggc atg   1555
Val Gly Met Ala Leu Ala Thr Ser Gly Asn Trp Ala Ile Ala Gly Met
470                 475                 480                 485

gtg atc aca gtg gcc tca tcc atg ggg gtc atc atc ttc acg att att   1603
Val Ile Thr Val Ala Ser Ser Met Gly Val Ile Ile Phe Thr Ile Ile
                490                 495                 500

gcg atg aag gtg cgc gga tct ttg gta tca ggt gtc gat gaa acc gtg   1651
Ala Met Lys Val Arg Gly Ser Leu Val Ser Gly Val Asp Glu Thr Val
            505                 510                 515

acc agt gtt att aac cgc ttc ttg gat aca cag gtc tct tct gca ggt   1699
Thr Ser Val Ile Asn Arg Phe Leu Asp Thr Gln Val Ser Ser Ala Gly
        520                 525                 530

gct acc tct ggt gac ggc atg atg cgt cgt gca gcc gca acg ggt ctt   1747
Ala Thr Ser Gly Asp Gly Met Met Arg Arg Ala Ala Ala Thr Gly Leu
    535                 540                 545

ggt att ggt gcg aca cat atg gta ctc aac cgt gat ggt gac ggt ggt   1795
Gly Ile Gly Ala Thr His Met Val Leu Asn Arg Asp Gly Asp Gly Gly
550                 555                 560                 565

gga tct gat tca ggc tct ggt gga tca ggt ggc ggt agc gat tca ggc   1843
Gly Ser Asp Ser Gly Ser Gly Gly Ser Gly Gly Gly Ser Asp Ser Gly
                570                 575                 580

ttg ggt gag aag gct gct ggt ctg gcg aag gtt gtc aca act gtg gct   1891
Leu Gly Glu Lys Ala Ala Gly Leu Ala Lys Val Val Thr Thr Val Ala
            585                 590                 595

ggt gcc gga tta gtc ggt aag tat gct acg gat gcg ctc gat aat tat   1939
Gly Ala Gly Leu Val Gly Lys Tyr Ala Thr Asp Ala Leu Asp Asn Tyr
        600                 605                 610

gca gat ggc gtt atc aac ggc gac ggt gat ggt gcg ttc gca gca ggt   1987
Ala Asp Gly Val Ile Asn Gly Asp Gly Asp Gly Ala Phe Ala Ala Gly
    615                 620                 625

ggt gac gct acc gtt gat ggc gac tat gta gca gat gga gat gca att   2035
Gly Asp Ala Thr Val Asp Gly Asp Tyr Val Ala Asp Gly Asp Ala Ile
630                 635                 640                 645

gct tct gct gat gct aac gct gat ttt gta gac ggg gtt gct gat ggt   2083
Ala Ser Ala Asp Ala Asn Ala Asp Phe Val Asp Gly Val Ala Asp Gly
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650 655 660

<210> 776
<211> 661
<212> PRT
<213> Corynebacterium glutamicum

<400> 776
Met Thr Asp Phe Phe Gly Leu Ile Tyr Asn Trp Ser Val Thr Val Gly
1 5 10 15

Trp Leu Ile Gly Ile Pro Val Ser Ile Gly Leu Phe Met Met Gly Ala
20 25 30

Leu Met Phe Arg Arg Met Asp Lys Gly Ser Ala Phe Lys Lys Val Val
35 40 45

Ile Arg Val Val Tyr Gly Val Val Gly Leu Pro Leu Leu Gly Val Ser
50 55 60

Tyr Thr Gly Ala Leu Asp Ser Phe Leu Asp Ser Gly Ser Ser Thr Ser
65 70 75 80

Ala Gly Ser Asn Ala Thr Lys Ile Val Leu Ser Thr Tyr Val Asp Phe
85 90 95

Gln Ser Trp Ala Glu Asn Thr Arg Met Arg Val Pro Asp Lys Val Thr
100 105 110

Leu Ala Trp Ser Leu Glu Asp Gln Ala Pro Thr Gly Gln Ser Met Arg
115 120 125

Met Val Arg Asn Ser Ala Leu Glu Ile Asn Ala Gln Ser Asn Glu Ser
130 135 140

Phe Thr Thr Phe Lys Asn Pro Gly Ser Met Asp Leu Gly Tyr Ser Met
145 150 155 160

Asp Trp Met Glu Lys Met Ala Asp Pro Ala Asn Ser Gly Thr Asp Gly
165 170 175

Thr Ser Ser Ser Ser Ala Thr Thr Ile Phe Gln Gly Thr Ile Ala Leu
180 185 190

Leu Ser Arg Tyr Ile Asp Asn Asp Ser Ile Ser Ser Gly Ser Phe Glu
195 200 205

Thr Ser Ile Arg Ser Ala Met Glu Ser Leu Thr Ser Lys Glu Gly Ser
210 215 220

Gly Glu Ala Val Ala Gly Gly Asp Val Met Ala Trp Val Thr Gly Tyr
225 230 235 240

Asn Thr Ala Ser Gly Leu Asn Glu Ile Thr Ala Ala Glu Leu Ala Asp
245 250 255

Ala Asn Asn Pro Leu Leu Glu Val Ser Asp Ser Ala Gly Leu Gln Gly
260 265 270

Arg Pro Ile Asp Arg Asn Ala Val Ser Phe Lys Ser Gly Asp Ala Thr

```
        275                 280                 285

Ala Ser Cys Asn Asn Ser Val Val Thr Gly Ser Arg Ala Val Val Gly
    290                 295                 300

Asp Tyr Arg Ser Asp Cys Asn Met Ser Pro Leu Thr Met Tyr Asn Phe
305                 310                 315                 320

Leu Asn Thr Ser Phe His Pro Ala Asp Ala Ser Val Phe Ser Thr Ser
                325                 330                 335

Thr Ser Ala Ser Ser Tyr Thr Arg Ala Ser His Ser Ala Val Ser Leu
            340                 345                 350

Ile Gly Ser Gly Ala Met Asn Phe Val Tyr Trp Phe Ser Ala Met Ser
        355                 360                 365

Leu Met Gly Ser Phe Ile Val Ile Gly Ile Gly Tyr Ala Gly Ala Met
    370                 375                 380

Leu Phe Asn Thr Ile Arg Arg Thr Leu Ser Leu Ile Gly Ala Val Pro
385                 390                 395                 400

Phe Ala Ala Met Gly Phe Ile Ala Gly Val Ala Lys Val Ile Val Tyr
                405                 410                 415

Thr Ile Ala Met Leu Val Glu Val Ile Gly Thr Ile Ile Leu Tyr Gln
            420                 425                 430

Leu Ile Thr Arg Phe Leu Met Ala Val Pro Ala Leu Phe Glu Gln Pro
        435                 440                 445

Leu Ala Asp Ser Leu Ser Ser Asn Glu Ser Ala Glu Leu Val Ala Gly
    450                 455                 460

Ala Gly Met Gly Leu Val Gly Met Ala Leu Ala Thr Ser Gly Asn Trp
465                 470                 475                 480

Ala Ile Ala Gly Met Val Ile Thr Val Ala Ser Ser Met Gly Val Ile
                485                 490                 495

Ile Phe Thr Ile Ile Ala Met Lys Val Arg Gly Ser Leu Val Ser Gly
            500                 505                 510

Val Asp Glu Thr Val Thr Ser Val Ile Asn Arg Phe Leu Asp Thr Gln
        515                 520                 525

Val Ser Ser Ala Gly Ala Thr Ser Gly Asp Gly Met Met Arg Arg Ala
    530                 535                 540

Ala Ala Thr Gly Leu Gly Ile Gly Ala Thr His Met Val Leu Asn Arg
545                 550                 555                 560

Asp Gly Asp Gly Gly Gly Ser Asp Ser Gly Ser Gly Gly Ser Gly Gly
                565                 570                 575

Gly Ser Asp Ser Gly Leu Gly Glu Lys Ala Ala Gly Leu Ala Lys Val
            580                 585                 590

Val Thr Thr Val Ala Gly Ala Gly Leu Val Gly Lys Tyr Ala Thr Asp
        595                 600                 605
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```
Ala Leu Asp Asn Tyr Ala Asp Gly Val Ile Asn Gly Asp Gly Asp Gly
    610                 615                 620

Ala Phe Ala Ala Gly Gly Asp Ala Thr Val Asp Gly Asp Tyr Val Ala
625                 630                 635                 640

Asp Gly Asp Ala Ile Ala Ser Ala Asp Ala Asn Ala Asp Phe Val Asp
                645                 650                 655

Gly Val Ala Asp Gly
            660


<210> 777
<211> 1541
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1518)
<223> FRXA01761

<400> 777
gct gat gct aac gct gat ttt gta gac ggt gtt gtt gat ggt gct ggt   48
Ala Asp Ala Asn Ala Asp Phe Val Asp Gly Val Val Asp Gly Ala Gly
  1               5                  10                  15

cgc gcg tca ttt agc aat gct gcg tat agc tcc gat gga acc act ctc   96
Arg Ala Ser Phe Ser Asn Ala Ala Tyr Ser Ser Asp Gly Thr Thr Leu
             20                  25                  30

gac ggt gag ggt gcg agc gtt gat gca cag ggt aac ccg ctt cat gct   144
Asp Gly Glu Gly Ala Ser Val Asp Ala Gln Gly Asn Pro Leu His Ala
         35                  40                  45

gat ggc aca cca atg agt gct gct gaa gct gaa atg aag atg gct ggt   192
Asp Gly Thr Pro Met Ser Ala Ala Glu Ala Glu Met Lys Met Ala Gly
     50                  55                  60

ctg agc tcg tca gga acc atg atg gag aaa tct ggt gtg aaa tcg agt   240
Leu Ser Ser Ser Gly Thr Met Met Glu Lys Ser Gly Val Lys Ser Ser
 65                  70                  75                  80

ggc att acc act gca gcg gat gtc atg gac gat cag tct ctg gca agc   288
Gly Ile Thr Thr Ala Ala Asp Val Met Asp Asp Gln Ser Leu Ala Ser
                 85                  90                  95

agt gtc act gag tct ggt ctg tcc aag att cca gac acc tat ggt gca   336
Ser Val Thr Glu Ser Gly Leu Ser Lys Ile Pro Asp Thr Tyr Gly Ala
            100                 105                 110

gat gtc tcg ggt gct gcg ggc aca gtc gga act acc ggt gct gat tac   384
Asp Val Ser Gly Ala Ala Gly Thr Val Gly Thr Thr Gly Ala Asp Tyr
        115                 120                 125

agt gcg acc gat tca agc gca ggt ctg aac atg agc gag gct gca ttg   432
Ser Ala Thr Asp Ser Ser Ala Gly Leu Asn Met Ser Glu Ala Ala Leu
    130                 135                 140
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cag agt ggc acc cca atg ggc gct ctc gct ggt gga tct gtg tcg agt   480
Gln Ser Gly Thr Pro Met Gly Ala Leu Ala Gly Gly Ser Val Ser Ser
145                 150                 155                 160

tcc gat cag gcc atg aat gac gca gct ctt cag att gca gcg tct cag   528
Ser Asp Gln Ala Met Asn Asp Ala Ala Leu Gln Ile Ala Ala Ser Gln
                165                 170                 175

ggt ctt gca cca gca ggt tcc ata gct ggt atg gag caa ctt agt gct   576
Gly Leu Ala Pro Ala Gly Ser Ile Ala Gly Met Glu Gln Leu Ser Ala
            180                 185                 190

caa gcc act gaa gca cct gct gga aag gcc ggc aag cag ctt ggc gat   624
Gln Ala Thr Glu Ala Pro Ala Gly Lys Ala Gly Lys Gln Leu Gly Asp
        195                 200                 205

ctt tct ggc tca gcg ctc aat act cag ctg gcg tcc atg gga cag cag   672
Leu Ser Gly Ser Ala Leu Asn Thr Gln Leu Ala Ser Met Gly Gln Gln
    210                 215                 220

gta ggt gac agt gtg aac agc gct tat gct gca ggc ggt atg ggt ggt   720
Val Gly Asp Ser Val Asn Ser Ala Tyr Ala Ala Gly Gly Met Gly Gly
225                 230                 235                 240

gtt gat gtg gct ggc aag gtc acc gag gca gca cag cac ttg tct cag   768
Val Asp Val Ala Gly Lys Val Thr Glu Ala Ala Gln His Leu Ser Gln
                245                 250                 255

gtt cca ggt cag att cag aat gct gtg acc aat gcg gat gct ggt tcc   816
Val Pro Gly Gln Ile Gln Asn Ala Val Thr Asn Ala Asp Ala Gly Ser
            260                 265                 270

tct ggc gca agc ttt ggt cag atg gca cag ggg gca gct ggt att gcc   864
Ser Gly Ala Ser Phe Gly Gln Met Ala Gln Gly Ala Ala Gly Ile Ala
        275                 280                 285

ggt gtc gca ggt gtg atc ggt gca gcg ggc gca gca agc tct gca gca   912
Gly Val Ala Gly Val Ile Gly Ala Ala Gly Ala Ala Ser Ser Ala Ala
    290                 295                 300

caa ggc gca ggt act gtc cag ggt gcg atg ggt aat gct gca gct ggt   960
Gln Gly Ala Gly Thr Val Gln Gly Ala Met Gly Asn Ala Ala Ala Gly
305                 310                 315                 320

gcg gga atg atc aac aac gct gtt tcc ggt gga gct act ggc tca aca   1008
Ala Gly Met Ile Asn Asn Ala Val Ser Gly Gly Ala Thr Gly Ser Thr
                325                 330                 335

ggt gcc gca cat gtg gtc aat gca tca cat gga cca gtg gcg cct ggt   1056
Gly Ala Ala His Val Val Asn Ala Ser His Gly Pro Val Ala Pro Gly
            340                 345                 350

cag gct cac tac caa gag tct ggt cat gca caa gca ttt gtg cag aac   1104
Gln Ala His Tyr Gln Glu Ser Gly His Ala Gln Ala Phe Val Gln Asn
        355                 360                 365

aac cag gcc aac acc gcg cac aca gca aac acg cgt gca ccg tca tca   1152
Asn Gln Ala Asn Thr Ala His Thr Ala Asn Thr Arg Ala Pro Ser Ser
    370                 375                 380

gct caa att atg ggc gcg aac gtt gct ggc tca ctg gca tca cag gct   1200
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```
Ala Gln Ile Met Gly Ala Asn Val Ala Gly Ser Leu Ala Ser Gln Ala
385                 390                 395                 400

gta cga gga atc ggt cag cct ggt cag atg ggt gct aat gtt cgc gac   1248
Val Arg Gly Ile Gly Gln Pro Gly Gln Met Gly Ala Asn Val Arg Asp
                405                 410                 415

gcg atg ggt ggc agc gga cgc tct ggt ggc cgt ggt gga gca act caa   1296
Ala Met Gly Gly Ser Gly Arg Ser Gly Gly Arg Gly Gly Ala Thr Gln
            420                 425                 430

ggc ggt cga ggc gca cag cgc agc ggt gtc agt gct aag aac ggt atc   1344
Gly Gly Arg Gly Ala Gln Arg Ser Gly Val Ser Ala Lys Asn Gly Ile
        435                 440                 445

cgt gca cag cga ggt cag aag cct tct gtg acc ggc cag gcg atg aat   1392
Arg Ala Gln Arg Gly Gln Lys Pro Ser Val Thr Gly Gln Ala Met Asn
    450                 455                 460

gca gca atg cgt tca gca gcg gta agc ggt cgc atg gca aac atg gac   1440
Ala Ala Met Arg Ser Ala Ala Val Ser Gly Arg Met Ala Asn Met Asp
465                 470                 475                 480

ggc aac agt gta ggt ggc act gaa gca gat cca cag cag ggg agt ggc   1488
Gly Asn Ser Val Gly Gly Thr Glu Ala Asp Pro Gln Gln Gly Ser Gly
                485                 490                 495

gta acc gag aag ggt gat aaa ggc gtt aaa tagcgtgtaa aacacaatga     1538
Val Thr Glu Lys Gly Asp Lys Gly Val Lys
            500                 505

ccg                                                               1541


<210> 778
<211> 506
<212> PRT
<213> Corynebacterium glutamicum

<400> 778
Ala Asp Ala Asn Ala Asp Phe Val Asp Gly Val Val Asp Gly Ala Gly
  1               5                  10                  15

Arg Ala Ser Phe Ser Asn Ala Ala Tyr Ser Ser Asp Gly Thr Thr Leu
            20                  25                  30

Asp Gly Glu Gly Ala Ser Val Asp Ala Gln Gly Asn Pro Leu His Ala
        35                  40                  45

Asp Gly Thr Pro Met Ser Ala Ala Glu Ala Glu Met Lys Met Ala Gly
    50                  55                  60

Leu Ser Ser Ser Gly Thr Met Met Glu Lys Ser Gly Val Lys Ser Ser
65                  70                  75                  80

Gly Ile Thr Thr Ala Ala Asp Val Met Asp Asp Gln Ser Leu Ala Ser
                85                  90                  95

Ser Val Thr Glu Ser Gly Leu Ser Lys Ile Pro Asp Thr Tyr Gly Ala
            100                 105                 110
```

```
Asp Val Ser Gly Ala Ala Gly Thr Val Gly Thr Thr Gly Ala Asp Tyr
        115                 120                 125

Ser Ala Thr Asp Ser Ser Ala Gly Leu Asn Met Ser Glu Ala Ala Leu
    130                 135                 140

Gln Ser Gly Thr Pro Met Gly Ala Leu Ala Gly Gly Ser Val Ser Ser
145                 150                 155                 160

Ser Asp Gln Ala Met Asn Asp Ala Ala Leu Gln Ile Ala Ala Ser Gln
                165                 170                 175

Gly Leu Ala Pro Ala Gly Ser Ile Ala Gly Met Glu Gln Leu Ser Ala
            180                 185                 190

Gln Ala Thr Glu Ala Pro Ala Gly Lys Ala Gly Lys Gln Leu Gly Asp
        195                 200                 205

Leu Ser Gly Ser Ala Leu Asn Thr Gln Leu Ala Ser Met Gly Gln Gln
    210                 215                 220

Val Gly Asp Ser Val Asn Ser Ala Tyr Ala Ala Gly Gly Met Gly Gly
225                 230                 235                 240

Val Asp Val Ala Gly Lys Val Thr Glu Ala Ala Gln His Leu Ser Gln
                245                 250                 255

Val Pro Gly Gln Ile Gln Asn Ala Val Thr Asn Ala Asp Ala Gly Ser
            260                 265                 270

Ser Gly Ala Ser Phe Gly Gln Met Ala Gln Gly Ala Ala Gly Ile Ala
        275                 280                 285

Gly Val Ala Gly Val Ile Gly Ala Ala Gly Ala Ala Ser Ser Ala Ala
    290                 295                 300

Gln Gly Ala Gly Thr Val Gln Gly Ala Met Gly Asn Ala Ala Ala Gly
305                 310                 315                 320

Ala Gly Met Ile Asn Asn Ala Val Ser Gly Gly Ala Thr Gly Ser Thr
                325                 330                 335

Gly Ala Ala His Val Val Asn Ala Ser His Gly Pro Val Ala Pro Gly
            340                 345                 350

Gln Ala His Tyr Gln Glu Ser Gly His Ala Gln Ala Phe Val Gln Asn
        355                 360                 365

Asn Gln Ala Asn Thr Ala His Thr Ala Asn Thr Arg Ala Pro Ser Ser
    370                 375                 380

Ala Gln Ile Met Gly Ala Asn Val Ala Gly Ser Leu Ala Ser Gln Ala
385                 390                 395                 400

Val Arg Gly Ile Gly Gln Pro Gly Gln Met Gly Ala Asn Val Arg Asp
                405                 410                 415

Ala Met Gly Gly Ser Gly Arg Ser Gly Gly Arg Gly Gly Ala Thr Gln
            420                 425                 430

Gly Gly Arg Gly Ala Gln Arg Ser Gly Val Ser Ala Lys Asn Gly Ile
```

```
        435                 440                 445

Arg Ala Gln Arg Gly Gln Lys Pro Ser Val Thr Gly Gln Ala Met Asn
    450                 455                 460

Ala Ala Met Arg Ser Ala Ala Val Ser Gly Arg Met Ala Asn Met Asp
465                 470                 475                 480

Gly Asn Ser Val Gly Gly Thr Glu Ala Asp Pro Gln Gln Gly Ser Gly
                485                 490                 495

Val Thr Glu Lys Gly Asp Lys Gly Val Lys
            500                 505


<210> 779
<211> 1065
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1042)
<223> RXN01765

<400> 779
gcagtccgtc ggtgtcgttt tccctgaact gccggcagag cttcagccac aaatcccagt 60

caaggcataa caccgcacac caagaatttt aggaggggtc atg agc aac aac gta   115
                                              Met Ser Asn Asn Val
                                                1               5

gtg aaa tat gag tgc gcg gtc gac gcc gac aac att gtc gca gtc gat   163
Val Lys Tyr Glu Cys Ala Val Asp Ala Asp Asn Ile Val Ala Val Asp
                10                  15                  20

atg cat gtg cac ttg gaa gtc gac agc tgc gga cac aaa tcg atg ccg   211
Met His Val His Leu Glu Val Asp Ser Cys Gly His Lys Ser Met Pro
            25                  30                  35

gca gac atc atg gcg gca tcc tcg aag tac ttt aag acc gcg gaa cga   259
Ala Asp Ile Met Ala Ala Ser Ser Lys Tyr Phe Lys Thr Ala Glu Arg
        40                  45                  50

act ccc tca gca gat gcc att gct gat att tat agg gaa cac aag atg   307
Thr Pro Ser Ala Asp Ala Ile Ala Asp Ile Tyr Arg Glu His Lys Met
    55                  60                  65

gcg gcg gtg gtt ttc acc atc gat gcg cgg acc caa atg ggg cat ctg   355
Ala Ala Val Val Phe Thr Ile Asp Ala Arg Thr Gln Met Gly His Leu
70                  75                  80                  85

ccg aac tcg att gat gat ttg gtg gca agc tgt gcc cgc aac aat gac   403
Pro Asn Ser Ile Asp Asp Leu Val Ala Ser Cys Ala Arg Asn Asn Asp
                90                  95                  100

gtg ctg atc cct ttt ggc agt gtg gat cct cgt acc ggc gag gac gcg   451
Val Leu Ile Pro Phe Gly Ser Val Asp Pro Arg Thr Gly Glu Asp Ala
            105                 110                 115

ctg gtg gaa gct cgc cga cag gtg gaa gaa ctc ggg gtg cga ggc ttc   499
```

```
Leu Val Glu Ala Arg Arg Gln Val Glu Glu Leu Gly Val Arg Gly Phe
        120                 125                 130

aaa ttc cat cca tcg gtt caa gga ttc gac cca tcc gcg cca gag ttc   547
Lys Phe His Pro Ser Val Gln Gly Phe Asp Pro Ser Ala Pro Glu Phe
    135                 140                 145

tac cca ctg tgg gaa ttg ctc gaa agt ttt gga ttg cca tgc gtg ttc   595
Tyr Pro Leu Trp Glu Leu Leu Glu Ser Phe Gly Leu Pro Cys Val Phe
150                 155                 160                 165

cat acc gga caa aac ggc atg ggt gca ggt ctt cca ggt ggt cga ggc   643
His Thr Gly Gln Asn Gly Met Gly Ala Gly Leu Pro Gly Gly Arg Gly
                170                 175                 180

att aag ctg cgc ttc tcc aac cca atg ttg ctt gat gat gtt gcg gcg   691
Ile Lys Leu Arg Phe Ser Asn Pro Met Leu Leu Asp Asp Val Ala Ala
            185                 190                 195

gac ttc ccg aac ctg acc atc atc atg gcg cac cct tct gtt cct tgg   739
Asp Phe Pro Asn Leu Thr Ile Ile Met Ala His Pro Ser Val Pro Trp
        200                 205                 210

cag gat gag gct aac tcg att gcc acc cac aag gcc aat gtg ttc att   787
Gln Asp Glu Ala Asn Ser Ile Ala Thr His Lys Ala Asn Val Phe Ile
    215                 220                 225

gat ctt tcc ggc tgg tcg ccg aag tat ttc cca gag tct ttg gtc aga   835
Asp Leu Ser Gly Trp Ser Pro Lys Tyr Phe Pro Glu Ser Leu Val Arg
230                 235                 240                 245

cag tcc aat aac gtg cta tcc aag aag gtg ctg ttt ggc acg gac ttc   883
Gln Ser Asn Asn Val Leu Ser Lys Lys Val Leu Phe Gly Thr Asp Phe
                250                 255                 260

ccg ctg att acc cca gag aaa tgg ctt gcg gct ttc gcg aat ctg cca   931
Pro Leu Ile Thr Pro Glu Lys Trp Leu Ala Ala Phe Ala Asn Leu Pro
            265                 270                 275

ctg aag gat gag gtt cgt ccg gga atc ctc aaa gac aat gcg gtg aag   979
Leu Lys Asp Glu Val Arg Pro Gly Ile Leu Lys Asp Asn Ala Val Lys
        280                 285                 290

gta ctt ggc cta gcc gct agc act gag cgc gga tct caa gca gaa aag   1027
Val Leu Gly Leu Ala Ala Ser Thr Glu Arg Gly Ser Gln Ala Glu Lys
    295                 300                 305

gtc gtg caa cat gcg tgatcccatt caaggtgctg tta                    1065
Val Val Gln His Ala
310
```

<210> 780
<211> 314
<212> PRT
<213> Corynebacterium glutamicum

<400> 780

```
Met Ser Asn Asn Val Val Lys Tyr Glu Cys Ala Val Asp Ala Asp Asn
  1               5                  10                  15
```

```
Ile Val Ala Val Asp Met His Val His Leu Glu Val Asp Ser Cys Gly
            20                  25                  30

His Lys Ser Met Pro Ala Asp Ile Met Ala Ala Ser Ser Lys Tyr Phe
        35                  40                  45

Lys Thr Ala Glu Arg Thr Pro Ser Ala Asp Ala Ile Ala Asp Ile Tyr
    50                  55                  60

Arg Glu His Lys Met Ala Ala Val Val Phe Thr Ile Asp Ala Arg Thr
65                  70                  75                  80

Gln Met Gly His Leu Pro Asn Ser Ile Asp Asp Leu Val Ala Ser Cys
                85                  90                  95

Ala Arg Asn Asn Asp Val Leu Ile Pro Phe Gly Ser Val Asp Pro Arg
            100                 105                 110

Thr Gly Glu Asp Ala Leu Val Glu Ala Arg Arg Gln Val Glu Glu Leu
        115                 120                 125

Gly Val Arg Gly Phe Lys Phe His Pro Ser Val Gln Gly Phe Asp Pro
    130                 135                 140

Ser Ala Pro Glu Phe Tyr Pro Leu Trp Glu Leu Leu Glu Ser Phe Gly
145                 150                 155                 160

Leu Pro Cys Val Phe His Thr Gly Gln Asn Gly Met Gly Ala Gly Leu
                165                 170                 175

Pro Gly Gly Arg Gly Ile Lys Leu Arg Phe Ser Asn Pro Met Leu Leu
            180                 185                 190

Asp Asp Val Ala Ala Asp Phe Pro Asn Leu Thr Ile Ile Met Ala His
        195                 200                 205

Pro Ser Val Pro Trp Gln Asp Glu Ala Asn Ser Ile Ala Thr His Lys
    210                 215                 220

Ala Asn Val Phe Ile Asp Leu Ser Gly Trp Ser Pro Lys Tyr Phe Pro
225                 230                 235                 240

Glu Ser Leu Val Arg Gln Ser Asn Asn Val Leu Ser Lys Lys Val Leu
                245                 250                 255

Phe Gly Thr Asp Phe Pro Leu Ile Thr Pro Glu Lys Trp Leu Ala Ala
            260                 265                 270

Phe Ala Asn Leu Pro Leu Lys Asp Glu Val Arg Pro Gly Ile Leu Lys
        275                 280                 285

Asp Asn Ala Val Lys Val Leu Gly Leu Ala Ala Ser Thr Glu Arg Gly
    290                 295                 300

Ser Gln Ala Glu Lys Val Val Gln His Ala
305                 310
```

<210> 781
<211> 1065
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1042)
<223> FRXA01765

<400> 781
gcagtccgtc ggtgtcgttt tccctgaact gccggcagag cttcagccac aaatcccagt 60

caaggcataa caccgcacac caagaatttt aggaggggtc atg agc aac aac gta 115
Met Ser Asn Asn Val
1 5

gtg aaa tat gag tgc gcg gtc gac gcc gac aac att gtc gca gtc gat 163
Val Lys Tyr Glu Cys Ala Val Asp Ala Asp Asn Ile Val Ala Val Asp
10 15 20

atg cat gtg cac ttg gaa gtc gac agc tgc gga cac aaa tcg atg ccg 211
Met His Val His Leu Glu Val Asp Ser Cys Gly His Lys Ser Met Pro
25 30 35

gca gac atc atg gcg gca tcc tcg aag tac ttt aag acc gcg gaa cga 259
Ala Asp Ile Met Ala Ala Ser Ser Lys Tyr Phe Lys Thr Ala Glu Arg
40 45 50

act ccc tca gca gat gcc att gct gat att tat agg gaa cac aag atg 307
Thr Pro Ser Ala Asp Ala Ile Ala Asp Ile Tyr Arg Glu His Lys Met
55 60 65

gcg gcg gtg gtt ttc acc atc gat gcg cgg acc caa atg ggg cat ctg 355
Ala Ala Val Val Phe Thr Ile Asp Ala Arg Thr Gln Met Gly His Leu
70 75 80 85

ccg aac tcg att gat gat ttg gtg gca agc tgt gcc cgc aac aat gac 403
Pro Asn Ser Ile Asp Asp Leu Val Ala Ser Cys Ala Arg Asn Asn Asp
90 95 100

gtg ctg atc cct ttt ggc agt gtg gat cct cgt acc ggc gag gac gcg 451
Val Leu Ile Pro Phe Gly Ser Val Asp Pro Arg Thr Gly Glu Asp Ala
105 110 115

ctg gtg gaa gct cgc cga cag gtg gaa gaa ctc ggg gtg cga ggc ttc 499
Leu Val Glu Ala Arg Arg Gln Val Glu Glu Leu Gly Val Arg Gly Phe
120 125 130

aaa ttc cat cca tcg gtt caa gga ttc gac cca tcc gcg cca gag ttc 547
Lys Phe His Pro Ser Val Gln Gly Phe Asp Pro Ser Ala Pro Glu Phe
135 140 145

tac cca ctg tgg gaa ttg ctc gaa agt ttt gga ttg cca tgc gtg ttc 595
Tyr Pro Leu Trp Glu Leu Leu Glu Ser Phe Gly Leu Pro Cys Val Phe
150 155 160 165

cat acc gga caa aac ggc atg ggt gca ggt ctt cca ggt ggt cga ggc 643
His Thr Gly Gln Asn Gly Met Gly Ala Gly Leu Pro Gly Gly Arg Gly
170 175 180

att aag ctg cgc ttc tcc aac cca atg ttg ctt gat gat gtt gcg gcg 691
Ile Lys Leu Arg Phe Ser Asn Pro Met Leu Leu Asp Asp Val Ala Ala
185 190 195

```
gac ttc ccg aac ctg acc atc atc atg gcg cac cct tct gtt cct tgg   739
Asp Phe Pro Asn Leu Thr Ile Ile Met Ala His Pro Ser Val Pro Trp
        200                 205                 210

cag gat gag gct aac tcg att gcc acc cac aag gcc aat gtg ttc att   787
Gln Asp Glu Ala Asn Ser Ile Ala Thr His Lys Ala Asn Val Phe Ile
    215                 220                 225

gat ctt tcc ggc tgg tcg ccg aag tat ttc cca gag tct ttg gtc aga   835
Asp Leu Ser Gly Trp Ser Pro Lys Tyr Phe Pro Glu Ser Leu Val Arg
230                 235                 240                 245

cag tcc aat aac gtg cta tcc aag aag gtg ctg ttt ggc acg gac ttc   883
Gln Ser Asn Asn Val Leu Ser Lys Lys Val Leu Phe Gly Thr Asp Phe
                250                 255                 260

ccg ctg att acc cca gag aaa tgg ctt gcg gct ttc gcg aat ctg cca   931
Pro Leu Ile Thr Pro Glu Lys Trp Leu Ala Ala Phe Ala Asn Leu Pro
            265                 270                 275

ctg aag gat gag gtt cgt ccg gga atc ctc aaa gac aat gcg gtg aag   979
Leu Lys Asp Glu Val Arg Pro Gly Ile Leu Lys Asp Asn Ala Val Lys
        280                 285                 290

gta ctt ggc cta gcc gct agc act gag cgc gga tct caa gca gaa aag   1027
Val Leu Gly Leu Ala Ala Ser Thr Glu Arg Gly Ser Gln Ala Glu Lys
    295                 300                 305

gtc gtg caa cat gcg tgatcccatt caaggtgctg tta                    1065
Val Val Gln His Ala
310
```

<210> 782
<211> 314
<212> PRT
<213> Corynebacterium glutamicum

<400> 782

```
Met Ser Asn Asn Val Val Lys Tyr Glu Cys Ala Val Asp Ala Asp Asn
  1               5                  10                  15

Ile Val Ala Val Asp Met His Val His Leu Glu Val Asp Ser Cys Gly
             20                  25                  30

His Lys Ser Met Pro Ala Asp Ile Met Ala Ala Ser Ser Lys Tyr Phe
         35                  40                  45

Lys Thr Ala Glu Arg Thr Pro Ser Ala Asp Ala Ile Ala Asp Ile Tyr
     50                  55                  60

Arg Glu His Lys Met Ala Ala Val Val Phe Thr Ile Asp Ala Arg Thr
 65                  70                  75                  80

Gln Met Gly His Leu Pro Asn Ser Ile Asp Asp Leu Val Ala Ser Cys
                 85                  90                  95

Ala Arg Asn Asn Asp Val Leu Ile Pro Phe Gly Ser Val Asp Pro Arg
            100                 105                 110
```

```
Thr Gly Glu Asp Ala Leu Val Glu Ala Arg Arg Gln Val Glu Glu Leu
        115                 120                 125

Gly Val Arg Gly Phe Lys Phe His Pro Ser Val Gln Gly Phe Asp Pro
    130                 135                 140

Ser Ala Pro Glu Phe Tyr Pro Leu Trp Glu Leu Leu Glu Ser Phe Gly
145                 150                 155                 160

Leu Pro Cys Val Phe His Thr Gly Gln Asn Gly Met Gly Ala Gly Leu
                165                 170                 175

Pro Gly Gly Arg Gly Ile Lys Leu Arg Phe Ser Asn Pro Met Leu Leu
            180                 185                 190

Asp Asp Val Ala Ala Asp Phe Pro Asn Leu Thr Ile Ile Met Ala His
        195                 200                 205

Pro Ser Val Pro Trp Gln Asp Glu Ala Asn Ser Ile Ala Thr His Lys
    210                 215                 220

Ala Asn Val Phe Ile Asp Leu Ser Gly Trp Ser Pro Lys Tyr Phe Pro
225                 230                 235                 240

Glu Ser Leu Val Arg Gln Ser Asn Asn Val Leu Ser Lys Lys Val Leu
                245                 250                 255

Phe Gly Thr Asp Phe Pro Leu Ile Thr Pro Glu Lys Trp Leu Ala Ala
            260                 265                 270

Phe Ala Asn Leu Pro Leu Lys Asp Glu Val Arg Pro Gly Ile Leu Lys
        275                 280                 285

Asp Asn Ala Val Lys Val Leu Gly Leu Ala Ala Ser Thr Glu Arg Gly
    290                 295                 300

Ser Gln Ala Glu Lys Val Val Gln His Ala
305                 310
```

<210> 783
<211> 588
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(565)
<223> RXN01767

<400> 783
acaccagccc tccacaagag cgtcgaagca atctacgctt cgacgctctt tttttcacta 60

cctactcatc ccccacataa gaaaaaaaga cgacaccacc atg att gac cat aaa 115
                                            Met Ile Asp His Lys
                                              1   5

ctg tgg ttt aac aca gta acc aac aac gcc tct gtc cga gaa gct gca 163
Leu Trp Phe Asn Thr Val Thr Asn Asn Ala Ser Val Arg Glu Ala Ala
                10   15   20

```
gga aaa tgc gac ata ccc atc aga acg ctc aac gag cag ctt aac cgt   211
Gly Lys Cys Asp Ile Pro Ile Arg Thr Leu Asn Glu Gln Leu Asn Arg
            25                  30                  35

cga ata ctc cct gaa aag acc gtc atc gct cta gca cgc gct tat gat   259
Arg Ile Leu Pro Glu Lys Thr Val Ile Ala Leu Ala Arg Ala Tyr Asp
        40                  45                  50

ctc tca cct gtt gat gcg ctc gtt cgc acc gga cac ctc acc gaa gaa   307
Leu Ser Pro Val Asp Ala Leu Val Arg Thr Gly His Leu Thr Glu Glu
    55                  60                  65

gag gct ggt agt cgt gaa gaa gat gcc agc cca gat tca gct gac gac   355
Glu Ala Gly Ser Arg Glu Glu Asp Ala Ser Pro Asp Ser Ala Asp Asp
70                  75                  80                  85

tac cct acc tgg gca ctg aac tcg cac ctt gac tat ggc att ctc gga   403
Tyr Pro Thr Trp Ala Leu Asn Ser His Leu Asp Tyr Gly Ile Leu Gly
                90                  95                  100

gct ttt ggc gac atc gct gaa gaa gta aac agc gaa aga gtt aac cgc   451
Ala Phe Gly Asp Ile Ala Glu Glu Val Asn Ser Glu Arg Val Asn Arg
            105                 110                 115

gac aac gcc ata gag caa att cgc gca tgg ctc gac gag ctt cca ggc   499
Asp Asn Ala Ile Glu Gln Ile Arg Ala Trp Leu Asp Glu Leu Pro Gly
        120                 125                 130

agc cta ttc aac aac ctc cgc agc act aaa aca ggc tac atc gaa cta   547
Ser Leu Phe Asn Asn Leu Arg Ser Thr Lys Thr Gly Tyr Ile Glu Leu
    135                 140                 145

ttc gag acc tat ctc gat taaacccaac cagcacaaca ata                588
Phe Glu Thr Tyr Leu Asp
150                 155


<210> 784
<211> 155
<212> PRT
<213> Corynebacterium glutamicum

<400> 784
Met Ile Asp His Lys Leu Trp Phe Asn Thr Val Thr Asn Asn Ala Ser
  1               5                  10                  15

Val Arg Glu Ala Ala Gly Lys Cys Asp Ile Pro Ile Arg Thr Leu Asn
            20                  25                  30

Glu Gln Leu Asn Arg Arg Ile Leu Pro Glu Lys Thr Val Ile Ala Leu
        35                  40                  45

Ala Arg Ala Tyr Asp Leu Ser Pro Val Asp Ala Leu Val Arg Thr Gly
    50                  55                  60

His Leu Thr Glu Glu Glu Ala Gly Ser Arg Glu Glu Asp Ala Ser Pro
65                  70                  75                  80

Asp Ser Ala Asp Asp Tyr Pro Thr Trp Ala Leu Asn Ser His Leu Asp
                85                  90                  95
```

```
Tyr Gly Ile Leu Gly Ala Phe Gly Asp Ile Ala Glu Glu Val Asn Ser
            100                 105                 110

Glu Arg Val Asn Arg Asp Asn Ala Ile Glu Gln Ile Arg Ala Trp Leu
        115                 120                 125

Asp Glu Leu Pro Gly Ser Leu Phe Asn Asn Leu Arg Ser Thr Lys Thr
    130                 135                 140

Gly Tyr Ile Glu Leu Phe Glu Thr Tyr Leu Asp
145                 150                 155


<210> 785
<211> 436
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(436)
<223> FRXA01767

<400> 785
acaccagccc tccacaagag cgtcgaagca atctacgctt cgacgctctt tttttcacta 60

cctactcatc ccccacataa gaaaaaaaga cgacaccacc atg att gac cat aaa   115
                                            Met Ile Asp His Lys
                                              1               5

ctg tgg ttt aac aca gta acc aac aac gcc tct gtc cga gaa gct gca   163
Leu Trp Phe Asn Thr Val Thr Asn Asn Ala Ser Val Arg Glu Ala Ala
                10                  15                  20

gga aaa tgc gac ata ccc atc aga acg ctc aac gag cag ctt aac cgt   211
Gly Lys Cys Asp Ile Pro Ile Arg Thr Leu Asn Glu Gln Leu Asn Arg
            25                  30                  35

cga ata ctc cct gaa aag acc gtc atc gct cta gca cgc gct tat gat   259
Arg Ile Leu Pro Glu Lys Thr Val Ile Ala Leu Ala Arg Ala Tyr Asp
        40                  45                  50

ctc tca cct gtt gat gcg ctc gtt cgc acc gga cac ctc acc gaa gaa   307
Leu Ser Pro Val Asp Ala Leu Val Arg Thr Gly His Leu Thr Glu Glu
    55                  60                  65

gag gct ggt agt cgt gaa gaa gat gcc agc cca gat tca gct gac gac   355
Glu Ala Gly Ser Arg Glu Glu Asp Ala Ser Pro Asp Ser Ala Asp Asp
70                  75                  80                  85

tac cct acc tgg gca ctg aac tcg cac ctt gac tat ggc att ctc gga   403
Tyr Pro Thr Trp Ala Leu Asn Ser His Leu Asp Tyr Gly Ile Leu Gly
                90                  95                  100

gct ttt ggc gac atc gct gaa gaa gta aac agc                      436
Ala Phe Gly Asp Ile Ala Glu Glu Val Asn Ser
            105                 110


<210> 786
<211> 112
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<212> PRT
<213> Corynebacterium glutamicum

<400> 786
Met Ile Asp His Lys Leu Trp Phe Asn Thr Val Thr Asn Asn Ala Ser
1 5 10 15

Val Arg Glu Ala Ala Gly Lys Cys Asp Ile Pro Ile Arg Thr Leu Asn
20 25 30

Glu Gln Leu Asn Arg Arg Ile Leu Pro Glu Lys Thr Val Ile Ala Leu
35 40 45

Ala Arg Ala Tyr Asp Leu Ser Pro Val Asp Ala Leu Val Arg Thr Gly
50 55 60

His Leu Thr Glu Glu Glu Ala Gly Ser Arg Glu Glu Asp Ala Ser Pro
65 70 75 80

Asp Ser Ala Asp Asp Tyr Pro Thr Trp Ala Leu Asn Ser His Leu Asp
85 90 95

Tyr Gly Ile Leu Gly Ala Phe Gly Asp Ile Ala Glu Glu Val Asn Ser
100 105 110

<210> 787
<211> 564
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(541)
<223> RXN01769

<400> 787
attttcaaca accaggacta aaacacctgc tgctgttgag cgcttctcac acatcatcct 60

cacaaccccg ttgcagcacc agcataaatc tatattcgct gtg acg ggg ttg ttg 115
Val Thr Gly Leu Leu
1 5

ggg cgc gcc cca cat tca ctc ttt ttc ccg att ggt ttc tac tac aca 163
Gly Arg Ala Pro His Ser Leu Phe Phe Pro Ile Gly Phe Tyr Tyr Thr
10 15 20

ccc atg acc tct att act act acc gat acc ccg cta tat aca gca ctg 211
Pro Met Thr Ser Ile Thr Thr Thr Asp Thr Pro Leu Tyr Thr Ala Leu
25 30 35

ccc cat acc cgt atc tct gat gcg gaa ttg ttg aca cca aca aca act 259
Pro His Thr Arg Ile Ser Asp Ala Glu Leu Leu Thr Pro Thr Thr Thr
40 45 50

gtg cac gag att ctc gtt tac gga ccg gct gag tgc cca ggg tgt aca 307
Val His Glu Ile Leu Val Tyr Gly Pro Ala Glu Cys Pro Gly Cys Thr
55 60 65

```
gca acg ctt gac ttc ttt gca cgc aaa aac atg ccg gcc acc aaa gtc   355
Ala Thr Leu Asp Phe Phe Ala Arg Lys Asn Met Pro Ala Thr Lys Val
 70                  75                  80                  85

act gta gct gcc ggt gat gta gca cat acc tac atc acc caa gac tta   403
Thr Val Ala Ala Gly Asp Val Ala His Thr Tyr Ile Thr Gln Asp Leu
                90                  95                 100

ggt tat ctc caa gca ccg att gtc act gtc cgt atc agt tcc tct gct   451
Gly Tyr Leu Gln Ala Pro Ile Val Thr Val Arg Ile Ser Ser Ser Ala
            105                 110                 115

tct aac cac gac aac gaa cac aac acc cag atc ctg cac tgg tcc ggc   499
Ser Asn His Asp Asn Glu His Asn Thr Gln Ile Leu His Trp Ser Gly
        120                 125                 130

gtt aat cgc tac ctc atg cag gca ctc tcc cgt act cat ttc           541
Val Asn Arg Tyr Leu Met Gln Ala Leu Ser Arg Thr His Phe
    135                 140                 145

tagaaaggtt tttcccgtca tgt                                        564


<210> 788
<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 788
Val Thr Gly Leu Leu Gly Arg Ala Pro His Ser Leu Phe Phe Pro Ile
  1               5                  10                  15

Gly Phe Tyr Tyr Thr Pro Met Thr Ser Ile Thr Thr Thr Asp Thr Pro
             20                  25                  30

Leu Tyr Thr Ala Leu Pro His Thr Arg Ile Ser Asp Ala Glu Leu Leu
         35                  40                  45

Thr Pro Thr Thr Thr Val His Glu Ile Leu Val Tyr Gly Pro Ala Glu
     50                  55                  60

Cys Pro Gly Cys Thr Ala Thr Leu Asp Phe Phe Ala Arg Lys Asn Met
 65                  70                  75                  80

Pro Ala Thr Lys Val Thr Val Ala Ala Gly Asp Val Ala His Thr Tyr
                85                  90                  95

Ile Thr Gln Asp Leu Gly Tyr Leu Gln Ala Pro Ile Val Thr Val Arg
            100                 105                 110

Ile Ser Ser Ser Ala Ser Asn His Asp Asn Glu His Asn Thr Gln Ile
        115                 120                 125

Leu His Trp Ser Gly Val Asn Arg Tyr Leu Met Gln Ala Leu Ser Arg
    130                 135                 140

Thr His Phe
145
```

<210> 789
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> FRXA01769

<400> 789
caggactaaa acacctgctg ctgttgagcg cttctcacac atcatcctca caaccccgtt 60

gcagcaccag cataaatcta tattcgctgt gacggggttg ttg ggg cgc gcc cca 115
Leu Gly Arg Ala Pro
1 5

cat tca ctc ttt ttc ccg att ggt ttc tac tac aca ccc atg acc tct 163
His Ser Leu Phe Phe Pro Ile Gly Phe Tyr Tyr Thr Pro Met Thr Ser
10 15 20

att act act acc gat acc ccg cta tat aca gca ctg ccc cat acc cgt 211
Ile Thr Thr Thr Asp Thr Pro Leu Tyr Thr Ala Leu Pro His Thr Arg
25 30 35

atc tct gat gcg gaa ttg ttg aca cca aca aca act gtg cac gag att 259
Ile Ser Asp Ala Glu Leu Leu Thr Pro Thr Thr Thr Val His Glu Ile
40 45 50

ctc gtt tac gga ccg gct gag tgc cca ggg tgt aca gca acg ctt gac 307
Leu Val Tyr Gly Pro Ala Glu Cys Pro Gly Cys Thr Ala Thr Leu Asp
55 60 65

ttc ttt gca cgc aaa aac atg ccg gcc acc aaa gtc act gta gct gcc 355
Phe Phe Ala Arg Lys Asn Met Pro Ala Thr Lys Val Thr Val Ala Ala
70 75 80 85

ggt gat gta gca cat acc tac atc acc caa gac tta ggt tat ctc caa 403
Gly Asp Val Ala His Thr Tyr Ile Thr Gln Asp Leu Gly Tyr Leu Gln
90 95 100

gca ccg att gtc act gtc cgt atc agt tcc tct gct tct aac cac gac 451
Ala Pro Ile Val Thr Val Arg Ile Ser Ser Ser Ala Ser Asn His Asp
105 110 115

aac gaa cac aac acc cag atc ctg cac tgg tcc ggc gtt aat cgc tac 499
Asn Glu His Asn Thr Gln Ile Leu His Trp Ser Gly Val Asn Arg Tyr
120 125 130

ctc atg cag gca ctc tcc cgt act cat ttc tagaaaggtt tttcccgtca 549
Leu Met Gln Ala Leu Ser Arg Thr His Phe
135 140

tgt 552

<210> 790
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 790
Leu Gly Arg Ala Pro His Ser Leu Phe Phe Pro Ile Gly Phe Tyr Tyr
1 5 10 15

Thr Pro Met Thr Ser Ile Thr Thr Thr Asp Thr Pro Leu Tyr Thr Ala
20 25 30

Leu Pro His Thr Arg Ile Ser Asp Ala Glu Leu Leu Thr Pro Thr Thr
35 40 45

Thr Val His Glu Ile Leu Val Tyr Gly Pro Ala Glu Cys Pro Gly Cys
50 55 60

Thr Ala Thr Leu Asp Phe Phe Ala Arg Lys Asn Met Pro Ala Thr Lys
65 70 75 80

Val Thr Val Ala Ala Gly Asp Val Ala His Thr Tyr Ile Thr Gln Asp
85 90 95

Leu Gly Tyr Leu Gln Ala Pro Ile Val Thr Val Arg Ile Ser Ser Ser
100 105 110

Ala Ser Asn His Asp Asn Glu His Asn Thr Gln Ile Leu His Trp Ser
115 120 125

Gly Val Asn Arg Tyr Leu Met Gln Ala Leu Ser Arg Thr His Phe
130 135 140

<210> 791
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> RXN01771

<400> 791
tgccccgctg ttggtggttc cggagcggcg ataatcgcta aacgtttgag gtgattgtat 60

gggtattttc aggtcgcggt cgcaggattt tgggtggagc atg cac cag gct ggc 115
Met His Gln Ala Gly
1 5

cag ctc atc aat gat ccc agt cag ggt ctg tgg cgc act tct gcc ctg 163
Gln Leu Ile Asn Asp Pro Ser Gln Gly Leu Trp Arg Thr Ser Ala Leu
10 15 20

cgc tcg ccg gtt gct cgg gtt gga cat gcc gtg ttg cgc cag cgt gcc 211
Arg Ser Pro Val Ala Arg Val Gly His Ala Val Leu Arg Gln Arg Ala
25 30 35

ggt gag atc tcg cgc atg caa ggt cgt gag ttt tct cgc cct ggg gat 259
Gly Glu Ile Ser Arg Met Gln Gly Arg Glu Phe Ser Arg Pro Gly Asp
40 45 50

cag ttc cga cag gta gat ttg cgc agg cga ctg att cag gtc cat ccc 307
Gln Phe Arg Gln Val Asp Leu Arg Arg Arg Leu Ile Gln Val His Pro
55 60 65

```
caa tca att cct aca gcg gat gcg atg gcc gta acc atc acc atg gcg   355
Gln Ser Ile Pro Thr Ala Asp Ala Met Ala Val Thr Ile Thr Met Ala
 70                  75                  80                  85

ctc acc gct gcc acg att gat ccg gtg aag ttc gtc gcg gat tca cag   403
Leu Thr Ala Ala Thr Ile Asp Pro Val Lys Phe Val Ala Asp Ser Gln
                90                  95                 100

aac ccg gat gaa gag att tat ttg gca gct cag atc gca ttg cgg gaa   451
Asn Pro Asp Glu Glu Ile Tyr Leu Ala Ala Gln Ile Ala Leu Arg Glu
            105                 110                 115

atg gtt atc gct atg cct ttg gag gat ttc atc ggg gtg cgc att gat   499
Met Val Ile Ala Met Pro Leu Glu Asp Phe Ile Gly Val Arg Ile Asp
        120                 125                 130

cta gag cct gtt ttg gtg gct gct caa gct gct gcg aag aat gtg ggc   547
Leu Glu Pro Val Leu Val Ala Ala Gln Ala Ala Ala Lys Asn Val Gly
    135                 140                 145

gtg gaa gtc tcg tca atc ttg ctg aag gat ctg aat ctt ccc cag gag   595
Val Glu Val Ser Ser Ile Leu Leu Lys Asp Leu Asn Leu Pro Gln Glu
150                 155                 160                 165

tac tcg gga gcg ttg cag gaa tcg atc gtt gcg aaa att caa gcc gaa   643
Tyr Ser Gly Ala Leu Gln Glu Ser Ile Val Ala Lys Ile Gln Ala Glu
                170                 175                 180

act gat ctg gaa cgt gca cga aat gaa gtg aaa act acc cgt gct cga   691
Thr Asp Leu Glu Arg Ala Arg Asn Glu Val Lys Thr Thr Arg Ala Arg
            185                 190                 195

ctt gcc agc gcg aaa gtg ttg gag caa aat ccg att ctt gcc aaa att   739
Leu Ala Ser Ala Lys Val Leu Glu Gln Asn Pro Ile Leu Ala Lys Ile
        200                 205                 210

cgg atg att gaa gcg ctc cca ccg gga tcc aca att gag gtt cgg gag   787
Arg Met Ile Glu Ala Leu Pro Pro Gly Ser Thr Ile Glu Val Arg Glu
    215                 220                 225

ggt gac tca aag gca taaagttgcc catttcggtg ccc                    825
Gly Asp Ser Lys Ala
230
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<210> 792
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 792

```
Met His Gln Ala Gly Gln Leu Ile Asn Asp Pro Ser Gln Gly Leu Trp
  1               5                  10                  15

Arg Thr Ser Ala Leu Arg Ser Pro Val Ala Arg Val Gly His Ala Val
             20                  25                  30

Leu Arg Gln Arg Ala Gly Glu Ile Ser Arg Met Gln Gly Arg Glu Phe
         35                  40                  45
```

```
Ser Arg Pro Gly Asp Gln Phe Arg Gln Val Asp Leu Arg Arg Arg Leu
     50                  55                  60

Ile Gln Val His Pro Gln Ser Ile Pro Thr Ala Asp Ala Met Ala Val
 65                  70                  75                  80

Thr Ile Thr Met Ala Leu Thr Ala Ala Thr Ile Asp Pro Val Lys Phe
                 85                  90                  95

Val Ala Asp Ser Gln Asn Pro Asp Glu Glu Ile Tyr Leu Ala Ala Gln
            100                 105                 110

Ile Ala Leu Arg Glu Met Val Ile Ala Met Pro Leu Glu Asp Phe Ile
        115                 120                 125

Gly Val Arg Ile Asp Leu Glu Pro Val Leu Val Ala Ala Gln Ala Ala
    130                 135                 140

Ala Lys Asn Val Gly Val Glu Val Ser Ser Ile Leu Leu Lys Asp Leu
145                 150                 155                 160

Asn Leu Pro Gln Glu Tyr Ser Gly Ala Leu Gln Glu Ser Ile Val Ala
                165                 170                 175

Lys Ile Gln Ala Glu Thr Asp Leu Glu Arg Ala Arg Asn Glu Val Lys
            180                 185                 190

Thr Thr Arg Ala Arg Leu Ala Ser Ala Lys Val Leu Glu Gln Asn Pro
        195                 200                 205

Ile Leu Ala Lys Ile Arg Met Ile Glu Ala Leu Pro Pro Gly Ser Thr
    210                 215                 220

Ile Glu Val Arg Glu Gly Asp Ser Lys Ala
225                 230
```

<210> 793
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> FRXA01771

<400> 793
tgccccgctg ttggtggttc cggagcggcg ataatcgcta aacgtttgag gtgattgtat 60

gggtattttc aggtcgcggt cgcaggattt tgggtggagc atg cac cag gct ggc 115
                                        Met His Gln Ala Gly
                                          1   5

cag ctc atc aat gat ccc agt cag ggt ctg tgg cgc act tct gcc ctg 163
Gln Leu Ile Asn Asp Pro Ser Gln Gly Leu Trp Arg Thr Ser Ala Leu
                10   15   20

cgc tcg ccg gtt gct cgg gtt gga cat gcc gtg ttg cgc cag cgt gcc 211
Arg Ser Pro Val Ala Arg Val Gly His Ala Val Leu Arg Gln Arg Ala
            25   30   35

```
ggt gag atc tcg cgc atg caa ggt cgt gag ttt tct cgc cct ggg gat   259
Gly Glu Ile Ser Arg Met Gln Gly Arg Glu Phe Ser Arg Pro Gly Asp
         40                  45                  50

cag ttc cga cag gta gat ttg cgc agg cga ctg att cag gtc cat ccc   307
Gln Phe Arg Gln Val Asp Leu Arg Arg Arg Leu Ile Gln Val His Pro
     55                  60                  65

caa tca att cct aca gcg gat gcg atg gcc gta acc atc acc atg gcg   355
Gln Ser Ile Pro Thr Ala Asp Ala Met Ala Val Thr Ile Thr Met Ala
 70                  75                  80                  85

ctc acc gct gcc acg att gat ccg gtg aag ttc gtc gcg gat tca cag   403
Leu Thr Ala Ala Thr Ile Asp Pro Val Lys Phe Val Ala Asp Ser Gln
                 90                  95                 100

aac ccg gat gaa gag att tat ttg gca gct cag atc gca ttg cgg gaa   451
Asn Pro Asp Glu Glu Ile Tyr Leu Ala Ala Gln Ile Ala Leu Arg Glu
            105                 110                 115

atg gtt atc gct atg cct ttg gag gat ttc atc ggg gtg cgc att gat   499
Met Val Ile Ala Met Pro Leu Glu Asp Phe Ile Gly Val Arg Ile Asp
        120                 125                 130

cta gag cct gtt ttg gtg gct gct caa gct gct gcg aag aat gtg ggc   547
Leu Glu Pro Val Leu Val Ala Ala Gln Ala Ala Ala Lys Asn Val Gly
    135                 140                 145

gtg gaa gtc tcg tca atc ttg ctg aag gat ctg aat ctt ccc cag gag   595
Val Glu Val Ser Ser Ile Leu Leu Lys Asp Leu Asn Leu Pro Gln Glu
150                 155                 160                 165

tac tcg gga gcg ttg cag gaa tcg atc gtt gcg aaa att caa gcc gaa   643
Tyr Ser Gly Ala Leu Gln Glu Ser Ile Val Ala Lys Ile Gln Ala Glu
                170                 175                 180

act gat ctg gaa cgt gca cga aat gaa gtg aaa act acc cgt gct cga   691
Thr Asp Leu Glu Arg Ala Arg Asn Glu Val Lys Thr Thr Arg Ala Arg
            185                 190                 195

ctt gcc agc gcg aaa gtg ttg gag caa aat ccg att ctt gcc aaa att   739
Leu Ala Ser Ala Lys Val Leu Glu Gln Asn Pro Ile Leu Ala Lys Ile
        200                 205                 210

cgg atg att gaa gcg ctc cca ccg gga tcc aca att gag gtt cgg gag   787
Arg Met Ile Glu Ala Leu Pro Pro Gly Ser Thr Ile Glu Val Arg Glu
    215                 220                 225

ggt gac tca aag gca taaagttgcc catttcggtg ccc                    825
Gly Asp Ser Lys Ala
230
```

<210> 794
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 794
Met His Gln Ala Gly Gln Leu Ile Asn Asp Pro Ser Gln Gly Leu Trp

```
  1               5                  10                  15

Arg Thr Ser Ala Leu Arg Ser Pro Val Ala Arg Val Gly His Ala Val
            20                  25                  30

Leu Arg Gln Arg Ala Gly Glu Ile Ser Arg Met Gln Gly Arg Glu Phe
        35                  40                  45

Ser Arg Pro Gly Asp Gln Phe Arg Gln Val Asp Leu Arg Arg Arg Leu
    50                  55                  60

Ile Gln Val His Pro Gln Ser Ile Pro Thr Ala Asp Ala Met Ala Val
65                  70                  75                  80

Thr Ile Thr Met Ala Leu Thr Ala Ala Thr Ile Asp Pro Val Lys Phe
                85                  90                  95

Val Ala Asp Ser Gln Asn Pro Asp Glu Glu Ile Tyr Leu Ala Ala Gln
            100                 105                 110

Ile Ala Leu Arg Glu Met Val Ile Ala Met Pro Leu Glu Asp Phe Ile
        115                 120                 125

Gly Val Arg Ile Asp Leu Glu Pro Val Leu Val Ala Ala Gln Ala Ala
    130                 135                 140

Ala Lys Asn Val Gly Val Glu Val Ser Ser Ile Leu Leu Lys Asp Leu
145                 150                 155                 160

Asn Leu Pro Gln Glu Tyr Ser Gly Ala Leu Gln Glu Ser Ile Val Ala
                165                 170                 175

Lys Ile Gln Ala Glu Thr Asp Leu Glu Arg Ala Arg Asn Glu Val Lys
            180                 185                 190

Thr Thr Arg Ala Arg Leu Ala Ser Ala Lys Val Leu Glu Gln Asn Pro
        195                 200                 205

Ile Leu Ala Lys Ile Arg Met Ile Glu Ala Leu Pro Pro Gly Ser Thr
    210                 215                 220

Ile Glu Val Arg Glu Gly Asp Ser Lys Ala
225                 230


<210> 795
<211> 849
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(826)
<223> RXN01774

<400> 795
ctgcgcaaga agagaaaaaa caacgacagc gaagctgcgt tcgggcgaat cggcgataat 60

cacacaccac tcttcctgag agaatcctga ggtcatcacc atg tca ccg aac ttc   115
                                               Met Ser Pro Asn Phe
                                                 1               5
```

```
caa gct cgc ggt act act gcg ccc act gtt gct ttg tcc atg cgc cag   163
Gln Ala Arg Gly Thr Thr Ala Pro Thr Val Ala Leu Ser Met Arg Gln
                 10                  15                  20

atc gcg cac atc cgt gaa gaa att aag aaa tca cca ctc gct gct tcc   211
Ile Ala His Ile Arg Glu Glu Ile Lys Lys Ser Pro Leu Ala Ala Ser
             25                  30                  35

gtt ttc atc aca ccc acc acc aaa caa atg gtt gtc cga gat cta gaa   259
Val Phe Ile Thr Pro Thr Thr Lys Gln Met Val Val Arg Asp Leu Glu
         40                  45                  50

tca ctg ttc cag cag ctc tac cac aca gat cta cct gaa cca tcc atc   307
Ser Leu Phe Gln Gln Leu Tyr His Thr Asp Leu Pro Glu Pro Ser Ile
     55                  60                  65

aaa gac agt ggt ctt atc agt gct atc ggc tct agc gcc ggc aat acc   355
Lys Asp Ser Gly Leu Ile Ser Ala Ile Gly Ser Ser Ala Gly Asn Thr
 70                  75                  80                  85

aat aat cca gca ctc gcc cta gaa act cag atg gct tac cac ctg gtg   403
Asn Asn Pro Ala Leu Ala Leu Glu Thr Gln Met Ala Tyr His Leu Val
                 90                  95                 100

ctt gct atg cac cac acc gat gtt gct acc tgg cac aag gtg gtg acc   451
Leu Ala Met His His Thr Asp Val Ala Thr Trp His Lys Val Val Thr
             105                 110                 115

aaa aac atc acc gaa tct gct gct gca caa gat gct gcg gtc gag cac   499
Lys Asn Ile Thr Glu Ser Ala Ala Ala Gln Asp Ala Ala Val Glu His
         120                 125                 130

agt gct aaa tac gat gct gtg tac gat gcc gca caa ctt atg ggc atc   547
Ser Ala Lys Tyr Asp Ala Val Tyr Asp Ala Ala Gln Leu Met Gly Ile
     135                 140                 145

act gtt gag gaa ggt aat gtc ggt agc atc gct att gcc ttt agc aca   595
Thr Val Glu Glu Gly Asn Val Gly Ser Ile Ala Ile Ala Phe Ser Thr
150                 155                 160                 165

gca cgt gca gac ggt aaa tct gat tgg tgt gtt tcc ggc atc agc cgc   643
Ala Arg Ala Asp Gly Lys Ser Asp Trp Cys Val Ser Gly Ile Ser Arg
                 170                 175                 180

tac atc gag gtc acc gaa gcc ttg gat gct gcg cga gct gtc act aaa   691
Tyr Ile Glu Val Thr Glu Ala Leu Asp Ala Ala Arg Ala Val Thr Lys
             185                 190                 195

aat act gat gcg ctc aat aaa act gct cta cca gac gtg cag ccg gcg   739
Asn Thr Asp Ala Leu Asn Lys Thr Ala Leu Pro Asp Val Gln Pro Ala
         200                 205                 210

ccg gtt gtg cat tca gca cag ttc atg aac aag tcc gca cac gat cat   787
Pro Val Val His Ser Ala Gln Phe Met Asn Lys Ser Ala His Asp His
     215                 220                 225

ggg gtt aat act gcg gaa aaa gat caa cca acc ctg ttt taaaagactg   836
Gly Val Asn Thr Ala Glu Lys Asp Gln Pro Thr Leu Phe
230                 235                 240
```

tccatttaac aac 849

<210> 796
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

<400> 796

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Met Ser Pro Asn Phe Gln Ala Arg Gly Thr Thr Ala Pro Thr Val Ala
  1               5                  10                  15

Leu Ser Met Arg Gln Ile Ala His Ile Arg Glu Glu Ile Lys Lys Ser
             20                  25                  30

Pro Leu Ala Ala Ser Val Phe Ile Thr Pro Thr Thr Lys Gln Met Val
         35                  40                  45

Val Arg Asp Leu Glu Ser Leu Phe Gln Gln Leu Tyr His Thr Asp Leu
     50                  55                  60

Pro Glu Pro Ser Ile Lys Asp Ser Gly Leu Ile Ser Ala Ile Gly Ser
 65                  70                  75                  80

Ser Ala Gly Asn Thr Asn Asn Pro Ala Leu Ala Leu Glu Thr Gln Met
                 85                  90                  95

Ala Tyr His Leu Val Leu Ala Met His His Thr Asp Val Ala Thr Trp
            100                 105                 110

His Lys Val Val Thr Lys Asn Ile Thr Glu Ser Ala Ala Ala Gln Asp
        115                 120                 125

Ala Ala Val Glu His Ser Ala Lys Tyr Asp Ala Val Tyr Asp Ala Ala
    130                 135                 140

Gln Leu Met Gly Ile Thr Val Glu Glu Gly Asn Val Gly Ser Ile Ala
145                 150                 155                 160

Ile Ala Phe Ser Thr Ala Arg Ala Asp Gly Lys Ser Asp Trp Cys Val
                165                 170                 175

Ser Gly Ile Ser Arg Tyr Ile Glu Val Thr Glu Ala Leu Asp Ala Ala
            180                 185                 190

Arg Ala Val Thr Lys Asn Thr Asp Ala Leu Asn Lys Thr Ala Leu Pro
        195                 200                 205

Asp Val Gln Pro Ala Pro Val Val His Ser Ala Gln Phe Met Asn Lys
    210                 215                 220

Ser Ala His Asp His Gly Val Asn Thr Ala Glu Lys Asp Gln Pro Thr
225                 230                 235                 240

Leu Phe
```

<210> 797
<211> 883
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(883)
<223> FRXA01774

<400> 797
ctgcgcaaga agagaaaaaa caacgacagc gaagctgcgt tcgggcgaat cggcgataat 60

cacacaccac tcttcctgag agaatcctga ggtcatcacc atg tca ccg aac ttc 115
Met Ser Pro Asn Phe
1 5

caa gct cgc ggt act act gcg ccc act gtt gct ttg tcc atg cgc cag 163
Gln Ala Arg Gly Thr Thr Ala Pro Thr Val Ala Leu Ser Met Arg Gln
10 15 20

atc gcg cac atc cgt gaa gaa att aag aaa tca cca ctc gct gct tcc 211
Ile Ala His Ile Arg Glu Glu Ile Lys Lys Ser Pro Leu Ala Ala Ser
25 30 35

gtt ttc atc aca ccc acc acc aaa caa atg gtt gtc cga gat cta gaa 259
Val Phe Ile Thr Pro Thr Thr Lys Gln Met Val Val Arg Asp Leu Glu
40 45 50

tca ctg ttc cag cag ctc tac cac aca gat cta cct gaa cca tcc atc 307
Ser Leu Phe Gln Gln Leu Tyr His Thr Asp Leu Pro Glu Pro Ser Ile
55 60 65

aaa gac agt ggt ctt atc agt gct atc ggc tct agc gcc ggc aat acc 355
Lys Asp Ser Gly Leu Ile Ser Ala Ile Gly Ser Ser Ala Gly Asn Thr
70 75 80 85

aat aat cca gca ctc gcc cta gaa act cag atg gct tac cac ctg gtg 403
Asn Asn Pro Ala Leu Ala Leu Glu Thr Gln Met Ala Tyr His Leu Val
90 95 100

ctt gct atg cac cac acc gat gtt gct acc tgg cac aag gtg gtg acc 451
Leu Ala Met His His Thr Asp Val Ala Thr Trp His Lys Val Val Thr
105 110 115

aaa aac atc acc gaa tct gct gct gca caa gat gct gcg gtc gag cac 499
Lys Asn Ile Thr Glu Ser Ala Ala Ala Gln Asp Ala Ala Val Glu His
120 125 130

agt gct aaa tac gat gct gtg tac gat gcc gca caa ctt atg ggc atc 547
Ser Ala Lys Tyr Asp Ala Val Tyr Asp Ala Ala Gln Leu Met Gly Ile
135 140 145

act gtt gag gaa ggt aat gtc ggt agc atc gct att gcc ttt agc aca 595
Thr Val Glu Glu Gly Asn Val Gly Ser Ile Ala Ile Ala Phe Ser Thr
150 155 160 165

gca cgt gca gac ggt aaa tct gat tgg tgt gtt tcc ggc atc agc cgc 643
Ala Arg Ala Asp Gly Lys Ser Asp Trp Cys Val Ser Gly Ile Ser Arg
170 175 180

tac atc gag gtc acc gaa gcc ttg gat gct gcg cga gct gtc act aaa 691
Tyr Ile Glu Val Thr Glu Ala Leu Asp Ala Ala Arg Ala Val Thr Lys
185 190 195

```
aat act gat gcg ctc aat aaa act gct cta cca gac gtg cag ccg gcg   739
Asn Thr Asp Ala Leu Asn Lys Thr Ala Leu Pro Asp Val Gln Pro Ala
        200                 205                 210

ccg gtt gtg cat tca gca cag ttc atg aac aag tcc gca cac gat cat   787
Pro Val Val His Ser Ala Gln Phe Met Asn Lys Ser Ala His Asp His
    215                 220                 225

ggg gtt aat act gcg gaa aaa gat caa cca acc tgt tta aag act gtg   835
Gly Val Asn Thr Ala Glu Lys Asp Gln Pro Thr Cys Leu Lys Thr Val
230                 235                 240                 245

cat tta caa cca cat cgt tac ccc cga aca ggc ttt aag gct att caa   883
His Leu Gln Pro His Arg Tyr Pro Arg Thr Gly Phe Lys Ala Ile Gln
                250                 255                 260
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<210> 798
<211> 261
<212> PRT
<213> Corynebacterium glutamicum

<400> 798

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Met Ser Pro Asn Phe Gln Ala Arg Gly Thr Thr Ala Pro Thr Val Ala
  1               5                  10                  15

Leu Ser Met Arg Gln Ile Ala His Ile Arg Glu Glu Ile Lys Lys Ser
            20                  25                  30

Pro Leu Ala Ala Ser Val Phe Ile Thr Pro Thr Thr Lys Gln Met Val
        35                  40                  45

Val Arg Asp Leu Glu Ser Leu Phe Gln Gln Leu Tyr His Thr Asp Leu
    50                  55                  60

Pro Glu Pro Ser Ile Lys Asp Ser Gly Leu Ile Ser Ala Ile Gly Ser
65                  70                  75                  80

Ser Ala Gly Asn Thr Asn Asn Pro Ala Leu Ala Leu Glu Thr Gln Met
                85                  90                  95

Ala Tyr His Leu Val Leu Ala Met His His Thr Asp Val Ala Thr Trp
            100                 105                 110

His Lys Val Val Thr Lys Asn Ile Thr Glu Ser Ala Ala Ala Gln Asp
        115                 120                 125

Ala Ala Val Glu His Ser Ala Lys Tyr Asp Ala Val Tyr Asp Ala Ala
    130                 135                 140

Gln Leu Met Gly Ile Thr Val Glu Glu Gly Asn Val Gly Ser Ile Ala
145                 150                 155                 160

Ile Ala Phe Ser Thr Ala Arg Ala Asp Gly Lys Ser Asp Trp Cys Val
                165                 170                 175

Ser Gly Ile Ser Arg Tyr Ile Glu Val Thr Glu Ala Leu Asp Ala Ala
            180                 185                 190

Arg Ala Val Thr Lys Asn Thr Asp Ala Leu Asn Lys Thr Ala Leu Pro
```

```
        195                 200                 205

Asp Val Gln Pro Ala Pro Val Val His Ser Ala Gln Phe Met Asn Lys
    210                 215                 220

Ser Ala His Asp His Gly Val Asn Thr Ala Glu Lys Asp Gln Pro Thr
225                 230                 235                 240

Cys Leu Lys Thr Val His Leu Gln Pro His Arg Tyr Pro Arg Thr Gly
                245                 250                 255

Phe Lys Ala Ile Gln
            260


<210> 799
<211> 816
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> RXN01787

<400> 799
cagaagcacg tattttcttc ttaactcgca cctcatctgg tgtgggtttt tttgcatttt 60

ttacacaccc cactccacac acactcgcaa aggattcatc atg agc aac aat gct   115
                                        Met Ser Asn Asn Ala
                                          1               5

ctt tta gta gca aac gaa gcc gac atc ggt ctc tac ctc cac tgg aat   163
Leu Leu Val Ala Asn Glu Ala Asp Ile Gly Leu Tyr Leu His Trp Asn
                10                  15                  20

ggt ggt cgc gac tcg att gag gcg ttt ctc gcc tac gcc gca tac gcg   211
Gly Gly Arg Asp Ser Ile Glu Ala Phe Leu Ala Tyr Ala Ala Tyr Ala
            25                  30                  35

cag tta cca ccc atc aac gaa aat aac gat tgg ttg cca ccg ttt att   259
Gln Leu Pro Pro Ile Asn Glu Asn Asn Asp Trp Leu Pro Pro Phe Ile
        40                  45                  50

act gtg ctg aag aac ttc ttc ggc aat gat ggt tct ggc gtc tac ctc   307
Thr Val Leu Lys Asn Phe Phe Gly Asn Asp Gly Ser Gly Val Tyr Leu
    55                  60                  65

gaa cct gtc aat cag gat tat ctc gac ggc atc gac tat gac aac ggt   355
Glu Pro Val Asn Gln Asp Tyr Leu Asp Gly Ile Asp Tyr Asp Asn Gly
70                  75                  80                  85

gtt tac atg ctt gac gat tat gag atc act gag cgt att aat cca ccc   403
Val Tyr Met Leu Asp Asp Tyr Glu Ile Thr Glu Arg Ile Asn Pro Pro
                90                  95                  100

gct gtt gag caa gac tcc cac gat ctc cac gac atg ttg atc aaa att   451
Ala Val Glu Gln Asp Ser His Asp Leu His Asp Met Leu Ile Lys Ile
            105                 110                 115

gat aaa gct caa cca cct gtc gat caa ctc ggg agt ttt ctc cat ggc   499
```

```
Asp Lys Ala Gln Pro Pro Val Asp Gln Leu Gly Ser Phe Leu His Gly
        120                 125                 130

cta gag acc tct gtc gca gat ttg ggg gtt ggt gat cgc gta ttt ttg   547
Leu Glu Thr Ser Val Ala Asp Leu Gly Val Gly Asp Arg Val Phe Leu
    135                 140                 145

cca cgt ttt agc acc ttt gat aag aaa ctc ggt cgc tac cgc atc cac   595
Pro Arg Phe Ser Thr Phe Asp Lys Lys Leu Gly Arg Tyr Arg Ile His
150                 155                 160                 165

act gtt ctc gga ttc gct gag aac gat ccg ttt aac cct atg acc agc   643
Thr Val Leu Gly Phe Ala Glu Asn Asp Pro Phe Asn Pro Met Thr Ser
                170                 175                 180

agc gag cga ttt aaa ggt aag ccc tat gtc gat atg ttc gac aat caa   691
Ser Glu Arg Phe Lys Gly Lys Pro Tyr Val Asp Met Phe Asp Asn Gln
            185                 190                 195

gac aac gcc ttt aac cca aat tcc tat atc act aca gat acc gtg cgc   739
Asp Asn Ala Phe Asn Pro Asn Ser Tyr Ile Thr Thr Asp Thr Val Arg
        200                 205                 210

atc gtt gtc gat cct gta ccg gaa act aat ccc gac gat gag aaa gca   787
Ile Val Val Asp Pro Val Pro Glu Thr Asn Pro Asp Asp Glu Lys Ala
    215                 220                 225

gga cgc tagccatgtc tcgcagctac ccc                                816
Gly Arg
230
```

<210> 800
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 800

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Met Ser Asn Asn Ala Leu Leu Val Ala Asn Glu Ala Asp Ile Gly Leu
  1               5                  10                  15

Tyr Leu His Trp Asn Gly Gly Arg Asp Ser Ile Glu Ala Phe Leu Ala
             20                  25                  30

Tyr Ala Ala Tyr Ala Gln Leu Pro Pro Ile Asn Glu Asn Asn Asp Trp
         35                  40                  45

Leu Pro Pro Phe Ile Thr Val Leu Lys Asn Phe Phe Gly Asn Asp Gly
     50                  55                  60

Ser Gly Val Tyr Leu Glu Pro Val Asn Gln Asp Tyr Leu Asp Gly Ile
 65                  70                  75                  80

Asp Tyr Asp Asn Gly Val Tyr Met Leu Asp Asp Tyr Glu Ile Thr Glu
                 85                  90                  95

Arg Ile Asn Pro Pro Ala Val Glu Gln Asp Ser His Asp Leu His Asp
            100                 105                 110

Met Leu Ile Lys Ile Asp Lys Ala Gln Pro Pro Val Asp Gln Leu Gly
        115                 120                 125
```

```
Ser Phe Leu His Gly Leu Glu Thr Ser Val Ala Asp Leu Gly Val Gly
    130                 135                 140

Asp Arg Val Phe Leu Pro Arg Phe Ser Thr Phe Asp Lys Lys Leu Gly
145                 150                 155                 160

Arg Tyr Arg Ile His Thr Val Leu Gly Phe Ala Glu Asn Asp Pro Phe
                165                 170                 175

Asn Pro Met Thr Ser Ser Glu Arg Phe Lys Gly Lys Pro Tyr Val Asp
            180                 185                 190

Met Phe Asp Asn Gln Asp Asn Ala Phe Asn Pro Asn Ser Tyr Ile Thr
        195                 200                 205

Thr Asp Thr Val Arg Ile Val Val Asp Pro Val Pro Glu Thr Asn Pro
    210                 215                 220

Asp Asp Glu Lys Ala Gly Arg
225                 230


<210> 801
<211> 377
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(354)
<223> FRXA01787

<400> 801
acc gag aaa att gat aaa gct caa cca cct gtc gat caa ctc ggg agt   48
Thr Glu Lys Ile Asp Lys Ala Gln Pro Pro Val Asp Gln Leu Gly Ser
  1               5                  10                  15

ttt ctc cat ggc cta gag acc tct gtc gca gat ttg ggg gtt ggt gat   96
Phe Leu His Gly Leu Glu Thr Ser Val Ala Asp Leu Gly Val Gly Asp
             20                  25                  30

cgc gta ttt ttg cca cgt ttt agc acc ttt gat aag aaa ctc ggt cgc   144
Arg Val Phe Leu Pro Arg Phe Ser Thr Phe Asp Lys Lys Leu Gly Arg
         35                  40                  45

tac cgc atc cac act gtt ctc gga ttc gct gag aac gat ccg ttt aac   192
Tyr Arg Ile His Thr Val Leu Gly Phe Ala Glu Asn Asp Pro Phe Asn
     50                  55                  60

cct atg acc agc agc gag cga ttt aaa ggt aag ccc tat gtc gat atg   240
Pro Met Thr Ser Ser Glu Arg Phe Lys Gly Lys Pro Tyr Val Asp Met
 65                  70                  75                  80

ttc gac aat caa gac aac gcc ttt aac cca aat tcc tat atc act aca   288
Phe Asp Asn Gln Asp Asn Ala Phe Asn Pro Asn Ser Tyr Ile Thr Thr
                 85                  90                  95

gat acc gtg cgc atc gtt gtc gat cct gta ccg gaa act aat ccc gac   336
Asp Thr Val Arg Ile Val Val Asp Pro Val Pro Glu Thr Asn Pro Asp
            100                 105                 110
```

```
gat gag aaa gca gga cgc tagccatgtc tcgcagctac ccc                  377
Asp Glu Lys Ala Gly Arg
        115


<210> 802
<211> 118
<212> PRT
<213> Corynebacterium glutamicum

<400> 802
Thr Glu Lys Ile Asp Lys Ala Gln Pro Pro Val Asp Gln Leu Gly Ser
  1               5                  10                  15

Phe Leu His Gly Leu Glu Thr Ser Val Ala Asp Leu Gly Val Gly Asp
             20                  25                  30

Arg Val Phe Leu Pro Arg Phe Ser Thr Phe Asp Lys Lys Leu Gly Arg
         35                  40                  45

Tyr Arg Ile His Thr Val Leu Gly Phe Ala Glu Asn Asp Pro Phe Asn
     50                  55                  60

Pro Met Thr Ser Ser Glu Arg Phe Lys Gly Lys Pro Tyr Val Asp Met
 65                  70                  75                  80

Phe Asp Asn Gln Asp Asn Ala Phe Asn Pro Asn Ser Tyr Ile Thr Thr
                 85                  90                  95

Asp Thr Val Arg Ile Val Val Asp Pro Val Pro Glu Thr Asn Pro Asp
            100                 105                 110

Asp Glu Lys Ala Gly Arg
        115


<210> 803
<211> 897
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> RXN01796

<400> 803
atgtaactcg atcaggtgga aatgcccgca aaagtggcgg cggtggccga gggatggccg 60

ttggtgcggc atcggtggcc tgctactagt cgggctcttc ttg ctc ctt ggc ggt   115
                                        Leu Leu Leu Gly Gly
                                          1               5

aac cct gcc gag atc gac cag gtt tta ggt ggc gat caa acc cag atc   163
Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly Asp Gln Thr Gln Ile
                 10                  15                  20

gag tct gga gag tcc acc gga gcc ggc gac ttt gat cac tgc caa acc   211
Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe Asp His Cys Gln Thr
             25                  30                  35
```

```
ggc gca gat gcc aac gcc agt gat gat tgt cgc ctt tac tac acc tca   259
Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg Leu Tyr Tyr Thr Ser
         40                  45                  50

ttc tcc gtc aat gaa atg tgg cag act ttg ctt cca gct cag gct ggt   307
Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu Pro Ala Gln Ala Gly
     55                  60                  65

atc gaa tac acc gag ccg aca ttg act ctt ttc aaa aac tcc acc caa   355
Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe Lys Asn Ser Thr Gln
 70                  75                  80                  85

acc ggc tgc ggt ttc gct tct gcg tcc act ggg ccg ttt tac tgt ccg   403
Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly Pro Phe Tyr Cys Pro
                 90                  95                 100

tca gac caa gat gct tat ttt gac ttg act ttc ttc gat cag atg cgt   451
Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe Phe Asp Gln Met Arg
            105                 110                 115

cag ttc ggt gca gaa aac gcc ccg ctt gcc cag atg tac atc gtg gcg   499
Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met Tyr Ile Val Ala
        120                 125                 130

cac gag tac ggc cac cac gtc caa aac ctc gag ggc aca ctc gga ctg   547
His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly Thr Leu Gly Leu
    135                 140                 145

tcc aat tac aac gat ccg ggc gct gat tcc aac gcc gtc aag atc gag   595
Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala Val Lys Ile Glu
150                 155                 160                 165

ttg cag gcc gat tgc tac gca ggc att tgg gct aat cac tcc agc gaa   643
Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn His Ser Ser Glu
                170                 175                 180

ggc ccg gat ccg cta ctc caa ccc atc acc gaa tct gag cta gat tcc   691
Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser Glu Leu Asp Ser
            185                 190                 195

gct ctc ctt gct gca agc gcc gtg ggc gac gac aat atc cag caa cga   739
Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn Ile Gln Gln Arg
        200                 205                 210

tcc ggt ggc gat gtc aat cct gaa agc tgg act cac ggc tca tcg cag   787
Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His Gly Ser Ser Gln
    215                 220                 225

cag cgc aaa gac gcg ttc ctc gcc ggc tac aac acc ggc cag atg agc   835
Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr Gly Gln Met Ser
230                 235                 240                 245

gcc tgc gac ttc ctc ggc cgg ggc gtc tac aac gac gct taaagcattg   884
Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp Ala
                250                 255

cttttcgacg tct                                                  897
```

<210> 804

<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 804

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Leu Leu Leu Gly Gly Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly
  1               5                  10                  15

Asp Gln Thr Gln Ile Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe
             20                  25                  30

Asp His Cys Gln Thr Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg
         35                  40                  45

Leu Tyr Tyr Thr Ser Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu
     50                  55                  60

Pro Ala Gln Ala Gly Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe
 65                  70                  75                  80

Lys Asn Ser Thr Gln Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly
                 85                  90                  95

Pro Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe
            100                 105                 110

Phe Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln
        115                 120                 125

Met Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu
    130                 135                 140

Gly Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn
145                 150                 155                 160

Ala Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala
                165                 170                 175

Asn His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu
            180                 185                 190

Ser Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp
        195                 200                 205

Asn Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr
    210                 215                 220

His Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn
225                 230                 235                 240

Thr Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn
                245                 250                 255

Asp Ala
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<210> 805
<211> 506
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(483)
<223> FRXA01796

<400> 805
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ttt tac tgt ccg tca gac caa gat gct tat gtt gac ttg act ttg ttc   48
Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Val Asp Leu Thr Leu Phe
  1               5                  10                  15

gat cag atg cgt cag ttc ggt gca gaa aac gcc ccg ctt gcc cag atg   96
Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met
             20                  25                  30

tac atc gtg gcg cac gag tac ggc cac cac gtc caa aac ctc gag ggc   144
Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly
         35                  40                  45

aca ctc gga ctg tcc aat tac aac gat ccg ggc gct gat tcc aac gcc   192
Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala
     50                  55                  60

gtc aag atc gag ttg cag gcc gat tgc tac gca ggc att tgg gct aat   240
Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn
 65                  70                  75                  80

cac tcc agc gaa ggc ccg gat ccg cta ctc caa ccc atc acc gaa tct   288
His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser
                 85                  90                  95

gag cta gat tcc gct ctc ctt gct gca agc gcc gtg ggc gac gac aat   336
Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn
            100                 105                 110

atc cag caa cga tcc ggt ggc gat gtc aat cct gaa agc tgg act cac   384
Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His
        115                 120                 125

ggc tca tcg cag cag cgc aaa gac gcg ttc ctc gcc ggc tac aac acc   432
Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr
    130                 135                 140

ggc cag atg agc gcc tgc gac ttc ctc ggc cgg ggc gtc tac aac gac   480
Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp
145                 150                 155                 160

gct taaagcattg cttttcgacg tct                                     506
Ala
```

<210> 806
<211> 161
<212> PRT
<213> Corynebacterium glutamicum

<400> 806
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Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Val Asp Leu Thr Leu Phe
  1               5                  10                  15
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```
Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met
            20                  25                  30

Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly
        35                  40                  45

Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala
    50                  55                  60

Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn
65                  70                  75                  80

His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser
                85                  90                  95

Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn
            100                 105                 110

Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His
        115                 120                 125

Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr
    130                 135                 140

Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp
145                 150                 155                 160

Ala
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<210> 807
<211> 1083
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1060)
<223> RXN01803

<400> 807

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ctagcggaaa ggctttagcg acaaggcttt ttgcatgttt taatgcaggg aatattaact 60

ttttgttaat ctctgaccat tgaccttgta cgcttaaaac atg cga aag aaa aaa   115
                                            Met Arg Lys Lys Lys
                                              1               5

gac ggt caa aat ctc cca gac ttc cgg aaa aat ccg cca aag ctg gat   163
Asp Gly Gln Asn Leu Pro Asp Phe Arg Lys Asn Pro Pro Lys Leu Asp
                10                  15                  20

aaa aag gct tat gaa aaa gaa cta aaa aga ctt caa gcc gaa ctc gtc   211
Lys Lys Ala Tyr Glu Lys Glu Leu Lys Arg Leu Gln Ala Glu Leu Val
            25                  30                  35

gat ttg caa caa tgg gtt gtg gaa acc ggt gcg cgc gtg gtc atc gtc   259
Asp Leu Gln Gln Trp Val Val Glu Thr Gly Ala Arg Val Val Ile Val
        40                  45                  50

atg gaa ggc cgc gac gcc gct ggt aaa ggt tct gcg atc aag cgc att   307
```

```
Met Glu Gly Arg Asp Ala Ala Gly Lys Gly Ser Ala Ile Lys Arg Ile
     55                  60                  65

acg cag tac ctc aac ccc cgg tcc gca agg atc gaa gcg ctg ccc acc   355
Thr Gln Tyr Leu Asn Pro Arg Ser Ala Arg Ile Glu Ala Leu Pro Thr
 70                  75                  80                  85

cca aac tct cgg gaa aaa ggg cag tgg tat ttc cag cgc tac atc gaa   403
Pro Asn Ser Arg Glu Lys Gly Gln Trp Tyr Phe Gln Arg Tyr Ile Glu
                 90                  95                 100

aaa ttg ccg act gct ggt gag atc gtt atc ttt gac cgc tcc tgg tac   451
Lys Leu Pro Thr Ala Gly Glu Ile Val Ile Phe Asp Arg Ser Trp Tyr
            105                 110                 115

aac cgt gca gga gtc gag cgc gtc atg gga ttt tgc acc tcc cag gag   499
Asn Arg Ala Gly Val Glu Arg Val Met Gly Phe Cys Thr Ser Gln Glu
        120                 125                 130

tac cgc cga ttc ctt cac cag gca cca atc ttt gaa cgc ctg ttg gtg   547
Tyr Arg Arg Phe Leu His Gln Ala Pro Ile Phe Glu Arg Leu Leu Val
    135                 140                 145

gaa gat ggc att cac ctg cgt aaa tac tgg ttc tct gta tct gat gaa   595
Glu Asp Gly Ile His Leu Arg Lys Tyr Trp Phe Ser Val Ser Asp Glu
150                 155                 160                 165

gag cag att gag cgt ttc gaa gac cgc ctg agc gat ccg ctg cgc cgg   643
Glu Gln Ile Glu Arg Phe Glu Asp Arg Leu Ser Asp Pro Leu Arg Arg
                170                 175                 180

tgg aag ttg tcg cca atg gat tta caa tcg atc acc cgc tgg gaa gat   691
Trp Lys Leu Ser Pro Met Asp Leu Gln Ser Ile Thr Arg Trp Glu Asp
            185                 190                 195

tac tca cgc gca aaa gat gag atg ttc atc cac acg gac atc ccg tca   739
Tyr Ser Arg Ala Lys Asp Glu Met Phe Ile His Thr Asp Ile Pro Ser
        200                 205                 210

gca ccg tgg tac acg gtg gaa tct gag gac aag aag cgt tcc cgc atc   787
Ala Pro Trp Tyr Thr Val Glu Ser Glu Asp Lys Lys Arg Ser Arg Ile
    215                 220                 225

aac gtc att tcg cat ctg ctc tcg acg att cct tat gag aag atc gat   835
Asn Val Ile Ser His Leu Leu Ser Thr Ile Pro Tyr Glu Lys Ile Asp
230                 235                 240                 245

cgt cca ttg ccg gaa atc cct cat cgc cca gat tct gaa tct gat tat   883
Arg Pro Leu Pro Glu Ile Pro His Arg Pro Asp Ser Glu Ser Asp Tyr
                250                 255                 260

gta cgt ccc cct cgc gat gag ttc cgt tat gtt cca gat gtg gca gca   931
Val Arg Pro Pro Arg Asp Glu Phe Arg Tyr Val Pro Asp Val Ala Ala
            265                 270                 275

cac ttg gaa gaa gag cgc atc aag aaa gaa gaa aaa gcc aag aag gca   979
His Leu Glu Glu Glu Arg Ile Lys Lys Glu Glu Lys Ala Lys Lys Ala
        280                 285                 290

aag aag cca gct aag gct gca gga aag aac tcg gat aag cag aag tct   1027
Lys Lys Pro Ala Lys Ala Ala Gly Lys Asn Ser Asp Lys Gln Lys Ser
```

295 300 305

tcc gga gga aaa ggc aag aag aag tcc aag aaa tagaacgcct tttaaggggt 1080
Ser Gly Gly Lys Gly Lys Lys Lys Ser Lys Lys
310 315 320

tga 1083

<210> 808
<211> 320
<212> PRT
<213> Corynebacterium glutamicum

<400> 808
Met Arg Lys Lys Lys Asp Gly Gln Asn Leu Pro Asp Phe Arg Lys Asn
1 5 10 15

Pro Pro Lys Leu Asp Lys Lys Ala Tyr Glu Lys Glu Leu Lys Arg Leu
20 25 30

Gln Ala Glu Leu Val Asp Leu Gln Gln Trp Val Val Glu Thr Gly Ala
35 40 45

Arg Val Val Ile Val Met Glu Gly Arg Asp Ala Ala Gly Lys Gly Ser
50 55 60

Ala Ile Lys Arg Ile Thr Gln Tyr Leu Asn Pro Arg Ser Ala Arg Ile
65 70 75 80

Glu Ala Leu Pro Thr Pro Asn Ser Arg Glu Lys Gly Gln Trp Tyr Phe
85 90 95

Gln Arg Tyr Ile Glu Lys Leu Pro Thr Ala Gly Glu Ile Val Ile Phe
100 105 110

Asp Arg Ser Trp Tyr Asn Arg Ala Gly Val Glu Arg Val Met Gly Phe
115 120 125

Cys Thr Ser Gln Glu Tyr Arg Arg Phe Leu His Gln Ala Pro Ile Phe
130 135 140

Glu Arg Leu Leu Val Glu Asp Gly Ile His Leu Arg Lys Tyr Trp Phe
145 150 155 160

Ser Val Ser Asp Glu Glu Gln Ile Glu Arg Phe Glu Asp Arg Leu Ser
165 170 175

Asp Pro Leu Arg Arg Trp Lys Leu Ser Pro Met Asp Leu Gln Ser Ile
180 185 190

Thr Arg Trp Glu Asp Tyr Ser Arg Ala Lys Asp Glu Met Phe Ile His
195 200 205

Thr Asp Ile Pro Ser Ala Pro Trp Tyr Thr Val Glu Ser Glu Asp Lys
210 215 220

Lys Arg Ser Arg Ile Asn Val Ile Ser His Leu Leu Ser Thr Ile Pro
225 230 235 240

Tyr Glu Lys Ile Asp Arg Pro Leu Pro Glu Ile Pro His Arg Pro Asp

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                245                 250                 255

Ser Glu Ser Asp Tyr Val Arg Pro Pro Arg Asp Glu Phe Arg Tyr Val
            260                 265                 270

Pro Asp Val Ala Ala His Leu Glu Glu Glu Arg Ile Lys Lys Glu Glu
        275                 280                 285

Lys Ala Lys Lys Ala Lys Lys Pro Ala Lys Ala Ala Gly Lys Asn Ser
    290                 295                 300

Asp Lys Gln Lys Ser Ser Gly Gly Lys Gly Lys Lys Lys Ser Lys Lys
305                 310                 315                 320
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<210> 809
<211> 1083
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1060)
<223> FRXA01803

<400> 809

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ctagcggaaa ggctttagcg acaaggcttt ttgcatgttt taatgcaggg aatattaact 60

ttttgttaat ctctgaccat tgaccttgta cgcttaaaac atg cga aag aaa aaa   115
                                            Met Arg Lys Lys Lys
                                              1               5

gac ggt caa aat ctc cca gac ttc cgg aaa aat ccg cca aag ctg gat   163
Asp Gly Gln Asn Leu Pro Asp Phe Arg Lys Asn Pro Pro Lys Leu Asp
                 10                  15                  20

aaa aag gct tat gaa aaa gaa cta aaa aga ctt caa gcc gaa ctc gtc   211
Lys Lys Ala Tyr Glu Lys Glu Leu Lys Arg Leu Gln Ala Glu Leu Val
             25                  30                  35

gat ttg caa caa tgg gtt gtg gaa acc ggt gcg cgc gtg gtc atc gtc   259
Asp Leu Gln Gln Trp Val Val Glu Thr Gly Ala Arg Val Val Ile Val
         40                  45                  50

atg gaa ggc cgc gac gcc gct ggt aaa ggt tct gcg atc aag cgc att   307
Met Glu Gly Arg Asp Ala Ala Gly Lys Gly Ser Ala Ile Lys Arg Ile
     55                  60                  65

acg cag tac ctc aac ccc cgg tcc gca agg atc gaa gcg ctg ccc acc   355
Thr Gln Tyr Leu Asn Pro Arg Ser Ala Arg Ile Glu Ala Leu Pro Thr
 70                  75                  80                  85

cca aac tct cgg gaa aaa ggg cag tgg tat ttc cag cgc tac atc gaa   403
Pro Asn Ser Arg Glu Lys Gly Gln Trp Tyr Phe Gln Arg Tyr Ile Glu
                 90                  95                 100

aaa ttg ccg act gct ggt gag atc gtt atc ttt gac cgc tcc tgg tac   451
Lys Leu Pro Thr Ala Gly Glu Ile Val Ile Phe Asp Arg Ser Trp Tyr
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            105                 110                 115

aac cgt gca gga gtc gag cgc gtc atg gga ttt tgc acc tcc cag gag   499
Asn Arg Ala Gly Val Glu Arg Val Met Gly Phe Cys Thr Ser Gln Glu
        120                 125                 130

tac cgc cga ttc ctt cac cag gca cca atc ttt gaa cgc ctg ttg gtg   547
Tyr Arg Arg Phe Leu His Gln Ala Pro Ile Phe Glu Arg Leu Leu Val
    135                 140                 145

gaa gat ggc att cac ctg cgt aaa tac tgg ttc tct gta tct gat gaa   595
Glu Asp Gly Ile His Leu Arg Lys Tyr Trp Phe Ser Val Ser Asp Glu
150                 155                 160                 165

gag cag att gag cgt ttc gaa gac cgc ctg agc gat ccg ctg cgc cgg   643
Glu Gln Ile Glu Arg Phe Glu Asp Arg Leu Ser Asp Pro Leu Arg Arg
                170                 175                 180

tgg aag ttg tcg cca atg gat tta caa tcg atc acc cgc tgg gaa gat   691
Trp Lys Leu Ser Pro Met Asp Leu Gln Ser Ile Thr Arg Trp Glu Asp
            185                 190                 195

tac tca cgc gca aaa gat gag atg ttc atc cac acg gac atc ccg tca   739
Tyr Ser Arg Ala Lys Asp Glu Met Phe Ile His Thr Asp Ile Pro Ser
        200                 205                 210

gca ccg tgg tac acg gtg gaa tct gag gac aag aag cgt tcc cgc atc   787
Ala Pro Trp Tyr Thr Val Glu Ser Glu Asp Lys Lys Arg Ser Arg Ile
    215                 220                 225

aac gtc att tcg cat ctg ctc tcg acg att cct tat gag aag atc gat   835
Asn Val Ile Ser His Leu Leu Ser Thr Ile Pro Tyr Glu Lys Ile Asp
230                 235                 240                 245

cgt cca ttg ccg gaa atc cct cat cgc cca gat tct gaa tct gat tat   883
Arg Pro Leu Pro Glu Ile Pro His Arg Pro Asp Ser Glu Ser Asp Tyr
                250                 255                 260

gta cgt ccc cct cgc gat gag ttc cgt tat gtt cca gat gtg gca gca   931
Val Arg Pro Pro Arg Asp Glu Phe Arg Tyr Val Pro Asp Val Ala Ala
            265                 270                 275

cac ttg gaa gaa gag cgc atc aag aaa gaa gaa aaa gcc aag aag gca   979
His Leu Glu Glu Glu Arg Ile Lys Lys Glu Glu Lys Ala Lys Lys Ala
        280                 285                 290

aag aag cca gct aag gct gca gga aag aac tcg gat aag cag aag tct  1027
Lys Lys Pro Ala Lys Ala Ala Gly Lys Asn Ser Asp Lys Gln Lys Ser
    295                 300                 305

tcc gga gga aaa ggc aag aag aag tcc aag aaa tagaacgcct tttaaggggt 1080
Ser Gly Gly Lys Gly Lys Lys Lys Ser Lys Lys
310                 315                 320

tga                                                             1083
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<210> 810
<211> 320
<212> PRT
<213> Corynebacterium glutamicum

<400> 810

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Met Arg Lys Lys Lys Asp Gly Gln Asn Leu Pro Asp Phe Arg Lys Asn
  1               5                  10                  15

Pro Pro Lys Leu Asp Lys Lys Ala Tyr Glu Lys Glu Leu Lys Arg Leu
            20                  25                  30

Gln Ala Glu Leu Val Asp Leu Gln Gln Trp Val Val Glu Thr Gly Ala
        35                  40                  45

Arg Val Val Ile Val Met Glu Gly Arg Asp Ala Ala Gly Lys Gly Ser
    50                  55                  60

Ala Ile Lys Arg Ile Thr Gln Tyr Leu Asn Pro Arg Ser Ala Arg Ile
65                  70                  75                  80

Glu Ala Leu Pro Thr Pro Asn Ser Arg Glu Lys Gly Gln Trp Tyr Phe
                85                  90                  95

Gln Arg Tyr Ile Glu Lys Leu Pro Thr Ala Gly Glu Ile Val Ile Phe
            100                 105                 110

Asp Arg Ser Trp Tyr Asn Arg Ala Gly Val Glu Arg Val Met Gly Phe
        115                 120                 125

Cys Thr Ser Gln Glu Tyr Arg Arg Phe Leu His Gln Ala Pro Ile Phe
    130                 135                 140

Glu Arg Leu Leu Val Glu Asp Gly Ile His Leu Arg Lys Tyr Trp Phe
145                 150                 155                 160

Ser Val Ser Asp Glu Glu Gln Ile Glu Arg Phe Glu Asp Arg Leu Ser
                165                 170                 175

Asp Pro Leu Arg Arg Trp Lys Leu Ser Pro Met Asp Leu Gln Ser Ile
            180                 185                 190

Thr Arg Trp Glu Asp Tyr Ser Arg Ala Lys Asp Glu Met Phe Ile His
        195                 200                 205

Thr Asp Ile Pro Ser Ala Pro Trp Tyr Thr Val Glu Ser Glu Asp Lys
    210                 215                 220

Lys Arg Ser Arg Ile Asn Val Ile Ser His Leu Leu Ser Thr Ile Pro
225                 230                 235                 240

Tyr Glu Lys Ile Asp Arg Pro Leu Pro Glu Ile Pro His Arg Pro Asp
                245                 250                 255

Ser Glu Ser Asp Tyr Val Arg Pro Pro Arg Asp Glu Phe Arg Tyr Val
            260                 265                 270

Pro Asp Val Ala Ala His Leu Glu Glu Glu Arg Ile Lys Lys Glu Glu
        275                 280                 285

Lys Ala Lys Lys Ala Lys Lys Pro Ala Lys Ala Ala Gly Lys Asn Ser
    290                 295                 300

Asp Lys Gln Lys Ser Ser Gly Gly Lys Gly Lys Lys Lys Ser Lys Lys
305                 310                 315                 320
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<210> 811
<211> 1299
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1276)
<223> RXN01809

<400> 811
acaacacgac agttgtaact agtggtttca acaccattat cggtatgact cgtggcgact 60

cgtatctctc tgatgatctc gatgacctgg gttaaacccg atg aac gag cag gaa 115
Met Asn Glu Gln Glu
1 5

cga gaa gcc tta gag gat gct gcc ctt gag gaa gct gcc tta gcc gat 163
Arg Glu Ala Leu Glu Asp Ala Ala Leu Glu Glu Ala Ala Leu Ala Asp
10 15 20

gaa tta gct gca tta gag gct gaa gct ggc gta caa ggg tca gtc gag 211
Glu Leu Ala Ala Leu Glu Ala Glu Ala Gly Val Gln Gly Ser Val Glu
25 30 35

cct tat gac tat gca gca gac ctt gat gat gag gac gag ttt gat gag 259
Pro Tyr Asp Tyr Ala Ala Asp Leu Asp Asp Glu Asp Glu Phe Asp Glu
40 45 50

gac cct ttt gct cag gat gaa ccc cgt gac gct ggt ccg cta ggt gag 307
Asp Pro Phe Ala Gln Asp Glu Pro Arg Asp Ala Gly Pro Leu Gly Glu
55 60 65

ttg agc agt gat aac cat gtc tct gag gct gtt gct gaa gac act ggg 355
Leu Ser Ser Asp Asn His Val Ser Glu Ala Val Ala Glu Asp Thr Gly
70 75 80 85

aca agt aca gaa gag tct gca caa gag ggc agt cac gaa gag tcg gta 403
Thr Ser Thr Glu Glu Ser Ala Gln Glu Gly Ser His Glu Glu Ser Val
90 95 100

gac aat ccc cgt gat ttc acc ggc act gcg aca gcg gtg cga tct ttt 451
Asp Asn Pro Arg Asp Phe Thr Gly Thr Ala Thr Ala Val Arg Ser Phe
105 110 115

cga ccc aga ctt ccc gta ccc aat gca ctg cga cca gga cca ccc atc 499
Arg Pro Arg Leu Pro Val Pro Asn Ala Leu Arg Pro Gly Pro Pro Ile
120 125 130

cga aca caa ccg gca gtg aac acc gac ata gat gat ggc ggg caa gag 547
Arg Thr Gln Pro Ala Val Asn Thr Asp Ile Asp Asp Gly Gly Gln Glu
135 140 145

aat aca gct ggc gcg act gcc gca gat gtg ggg gcg gga gtg ttt ttt 595
Asn Thr Ala Gly Ala Thr Ala Ala Asp Val Gly Ala Gly Val Phe Phe
150 155 160 165

```
ggt acg cat ttt gag ctg gct ttt ggg cag gtt gat gtt cac cgc cac   643
Gly Thr His Phe Glu Leu Ala Phe Gly Gln Val Asp Val His Arg His
               170                 175                 180

ata agg cat gag cag gct atg cga gat gga cac cag gat ctc agc gtc   691
Ile Arg His Glu Gln Ala Met Arg Asp Gly His Gln Asp Leu Ser Val
           185                 190                 195

ttt gtc ggt gct gat ggg gcg atc atg ctg gaa gaa ctt aaa aat cgt   739
Phe Val Gly Ala Asp Gly Ala Ile Met Leu Glu Glu Leu Lys Asn Arg
       200                 205                 210

tac cag cgc cca ccg gag aac gag ccc cat gat gat gat gtc acc gaa   787
Tyr Gln Arg Pro Pro Glu Asn Glu Pro His Asp Asp Asp Val Thr Glu
   215                 220                 225

atg ata aag acc acc gag gaa aca gag aag gag aac gta gag atg gat   835
Met Ile Lys Thr Thr Glu Glu Thr Glu Lys Glu Asn Val Glu Met Asp
230                 235                 240                 245

cag gat ata gct gta gta gac aac gtt gat gaa cag gtt gtg gtg aca   883
Gln Asp Ile Ala Val Val Asp Asn Val Asp Glu Gln Val Val Val Thr
               250                 255                 260

cct gct cat gac gct gac agc gta gcg gtt gtt gct gaa cag gtc gtt   931
Pro Ala His Asp Ala Asp Ser Val Ala Val Val Ala Glu Gln Val Val
           265                 270                 275

gcg tca gaa cca acg cca gag ccg gta ccc aag gtt gag cac gta gag   979
Ala Ser Glu Pro Thr Pro Glu Pro Val Pro Lys Val Glu His Val Glu
       280                 285                 290

atg agt gtc gat cta gcg ggt gag act att aca ccg att gat cag gca  1027
Met Ser Val Asp Leu Ala Gly Glu Thr Ile Thr Pro Ile Asp Gln Ala
   295                 300                 305

att cgg tct ttt atg cag ctc aac ggt att gag cac agc gtg gtg ttg  1075
Ile Arg Ser Phe Met Gln Leu Asn Gly Ile Glu His Ser Val Val Leu
310                 315                 320                 325

cga cgc ttg ggg ctg atg act cag gtg gca cat aat aag gaa ctt gat  1123
Arg Arg Leu Gly Leu Met Thr Gln Val Ala His Asn Lys Glu Leu Asp
               330                 335                 340

gag gtc tac gct aag gca ctt gcc gag ggt gaa tcc cat gct cag cag  1171
Glu Val Tyr Ala Lys Ala Leu Ala Glu Gly Glu Ser His Ala Gln Gln
           345                 350                 355

cag cat gaa tta gaa gca gaa aat gaa cgg ctt aaa aaa gaa gtt gat  1219
Gln His Glu Leu Glu Ala Glu Asn Glu Arg Leu Lys Lys Glu Val Asp
       360                 365                 370

gcg ctc gct gca gag ctt agt gct gcg ttg atg ggc gag ggt ggt ggt  1267
Ala Leu Ala Ala Glu Leu Ser Ala Ala Leu Met Gly Glu Gly Gly Gly
   375                 380                 385

gat cat gac taaggccgtg acaccaattg tgg                           1299
Asp His Asp
390
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<210> 812
<211> 392
<212> PRT
<213> Corynebacterium glutamicum

<400> 812
Met Asn Glu Gln Glu Arg Glu Ala Leu Glu Asp Ala Ala Leu Glu Glu
1 5 10 15

Ala Ala Leu Ala Asp Glu Leu Ala Ala Leu Glu Ala Glu Ala Gly Val
20 25 30

Gln Gly Ser Val Glu Pro Tyr Asp Tyr Ala Ala Asp Leu Asp Asp Glu
35 40 45

Asp Glu Phe Asp Glu Asp Pro Phe Ala Gln Asp Glu Pro Arg Asp Ala
50 55 60

Gly Pro Leu Gly Glu Leu Ser Ser Asp Asn His Val Ser Glu Ala Val
65 70 75 80

Ala Glu Asp Thr Gly Thr Ser Thr Glu Glu Ser Ala Gln Glu Gly Ser
85 90 95

His Glu Glu Ser Val Asp Asn Pro Arg Asp Phe Thr Gly Thr Ala Thr
100 105 110

Ala Val Arg Ser Phe Arg Pro Arg Leu Pro Val Pro Asn Ala Leu Arg
115 120 125

Pro Gly Pro Pro Ile Arg Thr Gln Pro Ala Val Asn Thr Asp Ile Asp
130 135 140

Asp Gly Gly Gln Glu Asn Thr Ala Gly Ala Thr Ala Ala Asp Val Gly
145 150 155 160

Ala Gly Val Phe Phe Gly Thr His Phe Glu Leu Ala Phe Gly Gln Val
165 170 175

Asp Val His Arg His Ile Arg His Glu Gln Ala Met Arg Asp Gly His
180 185 190

Gln Asp Leu Ser Val Phe Val Gly Ala Asp Gly Ala Ile Met Leu Glu
195 200 205

Glu Leu Lys Asn Arg Tyr Gln Arg Pro Pro Glu Asn Glu Pro His Asp
210 215 220

Asp Asp Val Thr Glu Met Ile Lys Thr Thr Glu Glu Thr Glu Lys Glu
225 230 235 240

Asn Val Glu Met Asp Gln Asp Ile Ala Val Val Asp Asn Val Asp Glu
245 250 255

Gln Val Val Val Thr Pro Ala His Asp Ala Asp Ser Val Ala Val Val
260 265 270

Ala Glu Gln Val Val Ala Ser Glu Pro Thr Pro Glu Pro Val Pro Lys
275 280 285

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Val Glu His Val Glu Met Ser Val Asp Leu Ala Gly Glu Thr Ile Thr
    290                 295                 300

Pro Ile Asp Gln Ala Ile Arg Ser Phe Met Gln Leu Asn Gly Ile Glu
305                 310                 315                 320

His Ser Val Val Leu Arg Arg Leu Gly Leu Met Thr Gln Val Ala His
                325                 330                 335

Asn Lys Glu Leu Asp Glu Val Tyr Ala Lys Ala Leu Ala Glu Gly Glu
            340                 345                 350

Ser His Ala Gln Gln Gln His Glu Leu Glu Ala Glu Asn Glu Arg Leu
        355                 360                 365

Lys Lys Glu Val Asp Ala Leu Ala Ala Glu Leu Ser Ala Ala Leu Met
    370                 375                 380

Gly Glu Gly Gly Gly Asp His Asp
385                 390
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<210> 813
<211> 586
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(586)
<223> FRXA01062

<400> 813

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acaacacgac agttgtaact agtggtttca acaccattat cggtatgact cgtggcgact 60

cgtatctctc tgatgatctc gatgacctgg gttaaacccg atg aac gag cag gaa   115
                                            Met Asn Glu Gln Glu
                                              1               5

cga gaa gcc tta gag gat gct gcc ctt gag gaa gct gcc tta gcc gat   163
Arg Glu Ala Leu Glu Asp Ala Ala Leu Glu Glu Ala Ala Leu Ala Asp
                 10                  15                  20

gaa tta gct gca tta gag gct gaa gct ggc gta caa ggg tca gtc gag   211
Glu Leu Ala Ala Leu Glu Ala Glu Ala Gly Val Gln Gly Ser Val Glu
             25                  30                  35

cct tat gac tat gca gca gac ctt gat gat gag gac gag ttt gat gag   259
Pro Tyr Asp Tyr Ala Ala Asp Leu Asp Asp Glu Asp Glu Phe Asp Glu
         40                  45                  50

gac cct ttt gct cag gat gaa ccc cgt gac gct ggt ccg cta ggt gag   307
Asp Pro Phe Ala Gln Asp Glu Pro Arg Asp Ala Gly Pro Leu Gly Glu
     55                  60                  65

ttg agc agt gat aac cat gtc tct gag gct gtt gct gaa gac act ggg   355
Leu Ser Ser Asp Asn His Val Ser Glu Ala Val Ala Glu Asp Thr Gly
 70                  75                  80                  85

aca agt aca gaa gag tct gca caa gag ggc agt cac gaa gag tcg gta   403
Thr Ser Thr Glu Glu Ser Ala Gln Glu Gly Ser His Glu Glu Ser Val
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                  90                  95                 100

gac aat ccc cgt gat ttc acc ggc act gcg aca gcg gtg cga tct ttt   451
Asp Asn Pro Arg Asp Phe Thr Gly Thr Ala Thr Ala Val Arg Ser Phe
            105                 110                 115

cga ccc aga ctt ccc gta ccc aat gca ctg cga cca gga cca ccc atc   499
Arg Pro Arg Leu Pro Val Pro Asn Ala Leu Arg Pro Gly Pro Pro Ile
        120                 125                 130

cga aca caa ccg gca gtg aac acc gac ata tat gat ggc ggg caa gag   547
Arg Thr Gln Pro Ala Val Asn Thr Asp Ile Tyr Asp Gly Gly Gln Glu
    135                 140                 145

aat aca gct ggc gcg act gcc gca gat gtg ggg gcg gga               586
Asn Thr Ala Gly Ala Thr Ala Ala Asp Val Gly Ala Gly
150                 155                 160


<210> 814
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 814
Met Asn Glu Gln Glu Arg Glu Ala Leu Glu Asp Ala Ala Leu Glu Glu
  1               5                  10                  15

Ala Ala Leu Ala Asp Glu Leu Ala Ala Leu Glu Ala Glu Ala Gly Val
             20                  25                  30

Gln Gly Ser Val Glu Pro Tyr Asp Tyr Ala Ala Asp Leu Asp Asp Glu
         35                  40                  45

Asp Glu Phe Asp Glu Asp Pro Phe Ala Gln Asp Glu Pro Arg Asp Ala
     50                  55                  60

Gly Pro Leu Gly Glu Leu Ser Ser Asp Asn His Val Ser Glu Ala Val
 65                  70                  75                  80

Ala Glu Asp Thr Gly Thr Ser Thr Glu Glu Ser Ala Gln Glu Gly Ser
                 85                  90                  95

His Glu Glu Ser Val Asp Asn Pro Arg Asp Phe Thr Gly Thr Ala Thr
            100                 105                 110

Ala Val Arg Ser Phe Arg Pro Arg Leu Pro Val Pro Asn Ala Leu Arg
        115                 120                 125

Pro Gly Pro Pro Ile Arg Thr Gln Pro Ala Val Asn Thr Asp Ile Tyr
    130                 135                 140

Asp Gly Gly Gln Glu Asn Thr Ala Gly Ala Thr Ala Ala Asp Val Gly
145                 150                 155                 160

Ala Gly


<210> 815
<211> 659
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(636)
<223> FRXA01809

<400> 815

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cac ata agg cat gag cag gct atg cga gat gga cac cag gat ctc agc   48
His Ile Arg His Glu Gln Ala Met Arg Asp Gly His Gln Asp Leu Ser
  1               5                  10                  15

gtc ttt gtc ggt gct gat ggg gcg atc atg ctg gaa gaa ctt aaa aat   96
Val Phe Val Gly Ala Asp Gly Ala Ile Met Leu Glu Glu Leu Lys Asn
             20                  25                  30

cgt tac cag cgc cca ccg gag aac gag ccc cat gat gat gat gtc acc   144
Arg Tyr Gln Arg Pro Pro Glu Asn Glu Pro His Asp Asp Asp Val Thr
         35                  40                  45

gaa atg ata aag acc acc gag gaa aca gag aag gag aac gta gag atg   192
Glu Met Ile Lys Thr Thr Glu Glu Thr Glu Lys Glu Asn Val Glu Met
     50                  55                  60

gat cag gat ata gct gta gta gac aac gtt gat gaa cag gtt gtg gtg   240
Asp Gln Asp Ile Ala Val Val Asp Asn Val Asp Glu Gln Val Val Val
 65                  70                  75                  80

aca cct gct cat gac gct gac agc gta gcg gtt gtt gct gaa cag gtc   288
Thr Pro Ala His Asp Ala Asp Ser Val Ala Val Val Ala Glu Gln Val
                 85                  90                  95

gtt gcg tca gaa cca acg cca gag ccg gta ccc aag gtt gag cac gta   336
Val Ala Ser Glu Pro Thr Pro Glu Pro Val Pro Lys Val Glu His Val
            100                 105                 110

gag atg agt gtc gat cta gcg ggt gag act att aca ccg att gat cag   384
Glu Met Ser Val Asp Leu Ala Gly Glu Thr Ile Thr Pro Ile Asp Gln
        115                 120                 125

gca att cgg tct ttt atg cag ctc aac ggt att gag cac agc gtg gtg   432
Ala Ile Arg Ser Phe Met Gln Leu Asn Gly Ile Glu His Ser Val Val
    130                 135                 140

ttg cga cgc ttg ggg ctg atg act cag gtg gca cat aat aag gaa ctt   480
Leu Arg Arg Leu Gly Leu Met Thr Gln Val Ala His Asn Lys Glu Leu
145                 150                 155                 160

gat gag gtc tac gct aag gca ctt gcc gag ggt gaa tcc cat gct cag   528
Asp Glu Val Tyr Ala Lys Ala Leu Ala Glu Gly Glu Ser His Ala Gln
                165                 170                 175

cag cag cat gaa tta gaa gca gaa aat gaa cgg ctt aaa aaa gaa gtt   576
Gln Gln His Glu Leu Glu Ala Glu Asn Glu Arg Leu Lys Lys Glu Val
            180                 185                 190

gat gcg ctc gct gca gag ctt agt gct gcg ttg atg ggc gag ggt ggt   624
Asp Ala Leu Ala Ala Glu Leu Ser Ala Ala Leu Met Gly Glu Gly Gly
        195                 200                 205
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ggt gat cat gac taaggccgtg acaccaattg tgg 659
Gly Asp His Asp
210

<210> 816
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 816
His Ile Arg His Glu Gln Ala Met Arg Asp Gly His Gln Asp Leu Ser
1 5 10 15

Val Phe Val Gly Ala Asp Gly Ala Ile Met Leu Glu Glu Leu Lys Asn
20 25 30

Arg Tyr Gln Arg Pro Pro Glu Asn Glu Pro His Asp Asp Asp Val Thr
35 40 45

Glu Met Ile Lys Thr Thr Glu Glu Thr Glu Lys Glu Asn Val Glu Met
50 55 60

Asp Gln Asp Ile Ala Val Val Asp Asn Val Asp Glu Gln Val Val Val
65 70 75 80

Thr Pro Ala His Asp Ala Asp Ser Val Ala Val Val Ala Glu Gln Val
85 90 95

Val Ala Ser Glu Pro Thr Pro Glu Pro Val Pro Lys Val Glu His Val
100 105 110

Glu Met Ser Val Asp Leu Ala Gly Glu Thr Ile Thr Pro Ile Asp Gln
115 120 125

Ala Ile Arg Ser Phe Met Gln Leu Asn Gly Ile Glu His Ser Val Val
130 135 140

Leu Arg Arg Leu Gly Leu Met Thr Gln Val Ala His Asn Lys Glu Leu
145 150 155 160

Asp Glu Val Tyr Ala Lys Ala Leu Ala Glu Gly Glu Ser His Ala Gln
165 170 175

Gln Gln His Glu Leu Glu Ala Glu Asn Glu Arg Leu Lys Lys Glu Val
180 185 190

Asp Ala Leu Ala Ala Glu Leu Ser Ala Ala Leu Met Gly Glu Gly Gly
195 200 205

Gly Asp His Asp
210

<210> 817
<211> 804
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(781)
<223> RXN01811

<400> 817
gaaggagaag agacattgtc tcaagaagag ctgacattag tcgcattgaa ttcttatgaa 60

aaaggagagt tgccaaagaa gaatatcatt atttgaaaac gtg ttt gaa ttt gat 115
Val Phe Glu Phe Asp
1 5

gat acc ttg gca aaa gat ata caa gta gac cgt acg tcc atg caa gta 163
Asp Thr Leu Ala Lys Asp Ile Gln Val Asp Arg Thr Ser Met Gln Val
10 15 20

ttc gaa gct tca gaa acc gtc aaa gaa gcg ata aaa gct tcg att gaa 211
Phe Glu Ala Ser Glu Thr Val Lys Glu Ala Ile Lys Ala Ser Ile Glu
25 30 35

caa gga cat act cgc tat ccg gtt atc tta gaa tca aaa gac aat gtt 259
Gln Gly His Thr Arg Tyr Pro Val Ile Leu Glu Ser Lys Asp Asn Val
40 45 50

tta ggt tat gtc acc ttg cca gat ttg atc aag caa tct tat aaa gat 307
Leu Gly Tyr Val Thr Leu Pro Asp Leu Ile Lys Gln Ser Tyr Lys Asp
55 60 65

gac cag ctg aca gta gaa cag ttg att gaa gag ccg atc gta aca act 355
Asp Gln Leu Thr Val Glu Gln Leu Ile Glu Glu Pro Ile Val Thr Thr
70 75 80 85

gaa acg atc cct ata aaa aaa tta ttg acg atc atg cga aaa aag gga 403
Glu Thr Ile Pro Ile Lys Lys Leu Leu Thr Ile Met Arg Lys Lys Gly
90 95 100

aag cat att gct atc tta aaa gat gaa tac gga ggg aca agc ggc tta 451
Lys His Ile Ala Ile Leu Lys Asp Glu Tyr Gly Gly Thr Ser Gly Leu
105 110 115

gtg acg att gaa gat att tta gaa gaa atc gtc ggg gaa atc cga gat 499
Val Thr Ile Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Arg Asp
120 125 130

gag aca gat ttg gac gaa gca ttg ata gcg gaa cag tca gat ggc tct 547
Glu Thr Asp Leu Asp Glu Ala Leu Ile Ala Glu Gln Ser Asp Gly Ser
135 140 145

tat atc atc tcc ggc aaa cta aca tta gat gat ttc cag cgt tat ttt 595
Tyr Ile Ile Ser Gly Lys Leu Thr Leu Asp Asp Phe Gln Arg Tyr Phe
150 155 160 165

cat gta gag att cca gag ttt gaa gaa acg aat ttt act aca ctt gcg 643
His Val Glu Ile Pro Glu Phe Glu Glu Thr Asn Phe Thr Thr Leu Ala
170 175 180

ggc ttt gct tct agc cga tat aaa gaa ata aaa gca gga aca atc att 691
Gly Phe Ala Ser Ser Arg Tyr Lys Glu Ile Lys Ala Gly Thr Ile Ile
185 190 195

gag att gca tca ttc cgt ttc acg gta tta gaa tac cag cat gca cat 739
Glu Ile Ala Ser Phe Arg Phe Thr Val Leu Glu Tyr Gln His Ala His
200 205 210

```
atc gat tat ttc aaa gta gag tcc acg gaa aga aaa aca gaa          781
Ile Asp Tyr Phe Lys Val Glu Ser Thr Glu Arg Lys Thr Glu
    215                 220                 225

taaaagaaaa aaggctgtga cat                                       804
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<210> 818
<211> 227
<212> PRT
<213> Corynebacterium glutamicum

<400> 818

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Val Phe Glu Phe Asp Asp Thr Leu Ala Lys Asp Ile Gln Val Asp Arg
  1               5                  10                  15

Thr Ser Met Gln Val Phe Glu Ala Ser Glu Thr Val Lys Glu Ala Ile
             20                  25                  30

Lys Ala Ser Ile Glu Gln Gly His Thr Arg Tyr Pro Val Ile Leu Glu
         35                  40                  45

Ser Lys Asp Asn Val Leu Gly Tyr Val Thr Leu Pro Asp Leu Ile Lys
     50                  55                  60

Gln Ser Tyr Lys Asp Asp Gln Leu Thr Val Glu Gln Leu Ile Glu Glu
 65                  70                  75                  80

Pro Ile Val Thr Thr Glu Thr Ile Pro Ile Lys Lys Leu Leu Thr Ile
                 85                  90                  95

Met Arg Lys Lys Gly Lys His Ile Ala Ile Leu Lys Asp Glu Tyr Gly
            100                 105                 110

Gly Thr Ser Gly Leu Val Thr Ile Glu Asp Ile Leu Glu Glu Ile Val
        115                 120                 125

Gly Glu Ile Arg Asp Glu Thr Asp Leu Asp Glu Ala Leu Ile Ala Glu
    130                 135                 140

Gln Ser Asp Gly Ser Tyr Ile Ile Ser Gly Lys Leu Thr Leu Asp Asp
145                 150                 155                 160

Phe Gln Arg Tyr Phe His Val Glu Ile Pro Glu Phe Glu Glu Thr Asn
                165                 170                 175

Phe Thr Thr Leu Ala Gly Phe Ala Ser Ser Arg Tyr Lys Glu Ile Lys
            180                 185                 190

Ala Gly Thr Ile Ile Glu Ile Ala Ser Phe Arg Phe Thr Val Leu Glu
        195                 200                 205

Tyr Gln His Ala His Ile Asp Tyr Phe Lys Val Glu Ser Thr Glu Arg
    210                 215                 220

Lys Thr Glu
225
```

<210> 819

<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(766)
<223> RXN01813

<400> 819
gcgagaattc aagaaaacaa aacagatcaa agtaaggcaa caagtgagca acaaagttca 60

gaatccgaac caaggtggaa gcaagaactt cctctgggca atg gtg gcg atc gtc 115
Met Val Ala Ile Val
1 5

gtc gtt gca atc gtc gtc gtc ggc ttc atc gtc atc caa ggc cag ggc 163
Val Val Ala Ile Val Val Val Gly Phe Ile Val Ile Gln Gly Gln Gly
10 15 20

tca aaa gca gcc aag ctt ggt gac cgc gac tac gaa gac acc tct ttg 211
Ser Lys Ala Ala Lys Leu Gly Asp Arg Asp Tyr Glu Asp Thr Ser Leu
25 30 35

gca atg gaa gta ggc tcc gac tcc atc acg ctg acc tcc gca aac acc 259
Ala Met Glu Val Gly Ser Asp Ser Ile Thr Leu Thr Ser Ala Asn Thr
40 45 50

tcc gcc gac gca aag tcc gtg cag ctt ttt gaa gac ttc tcc tgc tct 307
Ser Ala Asp Ala Lys Ser Val Gln Leu Phe Glu Asp Phe Ser Cys Ser
55 60 65

cac tgc tcc gag ctc tcc ctc gcc acc gac gct gac atg aag act cag 355
His Cys Ser Glu Leu Ser Leu Ala Thr Asp Ala Asp Met Lys Thr Gln
70 75 80 85

atc gaa gac ggc aac ctg gtc gtc gaa atc aag cca ctg aac ttc ctt 403
Ile Glu Asp Gly Asn Leu Val Val Glu Ile Lys Pro Leu Asn Phe Leu
90 95 100

gac cgc gaa aac atc gac ggc cac tcc acc cac gca ttg gca gca gcc 451
Asp Arg Glu Asn Ile Asp Gly His Ser Thr His Ala Leu Ala Ala Ala
105 110 115

ctt gca gtg gca gac tcc aac gac gca acc ctc tac tgg aac ttc cgc 499
Leu Ala Val Ala Asp Ser Asn Asp Ala Thr Leu Tyr Trp Asn Phe Arg
120 125 130

gca ttc ctc atg gaa gat cag tcc gag atc tac aac cag tgg tcc gat 547
Ala Phe Leu Met Glu Asp Gln Ser Glu Ile Tyr Asn Gln Trp Ser Asp
135 140 145

gat gac ttc gca gac ggc gtt gaa gcc ctt ggc gca gac tcc tcc gta 595
Asp Asp Phe Ala Asp Gly Val Glu Ala Leu Gly Ala Asp Ser Ser Val
150 155 160 165

gta gac gca atc cga aac ggc gac aac atc cag cgc gca tac gac ctg 643
Val Asp Ala Ile Arg Asn Gly Asp Asn Ile Gln Arg Ala Tyr Asp Leu
170 175 180

gca acc gca aac ggt gaa gaa ctc act gaa gaa acc ggc agc ctg tcc 691

```
Ala Thr Ala Asn Gly Glu Glu Leu Thr Glu Glu Thr Gly Ser Leu Ser
            185                 190                 195

tca cca cgc gtc ctc cag gac ggc aag gat gtt gaa ggc aac atc tcc   739
Ser Pro Arg Val Leu Gln Asp Gly Lys Asp Val Glu Gly Asn Ile Ser
        200                 205                 210

gac tgg atc acc act gtt cta gct tct taaagaactg atctagaagg         786
Asp Trp Ile Thr Thr Val Leu Ala Ser
    215                 220

aaa                                                               789


<210> 820
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 820
Met Val Ala Ile Val Val Val Ala Ile Val Val Val Gly Phe Ile Val
  1               5                  10                  15

Ile Gln Gly Gln Gly Ser Lys Ala Ala Lys Leu Gly Asp Arg Asp Tyr
             20                  25                  30

Glu Asp Thr Ser Leu Ala Met Glu Val Gly Ser Asp Ser Ile Thr Leu
         35                  40                  45

Thr Ser Ala Asn Thr Ser Ala Asp Ala Lys Ser Val Gln Leu Phe Glu
     50                  55                  60

Asp Phe Ser Cys Ser His Cys Ser Glu Leu Ser Leu Ala Thr Asp Ala
 65                  70                  75                  80

Asp Met Lys Thr Gln Ile Glu Asp Gly Asn Leu Val Val Glu Ile Lys
                 85                  90                  95

Pro Leu Asn Phe Leu Asp Arg Glu Asn Ile Asp Gly His Ser Thr His
            100                 105                 110

Ala Leu Ala Ala Ala Leu Ala Val Ala Asp Ser Asn Asp Ala Thr Leu
        115                 120                 125

Tyr Trp Asn Phe Arg Ala Phe Leu Met Glu Asp Gln Ser Glu Ile Tyr
    130                 135                 140

Asn Gln Trp Ser Asp Asp Asp Phe Ala Asp Gly Val Glu Ala Leu Gly
145                 150                 155                 160

Ala Asp Ser Ser Val Val Asp Ala Ile Arg Asn Gly Asp Asn Ile Gln
                165                 170                 175

Arg Ala Tyr Asp Leu Ala Thr Ala Asn Gly Glu Glu Leu Thr Glu Glu
            180                 185                 190

Thr Gly Ser Leu Ser Ser Pro Arg Val Leu Gln Asp Gly Lys Asp Val
        195                 200                 205

Glu Gly Asn Ile Ser Asp Trp Ile Thr Thr Val Leu Ala Ser
    210                 215                 220
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<210> 821
<211> 730
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(730)
<223> FRXA01813

<400> 821
gcgagaattc aagaaaacaa aacagatcaa agtaaggcaa caagtgagca acaaagttca 60

gaatccgaac caaggtggaa gcaagaactt cctctgggca atg gtg gcg atc gtc 115
Met Val Ala Ile Val
1 5

gtc gtt gca atc gtc gtc gtc ggc ttc atc gtc atc caa ggc cag ggc 163
Val Val Ala Ile Val Val Val Gly Phe Ile Val Ile Gln Gly Gln Gly
10 15 20

tca aaa gca gcc aag ctt ggt gac cgc gac tac gaa gac acc tct ttg 211
Ser Lys Ala Ala Lys Leu Gly Asp Arg Asp Tyr Glu Asp Thr Ser Leu
25 30 35

gca atg gaa gta ggc tcc gac tcc atc acg ctg acc tcc gca aac acc 259
Ala Met Glu Val Gly Ser Asp Ser Ile Thr Leu Thr Ser Ala Asn Thr
40 45 50

tcc gcc gac gca aag tcc gtg cag ctt ttt gaa gac ttc tcc tgc tct 307
Ser Ala Asp Ala Lys Ser Val Gln Leu Phe Glu Asp Phe Ser Cys Ser
55 60 65

cac tgc tcc gag ctc tcc ctc gcc acc gac gct gac atg aag act cag 355
His Cys Ser Glu Leu Ser Leu Ala Thr Asp Ala Asp Met Lys Thr Gln
70 75 80 85

atc gaa gac ggc aac ctg gtc gtc gaa atc aag cca ctg aac ttc ctt 403
Ile Glu Asp Gly Asn Leu Val Val Glu Ile Lys Pro Leu Asn Phe Leu
90 95 100

gac cgc gaa aac atc gac ggc cac tcc acc cac gca ttg gca gca gcc 451
Asp Arg Glu Asn Ile Asp Gly His Ser Thr His Ala Leu Ala Ala Ala
105 110 115

ctt gca gtg gca gac tcc aac gac gca acc ctc tac tgg aac ttc cgc 499
Leu Ala Val Ala Asp Ser Asn Asp Ala Thr Leu Tyr Trp Asn Phe Arg
120 125 130

gca ttc ctc atg gaa gat cag tcc gag atc tac aac cag tgg tcc gat 547
Ala Phe Leu Met Glu Asp Gln Ser Glu Ile Tyr Asn Gln Trp Ser Asp
135 140 145

gat gac ttc gca gac ggc gtt gaa gcc ctt ggc gca gac tcc tcc gta 595
Asp Asp Phe Ala Asp Gly Val Glu Ala Leu Gly Ala Asp Ser Ser Val
150 155 160 165

gta gac gca atc cga acg gcg aca aca tcc agc gcg cat acg acc tgg 643
Val Asp Ala Ile Arg Thr Ala Thr Thr Ser Ser Ala His Thr Thr Trp

```
                170                 175                 180

caa ccg caa acg gtg aag aac tca ctg aag aaa ccg gca gcc tgt tct   691
Gln Pro Gln Thr Val Lys Asn Ser Leu Lys Lys Pro Ala Ala Cys Ser
            185                 190                 195

tac cac gcg ttc ttc aag acg gca agg atg ttg aag gca               730
Tyr His Ala Phe Phe Lys Thr Ala Arg Met Leu Lys Ala
        200                 205                 210


<210> 822
<211> 210
<212> PRT
<213> Corynebacterium glutamicum

<400> 822
Met Val Ala Ile Val Val Val Ala Ile Val Val Val Gly Phe Ile Val
  1               5                  10                  15

Ile Gln Gly Gln Gly Ser Lys Ala Ala Lys Leu Gly Asp Arg Asp Tyr
             20                  25                  30

Glu Asp Thr Ser Leu Ala Met Glu Val Gly Ser Asp Ser Ile Thr Leu
         35                  40                  45

Thr Ser Ala Asn Thr Ser Ala Asp Ala Lys Ser Val Gln Leu Phe Glu
     50                  55                  60

Asp Phe Ser Cys Ser His Cys Ser Glu Leu Ser Leu Ala Thr Asp Ala
 65                  70                  75                  80

Asp Met Lys Thr Gln Ile Glu Asp Gly Asn Leu Val Val Glu Ile Lys
                 85                  90                  95

Pro Leu Asn Phe Leu Asp Arg Glu Asn Ile Asp Gly His Ser Thr His
            100                 105                 110

Ala Leu Ala Ala Ala Leu Ala Val Ala Asp Ser Asn Asp Ala Thr Leu
        115                 120                 125

Tyr Trp Asn Phe Arg Ala Phe Leu Met Glu Asp Gln Ser Glu Ile Tyr
    130                 135                 140

Asn Gln Trp Ser Asp Asp Asp Phe Ala Asp Gly Val Glu Ala Leu Gly
145                 150                 155                 160

Ala Asp Ser Ser Val Val Asp Ala Ile Arg Thr Ala Thr Thr Ser Ser
                165                 170                 175

Ala His Thr Thr Trp Gln Pro Gln Thr Val Lys Asn Ser Leu Lys Lys
            180                 185                 190

Pro Ala Ala Cys Ser Tyr His Ala Phe Phe Lys Thr Ala Arg Met Leu
        195                 200                 205

Lys Ala
    210


<210> 823
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<211> 915
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(892)
<223> RXN01815

<400> 823
gaatgaaaag aagtggtggc cgatgcttgg ctatctcagc ctgactttta cacttggata 60

ttctgctgtt tttctcggga tgcggctcta gaattgtaga atg aat cgt tca aca 115
Met Asn Arg Ser Thr
1 5

att tcc cca gtt gaa gcc cgc cag caa ttc cgc gca ggc ctt atc caa 163
Ile Ser Pro Val Glu Ala Arg Gln Gln Phe Arg Ala Gly Leu Ile Gln
10 15 20

ccc acc tcc ggc tgg tcc gcg ggt ttt gcc caa gcc aac ctc att tcc 211
Pro Thr Ser Gly Trp Ser Ala Gly Phe Ala Gln Ala Asn Leu Ile Ser
25 30 35

atg ccc cag gat ctg gct tat gat ttc ctg ctt ttt gct caa cgc aac 259
Met Pro Gln Asp Leu Ala Tyr Asp Phe Leu Leu Phe Ala Gln Arg Asn
40 45 50

ccc aag ccc tgc ccc atc ttg gaa gta tta aat gct ggc gaa acc ttc 307
Pro Lys Pro Cys Pro Ile Leu Glu Val Leu Asn Ala Gly Glu Thr Phe
55 60 65

ggc gga att ttc ggc tca aac gcc acc gaa gca gac atc cgc acc gac 355
Gly Gly Ile Phe Gly Ser Asn Ala Thr Glu Ala Asp Ile Arg Thr Asp
70 75 80 85

gcg ccc caa tac cgc att tac gca cac ggc gaa ctt atc gat tcc ccc 403
Ala Pro Gln Tyr Arg Ile Tyr Ala His Gly Glu Leu Ile Asp Ser Pro
90 95 100

gcc agc gcc gtc gat tat tgg cgc gac gac ctc gtc agt ttc atc atc 451
Ala Ser Ala Val Asp Tyr Trp Arg Asp Asp Leu Val Ser Phe Ile Ile
105 110 115

ggc tgc tcc ttt act ttt gaa cat ccc atg gtc caa gca ggc gtt ccc 499
Gly Cys Ser Phe Thr Phe Glu His Pro Met Val Gln Ala Gly Val Pro
120 125 130

gtc cgc cac ctc gag gcc ggc cgc aac gtc ccc atg tat gaa acc tca 547
Val Arg His Leu Glu Ala Gly Arg Asn Val Pro Met Tyr Glu Thr Ser
135 140 145

ctt gcc tgc cga cca gcc ggt tcc cta tca gga aac ctc gtg gtg tca 595
Leu Ala Cys Arg Pro Ala Gly Ser Leu Ser Gly Asn Leu Val Val Ser
150 155 160 165

ctg cgc atg atc ccc gca tcc caa gtc gcg gat gcc gtc cgc att acc 643
Leu Arg Met Ile Pro Ala Ser Gln Val Ala Asp Ala Val Arg Ile Thr
170 175 180

tcc cgc tac ccc gcg gtt cac gga gca cca gtc cac atc ggc gat cct 691

```
Ser Arg Tyr Pro Ala Val His Gly Ala Pro Val His Ile Gly Asp Pro
            185                 190                 195

tca ctg atc gga atc gat gac atc aac aac cct gat ttc ggc gat gcc   739
Ser Leu Ile Gly Ile Asp Asp Ile Asn Asn Pro Asp Phe Gly Asp Ala
        200                 205                 210

ccg ctg tcc gaa cca agc gac gtc ccc gtg ttt tgg gcc tgc gga gtt   787
Pro Leu Ser Glu Pro Ser Asp Val Pro Val Phe Trp Ala Cys Gly Val
    215                 220                 225

acc cct caa gca atg gtc atg tcc tcc aag cca ccg ctg gcg atc act   835
Thr Pro Gln Ala Met Val Met Ser Ser Lys Pro Pro Leu Ala Ile Thr
230                 235                 240                 245

cac gca ccc gga cac atg ctg atc acc gac gcc cca gat ctg gga ttc   883
His Ala Pro Gly His Met Leu Ile Thr Asp Ala Pro Asp Leu Gly Phe
                250                 255                 260

cag gtt cct taaacctgga tccaccgatg tga                            915
Gln Val Pro
```

09-05-2008

<210> 824
<211> 264
<212> PRT
<213> Corynebacterium glutamicum

<400> 824

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Met Asn Arg Ser Thr Ile Ser Pro Val Glu Ala Arg Gln Gln Phe Arg
  1               5                  10                  15

Ala Gly Leu Ile Gln Pro Thr Ser Gly Trp Ser Ala Gly Phe Ala Gln
             20                  25                  30

Ala Asn Leu Ile Ser Met Pro Gln Asp Leu Ala Tyr Asp Phe Leu Leu
         35                  40                  45

Phe Ala Gln Arg Asn Pro Lys Pro Cys Pro Ile Leu Glu Val Leu Asn
     50                  55                  60

Ala Gly Glu Thr Phe Gly Gly Ile Phe Gly Ser Asn Ala Thr Glu Ala
 65                  70                  75                  80

Asp Ile Arg Thr Asp Ala Pro Gln Tyr Arg Ile Tyr Ala His Gly Glu
                 85                  90                  95

Leu Ile Asp Ser Pro Ala Ser Ala Val Asp Tyr Trp Arg Asp Asp Leu
            100                 105                 110

Val Ser Phe Ile Ile Gly Cys Ser Phe Thr Phe Glu His Pro Met Val
        115                 120                 125

Gln Ala Gly Val Pro Val Arg His Leu Glu Ala Gly Arg Asn Val Pro
    130                 135                 140

Met Tyr Glu Thr Ser Leu Ala Cys Arg Pro Ala Gly Ser Leu Ser Gly
145                 150                 155                 160

Asn Leu Val Val Ser Leu Arg Met Ile Pro Ala Ser Gln Val Ala Asp
```

```
                165                 170                 175

Ala Val Arg Ile Thr Ser Arg Tyr Pro Ala Val His Gly Ala Pro Val
            180                 185                 190

His Ile Gly Asp Pro Ser Leu Ile Gly Ile Asp Asp Ile Asn Asn Pro
        195                 200                 205

Asp Phe Gly Asp Ala Pro Leu Ser Glu Pro Ser Asp Val Pro Val Phe
    210                 215                 220

Trp Ala Cys Gly Val Thr Pro Gln Ala Met Val Met Ser Ser Lys Pro
225                 230                 235                 240

Pro Leu Ala Ile Thr His Ala Pro Gly His Met Leu Ile Thr Asp Ala
                245                 250                 255

Pro Asp Leu Gly Phe Gln Val Pro
            260


<210> 825
<211> 915
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(892)
<223> FRXA01815

<400> 825
gaatgaaaag aagtggtggc cgatgcttgg ctatctcagc ctgactttta cacttggata 60

ttctgctgtt tttctcggga tgcggctcta gaattgtaga atg aat cgt tca aca   115
                                            Met Asn Arg Ser Thr
                                              1               5

att tcc cca gtt gaa gcc cgc cag caa ttc cgc gca ggc ctt atc caa   163
Ile Ser Pro Val Glu Ala Arg Gln Gln Phe Arg Ala Gly Leu Ile Gln
                 10                  15                  20

ccc acc tcc ggc tgg tcc gcg ggt ttt gcc caa gcc aac ctc att tcc   211
Pro Thr Ser Gly Trp Ser Ala Gly Phe Ala Gln Ala Asn Leu Ile Ser
             25                  30                  35

atg ccc cag gat ctg gct tat gat ttc ctg ctt ttt gct caa cgc aac   259
Met Pro Gln Asp Leu Ala Tyr Asp Phe Leu Leu Phe Ala Gln Arg Asn
         40                  45                  50

ccc aag ccc tgc ccc atc ttg gaa gta tta aat gct ggc gaa acc ttc   307
Pro Lys Pro Cys Pro Ile Leu Glu Val Leu Asn Ala Gly Glu Thr Phe
     55                  60                  65

ggc gga att ttc ggc tca aac gcc acc gaa gca gac atc cgc acc gac   355
Gly Gly Ile Phe Gly Ser Asn Ala Thr Glu Ala Asp Ile Arg Thr Asp
 70                  75                  80                  85

gcg ccc caa tac cgc att tac gca cac ggc gaa ctt atc gat tcc ccc   403
Ala Pro Gln Tyr Arg Ile Tyr Ala His Gly Glu Leu Ile Asp Ser Pro
                 90                  95                 100
```

```
gcc agc gcc gtc gat tat tgg cgc gac gac ctc gtc agt ttc atc atc   451
Ala Ser Ala Val Asp Tyr Trp Arg Asp Asp Leu Val Ser Phe Ile Ile
            105                 110                 115

ggc tgc tcc ttt act ttt gaa cat ccc atg gtc caa gca ggc gtt ccc   499
Gly Cys Ser Phe Thr Phe Glu His Pro Met Val Gln Ala Gly Val Pro
        120                 125                 130

gtc cgc cac ctc gag gcc ggc cgc aac gtc ccc atg tat gaa acc tca   547
Val Arg His Leu Glu Ala Gly Arg Asn Val Pro Met Tyr Glu Thr Ser
    135                 140                 145

ctt gcc tgc cga cca gcc ggt tcc cta tca gga aac ctc gtg gtg tca   595
Leu Ala Cys Arg Pro Ala Gly Ser Leu Ser Gly Asn Leu Val Val Ser
150                 155                 160                 165

ctg cgc atg atc ccc gca tcc caa gtc gcg gat gcc gtc cgc att acc   643
Leu Arg Met Ile Pro Ala Ser Gln Val Ala Asp Ala Val Arg Ile Thr
                170                 175                 180

tcc cgc tac ccc gcg gtt cac gga gca cca gtc cac atc ggc gat cct   691
Ser Arg Tyr Pro Ala Val His Gly Ala Pro Val His Ile Gly Asp Pro
            185                 190                 195

tca ctg atc gga atc gat gac atc aac aac cct gat ttc ggc gat gcc   739
Ser Leu Ile Gly Ile Asp Asp Ile Asn Asn Pro Asp Phe Gly Asp Ala
        200                 205                 210

ccg ctg tcc gaa cca agc gac gtc ccc gtg ttt tgg gcc tgc gga gtt   787
Pro Leu Ser Glu Pro Ser Asp Val Pro Val Phe Trp Ala Cys Gly Val
    215                 220                 225

acc cct caa gca atg gtc atg tcc tcc aag cca ccg ctg gcg atc act   835
Thr Pro Gln Ala Met Val Met Ser Ser Lys Pro Pro Leu Ala Ile Thr
230                 235                 240                 245

cac gca ccc gga cac atg ctg atc acc gac gcc cca gat ctg gga ttc   883
His Ala Pro Gly His Met Leu Ile Thr Asp Ala Pro Asp Leu Gly Phe
                250                 255                 260

cag gtt cct taaacctgga tccaccgatg tga                            915
Gln Val Pro
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<210> 826
<211> 264
<212> PRT
<213> Corynebacterium glutamicum

<400> 826

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Met Asn Arg Ser Thr Ile Ser Pro Val Glu Ala Arg Gln Gln Phe Arg
  1               5                  10                  15

Ala Gly Leu Ile Gln Pro Thr Ser Gly Trp Ser Ala Gly Phe Ala Gln
             20                  25                  30

Ala Asn Leu Ile Ser Met Pro Gln Asp Leu Ala Tyr Asp Phe Leu Leu
         35                  40                  45
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```
Phe Ala Gln Arg Asn Pro Lys Pro Cys Pro Ile Leu Glu Val Leu Asn
     50                  55                  60

Ala Gly Glu Thr Phe Gly Gly Ile Phe Gly Ser Asn Ala Thr Glu Ala
 65                  70                  75                  80

Asp Ile Arg Thr Asp Ala Pro Gln Tyr Arg Ile Tyr Ala His Gly Glu
                 85                  90                  95

Leu Ile Asp Ser Pro Ala Ser Ala Val Asp Tyr Trp Arg Asp Asp Leu
            100                 105                 110

Val Ser Phe Ile Ile Gly Cys Ser Phe Thr Phe Glu His Pro Met Val
        115                 120                 125

Gln Ala Gly Val Pro Val Arg His Leu Glu Ala Gly Arg Asn Val Pro
    130                 135                 140

Met Tyr Glu Thr Ser Leu Ala Cys Arg Pro Ala Gly Ser Leu Ser Gly
145                 150                 155                 160

Asn Leu Val Val Ser Leu Arg Met Ile Pro Ala Ser Gln Val Ala Asp
                165                 170                 175

Ala Val Arg Ile Thr Ser Arg Tyr Pro Ala Val His Gly Ala Pro Val
            180                 185                 190

His Ile Gly Asp Pro Ser Leu Ile Gly Ile Asp Asp Ile Asn Asn Pro
        195                 200                 205

Asp Phe Gly Asp Ala Pro Leu Ser Glu Pro Ser Asp Val Pro Val Phe
    210                 215                 220

Trp Ala Cys Gly Val Thr Pro Gln Ala Met Val Met Ser Ser Lys Pro
225                 230                 235                 240

Pro Leu Ala Ile Thr His Ala Pro Gly His Met Leu Ile Thr Asp Ala
                245                 250                 255

Pro Asp Leu Gly Phe Gln Val Pro
            260
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<210> 827
<211> 393
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(370)
<223> RXN01825

<400> 827
gtcaaggtag ctggcccggc aactgatacg ttaagctcaa acaagataag taccagttgc 60

tggggttttt ccaagacaat aaattatgaa ggtgtgaaca atg cca aag gca aga 115
                                                Met Pro Lys Ala Arg
                                                  1   5

gta act aaa aac gag acc gca ccg gtt tca agc aac cca agc gca aac 163

```
Val Thr Lys Asn Glu Thr Ala Pro Val Ser Ser Asn Pro Ser Ala Asn
                10                  15                  20

cgc acc ccg gtt aag atc aat tcc gcc gga acc cca atg tgg tac aag   211
Arg Thr Pro Val Lys Ile Asn Ser Ala Gly Thr Pro Met Trp Tyr Lys
            25                  30                  35

gtc atc atg ttt gcc ttc atg atc gtc ggc cta gcc tgg ttg atc att   259
Val Ile Met Phe Ala Phe Met Ile Val Gly Leu Ala Trp Leu Ile Ile
        40                  45                  50

aac tac ctc gtg ggc cca cag atc cca ttc atg gct gat ctt ggt gca   307
Asn Tyr Leu Val Gly Pro Gln Ile Pro Phe Met Ala Asp Leu Gly Ala
    55                  60                  65

tgg aac tat ggc atc ggc ttc ggt ctg atg atc atc ggc cta ctc atg   355
Trp Asn Tyr Gly Ile Gly Phe Gly Leu Met Ile Ile Gly Leu Leu Met
70                  75                  80                  85

acc atg ggt tgg cgt taatccttca aaaaagtgac tgc                     393
Thr Met Gly Trp Arg
                90
```

<210> 828
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

<400> 828

```
Met Pro Lys Ala Arg Val Thr Lys Asn Glu Thr Ala Pro Val Ser Ser
  1               5                  10                  15

Asn Pro Ser Ala Asn Arg Thr Pro Val Lys Ile Asn Ser Ala Gly Thr
            20                  25                  30

Pro Met Trp Tyr Lys Val Ile Met Phe Ala Phe Met Ile Val Gly Leu
        35                  40                  45

Ala Trp Leu Ile Ile Asn Tyr Leu Val Gly Pro Gln Ile Pro Phe Met
    50                  55                  60

Ala Asp Leu Gly Ala Trp Asn Tyr Gly Ile Gly Phe Gly Leu Met Ile
65                  70                  75                  80

Ile Gly Leu Leu Met Thr Met Gly Trp Arg
                85                  90
```

<210> 829
<211> 393
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(370)
<223> FRXA01825

<400> 829

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gtcaaggtag ctggcccggc aactgatacg ttaagctcaa acaagataag taccagttgc 60
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```
tggggttttt ccaagacaat aaattatgaa ggtgtgaaca atg cca aag gca aga   115
                                            Met Pro Lys Ala Arg
                                              1               5

gta act aaa aac gag acc gca ccg gtt tca agc aac cca agc gca aac   163
Val Thr Lys Asn Glu Thr Ala Pro Val Ser Ser Asn Pro Ser Ala Asn
                 10                  15                  20

cgc acc ccg gtt aag atc aat tcc gcc gga acc cca atg tgg tac aag   211
Arg Thr Pro Val Lys Ile Asn Ser Ala Gly Thr Pro Met Trp Tyr Lys
             25                  30                  35

gtc atc atg ttt gcc ttc atg atc gtc ggc cta gcc tgg ttg atc att   259
Val Ile Met Phe Ala Phe Met Ile Val Gly Leu Ala Trp Leu Ile Ile
         40                  45                  50

aac tac ctc gtg ggc cca cag atc cca ttc atg gct gat ctt ggt gca   307
Asn Tyr Leu Val Gly Pro Gln Ile Pro Phe Met Ala Asp Leu Gly Ala
     55                  60                  65

tgg aac tat ggc atc ggc ttc ggt ctg atg atc atc ggc cta ctc atg   355
Trp Asn Tyr Gly Ile Gly Phe Gly Leu Met Ile Ile Gly Leu Leu Met
 70                  75                  80                  85

acc atg ggt tgg cgt taatccttca aaaaagtgac tgc                    393
Thr Met Gly Trp Arg
                 90
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<210> 830
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

<400> 830

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Met Pro Lys Ala Arg Val Thr Lys Asn Glu Thr Ala Pro Val Ser Ser
  1               5                  10                  15

Asn Pro Ser Ala Asn Arg Thr Pro Val Lys Ile Asn Ser Ala Gly Thr
             20                  25                  30

Pro Met Trp Tyr Lys Val Ile Met Phe Ala Phe Met Ile Val Gly Leu
         35                  40                  45

Ala Trp Leu Ile Ile Asn Tyr Leu Val Gly Pro Gln Ile Pro Phe Met
     50                  55                  60

Ala Asp Leu Gly Ala Trp Asn Tyr Gly Ile Gly Phe Gly Leu Met Ile
 65                  70                  75                  80

Ile Gly Leu Leu Met Thr Met Gly Trp Arg
                 85                  90
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<210> 831
<211> 585
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(562)
<223> RXN01831

<400> 831
cctgtggata attggttgtt ggctgatggt gatgtcatta cggtgggtca ttccaatatc 60

gaagttcgta ttgttagtcc ctagagggag aggttgatca atg gat tct ctg gtc 115
Met Asp Ser Leu Val
1 5

ctt ctt ggg ctt cgc atc gct ttg ctt gtg gtg ttg tgg ttt ttc gtc 163
Leu Leu Gly Leu Arg Ile Ala Leu Leu Val Val Leu Trp Phe Phe Val
10 15 20

ttg atg gcg ctg cgc gct atg agg gca gat ttg aaa gtg acg ggt caa 211
Leu Met Ala Leu Arg Ala Met Arg Ala Asp Leu Lys Val Thr Gly Gln
25 30 35

gcg tcg aca agc agc tcc tcc gtc gcg gca ccg cag ggc ctt gcc cgg 259
Ala Ser Thr Ser Ser Ser Ser Val Ala Ala Pro Gln Gly Leu Ala Arg
40 45 50

gct ttt aat cgc tcc agc ccg cct cgt ctt ttg acg gtg gtc gag ggc 307
Ala Phe Asn Arg Ser Ser Pro Pro Arg Leu Leu Thr Val Val Glu Gly
55 60 65

ccg ttg gcg ggc tcc tcg att gag gtg tcg gag gat atg acg atg ggc 355
Pro Leu Ala Gly Ser Ser Ile Glu Val Ser Glu Asp Met Thr Met Gly
70 75 80 85

cgt agc cct gag tgc acg ttt gtg gtg ggc gat gat tac gcc tcc ggc 403
Arg Ser Pro Glu Cys Thr Phe Val Val Gly Asp Asp Tyr Ala Ser Gly
90 95 100

atg cat gcg cgg gtg ttt aag cgt ggt tcg gag tgg ttt gtg gag gat 451
Met His Ala Arg Val Phe Lys Arg Gly Ser Glu Trp Phe Val Glu Asp
105 110 115

ctg gat tcg cgc aac ggc act ttt gtc ggt ggt acg cgc att gat cag 499
Leu Asp Ser Arg Asn Gly Thr Phe Val Gly Gly Thr Arg Ile Asp Gln
120 125 130

cct gag cag att gcg gtg ggc acg gat atc cgt att ggt cgt aca gca 547
Pro Glu Gln Ile Ala Val Gly Thr Asp Ile Arg Ile Gly Arg Thr Ala
135 140 145

gtg agg ctt gtt ccc tgatgttgaa acttaaatat gcg 585
Val Arg Leu Val Pro
150

<210> 832
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 832
Met Asp Ser Leu Val Leu Leu Gly Leu Arg Ile Ala Leu Leu Val Val
1 5 10 15

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Leu Trp Phe Phe Val Leu Met Ala Leu Arg Ala Met Arg Ala Asp Leu
            20                  25                  30

Lys Val Thr Gly Gln Ala Ser Thr Ser Ser Ser Ser Val Ala Ala Pro
        35                  40                  45

Gln Gly Leu Ala Arg Ala Phe Asn Arg Ser Ser Pro Pro Arg Leu Leu
    50                  55                  60

Thr Val Val Glu Gly Pro Leu Ala Gly Ser Ser Ile Glu Val Ser Glu
65                  70                  75                  80

Asp Met Thr Met Gly Arg Ser Pro Glu Cys Thr Phe Val Val Gly Asp
                85                  90                  95

Asp Tyr Ala Ser Gly Met His Ala Arg Val Phe Lys Arg Gly Ser Glu
            100                 105                 110

Trp Phe Val Glu Asp Leu Asp Ser Arg Asn Gly Thr Phe Val Gly Gly
        115                 120                 125

Thr Arg Ile Asp Gln Pro Glu Gln Ile Ala Val Gly Thr Asp Ile Arg
    130                 135                 140

Ile Gly Arg Thr Ala Val Arg Leu Val Pro
145                 150
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<210> 833
<211> 585
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> FRXA01831

<400> 833

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cctgtggata attggttgtt ggctgatggt gatgtcatta cggtgggtca ttccaatatc 60

gaagttcgta ttgttagtcc ctagagggag aggttgatca atg gat tct ctg gtc   115
                                            Met Asp Ser Leu Val
                                              1               5

ctt ctt ggg ctt cgc atc gct ttg ctt gtg gtg ttg tgg ttt ttc gtc   163
Leu Leu Gly Leu Arg Ile Ala Leu Leu Val Val Leu Trp Phe Phe Val
                10                  15                  20

ttg atg gcg ctg cgc gct atg agg gca gat ttg aaa gtg acg ggt caa   211
Leu Met Ala Leu Arg Ala Met Arg Ala Asp Leu Lys Val Thr Gly Gln
            25                  30                  35

gcg tcg aca agc agc tcc tcc gtc gcg gca ccg cag ggc ctt gcc cgg   259
Ala Ser Thr Ser Ser Ser Ser Val Ala Ala Pro Gln Gly Leu Ala Arg
        40                  45                  50

gct ttt aat cgc tcc agc ccg cct cgt ctt ttg acg gtg gtc gag ggc   307
Ala Phe Asn Arg Ser Ser Pro Pro Arg Leu Leu Thr Val Val Glu Gly
    55                  60                  65
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```
ccg ttg gcg ggc tcc tcg att gag gtg tcg gag gat atg acg atg ggc   355
Pro Leu Ala Gly Ser Ser Ile Glu Val Ser Glu Asp Met Thr Met Gly
 70                  75                  80                  85

cgt agc cct gag tgc acg ttt gtg gtg ggc gat gat tac gcc tcc ggc   403
Arg Ser Pro Glu Cys Thr Phe Val Val Gly Asp Asp Tyr Ala Ser Gly
                 90                  95                 100

atg cat gcg cgg gtg ttt aag cgt ggt tcg gag tgg ttt gtg gag gat   451
Met His Ala Arg Val Phe Lys Arg Gly Ser Glu Trp Phe Val Glu Asp
            105                 110                 115

ctg gat tcg cgc aac ggc act ttt gtc ggt ggt acg cgc att gat cag   499
Leu Asp Ser Arg Asn Gly Thr Phe Val Gly Gly Thr Arg Ile Asp Gln
        120                 125                 130

cct gag cag att gcg gtg ggc acg gat atc cgt att ggt cgt aca gca   547
Pro Glu Gln Ile Ala Val Gly Thr Asp Ile Arg Ile Gly Arg Thr Ala
    135                 140                 145

gtg agg ctt gtt ccc tgatgttgaa acttaaatat gcg                     585
Val Arg Leu Val Pro
150
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10,000,000,000

<210> 835
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> RXN01834

<400> 835
actaagaacg tgagcttggt ttcataatac cccccagggt attgttagcc aggtgattct 60

agcccttctt ggcggcctaa taataggcct acttcttggc atg ctc ggt ggt ggc 115
Met Leu Gly Gly Gly
1 5

ggt gcc atc ctt gcc att ccg ctg ctt att tat gga ttt tct ttt agc 163
Gly Ala Ile Leu Ala Ile Pro Leu Leu Ile Tyr Gly Phe Ser Phe Ser
10 15 20

gcc acg caa gct act gca gct tca tta atc atc atc gga ctt ggc gcc 211
Ala Thr Gln Ala Thr Ala Ala Ser Leu Ile Ile Ile Gly Leu Gly Ala
25 30 35

ctc att gga ctg atc agc caa tac gct gcc ggg cac gtc cgc ctt aaa 259
Leu Ile Gly Leu Ile Ser Gln Tyr Ala Ala Gly His Val Arg Leu Lys
40 45 50

gag ggt cta agc ttt ggc ctt tta ggg ttg gtc ggc tca ttt gtg ggc 307
Glu Gly Leu Ser Phe Gly Leu Leu Gly Leu Val Gly Ser Phe Val Gly
55 60 65

agt cac ctt gct agc aat atc ccc gat tcc cta ctc ctg agc ggc ttt 355
Ser His Leu Ala Ser Asn Ile Pro Asp Ser Leu Leu Leu Ser Gly Phe
70 75 80 85

gcc atc ctc acg ctc gtg gtg gcg ttg acc atg att tct aaa tta aga 403
Ala Ile Leu Thr Leu Val Val Ala Leu Thr Met Ile Ser Lys Leu Arg
90 95 100

agc acc cga gaa tac ata acc aga agg cca agc atc ctt gcc att gct 451
Ser Thr Arg Glu Tyr Ile Thr Arg Arg Pro Ser Ile Leu Ala Ile Ala
105 110 115

ctt agt gcc acc ggc gtg gga ttt ttg acg gga ttt ttt ggt gtg ggt 499
Leu Ser Ala Thr Gly Val Gly Phe Leu Thr Gly Phe Phe Gly Val Gly
120 125 130

ggc ggt ttt gcc att gtg cca gcc ttg att ttt gcg ctc ggt ttt tcc 547
Gly Gly Phe Ala Ile Val Pro Ala Leu Ile Phe Ala Leu Gly Phe Ser
135 140 145

atg cgg cag gct agc gcc act tcc cta gtg gtg atc gcc gtt aac agc 595
Met Arg Gln Ala Ser Ala Thr Ser Leu Val Val Ile Ala Val Asn Ser
150 155 160 165

gct att gcc atg gga ttt aga tat tcc gat ttg gca agt att gac tgg 643
Ala Ile Ala Met Gly Phe Arg Tyr Ser Asp Leu Ala Ser Ile Asp Trp
170 175 180

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tca gtg atc tcg cca att atc atc acc acc gta ttg ggc gct ttt agt   691
Ser Val Ile Ser Pro Ile Ile Ile Thr Thr Val Leu Gly Ala Phe Ser
            185                 190                 195

ggc gta aaa cta gcc aaa aag gtc aaa gca tca tca ctg caa cta ggt   739
Gly Val Lys Leu Ala Lys Lys Val Lys Ala Ser Ser Leu Gln Leu Gly
        200                 205                 210

ttt gct ggc ttc ttg atc ttc att tcg atc tat atg gga ttt cag aat   787
Phe Ala Gly Phe Leu Ile Phe Ile Ser Ile Tyr Met Gly Phe Gln Asn
    215                 220                 225

ttc ccg gac ctt ttt taaaacttca aaatataccc ccc                    825
Phe Pro Asp Leu Phe
230
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<210> 836
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 836

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Met Leu Gly Gly Gly Gly Ala Ile Leu Ala Ile Pro Leu Leu Ile Tyr
  1               5                  10                  15

Gly Phe Ser Phe Ser Ala Thr Gln Ala Thr Ala Ala Ser Leu Ile Ile
             20                  25                  30

Ile Gly Leu Gly Ala Leu Ile Gly Leu Ile Ser Gln Tyr Ala Ala Gly
         35                  40                  45

His Val Arg Leu Lys Glu Gly Leu Ser Phe Gly Leu Leu Gly Leu Val
     50                  55                  60

Gly Ser Phe Val Gly Ser His Leu Ala Ser Asn Ile Pro Asp Ser Leu
 65                  70                  75                  80

Leu Leu Ser Gly Phe Ala Ile Leu Thr Leu Val Val Ala Leu Thr Met
                 85                  90                  95

Ile Ser Lys Leu Arg Ser Thr Arg Glu Tyr Ile Thr Arg Arg Pro Ser
            100                 105                 110

Ile Leu Ala Ile Ala Leu Ser Ala Thr Gly Val Gly Phe Leu Thr Gly
        115                 120                 125

Phe Phe Gly Val Gly Gly Gly Phe Ala Ile Val Pro Ala Leu Ile Phe
    130                 135                 140

Ala Leu Gly Phe Ser Met Arg Gln Ala Ser Ala Thr Ser Leu Val Val
145                 150                 155                 160

Ile Ala Val Asn Ser Ala Ile Ala Met Gly Phe Arg Tyr Ser Asp Leu
                165                 170                 175

Ala Ser Ile Asp Trp Ser Val Ile Ser Pro Ile Ile Ile Thr Thr Val
            180                 185                 190

Leu Gly Ala Phe Ser Gly Val Lys Leu Ala Lys Lys Val Lys Ala Ser
```

```
        195                 200                 205

Ser Leu Gln Leu Gly Phe Ala Gly Phe Leu Ile Phe Ile Ser Ile Tyr
    210                 215                 220

Met Gly Phe Gln Asn Phe Pro Asp Leu Phe
225                 230


<210> 837
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> FRXA01834

<400> 837
actaagaacg tgagcttggt ttcataatac cccccagggt attgttagcc aggtgattct 60

agcccttctt ggcggcctaa taataggcct acttcttggc atg ctc ggt ggt ggc   115
                                              Met Leu Gly Gly Gly
                                                1               5

ggt gcc atc ctt gcc att ccg ctg ctt att tat gga ttt tct ttt agc   163
Gly Ala Ile Leu Ala Ile Pro Leu Leu Ile Tyr Gly Phe Ser Phe Ser
                10                  15                  20

gcc acg caa gct act gca gct tca tta atc atc atc gga ctt ggc gcc   211
Ala Thr Gln Ala Thr Ala Ala Ser Leu Ile Ile Ile Gly Leu Gly Ala
            25                  30                  35

ctc att gga ctg atc agc caa tac gct gcc ggg cac gtc cgc ctt aaa   259
Leu Ile Gly Leu Ile Ser Gln Tyr Ala Ala Gly His Val Arg Leu Lys
        40                  45                  50

gag ggt cta agc ttt ggc ctt tta ggg ttg gtc ggc tca ttt gtg ggc   307
Glu Gly Leu Ser Phe Gly Leu Leu Gly Leu Val Gly Ser Phe Val Gly
    55                  60                  65

agt cac ctt gct agc aat atc ccc gat tcc cta ctc ctg agc ggc ttt   355
Ser His Leu Ala Ser Asn Ile Pro Asp Ser Leu Leu Leu Ser Gly Phe
70                  75                  80                  85

gcc atc ctc acg ctc gtg gtg gcg ttg acc atg att tct aaa tta aga   403
Ala Ile Leu Thr Leu Val Val Ala Leu Thr Met Ile Ser Lys Leu Arg
                90                  95                  100

agc acc cga gaa tac ata acc aga agg cca agc atc ctt gcc att gct   451
Ser Thr Arg Glu Tyr Ile Thr Arg Arg Pro Ser Ile Leu Ala Ile Ala
            105                 110                 115

ctt agt gcc acc ggc gtg gga ttt ttg acg gga ttt ttt ggt gtg ggt   499
Leu Ser Ala Thr Gly Val Gly Phe Leu Thr Gly Phe Phe Gly Val Gly
        120                 125                 130

ggc ggt ttt gcc att gtg cca gcc ttg att ttt gcg ctc ggt ttt tcc   547
Gly Gly Phe Ala Ile Val Pro Ala Leu Ile Phe Ala Leu Gly Phe Ser
    135                 140                 145
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atg cgg cag gct agc gcc act tcc cta gtg gtg atc gcc gtt aac agc   595
Met Arg Gln Ala Ser Ala Thr Ser Leu Val Val Ile Ala Val Asn Ser
150                 155                 160                 165

gct att gcc atg gga ttt aga tat tcc gat ttg gca agt att gac tgg   643
Ala Ile Ala Met Gly Phe Arg Tyr Ser Asp Leu Ala Ser Ile Asp Trp
                170                 175                 180

tca gtg atc tcg cca att atc atc acc acc gta ttg ggc gct ttt agt   691
Ser Val Ile Ser Pro Ile Ile Ile Thr Thr Val Leu Gly Ala Phe Ser
            185                 190                 195

ggc gta aaa cta gcc aaa aag gtc aaa gca tca tca ctg caa cta ggt   739
Gly Val Lys Leu Ala Lys Lys Val Lys Ala Ser Ser Leu Gln Leu Gly
        200                 205                 210

ttt gct ggc ttc ttg atc ttc att tcg atc tat atg gga ttt cag aat   787
Phe Ala Gly Phe Leu Ile Phe Ile Ser Ile Tyr Met Gly Phe Gln Asn
    215                 220                 225

ttc ccg gac ctt ttt taaaacttca aaatataccc ccc                    825
Phe Pro Asp Leu Phe
230
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09600 09650 09700 09750 09800 09850 09900 09950 10000 10050 10100 10150 10200 10250 10300 10350 10400 10450 10500 10550 10600 10650 10700 10750 10800 10850 10900 10950 11000 11050 11100 11150 11200 11250 11300 11350 11400 11450 11500 11550 11600

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Ile Ala Val Asn Ser Ala Ile Ala Met Gly Phe Arg Tyr Ser Asp Leu
                165                 170                 175

Ala Ser Ile Asp Trp Ser Val Ile Ser Pro Ile Ile Ile Thr Thr Val
            180                 185                 190

Leu Gly Ala Phe Ser Gly Val Lys Leu Ala Lys Lys Val Lys Ala Ser
        195                 200                 205

Ser Leu Gln Leu Gly Phe Ala Gly Phe Leu Ile Phe Ile Ser Ile Tyr
    210                 215                 220

Met Gly Phe Gln Asn Phe Pro Asp Leu Phe
225                 230
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<210> 839
<211> 382
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(382)
<223> RXN01846

<400> 839

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gtatttagga attgaaaccc actaaaaaac agactaagtt actaggtgat aacaaaagtt 60

gtttattact tatgggaata gtgtggaaag tagggtgaat atg tca att cct gga   115
                                            Met Ser Ile Pro Gly
                                              1               5

aat gtt agt tat gtt gca cag ggt ggc acc ggt tgg gat ggt gct gat   163
Asn Val Ser Tyr Val Ala Gln Gly Gly Thr Gly Trp Asp Gly Ala Asp
                  10                  15                  20

cag tac acc acg ggt gag agt tgg gat cta cag tcg ttc ctt gaa aac   211
Gln Tyr Thr Thr Gly Glu Ser Trp Asp Leu Gln Ser Phe Leu Glu Asn
              25                  30                  35

tcg act gac tac ctc atg att att ggt ggt tcg ctg ctg gca ctt gtt   259
Ser Thr Asp Tyr Leu Met Ile Ile Gly Gly Ser Leu Leu Ala Leu Val
          40                  45                  50

ggt ggt gct gct gtg att tgg ggc ttt gtc aac gtg atg cgc aag ctc   307
Gly Gly Ala Ala Val Ile Trp Gly Phe Val Asn Val Met Arg Lys Leu
      55                  60                  65

ttc ggt ggt cag agt ggt cag cag att cag tgg ttc acc act att ttg   355
Phe Gly Gly Gln Ser Gly Gln Gln Ile Gln Trp Phe Thr Thr Ile Leu
  70                  75                  80                  85

ctc atc att gtc ggt ggt gcg ttg cct                              382
Leu Ile Ile Val Gly Gly Ala Leu Pro
                  90
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<210> 840
<211> 94

<212> PRT
<213> Corynebacterium glutamicum

<400> 840
Met Ser Ile Pro Gly Asn Val Ser Tyr Val Ala Gln Gly Gly Thr Gly
1 5 10 15

Trp Asp Gly Ala Asp Gln Tyr Thr Thr Gly Glu Ser Trp Asp Leu Gln
20 25 30

Ser Phe Leu Glu Asn Ser Thr Asp Tyr Leu Met Ile Ile Gly Gly Ser
35 40 45

Leu Leu Ala Leu Val Gly Gly Ala Ala Val Ile Trp Gly Phe Val Asn
50 55 60

Val Met Arg Lys Leu Phe Gly Gly Gln Ser Gly Gln Gln Ile Gln Trp
65 70 75 80

Phe Thr Thr Ile Leu Leu Ile Ile Val Gly Gly Ala Leu Pro
85 90

<210> 841
<211> 358
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(358)
<223> FRXA01846

<400> 841
gtatttagga attgaaaccc actaaaaaac agactaagtt actaggtgat aacaaaagtt 60

gtttattact tatgggaata gtgtggaaag tagggtgaat atg tca att cct gga 115
Met Ser Ile Pro Gly
1 5

aat gtt agt tat gtt gca cag ggt ggc acc ggt tgg gat ggt gct gat 163
Asn Val Ser Tyr Val Ala Gln Gly Gly Thr Gly Trp Asp Gly Ala Asp
10 15 20

cag tac acc acg ggt gag agt tgg gat cta cag tcg ttc ctt gaa aac 211
Gln Tyr Thr Thr Gly Glu Ser Trp Asp Leu Gln Ser Phe Leu Glu Asn
25 30 35

tcg act gac tac ctc atg att att ggt ggt tcg ctg ctg gca ctt gtt 259
Ser Thr Asp Tyr Leu Met Ile Ile Gly Gly Ser Leu Leu Ala Leu Val
40 45 50

ggt ggt gct gct gtg att tgg ggc ttt gtc aac gtg atg cgc aag ctc 307
Gly Gly Ala Ala Val Ile Trp Gly Phe Val Asn Val Met Arg Lys Leu
55 60 65

ttc ggt ggt cag agt ggt cag cag att cag tgg ttc acc act att ttg 355
Phe Gly Gly Gln Ser Gly Gln Gln Ile Gln Trp Phe Thr Thr Ile Leu
70 75 80 85

ctc 358

Leu

<210> 842
<211> 86
<212> PRT
<213> Corynebacterium glutamicum

<400> 842
Met Ser Ile Pro Gly Asn Val Ser Tyr Val Ala Gln Gly Gly Thr Gly
1 5 10 15

Trp Asp Gly Ala Asp Gln Tyr Thr Thr Gly Glu Ser Trp Asp Leu Gln
20 25 30

Ser Phe Leu Glu Asn Ser Thr Asp Tyr Leu Met Ile Ile Gly Gly Ser
35 40 45

Leu Leu Ala Leu Val Gly Gly Ala Ala Val Ile Trp Gly Phe Val Asn
50 55 60

Val Met Arg Lys Leu Phe Gly Gly Gln Ser Gly Gln Gln Ile Gln Trp
65 70 75 80

Phe Thr Thr Ile Leu Leu
85

<210> 843
<211> 858
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(835)
<223> RXN01847

<400> 843
gacgtgtgat cataggtgac aaatataccc tctcaacttg gcttcgactg ccctgccccc 60

tcgatttaag aggcaaggct tttacagtat cctctcatgc atg ctt att gtg ttg 115
Met Leu Ile Val Leu
1 5

cct ccc tca gaa act aag acc cac ggc ggt tca gga aaa cct ctg gat 163
Pro Pro Ser Glu Thr Lys Thr His Gly Gly Ser Gly Lys Pro Leu Asp
10 15 20

ttt cac cat ttg agt ttc ccg tcg ctc acc aag gca cgc caa aca ata 211
Phe His His Leu Ser Phe Pro Ser Leu Thr Lys Ala Arg Gln Thr Ile
25 30 35

ctc gct gac ctg caa gct ttg gag gta gat gag gcg ctg aaa gtt ttg 259
Leu Ala Asp Leu Gln Ala Leu Glu Val Asp Glu Ala Leu Lys Val Leu
40 45 50

ggc att tct gaa aag ctc cgc cct gag gcc gaa tcc aat cgc gcg ctg 307
Gly Ile Ser Glu Lys Leu Arg Pro Glu Ala Glu Ser Asn Arg Ala Leu
55 60 65

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gag acc agc cct acg atg cct gcg att ttt cgg tat tcc gga gtg ctt   355
Glu Thr Ser Pro Thr Met Pro Ala Ile Phe Arg Tyr Ser Gly Val Leu
 70                  75                  80                  85

tat gat gcg ctc gac gct gca acg ctg ccg gag aaa gca ctg gaa cgc   403
Tyr Asp Ala Leu Asp Ala Ala Thr Leu Pro Glu Lys Ala Leu Glu Arg
                 90                  95                 100

ctc gcc atc ggc tcg gca ctt ttc ggc gtc atc cac gcc acc gat ccg   451
Leu Ala Ile Gly Ser Ala Leu Phe Gly Val Ile His Ala Thr Asp Pro
            105                 110                 115

atc ccg cat tac cgc ctg tcc ggc ggc aca aaa ctg ccc acc aaa agc   499
Ile Pro His Tyr Arg Leu Ser Gly Gly Thr Lys Leu Pro Thr Lys Ser
        120                 125                 130

ggc gag ctg ccc acc atg aag gcg cgt tgg ggc aca agc atc agc gaa   547
Gly Glu Leu Pro Thr Met Lys Ala Arg Trp Gly Thr Ser Ile Ser Glu
    135                 140                 145

gcg ctt atc gac gtc aac cag ctg gtg att gat ctt cgc agc ggg acc   595
Ala Leu Ile Asp Val Asn Gln Leu Val Ile Asp Leu Arg Ser Gly Thr
150                 155                 160                 165

tac caa cag ttg ggt cgc gta aaa gac gcc gtc acg gta cgc gtg gaa   643
Tyr Gln Gln Leu Gly Arg Val Lys Asp Ala Val Thr Val Arg Val Glu
                170                 175                 180

tca gtc atg gag gat ggc tcc cgc aaa gta gtc agc cac ttt aac aaa   691
Ser Val Met Glu Asp Gly Ser Arg Lys Val Val Ser His Phe Asn Lys
            185                 190                 195

cac tac aaa ggt gaa ctc gcc cgc gtg ctc gcg ctc tct gaa aaa gaa   739
His Tyr Lys Gly Glu Leu Ala Arg Val Leu Ala Leu Ser Glu Lys Glu
        200                 205                 210

gca cac acc gca gag gac gta atg agc att gcg cag gct gcg ggc ctt   787
Ala His Thr Ala Glu Asp Val Met Ser Ile Ala Gln Ala Ala Gly Leu
    215                 220                 225

gtg gtg gag gaa aac ccc aac cac aag gaa acc ctc act ctg gtt gtc   835
Val Val Glu Glu Asn Pro Asn His Lys Glu Thr Leu Thr Leu Val Val
230                 235                 240                 245

taggcgttaa tcaccatttt gat                                        858
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<210> 844
<211> 245
<212> PRT
<213> Corynebacterium glutamicum

<400> 844

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Met Leu Ile Val Leu Pro Pro Ser Glu Thr Lys Thr His Gly Gly Ser
  1               5                  10                  15

Gly Lys Pro Leu Asp Phe His His Leu Ser Phe Pro Ser Leu Thr Lys
             20                  25                  30

Ala Arg Gln Thr Ile Leu Ala Asp Leu Gln Ala Leu Glu Val Asp Glu
```

```
         35                  40                  45

Ala Leu Lys Val Leu Gly Ile Ser Glu Lys Leu Arg Pro Glu Ala Glu
     50                  55                  60

Ser Asn Arg Ala Leu Glu Thr Ser Pro Thr Met Pro Ala Ile Phe Arg
 65                  70                  75                  80

Tyr Ser Gly Val Leu Tyr Asp Ala Leu Asp Ala Ala Thr Leu Pro Glu
                 85                  90                  95

Lys Ala Leu Glu Arg Leu Ala Ile Gly Ser Ala Leu Phe Gly Val Ile
            100                 105                 110

His Ala Thr Asp Pro Ile Pro His Tyr Arg Leu Ser Gly Gly Thr Lys
        115                 120                 125

Leu Pro Thr Lys Ser Gly Glu Leu Pro Thr Met Lys Ala Arg Trp Gly
    130                 135                 140

Thr Ser Ile Ser Glu Ala Leu Ile Asp Val Asn Gln Leu Val Ile Asp
145                 150                 155                 160

Leu Arg Ser Gly Thr Tyr Gln Gln Leu Gly Arg Val Lys Asp Ala Val
                165                 170                 175

Thr Val Arg Val Glu Ser Val Met Glu Asp Gly Ser Arg Lys Val Val
            180                 185                 190

Ser His Phe Asn Lys His Tyr Lys Gly Glu Leu Ala Arg Val Leu Ala
        195                 200                 205

Leu Ser Glu Lys Glu Ala His Thr Ala Glu Asp Val Met Ser Ile Ala
    210                 215                 220

Gln Ala Ala Gly Leu Val Val Glu Glu Asn Pro Asn His Lys Glu Thr
225                 230                 235                 240

Leu Thr Leu Val Val
                245
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<210> 845
<211> 809
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (52)..(786)
<223> FRXA01847

<400> 845

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gccctgcccc ctcgatttaa gaggcaaggc ttttacagta tcctctcatg catg ctt   57
                                                          Met Leu
                                                            1

att gtg ttg cct ccc tca gaa act aag acc cac ggc ggt tca gga aaa   105
Ile Val Leu Pro Pro Ser Glu Thr Lys Thr His Gly Gly Ser Gly Lys
          5                  10                  15
```

```
cct ctg gat ttt cac cat ttg agt ttc ccg tcg ctc acc aag gca cgc   153
Pro Leu Asp Phe His His Leu Ser Phe Pro Ser Leu Thr Lys Ala Arg
     20                  25                  30

caa aca ata ctc gct gac ctg caa gct ttg gag gta gat gag gcg ctg   201
Gln Thr Ile Leu Ala Asp Leu Gln Ala Leu Glu Val Asp Glu Ala Leu
 35                  40                  45                  50

aaa gtt ttg ggc att tct gaa aag ctc cgc cct gag gcc gaa tcc aat   249
Lys Val Leu Gly Ile Ser Glu Lys Leu Arg Pro Glu Ala Glu Ser Asn
                 55                  60                  65

cgc gcg ctg gag acc agc cct acg atg cct gcg att ttt cgg tat tcc   297
Arg Ala Leu Glu Thr Ser Pro Thr Met Pro Ala Ile Phe Arg Tyr Ser
             70                  75                  80

gga gtg ctt tat gat gcg ctc gac gct gca acg ctg ccg gag aaa gca   345
Gly Val Leu Tyr Asp Ala Leu Asp Ala Ala Thr Leu Pro Glu Lys Ala
         85                  90                  95

ctg gaa cgc ctc gcc atc ggc tcg gca ctt ttc ggc gtc atc cac gcc   393
Leu Glu Arg Leu Ala Ile Gly Ser Ala Leu Phe Gly Val Ile His Ala
    100                 105                 110

acc gat ccg atc ccg cat tac cgc ctg tcc ggc ggc aca aaa ctg ccc   441
Thr Asp Pro Ile Pro His Tyr Arg Leu Ser Gly Gly Thr Lys Leu Pro
115                 120                 125                 130

acc aaa agc ggc gag ctg ccc acc atg aag gcg cgt tgg ggc aca agc   489
Thr Lys Ser Gly Glu Leu Pro Thr Met Lys Ala Arg Trp Gly Thr Ser
                135                 140                 145

atc agc gaa gcg ctt atc gac gtc aac cag ctg gtg att gat ctt cgc   537
Ile Ser Glu Ala Leu Ile Asp Val Asn Gln Leu Val Ile Asp Leu Arg
            150                 155                 160

agc ggg acc tac caa cag ttg ggt cgc gta aaa gac gcc gtc acg gta   585
Ser Gly Thr Tyr Gln Gln Leu Gly Arg Val Lys Asp Ala Val Thr Val
        165                 170                 175

cgc gtg gaa tca gtc atg gag gat ggc tcc cgc aaa gta gtc agc cac   633
Arg Val Glu Ser Val Met Glu Asp Gly Ser Arg Lys Val Val Ser His
    180                 185                 190

ttt aac aaa cac tac aaa ggt gaa ctc gcc cgc gtg ctc gcg ctc tct   681
Phe Asn Lys His Tyr Lys Gly Glu Leu Ala Arg Val Leu Ala Leu Ser
195                 200                 205                 210

gaa aaa gaa gca cac acc gca gag gac gta atg agc att gcg cag gct   729
Glu Lys Glu Ala His Thr Ala Glu Asp Val Met Ser Ile Ala Gln Ala
                215                 220                 225

gcg ggc ctt gtg gtg gag gaa aac ccc aac cac aag gaa acc ctc act   777
Ala Gly Leu Val Val Glu Glu Asn Pro Asn His Lys Glu Thr Leu Thr
            230                 235                 240

ctg gtt gtc taggcgttaa tcaccatttt gat                            809
Leu Val Val
        245
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<210> 846
<211> 245
<212> PRT
<213> Corynebacterium glutamicum

<400> 846
Met Leu Ile Val Leu Pro Pro Ser Glu Thr Lys Thr His Gly Gly Ser
1 5 10 15

Gly Lys Pro Leu Asp Phe His His Leu Ser Phe Pro Ser Leu Thr Lys
20 25 30

Ala Arg Gln Thr Ile Leu Ala Asp Leu Gln Ala Leu Glu Val Asp Glu
35 40 45

Ala Leu Lys Val Leu Gly Ile Ser Glu Lys Leu Arg Pro Glu Ala Glu
50 55 60

Ser Asn Arg Ala Leu Glu Thr Ser Pro Thr Met Pro Ala Ile Phe Arg
65 70 75 80

Tyr Ser Gly Val Leu Tyr Asp Ala Leu Asp Ala Ala Thr Leu Pro Glu
85 90 95

Lys Ala Leu Glu Arg Leu Ala Ile Gly Ser Ala Leu Phe Gly Val Ile
100 105 110

His Ala Thr Asp Pro Ile Pro His Tyr Arg Leu Ser Gly Gly Thr Lys
115 120 125

Leu Pro Thr Lys Ser Gly Glu Leu Pro Thr Met Lys Ala Arg Trp Gly
130 135 140

Thr Ser Ile Ser Glu Ala Leu Ile Asp Val Asn Gln Leu Val Ile Asp
145 150 155 160

Leu Arg Ser Gly Thr Tyr Gln Gln Leu Gly Arg Val Lys Asp Ala Val
165 170 175

Thr Val Arg Val Glu Ser Val Met Glu Asp Gly Ser Arg Lys Val Val
180 185 190

Ser His Phe Asn Lys His Tyr Lys Gly Glu Leu Ala Arg Val Leu Ala
195 200 205

Leu Ser Glu Lys Glu Ala His Thr Ala Glu Asp Val Met Ser Ile Ala
210 215 220

Gln Ala Ala Gly Leu Val Val Glu Glu Asn Pro Asn His Lys Glu Thr
225 230 235 240

Leu Thr Leu Val Val
245

<210> 847
<211> 448
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(448)
<223> RXN01874

<400> 847
agtgtcggcg cgacgattgt gggcggtgct ttggcgtggc acgcagcagt ttggcatcac 60

agttccggag cgcaaaacgc ggtcagcctt tcgcgtcgca gtg atc gcg tat gtt 115
Val Ile Ala Tyr Val
1 5

gcc agc gcg tgc tgc ctg ccg ttt ggc gca ttt gcc gga gcg ttg ttg 163
Ala Ser Ala Cys Cys Leu Pro Phe Gly Ala Phe Ala Gly Ala Leu Leu
10 15 20

tcc aag gag ctg tcg gga cat ctc cag gaa cga gtc ctt ctc acc cac 211
Ser Lys Glu Leu Ser Gly His Leu Gln Glu Arg Val Leu Leu Thr His
25 30 35

acg gtg att aat ttt cta ggt ttc gtg gga ttt gct gcg ctc ggt tcg 259
Thr Val Ile Asn Phe Leu Gly Phe Val Gly Phe Ala Ala Leu Gly Ser
40 45 50

ctg tcg gtg ctg ttc gcc gcg att tgg cgc acc aaa att cgc cac aat 307
Leu Ser Val Leu Phe Ala Ala Ile Trp Arg Thr Lys Ile Arg His Asn
55 60 65

ttc acc ccg tgg tct gtg ggg atc atg gcg gtg agc ctg ccg atc atc 355
Phe Thr Pro Trp Ser Val Gly Ile Met Ala Val Ser Leu Pro Ile Ile
70 75 80 85

gtc acg ggc atc ctg ctc aac aac ggc tat gtc gcc gcc aca ggc ctg 403
Val Thr Gly Ile Leu Leu Asn Asn Gly Tyr Val Ala Ala Thr Gly Leu
90 95 100

gcc gcg tac gtg gca gca tgg ttg ctg gcc atg gtg ggg tgg ggg 448
Ala Ala Tyr Val Ala Ala Trp Leu Leu Ala Met Val Gly Trp Gly
105 110 115

<210> 848
<211> 116
<212> PRT
<213> Corynebacterium glutamicum

<400> 848
Val Ile Ala Tyr Val Ala Ser Ala Cys Cys Leu Pro Phe Gly Ala Phe
1 5 10 15

Ala Gly Ala Leu Leu Ser Lys Glu Leu Ser Gly His Leu Gln Glu Arg
20 25 30

Val Leu Leu Thr His Thr Val Ile Asn Phe Leu Gly Phe Val Gly Phe
35 40 45

Ala Ala Leu Gly Ser Leu Ser Val Leu Phe Ala Ala Ile Trp Arg Thr
50 55 60

Lys Ile Arg His Asn Phe Thr Pro Trp Ser Val Gly Ile Met Ala Val
65 70 75 80

```
Ser Leu Pro Ile Ile Val Thr Gly Ile Leu Leu Asn Asn Gly Tyr Val
                 85                  90                  95

Ala Ala Thr Gly Leu Ala Ala Tyr Val Ala Ala Trp Leu Leu Ala Met
            100                 105                 110

Val Gly Trp Gly
        115
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<210> 849
<211> 448
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(448)
<223> FRXA01874

<400> 849

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agtgtcggcg cgacgattgt gggcggtgct ttggcgtggc acgcagcagt ttggcatcac 60

agttccggag cgcaaaacgc ggtcagcctt tcgcgtcgca gtg atc gcg tat gtt   115
                                              Val Ile Ala Tyr Val
                                                1               5

gcc agc gcg tgc tgc ctg ccg ttt ggc gca ttt gcc gga gcg ttg ttg   163
Ala Ser Ala Cys Cys Leu Pro Phe Gly Ala Phe Ala Gly Ala Leu Leu
                10                  15                  20

tcc aag gag ctg tcg gga cat ctc cag gaa cga gtc ctt ctc acc cac   211
Ser Lys Glu Leu Ser Gly His Leu Gln Glu Arg Val Leu Leu Thr His
            25                  30                  35

acg gtg att aat ttt cta ggt ttc gtg gga ttt gct gcg ctc ggt tcg   259
Thr Val Ile Asn Phe Leu Gly Phe Val Gly Phe Ala Ala Leu Gly Ser
        40                  45                  50

ctg tcg gtg ctg ttc gcc gcg att tgg cgc acc aaa att cgc cac aat   307
Leu Ser Val Leu Phe Ala Ala Ile Trp Arg Thr Lys Ile Arg His Asn
    55                  60                  65

ttc acc ccg tgg tct gtg ggg atc atg gcg gtg agc ctg ccg atc atc   355
Phe Thr Pro Trp Ser Val Gly Ile Met Ala Val Ser Leu Pro Ile Ile
70                  75                  80                  85

gtc acg ggc atc ctg ctc aac aac ggc tat gtc gcc gca cag gcc tgg   403
Val Thr Gly Ile Leu Leu Asn Asn Gly Tyr Val Ala Ala Gln Ala Trp
                90                  95                 100

ccg cgt acg tgg cag cat ggt tgc tgg cca tgg tgg ggt ggg gga       448
Pro Arg Thr Trp Gln His Gly Cys Trp Pro Trp Trp Gly Gly Gly
            105                 110                 115
```

<210> 850
<211> 116
<212> PRT
<213> Corynebacterium glutamicum

<400> 850
Val Ile Ala Tyr Val Ala Ser Ala Cys Cys Leu Pro Phe Gly Ala Phe
1 5 10 15

Ala Gly Ala Leu Leu Ser Lys Glu Leu Ser Gly His Leu Gln Glu Arg
20 25 30

Val Leu Leu Thr His Thr Val Ile Asn Phe Leu Gly Phe Val Gly Phe
35 40 45

Ala Ala Leu Gly Ser Leu Ser Val Leu Phe Ala Ala Ile Trp Arg Thr
50 55 60

Lys Ile Arg His Asn Phe Thr Pro Trp Ser Val Gly Ile Met Ala Val
65 70 75 80

Ser Leu Pro Ile Ile Val Thr Gly Ile Leu Leu Asn Asn Gly Tyr Val
85 90 95

Ala Ala Gln Ala Trp Pro Arg Thr Trp Gln His Gly Cys Trp Pro Trp
100 105 110

Trp Gly Gly Gly
115

<210> 851
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> RXN01875

<400> 851
aatcctatcc ctaaaaagtt tctaacaaaa gtattgcact tacttttttga tagtgctatc 60

ttcagttgtg tacttgaaac acacacgaat ggagcaagaa atg cgt att gca gta 115
Met Arg Ile Ala Val
1 5

act gga gca acg gga tct ttg ggt gga cat gtt gtg gat agt ctt cta 163
Thr Gly Ala Thr Gly Ser Leu Gly Gly His Val Val Asp Ser Leu Leu
10 15 20

aac aag ggc gtc gca gca tca gac atc gtt gcc att gtt cga aat gaa 211
Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala Ile Val Arg Asn Glu
25 30 35

gaa aag gca gca gac ctc aaa gcc cgt gga atc gct ctt ggt gtg gct 259
Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile Ala Leu Gly Val Ala
40 45 50

act ttt gaa gac gaa gcg gca ctg act gca gct ctt gaa ggt gtg gat 307
Thr Phe Glu Asp Glu Ala Ala Leu Thr Ala Ala Leu Glu Gly Val Asp
55 60 65

cgc ctt gtg ttt atc tct ggc agc gaa gtg ggg cag cgc gtt gcg cag 355
Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly Gln Arg Val Ala Gln

```
 70                  75                  80                  85

cac acc aat gtc atc aat gcc gct aaa gca gct ggc gtg aca ttc att   403
His Thr Asn Val Ile Asn Ala Ala Lys Ala Ala Gly Val Thr Phe Ile
                90                  95                 100

gca tac acc agc ttg ctc aac ctt ggt acc tca aag ctt gca ctt gct   451
Ala Tyr Thr Ser Leu Leu Asn Leu Gly Thr Ser Lys Leu Ala Leu Ala
            105                 110                 115

cca gag cac att gca acg gaa aag ctc ctg gca gaa agc ggc att gac   499
Pro Glu His Ile Ala Thr Glu Lys Leu Leu Ala Glu Ser Gly Ile Asp
        120                 125                 130

cac gcg ctg ctg cgc aat ggt tgg tac tgg gag aac tac gaa tct tca   547
His Ala Leu Leu Arg Asn Gly Trp Tyr Trp Glu Asn Tyr Glu Ser Ser
    135                 140                 145

att ggc gca gcg aag gcc acc ggg aag gta ttc ggc gca gct gaa ggc   595
Ile Gly Ala Ala Lys Ala Thr Gly Lys Val Phe Gly Ala Ala Glu Gly
150                 155                 160                 165

gca cgc gtt tcc gca gcc gca cgt aag gac tac gca gag gca gct gct   643
Ala Arg Val Ser Ala Ala Ala Arg Lys Asp Tyr Ala Glu Ala Ala Ala
                170                 175                 180

gtt gtc atc acc agc gac aac cag gca ggc aag gtc tat gag ctc gca   691
Val Val Ile Thr Ser Asp Asn Gln Ala Gly Lys Val Tyr Glu Leu Ala
            185                 190                 195

ggc gca cca gct ttg acc tac cca gag atc gca gct ggc att ggt gag   739
Gly Ala Pro Ala Leu Thr Tyr Pro Glu Ile Ala Ala Gly Ile Gly Glu
        200                 205                 210

gtc att ggt tct gag gca gaa tac gtc aac ctc tcc gtg gag gag tac   787
Val Ile Gly Ser Glu Ala Glu Tyr Val Asn Leu Ser Val Glu Glu Tyr
    215                 220                 225

caa aat gcg ctg gag cag gct ggc gtt cca gct gaa ttt gca gca ctt   835
Gln Asn Ala Leu Glu Gln Ala Gly Val Pro Ala Glu Phe Ala Ala Leu
230                 235                 240                 245

ctc gca ggc atg gat ccc atc att gca gag ggc gcg ctg tac tcc gac   883
Leu Ala Gly Met Asp Pro Ile Ile Ala Glu Gly Ala Leu Tyr Ser Asp
                250                 255                 260

agc acc gac cta cag gat ctc atc gga cgc ccg agc acc tca atc gtt   931
Ser Thr Asp Leu Gln Asp Leu Ile Gly Arg Pro Ser Thr Ser Ile Val
            265                 270                 275

gag gcc ctg agc tca taacctgcta ctcacctaaa atg                    969
Glu Ala Leu Ser Ser
        280
```

<210> 852
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 852

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Met Arg Ile Ala Val Thr Gly Ala Thr Gly Ser Leu Gly Gly His Val
 1               5                  10                  15

Val Asp Ser Leu Leu Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala
            20                  25                  30

Ile Val Arg Asn Glu Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile
        35                  40                  45

Ala Leu Gly Val Ala Thr Phe Glu Asp Glu Ala Ala Leu Thr Ala Ala
    50                  55                  60

Leu Glu Gly Val Asp Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly
65                  70                  75                  80

Gln Arg Val Ala Gln His Thr Asn Val Ile Asn Ala Ala Lys Ala Ala
                85                  90                  95

Gly Val Thr Phe Ile Ala Tyr Thr Ser Leu Leu Asn Leu Gly Thr Ser
            100                 105                 110

Lys Leu Ala Leu Ala Pro Glu His Ile Ala Thr Glu Lys Leu Leu Ala
        115                 120                 125

Glu Ser Gly Ile Asp His Ala Leu Leu Arg Asn Gly Trp Tyr Trp Glu
    130                 135                 140

Asn Tyr Glu Ser Ser Ile Gly Ala Ala Lys Ala Thr Gly Lys Val Phe
145                 150                 155                 160

Gly Ala Ala Glu Gly Ala Arg Val Ser Ala Ala Ala Arg Lys Asp Tyr
                165                 170                 175

Ala Glu Ala Ala Ala Val Val Ile Thr Ser Asp Asn Gln Ala Gly Lys
            180                 185                 190

Val Tyr Glu Leu Ala Gly Ala Pro Ala Leu Thr Tyr Pro Glu Ile Ala
        195                 200                 205

Ala Gly Ile Gly Glu Val Ile Gly Ser Glu Ala Glu Tyr Val Asn Leu
    210                 215                 220

Ser Val Glu Glu Tyr Gln Asn Ala Leu Glu Gln Ala Gly Val Pro Ala
225                 230                 235                 240

Glu Phe Ala Ala Leu Leu Ala Gly Met Asp Pro Ile Ile Ala Glu Gly
                245                 250                 255

Ala Leu Tyr Ser Asp Ser Thr Asp Leu Gln Asp Leu Ile Gly Arg Pro
            260                 265                 270

Ser Thr Ser Ile Val Glu Ala Leu Ser Ser
        275                 280
```

<210> 853
<211> 921
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(898)
<223> FRXA01875

<400> 853
ctwkcktsrs wtgtgtrsyw gawwmmcwyw cscagcatsr wgcwrgwwwy rmgkwktsca 60

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syaaacwggr gtcartcscg gatctttggg tggacatgtt gtg gat agt ctt cta   115
                                           Val Asp Ser Leu Leu
                                             1               5

aac aag ggc gtc gca gca tca gac atc gtt gcc att gtt cga aat gaa   163
Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala Ile Val Arg Asn Glu
                 10                  15                  20

gaa aag gca gca gac ctc aaa gcc cgt gga atc gct ctt ggt gtg gct   211
Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile Ala Leu Gly Val Ala
             25                  30                  35

act ttt gaa gac gaa gcg gca ctg act gca gct ctt gaa ggt gtg gat   259
Thr Phe Glu Asp Glu Ala Ala Leu Thr Ala Ala Leu Glu Gly Val Asp
         40                  45                  50

cgc ctt gtg ttt atc tct ggc agc gaa gtg ggg cag cgc gtt gcg cag   307
Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly Gln Arg Val Ala Gln
     55                  60                  65

cac acc aat gtc atc aat gcc gct aaa gca gct ggc gtg aca ttc att   355
His Thr Asn Val Ile Asn Ala Ala Lys Ala Ala Gly Val Thr Phe Ile
 70                  75                  80                  85

gca tac acc agc ttg ctc aac ctt ggt acc tca aag ctt gca ctt gct   403
Ala Tyr Thr Ser Leu Leu Asn Leu Gly Thr Ser Lys Leu Ala Leu Ala
                 90                  95                 100

cca gag cac att gca acg gaa aag ctc ctg gca gaa agc ggc att gac   451
Pro Glu His Ile Ala Thr Glu Lys Leu Leu Ala Glu Ser Gly Ile Asp
             105                 110                 115

cac gcg ctg ctg cgc aat ggt tgg tac tgg gag aac tac gaa tct tca   499
His Ala Leu Leu Arg Asn Gly Trp Tyr Trp Glu Asn Tyr Glu Ser Ser
         120                 125                 130

att ggc gca gcg aag gcc acc ggg aag gta ttc ggc gca gct gaa ggc   547
Ile Gly Ala Ala Lys Ala Thr Gly Lys Val Phe Gly Ala Ala Glu Gly
     135                 140                 145

gca cgc gtt tcc gca gcc gca cgt aag gac tac gca gag gca gct gct   595
Ala Arg Val Ser Ala Ala Ala Arg Lys Asp Tyr Ala Glu Ala Ala Ala
150                 155                 160                 165

gtt gtc atc acc agc gac aac cag gca ggc aag gtc tat gag ctc gca   643
Val Val Ile Thr Ser Asp Asn Gln Ala Gly Lys Val Tyr Glu Leu Ala
                 170                 175                 180

ggc gca cca gct ttg acc tac cca gag atc gca gct ggc att ggt gag   691
Gly Ala Pro Ala Leu Thr Tyr Pro Glu Ile Ala Ala Gly Ile Gly Glu
             185                 190                 195

gtc att ggt tct gag gca gaa tac gtc aac ctc tcc gtg gag gag tac   739
Val Ile Gly Ser Glu Ala Glu Tyr Val Asn Leu Ser Val Glu Glu Tyr
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```
        200                 205                 210
caa aat gcg ctg gag cag gct ggc gtt cca gct gaa ttt gca gca ctt   787
Gln Asn Ala Leu Glu Gln Ala Gly Val Pro Ala Glu Phe Ala Ala Leu
    215                 220                 225

ctc gca ggc atg gat ccc atc att gca gag ggc gcg ctg tac tcc gac   835
Leu Ala Gly Met Asp Pro Ile Ile Ala Glu Gly Ala Leu Tyr Ser Asp
230                 235                 240                 245

agc acc gac cta cag gat ctc atc gga cgc ccg agc acc tca atc gtt   883
Ser Thr Asp Leu Gln Asp Leu Ile Gly Arg Pro Ser Thr Ser Ile Val
                250                 255                 260

gag gcc ctg agc tca taacctgcta ctcacctaaa atg                    921
Glu Ala Leu Ser Ser
            265
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<210> 854
<211> 266
<212> PRT
<213> Corynebacterium glutamicum

<400> 854

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Val Asp Ser Leu Leu Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala
  1               5                  10                  15

Ile Val Arg Asn Glu Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile
             20                  25                  30

Ala Leu Gly Val Ala Thr Phe Glu Asp Glu Ala Ala Leu Thr Ala Ala
         35                  40                  45

Leu Glu Gly Val Asp Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly
     50                  55                  60

Gln Arg Val Ala Gln His Thr Asn Val Ile Asn Ala Ala Lys Ala Ala
 65                  70                  75                  80

Gly Val Thr Phe Ile Ala Tyr Thr Ser Leu Leu Asn Leu Gly Thr Ser
                 85                  90                  95

Lys Leu Ala Leu Ala Pro Glu His Ile Ala Thr Glu Lys Leu Leu Ala
            100                 105                 110

Glu Ser Gly Ile Asp His Ala Leu Leu Arg Asn Gly Trp Tyr Trp Glu
        115                 120                 125

Asn Tyr Glu Ser Ser Ile Gly Ala Ala Lys Ala Thr Gly Lys Val Phe
    130                 135                 140

Gly Ala Ala Glu Gly Ala Arg Val Ser Ala Ala Ala Arg Lys Asp Tyr
145                 150                 155                 160

Ala Glu Ala Ala Ala Val Val Ile Thr Ser Asp Asn Gln Ala Gly Lys
                165                 170                 175

Val Tyr Glu Leu Ala Gly Ala Pro Ala Leu Thr Tyr Pro Glu Ile Ala
            180                 185                 190
```

```
Ala Gly Ile Gly Glu Val Ile Gly Ser Glu Ala Glu Tyr Val Asn Leu
        195                 200                 205

Ser Val Glu Glu Tyr Gln Asn Ala Leu Glu Gln Ala Gly Val Pro Ala
    210                 215                 220

Glu Phe Ala Ala Leu Leu Ala Gly Met Asp Pro Ile Ile Ala Glu Gly
225                 230                 235                 240

Ala Leu Tyr Ser Asp Ser Thr Asp Leu Gln Asp Leu Ile Gly Arg Pro
                245                 250                 255

Ser Thr Ser Ile Val Glu Ala Leu Ser Ser
            260                 265


<210> 855
<211> 484
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(484)
<223> FRXA02734

<400> 855
aatcctatcc ctaaaaagtt tctaacaaaa gtattgcact tacttttga tagtgctatc 60

ttcagttgtg tacttgaaac acacacgaat ggagcaagaa atg cgt att gca gta   115
                                            Met Arg Ile Ala Val
                                              1               5

act gga gca acg gga tct ttg ggt gga cat gtt gtg gat agt ctt cta   163
Thr Gly Ala Thr Gly Ser Leu Gly Gly His Val Val Asp Ser Leu Leu
                 10                  15                  20

aac aag ggc gtc gca gca tca gac atc gtt gcc att gtt cga aat gaa   211
Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala Ile Val Arg Asn Glu
             25                  30                  35

gaa aag gca gca gac ctc aaa gcc cgt gga atc gct ctt ggt gtg gct   259
Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile Ala Leu Gly Val Ala
         40                  45                  50

act ttt gaa gac gaa acg gca ctg act gca gct ctt gaa ggt gtg gat   307
Thr Phe Glu Asp Glu Thr Ala Leu Thr Ala Ala Leu Glu Gly Val Asp
     55                  60                  65

cgc ctt gtg ttt atc tct ggc agc gaa gtg ggg cag cgc gtt gcg caa   355
Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly Gln Arg Val Ala Gln
 70                  75                  80                  85

cac acc aat gtc atc aat gcc gct aaa gca act ggc gtg aca ttc att   403
His Thr Asn Val Ile Asn Ala Ala Lys Ala Thr Gly Val Thr Phe Ile
                 90                  95                 100

gca tac acc agc ttg ctc aac ctt ggt cct caa agc ttg cac ttg ctc   451
Ala Tyr Thr Ser Leu Leu Asn Leu Gly Pro Gln Ser Leu His Leu Leu
            105                 110                 115
```

```
cag agc aca ttg caa ccg gaa aag ctc ctg gca                          484
Gln Ser Thr Leu Gln Pro Glu Lys Leu Leu Ala
        120                 125


<210> 856
<211> 128
<212> PRT
<213> Corynebacterium glutamicum

<400> 856
Met Arg Ile Ala Val Thr Gly Ala Thr Gly Ser Leu Gly Gly His Val
  1               5                  10                  15

Val Asp Ser Leu Leu Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala
             20                  25                  30

Ile Val Arg Asn Glu Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile
         35                  40                  45

Ala Leu Gly Val Ala Thr Phe Glu Asp Glu Thr Ala Leu Thr Ala Ala
     50                  55                  60

Leu Glu Gly Val Asp Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly
 65                  70                  75                  80

Gln Arg Val Ala Gln His Thr Asn Val Ile Asn Ala Ala Lys Ala Thr
                 85                  90                  95

Gly Val Thr Phe Ile Ala Tyr Thr Ser Leu Leu Asn Leu Gly Pro Gln
            100                 105                 110

Ser Leu His Leu Leu Gln Ser Thr Leu Gln Pro Glu Lys Leu Leu Ala
        115                 120                 125




<210> 857
<211> 1194
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1171)
<223> RXN01877

<400> 857
gtacccgtat tgtactaatt gtaattcccc ggagagggaa gaagtttaca tggcgcccca 60

tcagaagtca gggatcaacc ggatcaacag cacccgctcg gtg ccg ttg cgt ttg   115
                                          Val Pro Leu Arg Leu
                                            1               5

gct acc ggt ggc gtg ctc gcc acc ttg ctt atc ggc gga gtc acc gct   163
Ala Thr Gly Gly Val Leu Ala Thr Leu Leu Ile Gly Gly Val Thr Ala
                10                  15                  20

gca gct acc aaa aag gac atc att gtt gat gtc aac ggc gag cag atg   211
```

```
Ala Ala Thr Lys Lys Asp Ile Ile Val Asp Val Asn Gly Glu Gln Met
            25                  30                  35

tcc cta gtg act atg tcc ggc act gtt gaa ggt gtg ctg gcg caa gct   259
Ser Leu Val Thr Met Ser Gly Thr Val Glu Gly Val Leu Ala Gln Ala
        40                  45                  50

ggt gtg gaa ctt ggt gac cag gac att gtt tcc cct tca ctg gat tca   307
Gly Val Glu Leu Gly Asp Gln Asp Ile Val Ser Pro Ser Leu Asp Ser
    55                  60                  65

tcc atc agt gat gaa gac act gtg act gtt cgt act gcc aag cag gtg   355
Ser Ile Ser Asp Glu Asp Thr Val Thr Val Arg Thr Ala Lys Gln Val
70                  75                  80                  85

gcg ctc gtg gtg gaa ggt caa atc caa aac gtg acc acc act gcg gtt   403
Ala Leu Val Val Glu Gly Gln Ile Gln Asn Val Thr Thr Thr Ala Val
                90                  95                  100

tcc gtg gag gac ctc ctg cag gaa gtc ggt ggc att acc ggt gct gat   451
Ser Val Glu Asp Leu Leu Gln Glu Val Gly Gly Ile Thr Gly Ala Asp
            105                 110                 115

gcg gtg gac gct gat ctt tca gag acc atc cca gaa tct ggt ttg aag   499
Ala Val Asp Ala Asp Leu Ser Glu Thr Ile Pro Glu Ser Gly Leu Lys
        120                 125                 130

gtg agt gtt acc aag ccg aag att att tcc atc aat gat ggt ggc aag   547
Val Ser Val Thr Lys Pro Lys Ile Ile Ser Ile Asn Asp Gly Gly Lys
    135                 140                 145

gtc act tac gtt tct ttg gca gct cag aac gta cag gaa gcc cta gag   595
Val Thr Tyr Val Ser Leu Ala Ala Gln Asn Val Gln Glu Ala Leu Glu
150                 155                 160                 165

ctg cgg gat att gag ctg ggt gct cag gac cgc att aat gtg cct ctg   643
Leu Arg Asp Ile Glu Leu Gly Ala Gln Asp Arg Ile Asn Val Pro Leu
                170                 175                 180

gat cag cag ctg aag aac aac gct gcg atc cag atc gac cgc gtt gac   691
Asp Gln Gln Leu Lys Asn Asn Ala Ala Ile Gln Ile Asp Arg Val Asp
            185                 190                 195

aac acc gaa atc act gaa act gtg tct ttc gat gct gag cca acc tac   739
Asn Thr Glu Ile Thr Glu Thr Val Ser Phe Asp Ala Glu Pro Thr Tyr
        200                 205                 210

gtg gat gat cca gaa gct cca gct ggc gat gaa act gtg gtc gaa gaa   787
Val Asp Asp Pro Glu Ala Pro Ala Gly Asp Glu Thr Val Val Glu Glu
    215                 220                 225

ggc gct cct gga acc aag gaa gtt act cgc acc gta aca acc gtt aat   835
Gly Ala Pro Gly Thr Lys Glu Val Thr Arg Thr Val Thr Thr Val Asn
230                 235                 240                 245

ggt cag gaa gaa tct tcc acg gtg atc aat gaa gtt gaa atc acc gca   883
Gly Gln Glu Glu Ser Ser Thr Val Ile Asn Glu Val Glu Ile Thr Ala
                250                 255                 260

gca aag cca gca acc att agc cgt ggc acc aaa act gtc gct gca aac   931
Ala Lys Pro Ala Thr Ile Ser Arg Gly Thr Lys Thr Val Ala Ala Asn
```

```
            265                 270                 275

tcc gtg tgg gat cag ctg gca cag tgt gaa tcc ggc gga aac tgg gca   979
Ser Val Trp Asp Gln Leu Ala Gln Cys Glu Ser Gly Gly Asn Trp Ala
        280                 285                 290

atc aac aca ggt aat ggc ttc tcc ggc ggc cta cag ttc cac cca cag   1027
Ile Asn Thr Gly Asn Gly Phe Ser Gly Gly Leu Gln Phe His Pro Gln
    295                 300                 305

acc tgg ctc gca tac ggt ggt gga gct ttc tcc ggt gac gct tcc ggt   1075
Thr Trp Leu Ala Tyr Gly Gly Gly Ala Phe Ser Gly Asp Ala Ser Gly
310                 315                 320                 325

gca agc cgt gaa cag caa atc tcc atc gca gaa aag gtt cag gct gca   1123
Ala Ser Arg Glu Gln Gln Ile Ser Ile Ala Glu Lys Val Gln Ala Ala
                330                 335                 340

caa ggt tgg gga gca tgg cct gct tgc acc gca agc ttg ggc atc cga   1171
Gln Gly Trp Gly Ala Trp Pro Ala Cys Thr Ala Ser Leu Gly Ile Arg
            345                 350                 355

tagtagaaat ctggcatcca ata                                        1194


<210> 858
<211> 357
<212> PRT
<213> Corynebacterium glutamicum

<400> 858
Val Pro Leu Arg Leu Ala Thr Gly Gly Val Leu Ala Thr Leu Leu Ile
  1               5                  10                  15

Gly Gly Val Thr Ala Ala Ala Thr Lys Lys Asp Ile Ile Val Asp Val
             20                  25                  30

Asn Gly Glu Gln Met Ser Leu Val Thr Met Ser Gly Thr Val Glu Gly
         35                  40                  45

Val Leu Ala Gln Ala Gly Val Glu Leu Gly Asp Gln Asp Ile Val Ser
     50                  55                  60

Pro Ser Leu Asp Ser Ser Ile Ser Asp Glu Asp Thr Val Thr Val Arg
 65                  70                  75                  80

Thr Ala Lys Gln Val Ala Leu Val Val Glu Gly Gln Ile Gln Asn Val
                 85                  90                  95

Thr Thr Thr Ala Val Ser Val Glu Asp Leu Leu Gln Glu Val Gly Gly
            100                 105                 110

Ile Thr Gly Ala Asp Ala Val Asp Ala Asp Leu Ser Glu Thr Ile Pro
        115                 120                 125

Glu Ser Gly Leu Lys Val Ser Val Thr Lys Pro Lys Ile Ile Ser Ile
    130                 135                 140

Asn Asp Gly Gly Lys Val Thr Tyr Val Ser Leu Ala Ala Gln Asn Val
145                 150                 155                 160
```

```
Gln Glu Ala Leu Glu Leu Arg Asp Ile Glu Leu Gly Ala Gln Asp Arg
                165                 170                 175

Ile Asn Val Pro Leu Asp Gln Gln Leu Lys Asn Asn Ala Ala Ile Gln
            180                 185                 190

Ile Asp Arg Val Asp Asn Thr Glu Ile Thr Glu Thr Val Ser Phe Asp
        195                 200                 205

Ala Glu Pro Thr Tyr Val Asp Asp Pro Glu Ala Pro Ala Gly Asp Glu
    210                 215                 220

Thr Val Val Glu Glu Gly Ala Pro Gly Thr Lys Glu Val Thr Arg Thr
225                 230                 235                 240

Val Thr Thr Val Asn Gly Gln Glu Glu Ser Ser Thr Val Ile Asn Glu
                245                 250                 255

Val Glu Ile Thr Ala Ala Lys Pro Ala Thr Ile Ser Arg Gly Thr Lys
            260                 265                 270

Thr Val Ala Ala Asn Ser Val Trp Asp Gln Leu Ala Gln Cys Glu Ser
        275                 280                 285

Gly Gly Asn Trp Ala Ile Asn Thr Gly Asn Gly Phe Ser Gly Gly Leu
    290                 295                 300

Gln Phe His Pro Gln Thr Trp Leu Ala Tyr Gly Gly Gly Ala Phe Ser
305                 310                 315                 320

Gly Asp Ala Ser Gly Ala Ser Arg Glu Gln Gln Ile Ser Ile Ala Glu
                325                 330                 335

Lys Val Gln Ala Ala Gln Gly Trp Gly Ala Trp Pro Ala Cys Thr Ala
            340                 345                 350

Ser Leu Gly Ile Arg
        355
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20050130-0000-0000-0000-000000000000

<210> 859
<211> 1188
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1165)
<223> FRXA01877

<400> 859
gtattgtact aattgtaatt ccccggagag ggaagaagtt tacatggcgc cccatcagaa 60

gtcagggatc aaccggatca acagcacccg ctcggtgccg ttg cgt ttg gct acc 115
                                        Leu Arg Leu Ala Thr
                                          1   5

ggt ggc gtg ctc gcc acc ttg ctt atc ggc gga gtc acc gct gca gct 163
Gly Gly Val Leu Ala Thr Leu Leu Ile Gly Gly Val Thr Ala Ala Ala
                 10   15   20

```
acc aaa aag gac atc att gtt gat gtc aac ggc gag cag atg tcc cta   211
Thr Lys Lys Asp Ile Ile Val Asp Val Asn Gly Glu Gln Met Ser Leu
            25                  30                  35

gtg act atg tcc ggc act gtt gaa ggt gtg ctg gcg caa gct ggt gtg   259
Val Thr Met Ser Gly Thr Val Glu Gly Val Leu Ala Gln Ala Gly Val
        40                  45                  50

gaa ctt ggt gac cag gac att gtt tcc cct tca ctg gat tca tcc atc   307
Glu Leu Gly Asp Gln Asp Ile Val Ser Pro Ser Leu Asp Ser Ser Ile
    55                  60                  65

agt gat gaa gac act gtg act gtt cgt act gcc aag cag gtg gcg ctc   355
Ser Asp Glu Asp Thr Val Thr Val Arg Thr Ala Lys Gln Val Ala Leu
70                  75                  80                  85

gtg gtg gaa ggt caa atc caa aac gtg acc acc act gcg gtt tcc gtg   403
Val Val Glu Gly Gln Ile Gln Asn Val Thr Thr Thr Ala Val Ser Val
                90                  95                  100

gag gac ctc ctg cag gaa gtc ggt ggc att acc ggt gct gat gcg gtg   451
Glu Asp Leu Leu Gln Glu Val Gly Gly Ile Thr Gly Ala Asp Ala Val
            105                 110                 115

gac gct gat ctt tca gag acc atc cca gaa tct ggt ttg aag gtg agt   499
Asp Ala Asp Leu Ser Glu Thr Ile Pro Glu Ser Gly Leu Lys Val Ser
        120                 125                 130

gtt acc aag ccg aag att att tcc atc aat gat ggt ggc aag gtc act   547
Val Thr Lys Pro Lys Ile Ile Ser Ile Asn Asp Gly Gly Lys Val Thr
    135                 140                 145

tac gtt tct ttg gca gct cag aac gta cag gaa gcc cta gag ctg cgg   595
Tyr Val Ser Leu Ala Ala Gln Asn Val Gln Glu Ala Leu Glu Leu Arg
150                 155                 160                 165

gat att gag ctg ggt gct cag gac cgc att aat gtg cct ctg gat cag   643
Asp Ile Glu Leu Gly Ala Gln Asp Arg Ile Asn Val Pro Leu Asp Gln
                170                 175                 180

cag ctg aag aac aac gct gcg atc cag atc gac cgc gtt gac aac acc   691
Gln Leu Lys Asn Asn Ala Ala Ile Gln Ile Asp Arg Val Asp Asn Thr
            185                 190                 195

gaa atc act gaa act gtg tct ttc gat gct gag cca acc tac gtg gat   739
Glu Ile Thr Glu Thr Val Ser Phe Asp Ala Glu Pro Thr Tyr Val Asp
        200                 205                 210

gat cca gaa gct cca gct ggc gat gaa act gtg gtc gaa gaa ggc gct   787
Asp Pro Glu Ala Pro Ala Gly Asp Glu Thr Val Val Glu Glu Gly Ala
    215                 220                 225

cct gga acc aag gaa gtt act cgc acc gta aca acc gtt aat ggt cag   835
Pro Gly Thr Lys Glu Val Thr Arg Thr Val Thr Thr Val Asn Gly Gln
230                 235                 240                 245

gaa gaa tct tcc acg gtg atc aat gaa gtt gaa atc acc gca gca aag   883
Glu Glu Ser Ser Thr Val Ile Asn Glu Val Glu Ile Thr Ala Ala Lys
                250                 255                 260

cca gca acc att agc cgt ggc acc aaa act gtc gct gca aac tcc gtg   931
```

```
Pro Ala Thr Ile Ser Arg Gly Thr Lys Thr Val Ala Ala Asn Ser Val
            265                 270                 275

tgg gat cag ctg gca cag tgt gaa tcc ggc gga aac tgg gca atc aac   979
Trp Asp Gln Leu Ala Gln Cys Glu Ser Gly Gly Asn Trp Ala Ile Asn
        280                 285                 290

aca ggt aat ggc ttc tcc ggc ggc cta cag ttc cac cca cag acc tgg   1027
Thr Gly Asn Gly Phe Ser Gly Gly Leu Gln Phe His Pro Gln Thr Trp
    295                 300                 305

ctc gca tac ggt ggt gga gct ttc tcc ggt gac gct tcc ggt gca agc   1075
Leu Ala Tyr Gly Gly Gly Ala Phe Ser Gly Asp Ala Ser Gly Ala Ser
310                 315                 320                 325

cgt gaa cag caa atc tcc atc gca gaa aag gtt cag gct gca caa ggt   1123
Arg Glu Gln Gln Ile Ser Ile Ala Glu Lys Val Gln Ala Ala Gln Gly
                330                 335                 340

tgg gga gca tgg cct gct tgc acc gca agc ttg ggc atc cga           1165
Trp Gly Ala Trp Pro Ala Cys Thr Ala Ser Leu Gly Ile Arg
            345                 350                 355

tagtagaaat ctggcatcca ata                                        1188


<210> 860
<211> 355
<212> PRT
<213> Corynebacterium glutamicum

<400> 860
Leu Arg Leu Ala Thr Gly Gly Val Leu Ala Thr Leu Leu Ile Gly Gly
  1               5                  10                  15

Val Thr Ala Ala Ala Thr Lys Lys Asp Ile Ile Val Asp Val Asn Gly
             20                  25                  30

Glu Gln Met Ser Leu Val Thr Met Ser Gly Thr Val Glu Gly Val Leu
         35                  40                  45

Ala Gln Ala Gly Val Glu Leu Gly Asp Gln Asp Ile Val Ser Pro Ser
     50                  55                  60

Leu Asp Ser Ser Ile Ser Asp Glu Asp Thr Val Thr Val Arg Thr Ala
 65                  70                  75                  80

Lys Gln Val Ala Leu Val Val Glu Gly Gln Ile Gln Asn Val Thr Thr
                 85                  90                  95

Thr Ala Val Ser Val Glu Asp Leu Leu Gln Glu Val Gly Gly Ile Thr
            100                 105                 110

Gly Ala Asp Ala Val Asp Ala Asp Leu Ser Glu Thr Ile Pro Glu Ser
        115                 120                 125

Gly Leu Lys Val Ser Val Thr Lys Pro Lys Ile Ile Ser Ile Asn Asp
    130                 135                 140

Gly Gly Lys Val Thr Tyr Val Ser Leu Ala Ala Gln Asn Val Gln Glu
145                 150                 155                 160
```

```
Ala Leu Glu Leu Arg Asp Ile Glu Leu Gly Ala Gln Asp Arg Ile Asn
                165                 170                 175

Val Pro Leu Asp Gln Gln Leu Lys Asn Asn Ala Ala Ile Gln Ile Asp
            180                 185                 190

Arg Val Asp Asn Thr Glu Ile Thr Glu Thr Val Ser Phe Asp Ala Glu
        195                 200                 205

Pro Thr Tyr Val Asp Asp Pro Glu Ala Pro Ala Gly Asp Glu Thr Val
    210                 215                 220

Val Glu Glu Gly Ala Pro Gly Thr Lys Glu Val Thr Arg Thr Val Thr
225                 230                 235                 240

Thr Val Asn Gly Gln Glu Glu Ser Ser Thr Val Ile Asn Glu Val Glu
                245                 250                 255

Ile Thr Ala Ala Lys Pro Ala Thr Ile Ser Arg Gly Thr Lys Thr Val
            260                 265                 270

Ala Ala Asn Ser Val Trp Asp Gln Leu Ala Gln Cys Glu Ser Gly Gly
        275                 280                 285

Asn Trp Ala Ile Asn Thr Gly Asn Gly Phe Ser Gly Gly Leu Gln Phe
    290                 295                 300

His Pro Gln Thr Trp Leu Ala Tyr Gly Gly Gly Ala Phe Ser Gly Asp
305                 310                 315                 320

Ala Ser Gly Ala Ser Arg Glu Gln Gln Ile Ser Ile Ala Glu Lys Val
                325                 330                 335

Gln Ala Ala Gln Gly Trp Gly Ala Trp Pro Ala Cys Thr Ala Ser Leu
            340                 345                 350

Gly Ile Arg
        355
```

CONFIDENTIAL

<210> 861
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1033)
<223> RXN01879

<400> 861

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ctttgcgggc cgctgatatt gatccaacgc ttcgtggcga aaagcttgat gtcactgact 60

atgtgcgcct agctggggtg ttgcagcaaa aggatgagaa gtg aaa att acc gct   115
                                              Val Lys Ile Thr Ala
                                                1               5

aag gcg tgg gcg aaa acc aac ctg cat tta ggt gtg gga ccg gct cac   163
Lys Ala Trp Ala Lys Thr Asn Leu His Leu Gly Val Gly Pro Ala His
                10                  15                  20
```

```
gac gat gga ttt cac gag ctc atg acg gtg ttt caa acc att gat ctg   211
Asp Asp Gly Phe His Glu Leu Met Thr Val Phe Gln Thr Ile Asp Leu
            25                  30                  35

ttt gac acc gtc acc tta acc acc ctc gat gag gag ttg gtg gag gag   259
Phe Asp Thr Val Thr Leu Thr Thr Leu Asp Glu Glu Leu Val Glu Glu
        40                  45                  50

ggg agc gtc gtc aag caa tta tct gtg acc ggt gcc cgt ggc gtg cct   307
Gly Ser Val Val Lys Gln Leu Ser Val Thr Gly Ala Arg Gly Val Pro
    55                  60                  65

gag gac gcc agc aat ctt gcg tgg cgc gct gtg gat gcg ttg gtt aag   355
Glu Asp Ala Ser Asn Leu Ala Trp Arg Ala Val Asp Ala Leu Val Lys
70                  75                  80                  85

cgg cgc gcg gaa aag acg ccg ctg tct gca gtt tcg ctg cat att tcc   403
Arg Arg Ala Glu Lys Thr Pro Leu Ser Ala Val Ser Leu His Ile Ser
                90                  95                  100

aag ggg att ccg gtg gct ggc ggc atg gct ggc ggc tct gcg gat gcg   451
Lys Gly Ile Pro Val Ala Gly Gly Met Ala Gly Gly Ser Ala Asp Ala
            105                 110                 115

gct gcg aca ctg cgc gca gtg gat gcc tgg att ggg cct ttc ggc gag   499
Ala Ala Thr Leu Arg Ala Val Asp Ala Trp Ile Gly Pro Phe Gly Glu
        120                 125                 130

gac aca ttg ctg gag gtt gcc gcg gag ctc ggc tca gat gtg ccg ttt   547
Asp Thr Leu Leu Glu Val Ala Ala Glu Leu Gly Ser Asp Val Pro Phe
    135                 140                 145

tgc ctg ctt ggt ggc acc atg cgc ggt acc ggt cgc ggc gag cag ctg   595
Cys Leu Leu Gly Gly Thr Met Arg Gly Thr Gly Arg Gly Glu Gln Leu
150                 155                 160                 165

gta gat atg ttg acg cgc ggc aag cta cat tgg gtg gtg gcc gcg atg   643
Val Asp Met Leu Thr Arg Gly Lys Leu His Trp Val Val Ala Ala Met
                170                 175                 180

gcg cat ggc ctg tcc acg cct gag gta ttc aaa aag cat gat gag ctg   691
Ala His Gly Leu Ser Thr Pro Glu Val Phe Lys Lys His Asp Glu Leu
            185                 190                 195

aat ccg gaa tcg cat atg gat atc agc gac ctc agc gcc gca ctt ctc   739
Asn Pro Glu Ser His Met Asp Ile Ser Asp Leu Ser Ala Ala Leu Leu
        200                 205                 210

acc ggc aac acc gcc gag gtg ggg cag tgg ctg cac aat gat ctg acc   787
Thr Gly Asn Thr Ala Glu Val Gly Gln Trp Leu His Asn Asp Leu Thr
    215                 220                 225

agc gcc gca ctc agt ttg cgc cct gaa ctg cgc agc gtc ctc caa gaa   835
Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu Arg Ser Val Leu Gln Glu
230                 235                 240                 245

ggc atc cgc tcc ggc gcg cat gca gga att gtc tcc ggc tcc ggc ccg   883
Gly Ile Arg Ser Gly Ala His Ala Gly Ile Val Ser Gly Ser Gly Pro
                250                 255                 260
```

```
acc acg gta ttc ttg tgc gaa tcg gag cac aaa gcg caa gac gtt aaa   931
Thr Thr Val Phe Leu Cys Glu Ser Glu His Lys Ala Gln Asp Val Lys
            265                 270                 275

gag gcg cta atc gac gcc ggc cag gtg tac gct gct tac acc gcc acc   979
Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr Ala Ala Tyr Thr Ala Thr
        280                 285                 290

ggc cct gcg gcc tca acc gcc gac cag cgc ggc gca cac att ttg act   1027
Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg Gly Ala His Ile Leu Thr
    295             300                 305

gtt tca taataaagac aaacttaagt atc                                 1056
Val Ser
310
```

<210> 862
<211> 311
<212> PRT
<213> Corynebacterium glutamicum

<400> 862

```
Val Lys Ile Thr Ala Lys Ala Trp Ala Lys Thr Asn Leu His Leu Gly
  1               5                  10                  15

Val Gly Pro Ala His Asp Asp Gly Phe His Glu Leu Met Thr Val Phe
             20                  25                  30

Gln Thr Ile Asp Leu Phe Asp Thr Val Thr Leu Thr Thr Leu Asp Glu
         35                  40                  45

Glu Leu Val Glu Glu Gly Ser Val Val Lys Gln Leu Ser Val Thr Gly
     50                  55                  60

Ala Arg Gly Val Pro Glu Asp Ala Ser Asn Leu Ala Trp Arg Ala Val
 65                  70                  75                  80

Asp Ala Leu Val Lys Arg Arg Ala Glu Lys Thr Pro Leu Ser Ala Val
                 85                  90                  95

Ser Leu His Ile Ser Lys Gly Ile Pro Val Ala Gly Gly Met Ala Gly
            100                 105                 110

Gly Ser Ala Asp Ala Ala Ala Thr Leu Arg Ala Val Asp Ala Trp Ile
        115                 120                 125

Gly Pro Phe Gly Glu Asp Thr Leu Leu Glu Val Ala Ala Glu Leu Gly
    130                 135                 140

Ser Asp Val Pro Phe Cys Leu Leu Gly Gly Thr Met Arg Gly Thr Gly
145                 150                 155                 160

Arg Gly Glu Gln Leu Val Asp Met Leu Thr Arg Gly Lys Leu His Trp
                165                 170                 175

Val Val Ala Ala Met Ala His Gly Leu Ser Thr Pro Glu Val Phe Lys
            180                 185                 190

Lys His Asp Glu Leu Asn Pro Glu Ser His Met Asp Ile Ser Asp Leu
        195                 200                 205
```

```
Ser Ala Ala Leu Leu Thr Gly Asn Thr Ala Glu Val Gly Gln Trp Leu
    210                 215                 220

His Asn Asp Leu Thr Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu Arg
225                 230                 235                 240

Ser Val Leu Gln Glu Gly Ile Arg Ser Gly Ala His Ala Gly Ile Val
                245                 250                 255

Ser Gly Ser Gly Pro Thr Thr Val Phe Leu Cys Glu Ser Glu His Lys
            260                 265                 270

Ala Gln Asp Val Lys Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr Ala
        275                 280                 285

Ala Tyr Thr Ala Thr Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg Gly
    290                 295                 300

Ala His Ile Leu Thr Val Ser
305                 310
```

<210> 863
<211> 711
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(688)
<223> FRXA01879

<400> 863

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ctttgcgggc cgctgatatt gatccaacgc ttcgtggcga aaagcttgat gtcactgact 60

atgtgcgcct agctggggtg ttgcagcaaa aggatgagaa gtg aaa att acc gct   115
                                            Val Lys Ile Thr Ala
                                              1               5

aag gcg tgg gcg aaa acc aac ctg cat tta ggt gtg gga ccg gct cac   163
Lys Ala Trp Ala Lys Thr Asn Leu His Leu Gly Val Gly Pro Ala His
                  10                  15                  20

gac gat gga ttt cac gag ctc atg acg gtg ttt caa acc att gat ctg   211
Asp Asp Gly Phe His Glu Leu Met Thr Val Phe Gln Thr Ile Asp Leu
             25                  30                  35

ttt gac acc gtc acc tta acc acc ctc gat gag gag ttg gtg gag gag   259
Phe Asp Thr Val Thr Leu Thr Thr Leu Asp Glu Glu Leu Val Glu Glu
         40                  45                  50

ggg agc gtc gtc aag caa tta tct gtg acc ggt gcc cgt ggc gtg cct   307
Gly Ser Val Val Lys Gln Leu Ser Val Thr Gly Ala Arg Gly Val Pro
     55                  60                  65

gag gac gcc agc aat ctt gcg tgg cgc gct gtg gat gcg ttg gtt aag   355
Glu Asp Ala Ser Asn Leu Ala Trp Arg Ala Val Asp Ala Leu Val Lys
 70                  75                  80                  85

cgg cgc gcg gaa aag acg ccg ctg tct gca gtt tcg ctg cat att tcc   403
```

```
Arg Arg Ala Glu Lys Thr Pro Leu Ser Ala Val Ser Leu His Ile Ser
                 90                  95                 100

aag ggg att ccg gtg gct ggc ggc atg gct ggc ggc tct gcg gat gcg   451
Lys Gly Ile Pro Val Ala Gly Gly Met Ala Gly Gly Ser Ala Asp Ala
            105                 110                 115

gct gcg aca ctg cgc gca gtg gat gcc tgg att ggg cct ttc ggc gag   499
Ala Ala Thr Leu Arg Ala Val Asp Ala Trp Ile Gly Pro Phe Gly Glu
        120                 125                 130

gac aca ttg ctg gag gtt gcc gcg gag ctc ggc tca gat gtg ccg ttt   547
Asp Thr Leu Leu Glu Val Ala Ala Glu Leu Gly Ser Asp Val Pro Phe
    135                 140                 145

tgc ctg ctt ggt ggc acc atg cgc ggt acc ggt cgc ggc gag cag ctg   595
Cys Leu Leu Gly Gly Thr Met Arg Gly Thr Gly Arg Gly Glu Gln Leu
150                 155                 160                 165

gta gat atg ttg acg cgc ggc aag cta cat tgg gtg gtg gcc gcg atg   643
Val Asp Met Leu Thr Arg Gly Lys Leu His Trp Val Val Ala Ala Met
                170                 175                 180

gcg cat ggc ctg tcc acc ctg agg tat tca aaa agc atg atg agc       688
Ala His Gly Leu Ser Thr Leu Arg Tyr Ser Lys Ser Met Met Ser
            185                 190                 195

tgaatccgga atcgcatatg gat                                        711
```

<210> 864
<211> 196
<212> PRT
<213> Corynebacterium glutamicum

<400> 864

```
Val Lys Ile Thr Ala Lys Ala Trp Ala Lys Thr Asn Leu His Leu Gly
  1               5                  10                  15

Val Gly Pro Ala His Asp Asp Gly Phe His Glu Leu Met Thr Val Phe
             20                  25                  30

Gln Thr Ile Asp Leu Phe Asp Thr Val Thr Leu Thr Thr Leu Asp Glu
         35                  40                  45

Glu Leu Val Glu Glu Gly Ser Val Val Lys Gln Leu Ser Val Thr Gly
     50                  55                  60

Ala Arg Gly Val Pro Glu Asp Ala Ser Asn Leu Ala Trp Arg Ala Val
 65                  70                  75                  80

Asp Ala Leu Val Lys Arg Arg Ala Glu Lys Thr Pro Leu Ser Ala Val
                 85                  90                  95

Ser Leu His Ile Ser Lys Gly Ile Pro Val Ala Gly Gly Met Ala Gly
            100                 105                 110

Gly Ser Ala Asp Ala Ala Ala Thr Leu Arg Ala Val Asp Ala Trp Ile
        115                 120                 125

Gly Pro Phe Gly Glu Asp Thr Leu Leu Glu Val Ala Ala Glu Leu Gly
```

```
    130                 135                 140

Ser Asp Val Pro Phe Cys Leu Leu Gly Gly Thr Met Arg Gly Thr Gly
145                 150                 155                 160

Arg Gly Glu Gln Leu Val Asp Met Leu Thr Arg Gly Lys Leu His Trp
                165                 170                 175

Val Val Ala Ala Met Ala His Gly Leu Ser Thr Leu Arg Tyr Ser Lys
            180                 185                 190

Ser Met Met Ser
        195


<210> 865
<211> 531
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> FRXA01880

<400> 865
agctcggctc agatgtgccg ttttgcctgc ttggtggcac catgcgcggt accggtcgcg 60

gcgagcagct ggtagatatg ttgacgcgcg gcaagctaca ttg ggt ggt ggc cgc   115
                                            Leu Gly Gly Gly Arg
                                              1               5

gat ggc gca tgg cct gtc cac cct gag gta ttc aaa aag cat gat gag   163
Asp Gly Ala Trp Pro Val His Pro Glu Val Phe Lys Lys His Asp Glu
                 10                  15                  20

ctg aat ccg gaa tcg cat atg gat atc agc gac ctc agc gcc gca ctt   211
Leu Asn Pro Glu Ser His Met Asp Ile Ser Asp Leu Ser Ala Ala Leu
             25                  30                  35

ctc acc ggc aac acc gcc gag gtg ggg cag tgg ctg cac aat gat ctg   259
Leu Thr Gly Asn Thr Ala Glu Val Gly Gln Trp Leu His Asn Asp Leu
         40                  45                  50

acc agc gcc gca ctc agt ttg cgc cct gaa ctg cgc agc gtc ctc caa   307
Thr Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu Arg Ser Val Leu Gln
     55                  60                  65

gaa ggc atc cgc tcc ggc gcg cat gca gga att gtc tcc ggc tcc ggc   355
Glu Gly Ile Arg Ser Gly Ala His Ala Gly Ile Val Ser Gly Ser Gly
 70                  75                  80                  85

ccg acc acg gta ttc ttg tgc gaa tcg gag cac aaa gcg caa gac gtt   403
Pro Thr Thr Val Phe Leu Cys Glu Ser Glu His Lys Ala Gln Asp Val
                 90                  95                 100

aaa gag gcg cta atc gac gcc ggc cag gtg tac gct gct tac acc gcc   451
Lys Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr Ala Ala Tyr Thr Ala
            105                 110                 115

acc ggc cct gcg gcc tca acc gcc gac cag cgc ggc gca cac att ttg   499
```

```
Thr Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg Gly Ala His Ile Leu
        120                 125                 130

act gtt tca taataaagac aaacttaagt atc                              531
Thr Val Ser
    135
```

<210> 866
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 866

```
Leu Gly Gly Gly Arg Asp Gly Ala Trp Pro Val His Pro Glu Val Phe
  1               5                  10                  15

Lys Lys His Asp Glu Leu Asn Pro Glu Ser His Met Asp Ile Ser Asp
             20                  25                  30

Leu Ser Ala Ala Leu Leu Thr Gly Asn Thr Ala Glu Val Gly Gln Trp
         35                  40                  45

Leu His Asn Asp Leu Thr Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu
     50                  55                  60

Arg Ser Val Leu Gln Glu Gly Ile Arg Ser Gly Ala His Ala Gly Ile
 65                  70                  75                  80

Val Ser Gly Ser Gly Pro Thr Thr Val Phe Leu Cys Glu Ser Glu His
                 85                  90                  95

Lys Ala Gln Asp Val Lys Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr
            100                 105                 110

Ala Ala Tyr Thr Ala Thr Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg
        115                 120                 125

Gly Ala His Ile Leu Thr Val Ser
    130                 135
```

<210> 867
<211> 759
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(736)
<223> RXN01896

<400> 867

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ttattgggca gctcttttgg accgcgaagt caccccgag ctgcgccaca gcattgctta 60

ttggatccgc gcgaaccaca tcaaacgcta gagtgattcc atg acg cat gcg atc   115
                                            Met Thr His Ala Ile
                                              1               5

ctc ttt gac ctc gac ggc acc ctc gtt gat cac gct tcc gcc gcc cgc   163
Leu Phe Asp Leu Asp Gly Thr Leu Val Asp His Ala Ser Ala Ala Arg
```

```
                  10                  15                  20

gcc gcc ctg cac gcc tgg tcg ccg acc gtg ggc gtc gac acg gat gtt   211
Ala Ala Leu His Ala Trp Ser Pro Thr Val Gly Val Asp Thr Asp Val
            25                  30                  35

gag cgc tgg att gag ctg gat aag tgg ggt ttt gcc cgt ttt gag cgc   259
Glu Arg Trp Ile Glu Leu Asp Lys Trp Gly Phe Ala Arg Phe Glu Arg
        40                  45                  50

ggc gaa acc acg cat tta ggt cag cgg cgc gac cgc atc agg gcg tac   307
Gly Glu Thr Thr His Leu Gly Gln Arg Arg Asp Arg Ile Arg Ala Tyr
    55                  60                  65

ctc aac aga gag ctt gac gac gcc acc tgc gat gat att tac tcc ggc   355
Leu Asn Arg Glu Leu Asp Asp Ala Thr Cys Asp Asp Ile Tyr Ser Gly
70                  75                  80                  85

tac ctt aaa gca tat gag caa aac tgg act gcc tac ccc gat gcc aag   403
Tyr Leu Lys Ala Tyr Glu Gln Asn Trp Thr Ala Tyr Pro Asp Ala Lys
                90                  95                  100

ggc gtt ctc gat cgc gcg gta gcc acc ggt gcc cct gtg gga atc ctg   451
Gly Val Leu Asp Arg Ala Val Ala Thr Gly Ala Pro Val Gly Ile Leu
            105                 110                 115

acc aat ggc gca gcc ccc atg cag caa gac aag ctt gat cgc acc ggc   499
Thr Asn Gly Ala Ala Pro Met Gln Gln Asp Lys Leu Asp Arg Thr Gly
        120                 125                 130

ctt ggc ctg cca gaa ctc gtc atg ttg gcg gcg tcc act ctg gat tct   547
Leu Gly Leu Pro Glu Leu Val Met Leu Ala Ala Ser Thr Leu Asp Ser
    135                 140                 145

gcg aag cct cgc ccc gaa atg tat gcc cga gcg ctc acc cat ttg ggt   595
Ala Lys Pro Arg Pro Glu Met Tyr Ala Arg Ala Leu Thr His Leu Gly
150                 155                 160                 165

gcc cga acc gca aca att atc ggc gat gat tgg acc aac gat gtc gca   643
Ala Arg Thr Ala Thr Ile Ile Gly Asp Asp Trp Thr Asn Asp Val Ala
                170                 175                 180

gct ccc cgc gaa ctt ggc tgg aat gct ctc tat tta gat cgt tcc gga   691
Ala Pro Arg Glu Leu Gly Trp Asn Ala Leu Tyr Leu Asp Arg Ser Gly
            185                 190                 195

acc gat cca cgc gcc gat atc cac tcc ctg gat gaa ctc ttt cac       736
Thr Asp Pro Arg Ala Asp Ile His Ser Leu Asp Glu Leu Phe His
        200                 205                 210

taggctggcc tttattgttt ccg                                        759


<210> 868
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 868
Met Thr His Ala Ile Leu Phe Asp Leu Asp Gly Thr Leu Val Asp His
  1               5                  10                  15
```

```
Ala Ser Ala Ala Arg Ala Ala Leu His Ala Trp Ser Pro Thr Val Gly
            20                  25                  30

Val Asp Thr Asp Val Glu Arg Trp Ile Glu Leu Asp Lys Trp Gly Phe
        35                  40                  45

Ala Arg Phe Glu Arg Gly Glu Thr Thr His Leu Gly Gln Arg Arg Asp
    50                  55                  60

Arg Ile Arg Ala Tyr Leu Asn Arg Glu Leu Asp Asp Ala Thr Cys Asp
65                  70                  75                  80

Asp Ile Tyr Ser Gly Tyr Leu Lys Ala Tyr Glu Gln Asn Trp Thr Ala
                85                  90                  95

Tyr Pro Asp Ala Lys Gly Val Leu Asp Arg Ala Val Ala Thr Gly Ala
            100                 105                 110

Pro Val Gly Ile Leu Thr Asn Gly Ala Ala Pro Met Gln Gln Asp Lys
        115                 120                 125

Leu Asp Arg Thr Gly Leu Gly Leu Pro Glu Leu Val Met Leu Ala Ala
    130                 135                 140

Ser Thr Leu Asp Ser Ala Lys Pro Arg Pro Glu Met Tyr Ala Arg Ala
145                 150                 155                 160

Leu Thr His Leu Gly Ala Arg Thr Ala Thr Ile Ile Gly Asp Asp Trp
                165                 170                 175

Thr Asn Asp Val Ala Ala Pro Arg Glu Leu Gly Trp Asn Ala Leu Tyr
            180                 185                 190

Leu Asp Arg Ser Gly Thr Asp Pro Arg Ala Asp Ile His Ser Leu Asp
        195                 200                 205

Glu Leu Phe His
    210
```

<210> 869
<211> 602
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(579)
<223> FRXA01896

<400> 869

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gcc cgc gcc gcc ctg cac gcc tgg tcg ccg acc gtg ggc gtc gac acg   48
Ala Arg Ala Ala Leu His Ala Trp Ser Pro Thr Val Gly Val Asp Thr
  1               5                  10                  15

gat gtt gag cgc tgg att gag ctg gat aag tgg ggt ttt gcc cgt ttt   96
Asp Val Glu Arg Trp Ile Glu Leu Asp Lys Trp Gly Phe Ala Arg Phe
            20                  25                  30

gag cgc ggc gaa acc acg cat tta ggt cag cgg cgc gac cgc atc agg   144
```

```
Glu Arg Gly Glu Thr Thr His Leu Gly Gln Arg Arg Asp Arg Ile Arg
         35                  40                  45

gcg tac ctc aac aga gag ctt gac gac gcc acc tgc gat gat att tac   192
Ala Tyr Leu Asn Arg Glu Leu Asp Asp Ala Thr Cys Asp Asp Ile Tyr
     50                  55                  60

tcc ggc tac ctt aaa gca tat gag caa aac tgg act gcc tac ccc gat   240
Ser Gly Tyr Leu Lys Ala Tyr Glu Gln Asn Trp Thr Ala Tyr Pro Asp
 65                  70                  75                  80

gcc aag ggc gtt ctc gat cgc gcg gta gcc acc ggt gcc cct gtg gga   288
Ala Lys Gly Val Leu Asp Arg Ala Val Ala Thr Gly Ala Pro Val Gly
                 85                  90                  95

atc ctg acc aat ggc gca gcc ccc atg cag caa gac aag ctt gat cgc   336
Ile Leu Thr Asn Gly Ala Ala Pro Met Gln Gln Asp Lys Leu Asp Arg
            100                 105                 110

acc ggc ctt ggc ctg cca gaa ctc gtc atg ttg gcg gcg tcc act ctg   384
Thr Gly Leu Gly Leu Pro Glu Leu Val Met Leu Ala Ala Ser Thr Leu
        115                 120                 125

gat tct gcg aag cct cgc ccc gaa atg tat gcc cga gcg ctc acc cat   432
Asp Ser Ala Lys Pro Arg Pro Glu Met Tyr Ala Arg Ala Leu Thr His
    130                 135                 140

ttg ggt gcc cga acc gca aca att atc ggc gat gat tgg acc aac gat   480
Leu Gly Ala Arg Thr Ala Thr Ile Ile Gly Asp Asp Trp Thr Asn Asp
145                 150                 155                 160

gtc gca gct ccc cgc gaa ctt ggc tgg aat gct ctc tat tta gat cgt   528
Val Ala Ala Pro Arg Glu Leu Gly Trp Asn Ala Leu Tyr Leu Asp Arg
                165                 170                 175

tcc gga acc gat cca cgc gcc gat atc cac tcc ctg gat gaa ctc ttt   576
Ser Gly Thr Asp Pro Arg Ala Asp Ile His Ser Leu Asp Glu Leu Phe
            180                 185                 190

cac taggctggcc tttattgttt ccg                                    602
His
```

<210> 870
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 870

```
Ala Arg Ala Ala Leu His Ala Trp Ser Pro Thr Val Gly Val Asp Thr
  1               5                  10                  15

Asp Val Glu Arg Trp Ile Glu Leu Asp Lys Trp Gly Phe Ala Arg Phe
             20                  25                  30

Glu Arg Gly Glu Thr Thr His Leu Gly Gln Arg Arg Asp Arg Ile Arg
         35                  40                  45

Ala Tyr Leu Asn Arg Glu Leu Asp Asp Ala Thr Cys Asp Asp Ile Tyr
     50                  55                  60
```

```
Ser Gly Tyr Leu Lys Ala Tyr Glu Gln Asn Trp Thr Ala Tyr Pro Asp
 65                  70                  75                  80

Ala Lys Gly Val Leu Asp Arg Ala Val Ala Thr Gly Ala Pro Val Gly
                 85                  90                  95

Ile Leu Thr Asn Gly Ala Ala Pro Met Gln Gln Asp Lys Leu Asp Arg
            100                 105                 110

Thr Gly Leu Gly Leu Pro Glu Leu Val Met Leu Ala Ala Ser Thr Leu
        115                 120                 125

Asp Ser Ala Lys Pro Arg Pro Glu Met Tyr Ala Arg Ala Leu Thr His
    130                 135                 140

Leu Gly Ala Arg Thr Ala Thr Ile Ile Gly Asp Asp Trp Thr Asn Asp
145                 150                 155                 160

Val Ala Ala Pro Arg Glu Leu Gly Trp Asn Ala Leu Tyr Leu Asp Arg
                165                 170                 175

Ser Gly Thr Asp Pro Arg Ala Asp Ile His Ser Leu Asp Glu Leu Phe
            180                 185                 190

His
```

Date Recue/Date Received 2020-06-30

<210> 871
<211> 909
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(886)
<223> RXN01899

<400> 871

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cctcgcagca cttcgcgcag gcgaatccac agtggccgca accttgatca aagaacacat 60

cgaaggctac tacgaagaaa ccgctgccgc cgaggcctaa atg tcc cgc act ctg   115
                                              Met Ser Arg Thr Leu
                                                1               5

tgg gcg gtt tca gat cta cac gtc acc ttc gcc caa aac caa aac acc   163
Trp Ala Val Ser Asp Leu His Val Thr Phe Ala Gln Asn Gln Asn Thr
                10                  15                  20

gtt gat gcc ctc atg ccg cag gac ccc ggc gac tgg ctg atc gtc gct   211
Val Asp Ala Leu Met Pro Gln Asp Pro Gly Asp Trp Leu Ile Val Ala
            25                  30                  35

ggc gat gta gca gag aaa atc ccc gat gtg gta cgt acc tta tcc gcg   259
Gly Asp Val Ala Glu Lys Ile Pro Asp Val Val Arg Thr Leu Ser Ala
        40                  45                  50

ctg gtc aaa cgc ttt gac acc gtg att tgg gtg ccg ggc aac cac gaa   307
Leu Val Lys Arg Phe Asp Thr Val Ile Trp Val Pro Gly Asn His Glu
    55                  60                  65
```

```
ctc ttc aac cgg aaa aca gac cgc gtc aac ggc aaa gcc cgc tac cga   355
Leu Phe Asn Arg Lys Thr Asp Arg Val Asn Gly Lys Ala Arg Tyr Arg
 70                  75                  80                  85

gca tta gtc gga caa ctc cga gcc atc ggc gtg atc acc ccc gaa gat   403
Ala Leu Val Gly Gln Leu Arg Ala Ile Gly Val Ile Thr Pro Glu Asp
                90                  95                 100

ccc tat ccg atc ttt ggt ggc gtc acc atc tgc cca ctt ttc aca ctt   451
Pro Tyr Pro Ile Phe Gly Gly Val Thr Ile Cys Pro Leu Phe Thr Leu
            105                 110                 115

tac gat tac tct ttc cgt ccc ctc ggc ctc acc gcg aaa caa gcc ctc   499
Tyr Asp Tyr Ser Phe Arg Pro Leu Gly Leu Thr Ala Lys Gln Ala Leu
        120                 125                 130

gcc caa gca aaa ata aag cta gac gac gaa cta gcc atc gcc ccc tac   547
Ala Gln Ala Lys Ile Lys Leu Asp Asp Glu Leu Ala Ile Ala Pro Tyr
    135                 140                 145

gta gac atc ccc gcc tgg tgc gcc gaa cga gtc acc tac aca gaa gac   595
Val Asp Ile Pro Ala Trp Cys Ala Glu Arg Val Thr Tyr Thr Glu Asp
150                 155                 160                 165

cgc cta aaa gcc acc aaa ggc cca aaa gtc ctg gtc aat cac tgg ccg   643
Arg Leu Lys Ala Thr Lys Gly Pro Lys Val Leu Val Asn His Trp Pro
                170                 175                 180

ctg gtc att gag ccc acc cac cgg ctc ttc caa aaa gac atc gcg ctg   691
Leu Val Ile Glu Pro Thr His Arg Leu Phe Gln Lys Asp Ile Ala Leu
            185                 190                 195

tgg tgt gga acc acc gcc acc agg gat tgg gcc gta cga ttc aac gct   739
Trp Cys Gly Thr Thr Ala Thr Arg Asp Trp Ala Val Arg Phe Asn Ala
        200                 205                 210

ctc atg gcc att cac ggt cac cta cat att cct gcc gaa acc cgc gtt   787
Leu Met Ala Ile His Gly His Leu His Ile Pro Ala Glu Thr Arg Val
    215                 220                 225

gat ggg gta agc cac gtg gag gtt tct ttg ggt tac ccc ttt gaa aaa   835
Asp Gly Val Ser His Val Glu Val Ser Leu Gly Tyr Pro Phe Glu Lys
230                 235                 240                 245

cac cca cct cac atg aag cgt ccg tgg ccg ttt ccg gtc atg cag att   883
His Pro Pro His Met Lys Arg Pro Trp Pro Phe Pro Val Met Gln Ile
                250                 255                 260

aac taactctgtt gcttaaatgg ggg                                    909
Asn
```

<210> 872
<211> 262
<212> PRT
<213> Corynebacterium glutamicum

<400> 872
Met Ser Arg Thr Leu Trp Ala Val Ser Asp Leu His Val Thr Phe Ala

```
  1               5                  10                  15

Gln Asn Gln Asn Thr Val Asp Ala Leu Met Pro Gln Asp Pro Gly Asp
            20                  25                  30

Trp Leu Ile Val Ala Gly Asp Val Ala Glu Lys Ile Pro Asp Val Val
        35                  40                  45

Arg Thr Leu Ser Ala Leu Val Lys Arg Phe Asp Thr Val Ile Trp Val
    50                  55                  60

Pro Gly Asn His Glu Leu Phe Asn Arg Lys Thr Asp Arg Val Asn Gly
65                  70                  75                  80

Lys Ala Arg Tyr Arg Ala Leu Val Gly Gln Leu Arg Ala Ile Gly Val
                85                  90                  95

Ile Thr Pro Glu Asp Pro Tyr Pro Ile Phe Gly Gly Val Thr Ile Cys
            100                 105                 110

Pro Leu Phe Thr Leu Tyr Asp Tyr Ser Phe Arg Pro Leu Gly Leu Thr
        115                 120                 125

Ala Lys Gln Ala Leu Ala Gln Ala Lys Ile Lys Leu Asp Asp Glu Leu
    130                 135                 140

Ala Ile Ala Pro Tyr Val Asp Ile Pro Ala Trp Cys Ala Glu Arg Val
145                 150                 155                 160

Thr Tyr Thr Glu Asp Arg Leu Lys Ala Thr Lys Gly Pro Lys Val Leu
                165                 170                 175

Val Asn His Trp Pro Leu Val Ile Glu Pro Thr His Arg Leu Phe Gln
            180                 185                 190

Lys Asp Ile Ala Leu Trp Cys Gly Thr Thr Ala Thr Arg Asp Trp Ala
        195                 200                 205

Val Arg Phe Asn Ala Leu Met Ala Ile His Gly His Leu His Ile Pro
    210                 215                 220

Ala Glu Thr Arg Val Asp Gly Val Ser His Val Glu Val Ser Leu Gly
225                 230                 235                 240

Tyr Pro Phe Glu Lys His Pro Pro His Met Lys Arg Pro Trp Pro Phe
                245                 250                 255

Pro Val Met Gln Ile Asn
            260
```

<210> 873
<211> 909
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(886)
<223> FRXA01899

<400> 873
cctcgcagca cttcgcgcag gcgaatccac agtggccgca accttgatca aagaacacat 60

cgaaggctac tacgaagaaa ccgctgccgc cgaggcctaa atg tcc cgc act ctg 115
Met Ser Arg Thr Leu
1 5

tgg gcg gtt tca gat cta cac gtc acc ttc gcc caa aac caa aac acc 163
Trp Ala Val Ser Asp Leu His Val Thr Phe Ala Gln Asn Gln Asn Thr
10 15 20

gtt gat gcc ctc atg ccg cag gac ccc ggc gac tgg ctg atc gtc gct 211
Val Asp Ala Leu Met Pro Gln Asp Pro Gly Asp Trp Leu Ile Val Ala
25 30 35

ggc gat gta gca gag aaa atc ccc gat gtg gta cgt acc tta tcc gcg 259
Gly Asp Val Ala Glu Lys Ile Pro Asp Val Val Arg Thr Leu Ser Ala
40 45 50

ctg gtc aaa cgc ttt gac acc gtg att tgg gtg ccg ggc aac cac gaa 307
Leu Val Lys Arg Phe Asp Thr Val Ile Trp Val Pro Gly Asn His Glu
55 60 65

ctc ttc aac cgg aaa aca gac cgc gtc aac ggc aaa gcc cgc tac cga 355
Leu Phe Asn Arg Lys Thr Asp Arg Val Asn Gly Lys Ala Arg Tyr Arg
70 75 80 85

gca tta gtc gga caa ctc cga gcc atc ggc gtg atc acc ccc gaa gat 403
Ala Leu Val Gly Gln Leu Arg Ala Ile Gly Val Ile Thr Pro Glu Asp
90 95 100

ccc tat ccg atc ttt ggt ggc gtc acc atc tgc cca ctt ttc aca ctt 451
Pro Tyr Pro Ile Phe Gly Gly Val Thr Ile Cys Pro Leu Phe Thr Leu
105 110 115

tac gat tac tct ttc cgt ccc ctc ggc ctc acc gcg aaa caa gcc ctc 499
Tyr Asp Tyr Ser Phe Arg Pro Leu Gly Leu Thr Ala Lys Gln Ala Leu
120 125 130

gcc caa gca aaa ata aag cta gac gac gaa cta gcc atc gcc ccc tac 547
Ala Gln Ala Lys Ile Lys Leu Asp Asp Glu Leu Ala Ile Ala Pro Tyr
135 140 145

gta gac atc ccc gcc tgg tgc gcc gaa cga gtc acc tac aca gaa gac 595
Val Asp Ile Pro Ala Trp Cys Ala Glu Arg Val Thr Tyr Thr Glu Asp
150 155 160 165

cgc cta aaa gcc acc aaa ggc cca aaa gtc ctg gtc aat cac tgg ccg 643
Arg Leu Lys Ala Thr Lys Gly Pro Lys Val Leu Val Asn His Trp Pro
170 175 180

ctg gtc att gag ccc acc cac cgg ctc ttc caa aaa gac atc gcg ctg 691
Leu Val Ile Glu Pro Thr His Arg Leu Phe Gln Lys Asp Ile Ala Leu
185 190 195

tgg tgt gga acc acc gcc acc agg gat tgg gcc gta cga ttc aac gct 739
Trp Cys Gly Thr Thr Ala Thr Arg Asp Trp Ala Val Arg Phe Asn Ala
200 205 210

ctc atg gcc att cac ggt cac cta cat att cct gcc gaa acc cgc gtt 787
Leu Met Ala Ile His Gly His Leu His Ile Pro Ala Glu Thr Arg Val

```
    215                 220                 225

gat ggg gta agc cac gtg gag gtt tct ttg ggt tac ccc ttt gaa aaa   835
Asp Gly Val Ser His Val Glu Val Ser Leu Gly Tyr Pro Phe Glu Lys
230                 235                 240                 245

cac cca cct cac atg aag cgt ccg tgg ccg ttt ccg gtc atg cag att   883
His Pro Pro His Met Lys Arg Pro Trp Pro Phe Pro Val Met Gln Ile
                250                 255                 260

aac taactctgtt gcttaaatgg ggg                                     909
Asn
```

<210> 874
<211> 262
<212> PRT
<213> Corynebacterium glutamicum

<400> 874

```
Met Ser Arg Thr Leu Trp Ala Val Ser Asp Leu His Val Thr Phe Ala
  1               5                  10                  15

Gln Asn Gln Asn Thr Val Asp Ala Leu Met Pro Gln Asp Pro Gly Asp
             20                  25                  30

Trp Leu Ile Val Ala Gly Asp Val Ala Glu Lys Ile Pro Asp Val Val
         35                  40                  45

Arg Thr Leu Ser Ala Leu Val Lys Arg Phe Asp Thr Val Ile Trp Val
     50                  55                  60

Pro Gly Asn His Glu Leu Phe Asn Arg Lys Thr Asp Arg Val Asn Gly
 65                  70                  75                  80

Lys Ala Arg Tyr Arg Ala Leu Val Gly Gln Leu Arg Ala Ile Gly Val
                 85                  90                  95

Ile Thr Pro Glu Asp Pro Tyr Pro Ile Phe Gly Gly Val Thr Ile Cys
            100                 105                 110

Pro Leu Phe Thr Leu Tyr Asp Tyr Ser Phe Arg Pro Leu Gly Leu Thr
        115                 120                 125

Ala Lys Gln Ala Leu Ala Gln Ala Lys Ile Lys Leu Asp Asp Glu Leu
    130                 135                 140

Ala Ile Ala Pro Tyr Val Asp Ile Pro Ala Trp Cys Ala Glu Arg Val
145                 150                 155                 160

Thr Tyr Thr Glu Asp Arg Leu Lys Ala Thr Lys Gly Pro Lys Val Leu
                165                 170                 175

Val Asn His Trp Pro Leu Val Ile Glu Pro Thr His Arg Leu Phe Gln
            180                 185                 190

Lys Asp Ile Ala Leu Trp Cys Gly Thr Thr Ala Thr Arg Asp Trp Ala
        195                 200                 205

Val Arg Phe Asn Ala Leu Met Ala Ile His Gly His Leu His Ile Pro
```

```
    210                 215                 220

Ala Glu Thr Arg Val Asp Gly Val Ser His Val Glu Val Ser Leu Gly
225                 230                 235                 240

Tyr Pro Phe Glu Lys His Pro Pro His Met Lys Arg Pro Trp Pro Phe
                245                 250                 255

Pro Val Met Gln Ile Asn
            260


<210> 875
<211> 1182
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1159)
<223> RXN01902

<400> 875
ggctggtccg aagtgcaaac cttcaacacc ggcacctacg gtgacaactg gaacttcctc 60

ttcttcggcg acacccagct gtacaacacc cactccaacc gtg cag aag aag tcc   115
                                        Val Gln Lys Lys Ser
                                          1               5

aga act ggg caa aca acc tgg aac ggc ggc cca cca atc gaa aac cca   163
Arg Thr Gly Gln Thr Thr Trp Asn Gly Gly Pro Pro Ile Glu Asn Pro
                10                  15                  20

gga acc tcc ttc atc ctc tcc gcg ggt gat cag gca aac cac tcc agc   211
Gly Thr Ser Phe Ile Leu Ser Ala Gly Asp Gln Ala Asn His Ser Ser
            25                  30                  35

tgg gac gag cac tcc gca tac atc tcc cca gaa acc ctg cgc aac tac   259
Trp Asp Glu His Ser Ala Tyr Ile Ser Pro Glu Thr Leu Arg Asn Tyr
        40                  45                  50

cgt ctg gcc gtg aac aat gga aac cac gac cag tac aac tac gac gcc   307
Arg Leu Ala Val Asn Asn Gly Asn His Asp Gln Tyr Asn Tyr Asp Ala
    55                  60                  65

tac aac gcg atg tac cca cgc cct aac cag gtc gat gag aac tac ttc   355
Tyr Asn Ala Met Tyr Pro Arg Pro Asn Gln Val Asp Glu Asn Tyr Phe
70                  75                  80                  85

ttc gag tac aac aat gca ctc ttc ctg tcc ctg gac tcc aac gac tac   403
Phe Glu Tyr Asn Asn Ala Leu Phe Leu Ser Leu Asp Ser Asn Asp Tyr
                90                  95                  100

ttg gac atc gac gac gac atc gca ttc ctt cgc gac acc gtc gca gca   451
Leu Asp Ile Asp Asp Asp Ile Ala Phe Leu Arg Asp Thr Val Ala Ala
            105                 110                 115

cac ggt gac gac aag gac tgg atc gtc ctg acc tac cac cat tcc act   499
His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr Tyr His His Ser Thr
        120                 125                 130
```

```
ttc tcc cag gcc tac cac atg gat gac gct cgc att aag tac cag cgc   547
Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg Ile Lys Tyr Gln Arg
    135                 140                 145

gaa cgc ctc acc cca gtg atc tct gaa ctg aac gtt gac ttg gtt ctc   595
Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn Val Asp Leu Val Leu
150                 155                 160                 165

ggt gga cac gac cac atc tac acc cgc tcc cac ctg atg aac ggc ttc   643
Gly Gly His Asp His Ile Tyr Thr Arg Ser His Leu Met Asn Gly Phe
                170                 175                 180

acc cca gtc gat gca ggc cgc gaa gca gtt gtc ggt gaa act ctg aac   691
Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val Gly Glu Thr Leu Asn
            185                 190                 195

cct aag gcc ggc gaa gtt gtt tac ctt gca acc aac tct tcc tca ggc   739
Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr Asn Ser Ser Ser Gly
        200                 205                 210

tcc aag ttc tac gac ttc tac gac ttc cag ctc ggc cag cgt tac gac   787
Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu Gly Gln Arg Tyr Asp
    215                 220                 225

acc gga ctg gat ttc cag gaa acc gtc gat cag aag aag atc cgc acc   835
Thr Gly Leu Asp Phe Gln Glu Thr Val Asp Gln Lys Lys Ile Arg Thr
230                 235                 240                 245

tac acc gca gtc tgg aac cag gac cag gtt cag gac tac acc aac gtt   883
Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln Asp Tyr Thr Asn Val
                250                 255                 260

gaa ctg acc cca gaa ggc ctg act gtg acc act aag gac gca gtc tcc   931
Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr Lys Asp Ala Val Ser
            265                 270                 275

ggc gag ctg gtt gac cag ttc acc ctg agc aag cag gac cgc gac gaa   979
Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys Gln Asp Arg Asp Glu
        280                 285                 290

gaa tct gaa gtc cca gtt gaa gat gac aag gac gga gac aac gcg acc   1027
Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp Gly Asp Asn Ala Thr
    295                 300                 305

ggc tcc tcc aac ctt ggt cta gct gct atc ttg gct cca gtt ctg gcc   1075
Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu Ala Pro Val Leu Ala
310                 315                 320                 325

atc ttc ggt ttc gtc ggt gga ctc ttt gtt ggc ggc ggc tcc ctc gct   1123
Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly Gly Gly Ser Leu Ala
                330                 335                 340

gag ttc ttt gcc aac ctc ggc gtg aag atg cct ttc taatactgtc        1169
Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro Phe
            345                 350

tgagattcaa gca                                                   1182
```

<210> 876
<211> 353

<212> PRT
<213> Corynebacterium glutamicum

<400> 876

```
Val Gln Lys Lys Ser Arg Thr Gly Gln Thr Thr Trp Asn Gly Gly Pro
  1               5                  10                  15

Pro Ile Glu Asn Pro Gly Thr Ser Phe Ile Leu Ser Ala Gly Asp Gln
             20                  25                  30

Ala Asn His Ser Ser Trp Asp Glu His Ser Ala Tyr Ile Ser Pro Glu
         35                  40                  45

Thr Leu Arg Asn Tyr Arg Leu Ala Val Asn Asn Gly Asn His Asp Gln
     50                  55                  60

Tyr Asn Tyr Asp Ala Tyr Asn Ala Met Tyr Pro Arg Pro Asn Gln Val
 65                  70                  75                  80

Asp Glu Asn Tyr Phe Phe Glu Tyr Asn Asn Ala Leu Phe Leu Ser Leu
                 85                  90                  95

Asp Ser Asn Asp Tyr Leu Asp Ile Asp Asp Asp Ile Ala Phe Leu Arg
            100                 105                 110

Asp Thr Val Ala Ala His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr
        115                 120                 125

Tyr His His Ser Thr Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg
    130                 135                 140

Ile Lys Tyr Gln Arg Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn
145                 150                 155                 160

Val Asp Leu Val Leu Gly Gly His Asp His Ile Tyr Thr Arg Ser His
                165                 170                 175

Leu Met Asn Gly Phe Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val
            180                 185                 190

Gly Glu Thr Leu Asn Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr
        195                 200                 205

Asn Ser Ser Ser Gly Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu
    210                 215                 220

Gly Gln Arg Tyr Asp Thr Gly Leu Asp Phe Gln Glu Thr Val Asp Gln
225                 230                 235                 240

Lys Lys Ile Arg Thr Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln
                245                 250                 255

Asp Tyr Thr Asn Val Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr
            260                 265                 270

Lys Asp Ala Val Ser Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys
        275                 280                 285

Gln Asp Arg Asp Glu Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp
    290                 295                 300
```

```
Gly Asp Asn Ala Thr Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu
305                 310                 315                 320

Ala Pro Val Leu Ala Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly
                325                 330                 335

Gly Gly Ser Leu Ala Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro
            340                 345                 350

Phe
```

<210> 877
<211> 887
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(864)
<223> FRXA01902

<400> 877

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aac tac gac gcc tac aac gcg atg tac cca cgc cct aac cag gtc gat   48
Asn Tyr Asp Ala Tyr Asn Ala Met Tyr Pro Arg Pro Asn Gln Val Asp
  1               5                  10                  15

gag aac tac ttc ttc gag tac aac aat gca ctc ttc ctg tcc ctg gac   96
Glu Asn Tyr Phe Phe Glu Tyr Asn Asn Ala Leu Phe Leu Ser Leu Asp
             20                  25                  30

tcc aac gac tac ttg gac atc gac gac gac atc gca ttc ctt cgc gac   144
Ser Asn Asp Tyr Leu Asp Ile Asp Asp Asp Ile Ala Phe Leu Arg Asp
         35                  40                  45

acc gtc gca gca cac ggt gac gac aag gac tgg atc gtc ctg acc tac   192
Thr Val Ala Ala His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr Tyr
     50                  55                  60

cac cat tcc act ttc tcc cag gcc tac cac atg gat gac gct cgc att   240
His His Ser Thr Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg Ile
 65                  70                  75                  80

aag tac cag cgc gaa cgc ctc acc cca gtg atc tct gaa ctg aac gtt   288
Lys Tyr Gln Arg Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn Val
                 85                  90                  95

gac ttg gtt ctc ggt gga cac gac cac atc tac acc cgc tcc cac ctg   336
Asp Leu Val Leu Gly Gly His Asp His Ile Tyr Thr Arg Ser His Leu
            100                 105                 110

atg aac ggc ttc acc cca gtc gat gca ggc cgc gaa gca gtt gtc ggt   384
Met Asn Gly Phe Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val Gly
        115                 120                 125

gaa act ctg aac cct aag gcc ggc gaa gtt gtt tac ctt gca acc aac   432
Glu Thr Leu Asn Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr Asn
    130                 135                 140

tct tcc tca ggc tcc aag ttc tac gac ttc tac gac ttc cag ctc ggc   480
```

```
Ser Ser Ser Gly Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu Gly
145                 150                 155                 160

cag cgt tac gac acc gga ctg gat ttc cag gaa acc gtc gat cag aag   528
Gln Arg Tyr Asp Thr Gly Leu Asp Phe Gln Glu Thr Val Asp Gln Lys
                165                 170                 175

aag atc cgc acc tac acc gca gtc tgg aac cag gac cag gtt cag gac   576
Lys Ile Arg Thr Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln Asp
            180                 185                 190

tac acc aac gtt gaa ctg acc cca gaa ggc ctg act gtg acc act aag   624
Tyr Thr Asn Val Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr Lys
        195                 200                 205

gac gca gtc tcc ggc gag ctg gtt gac cag ttc acc ctg agc aag cag   672
Asp Ala Val Ser Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys Gln
    210                 215                 220

gac cgc gac gaa gaa tct gaa gtc cca gtt gaa gat gac aag gac gga   720
Asp Arg Asp Glu Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp Gly
225                 230                 235                 240

gac aac gcg acc ggc tcc tcc aac ctt ggt cta gct gct atc ttg gct   768
Asp Asn Ala Thr Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu Ala
                245                 250                 255

cca gtt ctg gcc atc ttc ggt ttc gtc ggt gga ctc ttt gtt ggc ggc   816
Pro Val Leu Ala Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly Gly
            260                 265                 270

ggc tcc ctc gct gag ttc ttt gcc aac ctc ggc gtg aag atg cct ttc   864
Gly Ser Leu Ala Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro Phe
        275                 280                 285

taatactgtc tgagattcaa gca                                        887


<210> 878
<211> 288
<212> PRT
<213> Corynebacterium glutamicum

<400> 878
Asn Tyr Asp Ala Tyr Asn Ala Met Tyr Pro Arg Pro Asn Gln Val Asp
  1               5                  10                  15

Glu Asn Tyr Phe Phe Glu Tyr Asn Asn Ala Leu Phe Leu Ser Leu Asp
             20                  25                  30

Ser Asn Asp Tyr Leu Asp Ile Asp Asp Asp Ile Ala Phe Leu Arg Asp
         35                  40                  45

Thr Val Ala Ala His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr Tyr
     50                  55                  60

His His Ser Thr Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg Ile
 65                  70                  75                  80

Lys Tyr Gln Arg Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn Val
                 85                  90                  95
```

```
Asp Leu Val Leu Gly Gly His Asp His Ile Tyr Thr Arg Ser His Leu
            100                 105                 110

Met Asn Gly Phe Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val Gly
        115                 120                 125

Glu Thr Leu Asn Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr Asn
    130                 135                 140

Ser Ser Ser Gly Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu Gly
145                 150                 155                 160

Gln Arg Tyr Asp Thr Gly Leu Asp Phe Gln Glu Thr Val Asp Gln Lys
                165                 170                 175

Lys Ile Arg Thr Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln Asp
            180                 185                 190

Tyr Thr Asn Val Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr Lys
        195                 200                 205

Asp Ala Val Ser Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys Gln
    210                 215                 220

Asp Arg Asp Glu Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp Gly
225                 230                 235                 240

Asp Asn Ala Thr Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu Ala
                245                 250                 255

Pro Val Leu Ala Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly Gly
            260                 265                 270

Gly Ser Leu Ala Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro Phe
        275                 280                 285
```

CONFIDENTIAL

<210> 879
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> RXN01908

<400> 879
tccacgacat ctgacacaga aagaagattc accatgtcta agaacaacgc agctcacccg 60

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cagtctgtct tccatatttc atatcccagc acataccact atg cac tct gac cgc   115
                                              Met His Ser Asp Arg
                                                1               5

ttt gag cac cca gac aac ggc tat ggc tac acc att cgt cag gac act   163
Phe Glu His Pro Asp Asn Gly Tyr Gly Tyr Thr Ile Arg Gln Asp Thr
                10                  15                  20
```

```
gat gca gag aac ccg atg acc cat cac gat acg aaa gat gca gct ctc   211
Asp Ala Glu Asn Pro Met Thr His His Asp Thr Lys Asp Ala Ala Leu
            25                  30                  35

tgg gtt cac aac cga cca cga cgc gga gat acc gtc gcc gat aag cca   259
Trp Val His Asn Arg Pro Arg Arg Gly Asp Thr Val Ala Asp Lys Pro
        40                  45                  50

gaa ggc aat gag att ctc gac atc ttt gcc aag ttc atc tgc ggc cag   307
Glu Gly Asn Glu Ile Leu Asp Ile Phe Ala Lys Phe Ile Cys Gly Gln
    55                  60                  65

cac gat aat gat gac aac ccg ttc gaa gtc tgg tcc gac ggt gac tcg   355
His Asp Asn Asp Asp Asn Pro Phe Glu Val Trp Ser Asp Gly Asp Ser
70                  75                  80                  85

gat gca tca ctc atc cgc acc aag gcg tat gtt gcc gag cac cac ccc   403
Asp Ala Ser Leu Ile Arg Thr Lys Ala Tyr Val Ala Glu His His Pro
                90                  95                  100

gaa ctt ata ttc gac atc tct gcg aaa acc atc acg ggt tat tcc caa   451
Glu Leu Ile Phe Asp Ile Ser Ala Lys Thr Ile Thr Gly Tyr Ser Gln
            105                 110                 115

ggc gat tgg ctc gat gtg gtc tgt gtt act act gcc gcc act tgc gac   499
Gly Asp Trp Leu Asp Val Val Cys Val Thr Thr Ala Ala Thr Cys Asp
        120                 125                 130

gaa ctt atc cct gct gac agt ctt att gac atc tac cgc cag tgg gct   547
Glu Leu Ile Pro Ala Asp Ser Leu Ile Asp Ile Tyr Arg Gln Trp Ala
    135                 140                 145

ttt ggt gat gtg tgg aca gtg att cct gat tct cag cca ggt ctc gca   595
Phe Gly Asp Val Trp Thr Val Ile Pro Asp Ser Gln Pro Gly Leu Ala
150                 155                 160                 165

ggt att tat gct gac gat cca gct gac gcc ctt gcg tac tat caa gag   643
Gly Ile Tyr Ala Asp Asp Pro Ala Asp Ala Leu Ala Tyr Tyr Gln Glu
                170                 175                 180

aat ttc gaa gat gaa ccc atc tgg gat ctc tta agc cgc cac gac gct   691
Asn Phe Glu Asp Glu Pro Ile Trp Asp Leu Leu Ser Arg His Asp Ala
            185                 190                 195

gac aaa gac gcc gca gca ctg gca gct gcc tct gct gca gaa aac cac   739
Asp Lys Asp Ala Ala Ala Leu Ala Ala Ala Ser Ala Ala Glu Asn His
        200                 205                 210

gca cta gcg cga ggt act acc cca gtc gtt atc cgt acc caa gac atc   787
Ala Leu Ala Arg Gly Thr Thr Pro Val Val Ile Arg Thr Gln Asp Ile
    215                 220                 225

atc act aac gcg cga tac ctc atg tct gat agt gct gat gac aat cca   835
Ile Thr Asn Ala Arg Tyr Leu Met Ser Asp Ser Ala Asp Asp Asn Pro
230                 235                 240                 245

gaa tac gat cgc gcc ttg gtc gaa ctt agt gct tat ctc tta agt atc   883
Glu Tyr Asp Arg Ala Leu Val Glu Leu Ser Ala Tyr Leu Leu Ser Ile
                250                 255                 260
```

```
gac ctc gat gat cgc gtt gct gca gag atg acc att tta ggt cgc cct   931
Asp Leu Asp Asp Arg Val Ala Ala Glu Met Thr Ile Leu Gly Arg Pro
            265                 270                 275

gtg cct aaa gaa gga taaccaccac accagaaaag aag                    969
Val Pro Lys Glu Gly
        280


<210> 880
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 880
Met His Ser Asp Arg Phe Glu His Pro Asp Asn Gly Tyr Gly Tyr Thr
  1               5                  10                  15

Ile Arg Gln Asp Thr Asp Ala Glu Asn Pro Met Thr His His Asp Thr
             20                  25                  30

Lys Asp Ala Ala Leu Trp Val His Asn Arg Pro Arg Arg Gly Asp Thr
         35                  40                  45

Val Ala Asp Lys Pro Glu Gly Asn Glu Ile Leu Asp Ile Phe Ala Lys
     50                  55                  60

Phe Ile Cys Gly Gln His Asp Asn Asp Asp Asn Pro Phe Glu Val Trp
 65                  70                  75                  80

Ser Asp Gly Asp Ser Asp Ala Ser Leu Ile Arg Thr Lys Ala Tyr Val
                 85                  90                  95

Ala Glu His His Pro Glu Leu Ile Phe Asp Ile Ser Ala Lys Thr Ile
            100                 105                 110

Thr Gly Tyr Ser Gln Gly Asp Trp Leu Asp Val Val Cys Val Thr Thr
        115                 120                 125

Ala Ala Thr Cys Asp Glu Leu Ile Pro Ala Asp Ser Leu Ile Asp Ile
    130                 135                 140

Tyr Arg Gln Trp Ala Phe Gly Asp Val Trp Thr Val Ile Pro Asp Ser
145                 150                 155                 160

Gln Pro Gly Leu Ala Gly Ile Tyr Ala Asp Asp Pro Ala Asp Ala Leu
                165                 170                 175

Ala Tyr Tyr Gln Glu Asn Phe Glu Asp Glu Pro Ile Trp Asp Leu Leu
            180                 185                 190

Ser Arg His Asp Ala Asp Lys Asp Ala Ala Ala Leu Ala Ala Ala Ser
        195                 200                 205

Ala Ala Glu Asn His Ala Leu Ala Arg Gly Thr Thr Pro Val Val Ile
    210                 215                 220

Arg Thr Gln Asp Ile Ile Thr Asn Ala Arg Tyr Leu Met Ser Asp Ser
225                 230                 235                 240

Ala Asp Asp Asn Pro Glu Tyr Asp Arg Ala Leu Val Glu Leu Ser Ala
```

```
                245                 250                 255

Tyr Leu Leu Ser Ile Asp Leu Asp Asp Arg Val Ala Ala Glu Met Thr
            260                 265                 270

Ile Leu Gly Arg Pro Val Pro Lys Glu Gly
        275                 280


<210> 881
<211> 583
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(583)
<223> FRXA01908

<400> 881
tccacgacat ctgacacaga aagaagattc accatgtcta agaacaacgc agctcacccg 60

cagtctgtct tccatatttc atatcccagc acataccact atg cac tct gac cgc   115
                                            Met His Ser Asp Arg
                                              1               5

ttt gag cac cca gac aac ggc tat ggc tac acc att cgt cag gac act   163
Phe Glu His Pro Asp Asn Gly Tyr Gly Tyr Thr Ile Arg Gln Asp Thr
                10                  15                  20

gat gca gag aac ccg atg acc cat cac gat acg aaa gat gca gct ctc   211
Asp Ala Glu Asn Pro Met Thr His His Asp Thr Lys Asp Ala Ala Leu
            25                  30                  35

tgg gtt cac aac cga cca cga cgc gga gat acc gtc gcc gat aag cca   259
Trp Val His Asn Arg Pro Arg Arg Gly Asp Thr Val Ala Asp Lys Pro
        40                  45                  50

gaa ggc aat gag att ctc gac atc ttt gcc aag ttc atc tgc ggc cag   307
Glu Gly Asn Glu Ile Leu Asp Ile Phe Ala Lys Phe Ile Cys Gly Gln
    55                  60                  65

cac gat aat gat gac aac ccg ttc gaa gtc tgg tcc gac ggt gac tcg   355
His Asp Asn Asp Asp Asn Pro Phe Glu Val Trp Ser Asp Gly Asp Ser
70                  75                  80                  85

gat gca tca ctc atc cgc acc aag gcg tat gtt gcc gag cac cac ccc   403
Asp Ala Ser Leu Ile Arg Thr Lys Ala Tyr Val Ala Glu His His Pro
                90                  95                  100

gaa ctt ata ttc gac atc tct gcg aaa acc atc acg ggt tat tcc caa   451
Glu Leu Ile Phe Asp Ile Ser Ala Lys Thr Ile Thr Gly Tyr Ser Gln
            105                 110                 115

ggc gat tgg ctc gat gtg gtc tgt gtt act act gcc gcc act tgc gac   499
Gly Asp Trp Leu Asp Val Val Cys Val Thr Thr Ala Ala Thr Cys Asp
        120                 125                 130

gaa ctt atc cct gct gac agt ctt att gac atc tac cgc cag tgg gct   547
Glu Leu Ile Pro Ala Asp Ser Leu Ile Asp Ile Tyr Arg Gln Trp Ala
    135                 140                 145
```

```
ttt ggt gat gtg tgg aca gtg att cct gat tct cag                    583
Phe Gly Asp Val Trp Thr Val Ile Pro Asp Ser Gln
150                 155                 160


<210> 882
<211> 161
<212> PRT
<213> Corynebacterium glutamicum

<400> 882
Met His Ser Asp Arg Phe Glu His Pro Asp Asn Gly Tyr Gly Tyr Thr
  1               5                  10                  15

Ile Arg Gln Asp Thr Asp Ala Glu Asn Pro Met Thr His His Asp Thr
             20                  25                  30

Lys Asp Ala Ala Leu Trp Val His Asn Arg Pro Arg Arg Gly Asp Thr
         35                  40                  45

Val Ala Asp Lys Pro Glu Gly Asn Glu Ile Leu Asp Ile Phe Ala Lys
     50                  55                  60

Phe Ile Cys Gly Gln His Asp Asn Asp Asp Asn Pro Phe Glu Val Trp
 65                  70                  75                  80

Ser Asp Gly Asp Ser Asp Ala Ser Leu Ile Arg Thr Lys Ala Tyr Val
                 85                  90                  95

Ala Glu His His Pro Glu Leu Ile Phe Asp Ile Ser Ala Lys Thr Ile
            100                 105                 110

Thr Gly Tyr Ser Gln Gly Asp Trp Leu Asp Val Val Cys Val Thr Thr
        115                 120                 125

Ala Ala Thr Cys Asp Glu Leu Ile Pro Ala Asp Ser Leu Ile Asp Ile
    130                 135                 140

Tyr Arg Gln Trp Ala Phe Gly Asp Val Trp Thr Val Ile Pro Asp Ser
145                 150                 155                 160

Gln


<210> 883
<211> 970
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (69)..(947)
<223> RXN01909

<400> 883
ttaataagaa ttgttctggg aagtaatata aaaagtcccg aacaaattag tgtgaaaggg 60

tttgtatcatg gct aat ttt cga agc aag gat aaa gat ggc aat gtc atc   110
        Met Ala Asn Phe Arg Ser Lys Asp Lys Asp Gly Asn Val Ile
```

```
          1               5                  10

aat ccg aac gcg tct act aaa ggt gta gat ctt gtt gtc aac gtc tac   158
Asn Pro Asn Ala Ser Thr Lys Gly Val Asp Leu Val Val Asn Val Tyr
 15                  20                  25                  30

gac agc gcc aag cat gtg acc gaa aag ggt aac act gtc cac ttt gtg   206
Asp Ser Ala Lys His Val Thr Glu Lys Gly Asn Thr Val His Phe Val
                 35                  40                  45

gat gtt cag gta gcg caa att ccg att gac gct gac ggc act cgt gcg   254
Asp Val Gln Val Ala Gln Ile Pro Ile Asp Ala Asp Gly Thr Arg Ala
             50                  55                  60

aat gcg aat ctt gca cca cag act atg cct cat ctg cat ctt gac act   302
Asn Ala Asn Leu Ala Pro Gln Thr Met Pro His Leu His Leu Asp Thr
         65                  70                  75

aag gac ggt cag cgc aac aca ggt gtt gcg tat tct gat gcg cag att   350
Lys Asp Gly Gln Arg Asn Thr Gly Val Ala Tyr Ser Asp Ala Gln Ile
     80                  85                  90

caa gcg atg cag acg gtg gca gca cag ggg cgc aac cat atg acc ccg   398
Gln Ala Met Gln Thr Val Ala Ala Gln Gly Arg Asn His Met Thr Pro
 95                 100                 105                 110

ctc ttg agc aaa gac ggt gag aca gtt ggt tac tcc atg ttg gtc aag   446
Leu Leu Ser Lys Asp Gly Glu Thr Val Gly Tyr Ser Met Leu Val Lys
                115                 120                 125

gct gat gtc atg ttc ccg aag acc aag gac ggc aag tct ctc cct gcg   494
Ala Asp Val Met Phe Pro Lys Thr Lys Asp Gly Lys Ser Leu Pro Ala
            130                 135                 140

gtc atg aac act aag tct ctg cag cca tct ggg gtt cct att tcg gac   542
Val Met Asn Thr Lys Ser Leu Gln Pro Ser Gly Val Pro Ile Ser Asp
        145                 150                 155

gcg atg aat att cag cag cag cag ttt atg gct gtg gca atg aat cgc   590
Ala Met Asn Ile Gln Gln Gln Gln Phe Met Ala Val Ala Met Asn Arg
    160                 165                 170

caa gca gca gaa gcg cag aag gct gca caa gcc caa gcg acc cag gct   638
Gln Ala Ala Glu Ala Gln Lys Ala Ala Gln Ala Gln Ala Thr Gln Ala
175                 180                 185                 190

caa gca cca cag gtg gca ccg cag cca gtt atg cag aat cag caa ttc   686
Gln Ala Pro Gln Val Ala Pro Gln Pro Val Met Gln Asn Gln Gln Phe
                195                 200                 205

cag gca cca gtg cca cag ggc cag cag cca gca tat gca gga gcc cct   734
Gln Ala Pro Val Pro Gln Gly Gln Gln Pro Ala Tyr Ala Gly Ala Pro
            210                 215                 220

gtc tat gca gac gcg gta gct cat gca acc gcg cag cag cag gca gca   782
Val Tyr Ala Asp Ala Val Ala His Ala Thr Ala Gln Gln Gln Ala Ala
        225                 230                 235

gca gct cag gca ccg cag gca cct gct ggg aat ccg ttt aac cag ccg   830
Ala Ala Gln Ala Pro Gln Ala Pro Ala Gly Asn Pro Phe Asn Gln Pro
    240                 245                 250
```

```
cca gca gta gca gca gct ctg gca ccg cag acg cag ccg cca gca gta   878
Pro Ala Val Ala Ala Ala Leu Ala Pro Gln Thr Gln Pro Pro Ala Val
255                 260                 265                 270

gca gca gct ctg gca ccg cag acg cag cag ccg gca gca caa cct cag   926
Ala Ala Ala Leu Ala Pro Gln Thr Gln Gln Pro Ala Ala Gln Pro Gln
                275                 280                 285

atg gat aac gag cca ccg ttt taaaggcgca atacaccaca ccc             970
Met Asp Asn Glu Pro Pro Phe
            290
```

<210> 884
<211> 293
<212> PRT
<213> Corynebacterium glutamicum

<400> 884

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Met Ala Asn Phe Arg Ser Lys Asp Lys Asp Gly Asn Val Ile Asn Pro
  1               5                  10                  15

Asn Ala Ser Thr Lys Gly Val Asp Leu Val Val Asn Val Tyr Asp Ser
             20                  25                  30

Ala Lys His Val Thr Glu Lys Gly Asn Thr Val His Phe Val Asp Val
         35                  40                  45

Gln Val Ala Gln Ile Pro Ile Asp Ala Asp Gly Thr Arg Ala Asn Ala
     50                  55                  60

Asn Leu Ala Pro Gln Thr Met Pro His Leu His Leu Asp Thr Lys Asp
 65                  70                  75                  80

Gly Gln Arg Asn Thr Gly Val Ala Tyr Ser Asp Ala Gln Ile Gln Ala
                 85                  90                  95

Met Gln Thr Val Ala Ala Gln Gly Arg Asn His Met Thr Pro Leu Leu
            100                 105                 110

Ser Lys Asp Gly Glu Thr Val Gly Tyr Ser Met Leu Val Lys Ala Asp
        115                 120                 125

Val Met Phe Pro Lys Thr Lys Asp Gly Lys Ser Leu Pro Ala Val Met
    130                 135                 140

Asn Thr Lys Ser Leu Gln Pro Ser Gly Val Pro Ile Ser Asp Ala Met
145                 150                 155                 160

Asn Ile Gln Gln Gln Gln Phe Met Ala Val Ala Met Asn Arg Gln Ala
                165                 170                 175

Ala Glu Ala Gln Lys Ala Ala Gln Ala Gln Ala Thr Gln Ala Gln Ala
            180                 185                 190

Pro Gln Val Ala Pro Gln Pro Val Met Gln Asn Gln Gln Phe Gln Ala
        195                 200                 205

Pro Val Pro Gln Gly Gln Gln Pro Ala Tyr Ala Gly Ala Pro Val Tyr
    210                 215                 220
```

```
Ala Asp Ala Val Ala His Ala Thr Ala Gln Gln Gln Ala Ala Ala Ala
225                 230                 235                 240

Gln Ala Pro Gln Ala Pro Ala Gly Asn Pro Phe Asn Gln Pro Pro Ala
                245                 250                 255

Val Ala Ala Ala Leu Ala Pro Gln Thr Gln Pro Pro Ala Val Ala Ala
            260                 265                 270

Ala Leu Ala Pro Gln Thr Gln Gln Pro Ala Ala Gln Pro Gln Met Asp
        275                 280                 285

Asn Glu Pro Pro Phe
    290
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<210> 885
<211> 960
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (59)..(937)
<223> FRXA01909

<400> 885

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ttgttctggg aagtaatata aaaagtcccg aacaaattag tgtgaaaggg tttgtatcatg 61
                                                              Met
                                                               1

gct aat ttt cga agc aag gat aaa gat ggc aat gtc atc aat ccg aac  109
Ala Asn Phe Arg Ser Lys Asp Lys Asp Gly Asn Val Ile Asn Pro Asn
              5                  10                  15

gcg tct act aaa ggt gta gat ctt gtt gtc aac gtc tac gac agc gcc  157
Ala Ser Thr Lys Gly Val Asp Leu Val Val Asn Val Tyr Asp Ser Ala
         20                  25                  30

aag cat gtg acc gaa aag ggt aac act gtc cac ttt gtg gat gtt cag  205
Lys His Val Thr Glu Lys Gly Asn Thr Val His Phe Val Asp Val Gln
     35                  40                  45

gta gcg caa att ccg att gac gct gac ggc act cgt gcg aat gcg aat  253
Val Ala Gln Ile Pro Ile Asp Ala Asp Gly Thr Arg Ala Asn Ala Asn
 50                  55                  60                  65

ctt gca cca cag act atg cct cat ctg cat ctt gac act aag gac ggt  301
Leu Ala Pro Gln Thr Met Pro His Leu His Leu Asp Thr Lys Asp Gly
                 70                  75                  80

cag cgc aac aca ggt gtt gcg tat tct gat gcg cag att caa gcg atg  349
Gln Arg Asn Thr Gly Val Ala Tyr Ser Asp Ala Gln Ile Gln Ala Met
             85                  90                  95

cag acg gtg gca gca cag ggg cgc aac cat atg acc ccg ctc ttg agc  397
Gln Thr Val Ala Ala Gln Gly Arg Asn His Met Thr Pro Leu Leu Ser
        100                 105                 110

aaa gac ggt gag aca gtt ggt tac tcc atg ttg gtc aag gct gat gtc  445
```

```
Lys Asp Gly Glu Thr Val Gly Tyr Ser Met Leu Val Lys Ala Asp Val
    115                 120                 125

atg ttc ccg aag acc aag gac ggc aag tct ctc cct gcg gtc atg aac   493
Met Phe Pro Lys Thr Lys Asp Gly Lys Ser Leu Pro Ala Val Met Asn
130                 135                 140                 145

act aag tct ctg cag cca tct ggg gtt cct att tcg gac gcg atg aat   541
Thr Lys Ser Leu Gln Pro Ser Gly Val Pro Ile Ser Asp Ala Met Asn
                150                 155                 160

att cag cag cag cag ttt atg gct gtg gca atg aat cgc caa gca gca   589
Ile Gln Gln Gln Gln Phe Met Ala Val Ala Met Asn Arg Gln Ala Ala
            165                 170                 175

gaa gcg cag aag gct gca caa gcc caa gcg acc cag gct caa gca cca   637
Glu Ala Gln Lys Ala Ala Gln Ala Gln Ala Thr Gln Ala Gln Ala Pro
        180                 185                 190

cag gtg gca ccg cag cca gtt atg cag aat cag caa ttc cag gca cca   685
Gln Val Ala Pro Gln Pro Val Met Gln Asn Gln Gln Phe Gln Ala Pro
    195                 200                 205

gtg cca cag ggc cag cag cca gca tat gca gga gcc cct gtc tat gca   733
Val Pro Gln Gly Gln Gln Pro Ala Tyr Ala Gly Ala Pro Val Tyr Ala
210                 215                 220                 225

gac gcg gta gct cat gca acc gcg cag cag cag gca gca gca gct cag   781
Asp Ala Val Ala His Ala Thr Ala Gln Gln Gln Ala Ala Ala Ala Gln
                230                 235                 240

gca ccg cag gca cct gct ggg aat ccg ttt aac cag ccg cca gca gta   829
Ala Pro Gln Ala Pro Ala Gly Asn Pro Phe Asn Gln Pro Pro Ala Val
            245                 250                 255

gca gca gct ctg gca ccg cag acg cag ccg cca gca gta gca gca gct   877
Ala Ala Ala Leu Ala Pro Gln Thr Gln Pro Pro Ala Val Ala Ala Ala
        260                 265                 270

ctg gca ccg cag acg cag cag ccg gca gca caa cct cag atg gat aac   925
Leu Ala Pro Gln Thr Gln Gln Pro Ala Ala Gln Pro Gln Met Asp Asn
    275                 280                 285

gag cca ccg ttt taaaggcgca atacaccaca ccc                        960
Glu Pro Pro Phe
290
```

<210> 886
<211> 293
<212> PRT
<213> Corynebacterium glutamicum

<400> 886

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Met Ala Asn Phe Arg Ser Lys Asp Lys Asp Gly Asn Val Ile Asn Pro
  1               5                  10                  15

Asn Ala Ser Thr Lys Gly Val Asp Leu Val Val Asn Val Tyr Asp Ser
             20                  25                  30

Ala Lys His Val Thr Glu Lys Gly Asn Thr Val His Phe Val Asp Val
```

```
          35                  40                  45

Gln Val Ala Gln Ile Pro Ile Asp Ala Asp Gly Thr Arg Ala Asn Ala
      50                  55                  60

Asn Leu Ala Pro Gln Thr Met Pro His Leu His Leu Asp Thr Lys Asp
 65                  70                  75                  80

Gly Gln Arg Asn Thr Gly Val Ala Tyr Ser Asp Ala Gln Ile Gln Ala
                 85                  90                  95

Met Gln Thr Val Ala Ala Gln Gly Arg Asn His Met Thr Pro Leu Leu
            100                 105                 110

Ser Lys Asp Gly Glu Thr Val Gly Tyr Ser Met Leu Val Lys Ala Asp
        115                 120                 125

Val Met Phe Pro Lys Thr Lys Asp Gly Lys Ser Leu Pro Ala Val Met
    130                 135                 140

Asn Thr Lys Ser Leu Gln Pro Ser Gly Val Pro Ile Ser Asp Ala Met
145                 150                 155                 160

Asn Ile Gln Gln Gln Gln Phe Met Ala Val Ala Met Asn Arg Gln Ala
                165                 170                 175

Ala Glu Ala Gln Lys Ala Ala Gln Ala Gln Ala Thr Gln Ala Gln Ala
            180                 185                 190

Pro Gln Val Ala Pro Gln Pro Val Met Gln Asn Gln Gln Phe Gln Ala
        195                 200                 205

Pro Val Pro Gln Gly Gln Gln Pro Ala Tyr Ala Gly Ala Pro Val Tyr
    210                 215                 220

Ala Asp Ala Val Ala His Ala Thr Ala Gln Gln Gln Ala Ala Ala Ala
225                 230                 235                 240

Gln Ala Pro Gln Ala Pro Ala Gly Asn Pro Phe Asn Gln Pro Pro Ala
                245                 250                 255

Val Ala Ala Ala Leu Ala Pro Gln Thr Gln Pro Pro Ala Val Ala Ala
            260                 265                 270

Ala Leu Ala Pro Gln Thr Gln Gln Pro Ala Ala Gln Pro Gln Met Asp
        275                 280                 285

Asn Glu Pro Pro Phe
    290
```

<210> 887
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> RXN01910

<400> 887
caccgtttta aaggcgcaat acaccacacc ccaacaaact ttttgattgt tggggtgttt 60

gtctcagatc atgaacagca caatgtagga gaagattgat atg gca ttt ccg ctt 115
Met Ala Phe Pro Leu
1 5

cta gcg gtt gct ggc aca gtt gcc ccc gtt gca gca gga tgg gca aaa 163
Leu Ala Val Ala Gly Thr Val Ala Pro Val Ala Ala Gly Trp Ala Lys
10 15 20

gat aag ttt ctc agc aac tct cag aat aat cag cag gcc cag aat cag 211
Asp Lys Phe Leu Ser Asn Ser Gln Asn Asn Gln Gln Ala Gln Asn Gln
25 30 35

cag atg agt ttt gga cag gtc aac aac agc gca cag aat tct gga tca 259
Gln Met Ser Phe Gly Gln Val Asn Asn Ser Ala Gln Asn Ser Gly Ser
40 45 50

gaa aac agc ggt ttc atg ggt caa tac ggc aat ctg ggt gca ggt ttg 307
Glu Asn Ser Gly Phe Met Gly Gln Tyr Gly Asn Leu Gly Ala Gly Leu
55 60 65

gca ggt gct gct aca ggc gca ggg ctt gcg tat agc gat ttt gaa gat 355
Ala Gly Ala Ala Thr Gly Ala Gly Leu Ala Tyr Ser Asp Phe Glu Asp
70 75 80 85

ggt caa agt ttg tcc tcg aag gcc cgc aac atg gtc ggc aaa ggg ctc 403
Gly Gln Ser Leu Ser Ser Lys Ala Arg Asn Met Val Gly Lys Gly Leu
90 95 100

gct ggt gcc gga gct ggt gtg ttc acc aag ctt gcc aat gat gca att 451
Ala Gly Ala Gly Ala Gly Val Phe Thr Lys Leu Ala Asn Asp Ala Ile
105 110 115

cag gcc gag ggt ggc tcg atg aag gct agt gct tat tct gcc att gca 499
Gln Ala Glu Gly Gly Ser Met Lys Ala Ser Ala Tyr Ser Ala Ile Ala
120 125 130

ggc ggc ttg gga tcg tat ctc aaa gac ggc ggt ccg ggt gtg att aaa 547
Gly Gly Leu Gly Ser Tyr Leu Lys Asp Gly Gly Pro Gly Val Ile Lys
135 140 145

tcc gcg atg gcc agc ggt gca gcc ggt ttt ggt gcg gat aaa gtg cac 595
Ser Ala Met Ala Ser Gly Ala Ala Gly Phe Gly Ala Asp Lys Val His
150 155 160 165

gat aaa tta gct gag tct ggt cat gag ggg ttg gct gat tcc ttg tcg 643
Asp Lys Leu Ala Glu Ser Gly His Glu Gly Leu Ala Asp Ser Leu Ser
170 175 180

ggc gct att caa gga ggt ggt ctt ggt tac tcc acg ctt ggc ggt gtc 691
Gly Ala Ile Gln Gly Gly Gly Leu Gly Tyr Ser Thr Leu Gly Gly Val
185 190 195

act ggt gct ggt att ggc ggt gcg acg ggc ggt ctc gca gga cta gca 739
Thr Gly Ala Gly Ile Gly Gly Ala Thr Gly Gly Leu Ala Gly Leu Ala
200 205 210

caa aac tac ttt ggt ggt ggc gat gac tac agc aac gct ggg gca tct 787
Gln Asn Tyr Phe Gly Gly Gly Asp Asp Tyr Ser Asn Ala Gly Ala Ser

```
    215                 220                 225

gca tcg ggg ttt agt gcc aac cag gtt aat agt gag atc agc acc gag   835
Ala Ser Gly Phe Ser Ala Asn Gln Val Asn Ser Glu Ile Ser Thr Glu
230                 235                 240                 245

att ccg cag ttt gcg aat ctt ggt caa cca cag cga tcc gag ctt gaa   883
Ile Pro Gln Phe Ala Asn Leu Gly Gln Pro Gln Arg Ser Glu Leu Glu
                250                 255                 260

caa tta gcg cta cct caa gaa tca cgg tct gta gat aag agc tac gac   931
Gln Leu Ala Leu Pro Gln Glu Ser Arg Ser Val Asp Lys Ser Tyr Asp
            265                 270                 275

caa ggc tac gaa gcg taagcgcttt ataacaaccc cgt                    969
Gln Gly Tyr Glu Ala
        280


<210> 888
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 888
Met Ala Phe Pro Leu Leu Ala Val Ala Gly Thr Val Ala Pro Val Ala
  1               5                  10                  15

Ala Gly Trp Ala Lys Asp Lys Phe Leu Ser Asn Ser Gln Asn Asn Gln
             20                  25                  30

Gln Ala Gln Asn Gln Gln Met Ser Phe Gly Gln Val Asn Asn Ser Ala
         35                  40                  45

Gln Asn Ser Gly Ser Glu Asn Ser Gly Phe Met Gly Gln Tyr Gly Asn
     50                  55                  60

Leu Gly Ala Gly Leu Ala Gly Ala Ala Thr Gly Ala Gly Leu Ala Tyr
 65                  70                  75                  80

Ser Asp Phe Glu Asp Gly Gln Ser Leu Ser Ser Lys Ala Arg Asn Met
                 85                  90                  95

Val Gly Lys Gly Leu Ala Gly Ala Gly Ala Gly Val Phe Thr Lys Leu
            100                 105                 110

Ala Asn Asp Ala Ile Gln Ala Glu Gly Gly Ser Met Lys Ala Ser Ala
        115                 120                 125

Tyr Ser Ala Ile Ala Gly Gly Leu Gly Ser Tyr Leu Lys Asp Gly Gly
    130                 135                 140

Pro Gly Val Ile Lys Ser Ala Met Ala Ser Gly Ala Ala Gly Phe Gly
145                 150                 155                 160

Ala Asp Lys Val His Asp Lys Leu Ala Glu Ser Gly His Glu Gly Leu
                165                 170                 175

Ala Asp Ser Leu Ser Gly Ala Ile Gln Gly Gly Gly Leu Gly Tyr Ser
            180                 185                 190
```

```
Thr Leu Gly Gly Val Thr Gly Ala Gly Ile Gly Gly Ala Thr Gly Gly
        195                 200                 205

Leu Ala Gly Leu Ala Gln Asn Tyr Phe Gly Gly Gly Asp Asp Tyr Ser
    210                 215                 220

Asn Ala Gly Ala Ser Ala Ser Gly Phe Ser Ala Asn Gln Val Asn Ser
225                 230                 235                 240

Glu Ile Ser Thr Glu Ile Pro Gln Phe Ala Asn Leu Gly Gln Pro Gln
                245                 250                 255

Arg Ser Glu Leu Glu Gln Leu Ala Leu Pro Gln Glu Ser Arg Ser Val
            260                 265                 270

Asp Lys Ser Tyr Asp Gln Gly Tyr Glu Ala
        275                 280
```

<210> 889
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> FRXA01910

<400> 889

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caccgtttta aaggcgcaat acaccacacc ccaacaaact ttttgattgt tggggtgttt 60

gtctcagatc atgaacagca caatgtagga gaagattgat atg gca ttt ccg ctt   115
                                            Met Ala Phe Pro Leu
                                              1               5

cta gcg gtt gct ggc aca gtt gcc ccc gtt gca gca gga tgg gca aaa   163
Leu Ala Val Ala Gly Thr Val Ala Pro Val Ala Ala Gly Trp Ala Lys
                 10                  15                  20

gat aag ttt ctc agc aac tct cag aat aat cag cag gcc cag aat cag   211
Asp Lys Phe Leu Ser Asn Ser Gln Asn Asn Gln Gln Ala Gln Asn Gln
             25                  30                  35

cag atg agt ttt gga cag gtc aac aac agc gca cag aat tct gga tca   259
Gln Met Ser Phe Gly Gln Val Asn Asn Ser Ala Gln Asn Ser Gly Ser
         40                  45                  50

gaa aac agc ggt ttc atg ggt caa tac ggc aat ctg ggt gca ggt ttg   307
Glu Asn Ser Gly Phe Met Gly Gln Tyr Gly Asn Leu Gly Ala Gly Leu
     55                  60                  65

gca ggt gct gct aca ggc gca ggg ctt gcg tat agc gat ttt gaa gat   355
Ala Gly Ala Ala Thr Gly Ala Gly Leu Ala Tyr Ser Asp Phe Glu Asp
 70                  75                  80                  85

ggt caa agt ttg tcc tcg aag gcc cgc aac atg gtc ggc aaa ggg ctc   403
Gly Gln Ser Leu Ser Ser Lys Ala Arg Asn Met Val Gly Lys Gly Leu
                 90                  95                 100

gct ggt gcc gga gct ggt gtg ttc acc aag ctt gcc aat gat gca att   451
```

```
Ala Gly Ala Gly Ala Gly Val Phe Thr Lys Leu Ala Asn Asp Ala Ile
            105                 110                 115

cag gcc gag ggt ggc tcg atg aag gct agt gct tat tct gcc att gca   499
Gln Ala Glu Gly Gly Ser Met Lys Ala Ser Ala Tyr Ser Ala Ile Ala
        120                 125                 130

agc ggc ttg gga tcg tat ctc aaa aac ggc ggt ccg ggt gtg att aaa   547
Ser Gly Leu Gly Ser Tyr Leu Lys Asn Gly Gly Pro Gly Val Ile Lys
    135                 140                 145

tcc gcg atg gcc agc ggt gca gcc ggt ttt ggt gcg gat aaa gtg cac   595
Ser Ala Met Ala Ser Gly Ala Ala Gly Phe Gly Ala Asp Lys Val His
150                 155                 160                 165

gat aaa tta gct gag tct ggt cat gag ggg ttg gct gat tcc ttg tcg   643
Asp Lys Leu Ala Glu Ser Gly His Glu Gly Leu Ala Asp Ser Leu Ser
                170                 175                 180

ggc gct att caa gga ggt ggt ctt ggt tac tcc acg ctt ggc ggt gtc   691
Gly Ala Ile Gln Gly Gly Gly Leu Gly Tyr Ser Thr Leu Gly Gly Val
            185                 190                 195

act ggt gct ggt att ggc ggt gcg acg ggc ggt ctc gca gga cta gca   739
Thr Gly Ala Gly Ile Gly Gly Ala Thr Gly Gly Leu Ala Gly Leu Ala
        200                 205                 210

caa aac tac ttt ggt ggt ggc gat gac tac agc aac gct ggg gca tct   787
Gln Asn Tyr Phe Gly Gly Gly Asp Asp Tyr Ser Asn Ala Gly Ala Ser
    215                 220                 225

gca tcg ggg ttt agt gcc aac cag gtt aat agt gag atc agc acc gag   835
Ala Ser Gly Phe Ser Ala Asn Gln Val Asn Ser Glu Ile Ser Thr Glu
230                 235                 240                 245

att ccg cag ttt gcg aat ctt ggt caa cca cag cga tcc gag ctt gaa   883
Ile Pro Gln Phe Ala Asn Leu Gly Gln Pro Gln Arg Ser Glu Leu Glu
                250                 255                 260

caa tta gcg cta cct caa gaa tca cgg tct gta gat aag agc tac gac   931
Gln Leu Ala Leu Pro Gln Glu Ser Arg Ser Val Asp Lys Ser Tyr Asp
            265                 270                 275

caa ggc tac gaa gcg taagcgcttt ataacaaccc cgt                     969
Gln Gly Tyr Glu Ala
        280
```

5d4d5d5d5

```
         35                  40                  45

Gln Asn Ser Gly Ser Glu Asn Ser Gly Phe Met Gly Gln Tyr Gly Asn
     50                  55                  60

Leu Gly Ala Gly Leu Ala Gly Ala Ala Thr Gly Ala Gly Leu Ala Tyr
 65                  70                  75                  80

Ser Asp Phe Glu Asp Gly Gln Ser Leu Ser Ser Lys Ala Arg Asn Met
                 85                  90                  95

Val Gly Lys Gly Leu Ala Gly Ala Gly Ala Gly Val Phe Thr Lys Leu
            100                 105                 110

Ala Asn Asp Ala Ile Gln Ala Glu Gly Gly Ser Met Lys Ala Ser Ala
        115                 120                 125

Tyr Ser Ala Ile Ala Ser Gly Leu Gly Ser Tyr Leu Lys Asn Gly Gly
    130                 135                 140

Pro Gly Val Ile Lys Ser Ala Met Ala Ser Gly Ala Ala Gly Phe Gly
145                 150                 155                 160

Ala Asp Lys Val His Asp Lys Leu Ala Glu Ser Gly His Glu Gly Leu
                165                 170                 175

Ala Asp Ser Leu Ser Gly Ala Ile Gln Gly Gly Gly Leu Gly Tyr Ser
            180                 185                 190

Thr Leu Gly Gly Val Thr Gly Ala Gly Ile Gly Gly Ala Thr Gly Gly
        195                 200                 205

Leu Ala Gly Leu Ala Gln Asn Tyr Phe Gly Gly Gly Asp Asp Tyr Ser
    210                 215                 220

Asn Ala Gly Ala Ser Ala Ser Gly Phe Ser Ala Asn Gln Val Asn Ser
225                 230                 235                 240

Glu Ile Ser Thr Glu Ile Pro Gln Phe Ala Asn Leu Gly Gln Pro Gln
                245                 250                 255

Arg Ser Glu Leu Glu Gln Leu Ala Leu Pro Gln Glu Ser Arg Ser Val
            260                 265                 270

Asp Lys Ser Tyr Asp Gln Gly Tyr Glu Ala
        275                 280
```

<210> 891
<211> 1062
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1039)
<223> RXN01911

<400> 891
agatgccgca gatcaccgag tgagcgttac tgagatcact gagtctcgat gggtaatcca 60

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tataattgtg agcgggattc ttagtgcgct cgcggttctg gtg ttt att att ggc   115
                                            Val Phe Ile Ile Gly
                                              1               5

gcc ggc ttg cca ctg ttg tac gtg ccg att ttt gtg act gtc atc gtc   163
Ala Gly Leu Pro Leu Leu Tyr Val Pro Ile Phe Val Thr Val Ile Val
                 10                  15                  20

atg gtg gtg tat gcg cta ttg cgc tat gag cag cgc atg tca ggc aca   211
Met Val Val Tyr Ala Leu Leu Arg Tyr Glu Gln Arg Met Ser Gly Thr
             25                  30                  35

gtc tac gag gaa gca gat cct gtc gaa atg gat tca gtg atc tgg gag   259
Val Tyr Glu Glu Ala Asp Pro Val Glu Met Asp Ser Val Ile Trp Glu
         40                  45                  50

ggc atc aag tgc gat att gcc tcg gat att gca gcc cga gca gaa gcg   307
Gly Ile Lys Cys Asp Ile Ala Ser Asp Ile Ala Ala Arg Ala Glu Ala
     55                  60                  65

aaa aaa gcg aaa aag cca gtt gcg tca gat gct gtt gct gtt ggt aac   355
Lys Lys Ala Lys Lys Pro Val Ala Ser Asp Ala Val Ala Val Gly Asn
 70                  75                  80                  85

tat atc gcg tcc ttg cgt cag cat atg ttg gta gaa acc cag cga cgt   403
Tyr Ile Ala Ser Leu Arg Gln His Met Leu Val Glu Thr Gln Arg Arg
                 90                  95                 100

tat cac cac aag ctt ggt cgt gag ctg cat aat gat cca gcg caa cta   451
Tyr His His Lys Leu Gly Arg Glu Leu His Asn Asp Pro Ala Gln Leu
             105                 110                 115

gag gat tat ggc tct ggt ctg cgt gac tgt gag tgt cgg gca tgt gtg   499
Glu Asp Tyr Gly Ser Gly Leu Arg Asp Cys Glu Cys Arg Ala Cys Val
         120                 125                 130

gtg gct cag aaa ttg ggt gtc acg gtg cac gct cat ggt gtg gtg cag   547
Val Ala Gln Lys Leu Gly Val Thr Val His Ala His Gly Val Val Gln
     135                 140                 145

gcg agc gca cgt aaa aaa gat cgc gtc att att ggg cga gcc gat ggt   595
Ala Ser Ala Arg Lys Lys Asp Arg Val Ile Ile Gly Arg Ala Asp Gly
150                 155                 160                 165

att gat gtg gcc ggc tgg tgg aac cac cgc caa gaa gct cga cgt aaa   643
Ile Asp Val Ala Gly Trp Trp Asn His Arg Gln Glu Ala Arg Arg Lys
                 170                 175                 180

acg agc gcg gct aag cag ttg gag cgc gat gca caa cgc aag cga acc   691
Thr Ser Ala Ala Lys Gln Leu Glu Arg Asp Ala Gln Arg Lys Arg Thr
             185                 190                 195

caa gct gag cgc gat aaa gag att gag cgt aag cgt aag gct caa gaa   739
Gln Ala Glu Arg Asp Lys Glu Ile Glu Arg Lys Arg Lys Ala Gln Glu
         200                 205                 210

ttt gta gcg gag cag tca ggg aaa gct gct gca gca caa cgg cgg gcc   787
Phe Val Ala Glu Gln Ser Gly Lys Ala Ala Ala Ala Gln Arg Arg Ala
     215                 220                 225

gag aaa aag gct gcg aag caa gcg cgt gta gat gaa ctg gtg gcg cag   835
```

```
Glu Lys Lys Ala Ala Lys Gln Ala Arg Val Asp Glu Leu Val Ala Gln
230                 235                 240                 245

aaa cag gct gct cag gag cag aaa act cac tgt aag cgg gac aag cag   883
Lys Gln Ala Ala Gln Glu Gln Lys Thr His Cys Lys Arg Asp Lys Gln
                250                 255                 260

cgt gcg aag aaa gca caa ggg cgc aaa gtt ggt gcc gtt gat aat tcc   931
Arg Ala Lys Lys Ala Gln Gly Arg Lys Val Gly Ala Val Asp Asn Ser
            265                 270                 275

gct gtg gac gat gtg ttg gcg tat gcg gag aaa acc cgc agt ata gct   979
Ala Val Asp Asp Val Leu Ala Tyr Ala Glu Lys Thr Arg Ser Ile Ala
        280                 285                 290

ggc tgt aga gat gac gac agc gtt gtg cac gtt gat atg gca gcg ggt   1027
Gly Cys Arg Asp Asp Asp Ser Val Val His Val Asp Met Ala Ala Gly
    295                 300                 305

gtc cgc gat gtc taaatcgcag gatgatcgaa aaa                        1062
Val Arg Asp Val
310
```

<210> 892
<211> 313
<212> PRT
<213> Corynebacterium glutamicum

<400> 892

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Val Phe Ile Ile Gly Ala Gly Leu Pro Leu Leu Tyr Val Pro Ile Phe
  1               5                  10                  15

Val Thr Val Ile Val Met Val Val Tyr Ala Leu Leu Arg Tyr Glu Gln
             20                  25                  30

Arg Met Ser Gly Thr Val Tyr Glu Glu Ala Asp Pro Val Glu Met Asp
         35                  40                  45

Ser Val Ile Trp Glu Gly Ile Lys Cys Asp Ile Ala Ser Asp Ile Ala
     50                  55                  60

Ala Arg Ala Glu Ala Lys Lys Ala Lys Lys Pro Val Ala Ser Asp Ala
 65                  70                  75                  80

Val Ala Val Gly Asn Tyr Ile Ala Ser Leu Arg Gln His Met Leu Val
                 85                  90                  95

Glu Thr Gln Arg Arg Tyr His His Lys Leu Gly Arg Glu Leu His Asn
            100                 105                 110

Asp Pro Ala Gln Leu Glu Asp Tyr Gly Ser Gly Leu Arg Asp Cys Glu
        115                 120                 125

Cys Arg Ala Cys Val Val Ala Gln Lys Leu Gly Val Thr Val His Ala
    130                 135                 140

His Gly Val Val Gln Ala Ser Ala Arg Lys Lys Asp Arg Val Ile Ile
145                 150                 155                 160

Gly Arg Ala Asp Gly Ile Asp Val Ala Gly Trp Trp Asn His Arg Gln
```

```
                 165                 170                 175

Glu Ala Arg Arg Lys Thr Ser Ala Ala Lys Gln Leu Glu Arg Asp Ala
            180                 185                 190

Gln Arg Lys Arg Thr Gln Ala Glu Arg Asp Lys Glu Ile Glu Arg Lys
        195                 200                 205

Arg Lys Ala Gln Glu Phe Val Ala Glu Gln Ser Gly Lys Ala Ala Ala
    210                 215                 220

Ala Gln Arg Arg Ala Glu Lys Lys Ala Ala Lys Gln Ala Arg Val Asp
225                 230                 235                 240

Glu Leu Val Ala Gln Lys Gln Ala Ala Gln Glu Gln Lys Thr His Cys
                245                 250                 255

Lys Arg Asp Lys Gln Arg Ala Lys Lys Ala Gln Gly Arg Lys Val Gly
            260                 265                 270

Ala Val Asp Asn Ser Ala Val Asp Asp Val Leu Ala Tyr Ala Glu Lys
        275                 280                 285

Thr Arg Ser Ile Ala Gly Cys Arg Asp Asp Asp Ser Val Val His Val
    290                 295                 300

Asp Met Ala Ala Gly Val Arg Asp Val
305                 310
```

<210> 893
<211> 946
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> FRXA01911

<400> 893

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agatgccgca gatcaccgag tgagcgttac tgagatcact gagtctcgat gggtaatcca 60

tataattgtg agcgggattc ttagtgcgct cgcggttctg gtg ttt att att ggc   115
                                            Val Phe Ile Ile Gly
                                              1               5

gcc ggc ttg cca ctg ttg tac gtg ccg att ttt gtg act gtc atc gtc   163
Ala Gly Leu Pro Leu Leu Tyr Val Pro Ile Phe Val Thr Val Ile Val
                  10                  15                  20

atg gtg gtg tat gcg cta ttg cgc tat gag cag cgc atg tca ggc aca   211
Met Val Val Tyr Ala Leu Leu Arg Tyr Glu Gln Arg Met Ser Gly Thr
             25                  30                  35

gtc tac gag gaa gca gat cct gtc gaa atg gat tca gtg atc tgg gag   259
Val Tyr Glu Glu Ala Asp Pro Val Glu Met Asp Ser Val Ile Trp Glu
         40                  45                  50

ggc atc aag tgc gat att gcc tcg gat att gca gcc cga gca gaa gcg   307
Gly Ile Lys Cys Asp Ile Ala Ser Asp Ile Ala Ala Arg Ala Glu Ala
```

```
     55                  60                  65

aaa aaa gcg aaa aag cca gtt gcg tca gat gct gtt gct gtt ggt aac   355
Lys Lys Ala Lys Lys Pro Val Ala Ser Asp Ala Val Ala Val Gly Asn
 70                  75                  80                  85

tat atc gcg tcc ttg cgt cag cat atg ttg gta gaa acc cag cga cgt   403
Tyr Ile Ala Ser Leu Arg Gln His Met Leu Val Glu Thr Gln Arg Arg
                 90                  95                 100

tat cac cac aag ctt ggt cgt gag ctg cat aat gat cca gcg caa cta   451
Tyr His His Lys Leu Gly Arg Glu Leu His Asn Asp Pro Ala Gln Leu
            105                 110                 115

gag gat tat ggc tct ggt ctg cgt gac tgt gag tgt cgg gca tgt gtg   499
Glu Asp Tyr Gly Ser Gly Leu Arg Asp Cys Glu Cys Arg Ala Cys Val
        120                 125                 130

gtg gct cag aaa ttg ggt gtc acg gtg cac gct cat ggt gtg gtg cag   547
Val Ala Gln Lys Leu Gly Val Thr Val His Ala His Gly Val Val Gln
    135                 140                 145

gcg agc gca cgt aaa aaa gat cgc gtc att att ggg cga gcc gat ggt   595
Ala Ser Ala Arg Lys Lys Asp Arg Val Ile Ile Gly Arg Ala Asp Gly
150                 155                 160                 165

att gat gtg gcc ggc tgg tgg aac cac cgc caa gaa gct cga cgt aaa   643
Ile Asp Val Ala Gly Trp Trp Asn His Arg Gln Glu Ala Arg Arg Lys
                170                 175                 180

acg agc gcg gct aag cag ttg gag cgc gat gca caa cgc aag cga acc   691
Thr Ser Ala Ala Lys Gln Leu Glu Arg Asp Ala Gln Arg Lys Arg Thr
            185                 190                 195

caa gct gag cgc gat aaa gag att gag cgt aag cgt aag gct caa gaa   739
Gln Ala Glu Arg Asp Lys Glu Ile Glu Arg Lys Arg Lys Ala Gln Glu
        200                 205                 210

ttt gta gcg gag cag tca ggg aaa gct gct gca gca caa cgg cgg gcc   787
Phe Val Ala Glu Gln Ser Gly Lys Ala Ala Ala Ala Gln Arg Arg Ala
    215                 220                 225

gag aaa aag gct gcg aag caa gcg cgt gta gat gaa ctg gtg gcg cag   835
Glu Lys Lys Ala Ala Lys Gln Ala Arg Val Asp Glu Leu Val Ala Gln
230                 235                 240                 245

aaa cag gct gct cag gag cag aaa act cac tgt aag cgg gac aag cag   883
Lys Gln Ala Ala Gln Glu Gln Lys Thr His Cys Lys Arg Asp Lys Gln
                250                 255                 260

cgt gcg aag aaa gca caa ggg cgc aaa gtt ggt gcc gtt gat aat tcc   931
Arg Ala Lys Lys Ala Gln Gly Arg Lys Val Gly Ala Val Asp Asn Ser
            265                 270                 275

gct gtg gac gat gtg                                              946
Ala Val Asp Asp Val
        280
```

<210> 894
<211> 282

<212> PRT
<213> Corynebacterium glutamicum

<400> 894

```
Val Phe Ile Ile Gly Ala Gly Leu Pro Leu Leu Tyr Val Pro Ile Phe
  1               5                  10                  15

Val Thr Val Ile Val Met Val Val Tyr Ala Leu Leu Arg Tyr Glu Gln
             20                  25                  30

Arg Met Ser Gly Thr Val Tyr Glu Glu Ala Asp Pro Val Glu Met Asp
         35                  40                  45

Ser Val Ile Trp Glu Gly Ile Lys Cys Asp Ile Ala Ser Asp Ile Ala
     50                  55                  60

Ala Arg Ala Glu Ala Lys Lys Ala Lys Lys Pro Val Ala Ser Asp Ala
 65                  70                  75                  80

Val Ala Val Gly Asn Tyr Ile Ala Ser Leu Arg Gln His Met Leu Val
                 85                  90                  95

Glu Thr Gln Arg Arg Tyr His His Lys Leu Gly Arg Glu Leu His Asn
            100                 105                 110

Asp Pro Ala Gln Leu Glu Asp Tyr Gly Ser Gly Leu Arg Asp Cys Glu
        115                 120                 125

Cys Arg Ala Cys Val Val Ala Gln Lys Leu Gly Val Thr Val His Ala
    130                 135                 140

His Gly Val Val Gln Ala Ser Ala Arg Lys Lys Asp Arg Val Ile Ile
145                 150                 155                 160

Gly Arg Ala Asp Gly Ile Asp Val Ala Gly Trp Trp Asn His Arg Gln
                165                 170                 175

Glu Ala Arg Arg Lys Thr Ser Ala Ala Lys Gln Leu Glu Arg Asp Ala
            180                 185                 190

Gln Arg Lys Arg Thr Gln Ala Glu Arg Asp Lys Glu Ile Glu Arg Lys
        195                 200                 205

Arg Lys Ala Gln Glu Phe Val Ala Glu Gln Ser Gly Lys Ala Ala Ala
    210                 215                 220

Ala Gln Arg Arg Ala Glu Lys Lys Ala Ala Lys Gln Ala Arg Val Asp
225                 230                 235                 240

Glu Leu Val Ala Gln Lys Gln Ala Ala Gln Glu Gln Lys Thr His Cys
                245                 250                 255

Lys Arg Asp Lys Gln Arg Ala Lys Lys Ala Gln Gly Arg Lys Val Gly
            260                 265                 270

Ala Val Asp Asn Ser Ala Val Asp Asp Val
        275                 280
```

<210> 895
<211> 1074

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1051)
<223> RXN01930

<400> 895
cgaaagaagc cataatttag agaggacaat tctctactat tggtcaaggc tcccacccgg 60

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tgtcattcga cattattacc gctcactcac aatcgatgaa gtg att tca aca aat   115
                                          Val Ile Ser Thr Asn
                                            1               5

gag att gaa aat att cac tca act cgt cgg gat att gaa ata gcg ctt   163
Glu Ile Glu Asn Ile His Ser Thr Arg Arg Asp Ile Glu Ile Ala Leu
                 10                  15                  20

gat gaa tct tcc act agt gag cca aag aga ttt tcg gaa att tca cac   211
Asp Glu Ser Ser Thr Ser Glu Pro Lys Arg Phe Ser Glu Ile Ser His
             25                  30                  35

ctt tac ctc gca ctt gcc gaa ggt aaa ata tcc ttt ccg gaa agc cca   259
Leu Tyr Leu Ala Leu Ala Glu Gly Lys Ile Ser Phe Pro Glu Ser Pro
         40                  45                  50

agt gaa ctt cga gaa ctc tat gac cat tta atg cac ggc gag cta ggt   307
Ser Glu Leu Arg Glu Leu Tyr Asp His Leu Met His Gly Glu Leu Gly
     55                  60                  65

aaa gaa aat gaa tta gat ggt gag att ttc cgc caa gga ccc gtg gaa   355
Lys Glu Asn Glu Leu Asp Gly Glu Ile Phe Arg Gln Gly Pro Val Glu
 70                  75                  80                  85

atc cgc gat agt cgg caa aaa gtg att cat tca ggt ttt tct cca gaa   403
Ile Arg Asp Ser Arg Gln Lys Val Ile His Ser Gly Phe Ser Pro Glu
                 90                  95                 100

tca cag atc atc gaa gga atc aac gca att att aag ctg gcg cac tca   451
Ser Gln Ile Ile Glu Gly Ile Asn Ala Ile Ile Lys Leu Ala His Ser
            105                 110                 115

gaa gag gaa tcc aac ctt gtt ggc atc atg atg tca cac ttc atg ttt   499
Glu Glu Glu Ser Asn Leu Val Gly Ile Met Met Ser His Phe Met Phe
        120                 125                 130

gaa tca att cac ccg ttt tat gat gga aac gga aga act ggg cgc tac   547
Glu Ser Ile His Pro Phe Tyr Asp Gly Asn Gly Arg Thr Gly Arg Tyr
    135                 140                 145

ctt ctc ggg ata caa tta agc aaa att ctc tcc cct gct aca gca ctg   595
Leu Leu Gly Ile Gln Leu Ser Lys Ile Leu Ser Pro Ala Thr Ala Leu
150                 155                 160                 165

aca atg tct tcg gca att aat caa ttt cga aac aag tac tac aaa gcg   643
Thr Met Ser Ser Ala Ile Asn Gln Phe Arg Asn Lys Tyr Tyr Lys Ala
                170                 175                 180

ttt cat gcc gta gaa cac cga tta aat cgc gga gac gga aca ccg ttt   691
Phe His Ala Val Glu His Arg Leu Asn Arg Gly Asp Gly Thr Pro Phe
```

```
            185                 190                 195

gtt att tcc atg ctt gag ctg tta att gca gcg caa gaa ggt ctc att   739
Val Ile Ser Met Leu Glu Leu Leu Ile Ala Ala Gln Glu Gly Leu Ile
        200                 205                 210

gag aat ata aaa caa aga atc gac ttt ttg gca agc ctt gag gac gcc   787
Glu Asn Ile Lys Gln Arg Ile Asp Phe Leu Ala Ser Leu Glu Asp Ala
    215                 220                 225

att aaa acg ctt cgg ggt acc aat tcc ttt aag aac cat cag atc aat   835
Ile Lys Thr Leu Arg Gly Thr Asn Ser Phe Lys Asn His Gln Ile Asn
230                 235                 240                 245

ctg ttg tac att ctc ggc cag att cag ctt ttc ggt aag gac gaa aca   883
Leu Leu Tyr Ile Leu Gly Gln Ile Gln Leu Phe Gly Lys Asp Glu Thr
                250                 255                 260

ctt tca ctt gaa tcg gca gca aag ttt ctt aaa gtt tct aag gca act   931
Leu Ser Leu Glu Ser Ala Ala Lys Phe Leu Lys Val Ser Lys Ala Thr
            265                 270                 275

gca acg agg tat ttt aga act ctc cga gaa atg gaa tta gtt cac gag   979
Ala Thr Arg Tyr Phe Arg Thr Leu Arg Glu Met Glu Leu Val His Glu
        280                 285                 290

gtc agc aaa cgc cct ttg cgg ttt gcg ctc acg gat aaa ggt cgt gag   1027
Val Ser Lys Arg Pro Leu Arg Phe Ala Leu Thr Asp Lys Gly Arg Glu
    295                 300                 305

ata gta ggt ctt gag gta aaa att tgactccata acgagaactt aat         1074
Ile Val Gly Leu Glu Val Lys Ile
310                 315
```

<210> 896
<211> 317
<212> PRT
<213> Corynebacterium glutamicum

<400> 896

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Val Ile Ser Thr Asn Glu Ile Glu Asn Ile His Ser Thr Arg Arg Asp
  1               5                  10                  15

Ile Glu Ile Ala Leu Asp Glu Ser Ser Thr Ser Glu Pro Lys Arg Phe
             20                  25                  30

Ser Glu Ile Ser His Leu Tyr Leu Ala Leu Ala Glu Gly Lys Ile Ser
         35                  40                  45

Phe Pro Glu Ser Pro Ser Glu Leu Arg Glu Leu Tyr Asp His Leu Met
     50                  55                  60

His Gly Glu Leu Gly Lys Glu Asn Glu Leu Asp Gly Glu Ile Phe Arg
 65                  70                  75                  80

Gln Gly Pro Val Glu Ile Arg Asp Ser Arg Gln Lys Val Ile His Ser
                 85                  90                  95

Gly Phe Ser Pro Glu Ser Gln Ile Ile Glu Gly Ile Asn Ala Ile Ile
            100                 105                 110
```

```
Lys Leu Ala His Ser Glu Glu Glu Ser Asn Leu Val Gly Ile Met Met
        115                 120                 125

Ser His Phe Met Phe Glu Ser Ile His Pro Phe Tyr Asp Gly Asn Gly
    130                 135                 140

Arg Thr Gly Arg Tyr Leu Leu Gly Ile Gln Leu Ser Lys Ile Leu Ser
145                 150                 155                 160

Pro Ala Thr Ala Leu Thr Met Ser Ser Ala Ile Asn Gln Phe Arg Asn
                165                 170                 175

Lys Tyr Tyr Lys Ala Phe His Ala Val Glu His Arg Leu Asn Arg Gly
            180                 185                 190

Asp Gly Thr Pro Phe Val Ile Ser Met Leu Glu Leu Leu Ile Ala Ala
        195                 200                 205

Gln Glu Gly Leu Ile Glu Asn Ile Lys Gln Arg Ile Asp Phe Leu Ala
    210                 215                 220

Ser Leu Glu Asp Ala Ile Lys Thr Leu Arg Gly Thr Asn Ser Phe Lys
225                 230                 235                 240

Asn His Gln Ile Asn Leu Leu Tyr Ile Leu Gly Gln Ile Gln Leu Phe
                245                 250                 255

Gly Lys Asp Glu Thr Leu Ser Leu Glu Ser Ala Ala Lys Phe Leu Lys
            260                 265                 270

Val Ser Lys Ala Thr Ala Thr Arg Tyr Phe Arg Thr Leu Arg Glu Met
        275                 280                 285

Glu Leu Val His Glu Val Ser Lys Arg Pro Leu Arg Phe Ala Leu Thr
    290                 295                 300

Asp Lys Gly Arg Glu Ile Val Gly Leu Glu Val Lys Ile
305                 310                 315
```

20050250090

<210> 897
<211> 1074
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1051)
<223> FRXA01930

<400> 897
cgaaagaagc cataatttag agaggacaat tctctactat tggtcaaggc tcccacccgg 60

```
tgtcattcga cattattacc gctcactcac aatcgatgaa gtg att tca aca aat   115
                                          Val Ile Ser Thr Asn
                                            1               5

gag att gaa aat att cac tca act cgt cgg gat att gaa ata gcg ctt   163
Glu Ile Glu Asn Ile His Ser Thr Arg Arg Asp Ile Glu Ile Ala Leu
            10                  15                  20
```

```
gat gaa tct tcc act agt gag cca aag aga ttt tcg gaa att tca cac   211
Asp Glu Ser Ser Thr Ser Glu Pro Lys Arg Phe Ser Glu Ile Ser His
            25                  30                  35

ctt tac ctc gca ctt gcc gaa ggt aaa ata tcc ttt ccg gaa agc cca   259
Leu Tyr Leu Ala Leu Ala Glu Gly Lys Ile Ser Phe Pro Glu Ser Pro
        40                  45                  50

agt gaa ctt cga gaa ctc tat gac cat tta atg cac ggc gag cta ggt   307
Ser Glu Leu Arg Glu Leu Tyr Asp His Leu Met His Gly Glu Leu Gly
    55                  60                  65

aaa gaa aat gaa tta gat ggt gag att ttc cgc caa gga ccc gtg gaa   355
Lys Glu Asn Glu Leu Asp Gly Glu Ile Phe Arg Gln Gly Pro Val Glu
70                  75                  80                  85

atc cgc gat agt cgg caa aaa gtg att cat tca ggt ttt tct cca gaa   403
Ile Arg Asp Ser Arg Gln Lys Val Ile His Ser Gly Phe Ser Pro Glu
                90                  95                  100

tca cag atc atc gaa gga atc aac gca att att aag ctg gcg cac tca   451
Ser Gln Ile Ile Glu Gly Ile Asn Ala Ile Ile Lys Leu Ala His Ser
            105                 110                 115

gaa gag gaa tcc aac ctt gtt ggc atc atg atg tca cac ttc atg ttt   499
Glu Glu Glu Ser Asn Leu Val Gly Ile Met Met Ser His Phe Met Phe
        120                 125                 130

gaa tca att cac ccg ttt tat gat gga aac gga aga act ggg cgc tac   547
Glu Ser Ile His Pro Phe Tyr Asp Gly Asn Gly Arg Thr Gly Arg Tyr
    135                 140                 145

ctt ctc ggg ata caa tta agc aaa att ctc tcc cct gct aca gca ctg   595
Leu Leu Gly Ile Gln Leu Ser Lys Ile Leu Ser Pro Ala Thr Ala Leu
150                 155                 160                 165

aca atg tct tcg gca att aat caa ttt cga aac aag tac tac aaa gcg   643
Thr Met Ser Ser Ala Ile Asn Gln Phe Arg Asn Lys Tyr Tyr Lys Ala
                170                 175                 180

ttt cat gcc gta gaa cac cga tta aat cgc gga gac gga aca ccg ttt   691
Phe His Ala Val Glu His Arg Leu Asn Arg Gly Asp Gly Thr Pro Phe
            185                 190                 195

gtt att tcc atg ctt gag ctg tta att gca gcg caa gaa ggt ctc att   739
Val Ile Ser Met Leu Glu Leu Leu Ile Ala Ala Gln Glu Gly Leu Ile
        200                 205                 210

gag aat ata aaa caa aga atc gac ttt ttg gca agc ctt gag gac gcc   787
Glu Asn Ile Lys Gln Arg Ile Asp Phe Leu Ala Ser Leu Glu Asp Ala
    215                 220                 225

att aaa acg ctt cgg ggt acc aat tcc ttt aag aac cat cag atc aat   835
Ile Lys Thr Leu Arg Gly Thr Asn Ser Phe Lys Asn His Gln Ile Asn
230                 235                 240                 245

ctg ttg tac att ctc ggc cag att cag ctt ttc ggt aag gac gaa aca   883
Leu Leu Tyr Ile Leu Gly Gln Ile Gln Leu Phe Gly Lys Asp Glu Thr
                250                 255                 260
```

```
ctt tca ctt gaa tcg gca gca aag ttt ctt aaa gtt tct aag gca act   931
Leu Ser Leu Glu Ser Ala Ala Lys Phe Leu Lys Val Ser Lys Ala Thr
            265                 270                 275

gca acg agg tat ttt aga act ctc cga gaa atg gaa tta gtt cac gag   979
Ala Thr Arg Tyr Phe Arg Thr Leu Arg Glu Met Glu Leu Val His Glu
        280                 285                 290

gtc agc aaa cgc cct ttg cgg ttt gcg ctc acg gat aaa ggt cgt gag   1027
Val Ser Lys Arg Pro Leu Arg Phe Ala Leu Thr Asp Lys Gly Arg Glu
    295                 300                 305

ata gta ggt ctt gag gta aaa att tgactccata acgagaactt aat         1074
Ile Val Gly Leu Glu Val Lys Ile
310                 315
```

<210> 898
<211> 317
<212> PRT
<213> Corynebacterium glutamicum

<400> 898

```
Val Ile Ser Thr Asn Glu Ile Glu Asn Ile His Ser Thr Arg Arg Asp
  1               5                  10                  15

Ile Glu Ile Ala Leu Asp Glu Ser Ser Thr Ser Glu Pro Lys Arg Phe
             20                  25                  30

Ser Glu Ile Ser His Leu Tyr Leu Ala Leu Ala Glu Gly Lys Ile Ser
         35                  40                  45

Phe Pro Glu Ser Pro Ser Glu Leu Arg Glu Leu Tyr Asp His Leu Met
     50                  55                  60

His Gly Glu Leu Gly Lys Glu Asn Glu Leu Asp Gly Glu Ile Phe Arg
 65                  70                  75                  80

Gln Gly Pro Val Glu Ile Arg Asp Ser Arg Gln Lys Val Ile His Ser
                 85                  90                  95

Gly Phe Ser Pro Glu Ser Gln Ile Ile Glu Gly Ile Asn Ala Ile Ile
            100                 105                 110

Lys Leu Ala His Ser Glu Glu Glu Ser Asn Leu Val Gly Ile Met Met
        115                 120                 125

Ser His Phe Met Phe Glu Ser Ile His Pro Phe Tyr Asp Gly Asn Gly
    130                 135                 140

Arg Thr Gly Arg Tyr Leu Leu Gly Ile Gln Leu Ser Lys Ile Leu Ser
145                 150                 155                 160

Pro Ala Thr Ala Leu Thr Met Ser Ser Ala Ile Asn Gln Phe Arg Asn
                165                 170                 175

Lys Tyr Tyr Lys Ala Phe His Ala Val Glu His Arg Leu Asn Arg Gly
            180                 185                 190

Asp Gly Thr Pro Phe Val Ile Ser Met Leu Glu Leu Leu Ile Ala Ala
        195                 200                 205
```

```
Gln Glu Gly Leu Ile Glu Asn Ile Lys Gln Arg Ile Asp Phe Leu Ala
    210                 215                 220

Ser Leu Glu Asp Ala Ile Lys Thr Leu Arg Gly Thr Asn Ser Phe Lys
225                 230                 235                 240

Asn His Gln Ile Asn Leu Leu Tyr Ile Leu Gly Gln Ile Gln Leu Phe
                245                 250                 255

Gly Lys Asp Glu Thr Leu Ser Leu Glu Ser Ala Ala Lys Phe Leu Lys
            260                 265                 270

Val Ser Lys Ala Thr Ala Thr Arg Tyr Phe Arg Thr Leu Arg Glu Met
        275                 280                 285

Glu Leu Val His Glu Val Ser Lys Arg Pro Leu Arg Phe Ala Leu Thr
    290                 295                 300

Asp Lys Gly Arg Glu Ile Val Gly Leu Glu Val Lys Ile
305                 310                 315
```

<210> 899
<211> 1095
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1072)
<223> RXN01944

<400> 899

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gctgattctt ctgtaccact catcacagat aataccgcaa ccagtatcaa ccctgcggag 60

ccgtttacct tcgccttcaa atatcaccga tgatgtccag gtg cgc acg gca aca   115
                                            Val Arg Thr Ala Thr
                                              1               5

ctg cat gtt act tcc agt gct ggc gaa gcc gcg aca acc atc aac ctc   163
Leu His Val Thr Ser Ser Ala Gly Glu Ala Ala Thr Thr Ile Asn Leu
                 10                  15                  20

acc gag gat gac ggc tct ttc aat tgg gct ctg cct gca gcg gat ctc   211
Thr Glu Asp Asp Gly Ser Phe Asn Trp Ala Leu Pro Ala Ala Asp Leu
             25                  30                  35

acc gga aaa tcc tgg ttc gaa tac acc gta acc gcc acc gac gga ttc   259
Thr Gly Lys Ser Trp Phe Glu Tyr Thr Val Thr Ala Thr Asp Gly Phe
         40                  45                  50

aac agc gtt acc acc gag ccg gta cgc gtc acc gtc gac ggc gcc aac   307
Asn Ser Val Thr Thr Glu Pro Val Arg Val Thr Val Asp Gly Ala Asn
     55                  60                  65

acc gac ccg ctg cgc ctc aac ctg gaa gaa aac caa tgg gtc agt ggc   355
Thr Asp Pro Leu Arg Leu Asn Leu Glu Glu Asn Gln Trp Val Ser Gly
 70                  75                  80                  85

acc acc gat gtt atc ggt gct tca gat gtc ttc ggc gac aag ctt gaa   403
```

```
Thr Thr Asp Val Ile Gly Ala Ser Asp Val Phe Gly Asp Lys Leu Glu
                 90                  95                 100

ttg ctt atc gac gac gcg cct gca gtc acc aac tcc agc ctg tct gcg   451
Leu Leu Ile Asp Asp Ala Pro Ala Val Thr Asn Ser Ser Leu Ser Ala
            105                 110                 115

gcc ccg acg ttt gcg atg gaa gta acc caa act gat gtg ttc ttc cgc   499
Ala Pro Thr Phe Ala Met Glu Val Thr Gln Thr Asp Val Phe Phe Arg
        120                 125                 130

aac ggc atc ctt gcc ggt ggg gaa gaa ctc cgc att ttc gat caa gga   547
Asn Gly Ile Leu Ala Gly Gly Glu Glu Leu Arg Ile Phe Asp Gln Gly
    135                 140                 145

act tac gcc aac acc gaa acc atc tcc aca cca gtc ccg ctg tat cac   595
Thr Tyr Ala Asn Thr Glu Thr Ile Ser Thr Pro Val Pro Leu Tyr His
150                 155                 160                 165

atc aat gag gac ggt acc ctc aca gtc agt gtg tat gcg gga act aaa   643
Ile Asn Glu Asp Gly Thr Leu Thr Val Ser Val Tyr Ala Gly Thr Lys
                170                 175                 180

gca gca cca gaa att gac ctc aac gag aac aat gac gat ttc cag atc   691
Ala Ala Pro Glu Ile Asp Leu Asn Glu Asn Asn Asp Asp Phe Gln Ile
            185                 190                 195

aga aac ctt cga cta att ctg cct gat ggc cgg acc ctc acc cct gcc   739
Arg Asn Leu Arg Leu Ile Leu Pro Asp Gly Arg Thr Leu Thr Pro Ala
        200                 205                 210

gga att tcc gat tct aat gcg tgg ctc aac atg gga gac agc gct gga   787
Gly Ile Ser Asp Ser Asn Ala Trp Leu Asn Met Gly Asp Ser Ala Gly
    215                 220                 225

aaa ctc gat ttc ttc gat gcc acc ttc gcc ctc cct gag gat gct ttc   835
Lys Leu Asp Phe Phe Asp Ala Thr Phe Ala Leu Pro Glu Asp Ala Phe
230                 235                 240                 245

acc ggt gtg gca cac gca tgg gat acc acc caa agc aca gat gga gaa   883
Thr Gly Val Ala His Ala Trp Asp Thr Thr Gln Ser Thr Asp Gly Glu
                250                 255                 260

cac cac atc acc att tcc cgc gaa gac ggc ggg gaa atc agc cgc acc   931
His His Ile Thr Ile Ser Arg Glu Asp Gly Gly Glu Ile Ser Arg Thr
            265                 270                 275

atc cgg gtt gat aat act gcc cca gaa ctc acc gtt tct gga gtt gaa   979
Ile Arg Val Asp Asn Thr Ala Pro Glu Leu Thr Val Ser Gly Val Glu
        280                 285                 290

gaa gga caa gaa ctg cgc ggc acc gta gaa att gat gcc cag gca acc   1027
Glu Gly Gln Glu Leu Arg Gly Thr Val Glu Ile Asp Ala Gln Ala Thr
    295                 300                 305

gat gcg ggt gcg ggc gtg aag agc gtc gag acg ctt ctc gac ggc       1072
Asp Ala Gly Ala Gly Val Lys Ser Val Glu Thr Leu Leu Asp Gly
310                 315                 320

taacgcgtgc aacttccact aac                                        1095
```

<210> 900
<211> 324
<212> PRT
<213> Corynebacterium glutamicum

<400> 900

```
Val Arg Thr Ala Thr Leu His Val Thr Ser Ser Ala Gly Glu Ala Ala
 1               5                  10                  15

Thr Thr Ile Asn Leu Thr Glu Asp Asp Gly Ser Phe Asn Trp Ala Leu
            20                  25                  30

Pro Ala Ala Asp Leu Thr Gly Lys Ser Trp Phe Glu Tyr Thr Val Thr
        35                  40                  45

Ala Thr Asp Gly Phe Asn Ser Val Thr Thr Glu Pro Val Arg Val Thr
    50                  55                  60

Val Asp Gly Ala Asn Thr Asp Pro Leu Arg Leu Asn Leu Glu Glu Asn
65                  70                  75                  80

Gln Trp Val Ser Gly Thr Thr Asp Val Ile Gly Ala Ser Asp Val Phe
                85                  90                  95

Gly Asp Lys Leu Glu Leu Leu Ile Asp Asp Ala Pro Ala Val Thr Asn
            100                 105                 110

Ser Ser Leu Ser Ala Ala Pro Thr Phe Ala Met Glu Val Thr Gln Thr
        115                 120                 125

Asp Val Phe Phe Arg Asn Gly Ile Leu Ala Gly Gly Glu Glu Leu Arg
    130                 135                 140

Ile Phe Asp Gln Gly Thr Tyr Ala Asn Thr Glu Thr Ile Ser Thr Pro
145                 150                 155                 160

Val Pro Leu Tyr His Ile Asn Glu Asp Gly Thr Leu Thr Val Ser Val
                165                 170                 175

Tyr Ala Gly Thr Lys Ala Ala Pro Glu Ile Asp Leu Asn Glu Asn Asn
            180                 185                 190

Asp Asp Phe Gln Ile Arg Asn Leu Arg Leu Ile Leu Pro Asp Gly Arg
        195                 200                 205

Thr Leu Thr Pro Ala Gly Ile Ser Asp Ser Asn Ala Trp Leu Asn Met
    210                 215                 220

Gly Asp Ser Ala Gly Lys Leu Asp Phe Phe Asp Ala Thr Phe Ala Leu
225                 230                 235                 240

Pro Glu Asp Ala Phe Thr Gly Val Ala His Ala Trp Asp Thr Thr Gln
                245                 250                 255

Ser Thr Asp Gly Glu His His Ile Thr Ile Ser Arg Glu Asp Gly Gly
            260                 265                 270

Glu Ile Ser Arg Thr Ile Arg Val Asp Asn Thr Ala Pro Glu Leu Thr
        275                 280                 285
```

```
Val Ser Gly Val Glu Glu Gly Gln Glu Leu Arg Gly Thr Val Glu Ile
    290                 295                 300

Asp Ala Gln Ala Thr Asp Ala Gly Ala Gly Val Lys Ser Val Glu Thr
305                 310                 315                 320

Leu Leu Asp Gly
```

<210> 901
<211> 407
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(384)
<223> FRXA01944

<400> 901

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atc aga aac ctt cga cta att ctg cct gat ggc cgg acc ctc acc cct   48
Ile Arg Asn Leu Arg Leu Ile Leu Pro Asp Gly Arg Thr Leu Thr Pro
  1               5                  10                  15

gcc gga att tcc gat tct aat gcg tgg ctc aac atg gga gac agc gct   96
Ala Gly Ile Ser Asp Ser Asn Ala Trp Leu Asn Met Gly Asp Ser Ala
             20                  25                  30

gga aaa ctc gat ttc ttc gat gcc acc ttc gcc ctc cct gag gat gct  144
Gly Lys Leu Asp Phe Phe Asp Ala Thr Phe Ala Leu Pro Glu Asp Ala
         35                  40                  45

ttc acc ggt gtg gca cac gca tgg gat acc acc caa agc aca gat gga  192
Phe Thr Gly Val Ala His Ala Trp Asp Thr Thr Gln Ser Thr Asp Gly
     50                  55                  60

gaa cac cac atc acc att tcc cgc gaa gac ggc ggg gaa atc agc cgc  240
Glu His His Ile Thr Ile Ser Arg Glu Asp Gly Gly Glu Ile Ser Arg
 65                  70                  75                  80

acc atc cgg gtt gat aat act gcc cca gaa ctc acc gtt tct gga gtt  288
Thr Ile Arg Val Asp Asn Thr Ala Pro Glu Leu Thr Val Ser Gly Val
                 85                  90                  95

gaa gaa gga caa gaa ctg cgc ggc acc gta gaa att gat gcc cag gca  336
Glu Glu Gly Gln Glu Leu Arg Gly Thr Val Glu Ile Asp Ala Gln Ala
            100                 105                 110

acc gat gcg ggt gcg ggc gtg aag agc gtc gag acg ctt ctc gac ggc  384
Thr Asp Ala Gly Ala Gly Val Lys Ser Val Glu Thr Leu Leu Asp Gly
        115                 120                 125

taacgcgtgc aacttccact aac                                       407
```

<210> 902
<211> 128
<212> PRT
<213> Corynebacterium glutamicum

<400> 902
Ile Arg Asn Leu Arg Leu Ile Leu Pro Asp Gly Arg Thr Leu Thr Pro
1 5 10 15

Ala Gly Ile Ser Asp Ser Asn Ala Trp Leu Asn Met Gly Asp Ser Ala
20 25 30

Gly Lys Leu Asp Phe Phe Asp Ala Thr Phe Ala Leu Pro Glu Asp Ala
35 40 45

Phe Thr Gly Val Ala His Ala Trp Asp Thr Thr Gln Ser Thr Asp Gly
50 55 60

Glu His His Ile Thr Ile Ser Arg Glu Asp Gly Gly Glu Ile Ser Arg
65 70 75 80

Thr Ile Arg Val Asp Asn Thr Ala Pro Glu Leu Thr Val Ser Gly Val
85 90 95

Glu Glu Gly Gln Glu Leu Arg Gly Thr Val Glu Ile Asp Ala Gln Ala
100 105 110

Thr Asp Ala Gly Ala Gly Val Lys Ser Val Glu Thr Leu Leu Asp Gly
115 120 125

<210> 903
<211> 673
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(673)
<223> FRXA01636

<400> 903
gctgattctt ctgtaccact catcacagat aataccgcaa ccagtatcaa ccctgcggag 60

ccgtttacct tcgccttcaa atatcaccga tgatgtccag gtg cgc acg gca aca 115
Val Arg Thr Ala Thr
1 5

ctg cat gtt act tcc agt gct ggc gaa gcc gcg aca acc atc aac ctc 163
Leu His Val Thr Ser Ser Ala Gly Glu Ala Ala Thr Thr Ile Asn Leu
10 15 20

acc gag gat gac ggc tct ttc aat tgg gct ctg cct gca gcg gat ctc 211
Thr Glu Asp Asp Gly Ser Phe Asn Trp Ala Leu Pro Ala Ala Asp Leu
25 30 35

acc gga aaa tcc tgg ttc gaa tac acc gta acc gcc acc gac gga ttc 259
Thr Gly Lys Ser Trp Phe Glu Tyr Thr Val Thr Ala Thr Asp Gly Phe
40 45 50

aac agc gtt acc acc gag ccg gta cgc gtc acc gtc gac ggc gcc aac 307
Asn Ser Val Thr Thr Glu Pro Val Arg Val Thr Val Asp Gly Ala Asn
55 60 65

```
acc gac ccg ctg cgc ctc aac ctg gaa gaa aac caa tgg gtc agt ggc   355
Thr Asp Pro Leu Arg Leu Asn Leu Glu Glu Asn Gln Trp Val Ser Gly
 70                  75                  80                  85

acc acc gat gtt atc ggt gct tca gat gtc ttc ggc gac aag ctt gaa   403
Thr Thr Asp Val Ile Gly Ala Ser Asp Val Phe Gly Asp Lys Leu Glu
                90                  95                 100

ttg ctt atc gac gac gcg cct gca gtc acc aac tcc agc ctg tct gcg   451
Leu Leu Ile Asp Asp Ala Pro Ala Val Thr Asn Ser Ser Leu Ser Ala
            105                 110                 115

gcc ccg acg ttt gcg atg gaa gta acc caa act gat gtg ttc ttc cgc   499
Ala Pro Thr Phe Ala Met Glu Val Thr Gln Thr Asp Val Phe Phe Arg
        120                 125                 130

aac ggc atc ctt gcc ggt ggg gaa gaa ctc cgc att ttc gat caa gga   547
Asn Gly Ile Leu Ala Gly Gly Glu Glu Leu Arg Ile Phe Asp Gln Gly
    135                 140                 145

act tac gcc aac acc gaa acc atc tcc aca cca gtc ccg ctg tat cac   595
Thr Tyr Ala Asn Thr Glu Thr Ile Ser Thr Pro Val Pro Leu Tyr His
150                 155                 160                 165

atc aat gag gac ggt acc ctc aca gtc agt gtg tat gcg gga act aaa   643
Ile Asn Glu Asp Gly Thr Leu Thr Val Ser Val Tyr Ala Gly Thr Lys
                170                 175                 180

gca gca cca gaa att gac ctc aac gag aac                          673
Ala Ala Pro Glu Ile Asp Leu Asn Glu Asn
            185                 190
```

5050450 "5050550

<210> 904
<211> 191
<212> PRT
<213> Corynebacterium glutamicum

<400> 904

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Val Arg Thr Ala Thr Leu His Val Thr Ser Ser Ala Gly Glu Ala Ala
  1               5                  10                  15

Thr Thr Ile Asn Leu Thr Glu Asp Asp Gly Ser Phe Asn Trp Ala Leu
             20                  25                  30

Pro Ala Ala Asp Leu Thr Gly Lys Ser Trp Phe Glu Tyr Thr Val Thr
         35                  40                  45

Ala Thr Asp Gly Phe Asn Ser Val Thr Thr Glu Pro Val Arg Val Thr
     50                  55                  60

Val Asp Gly Ala Asn Thr Asp Pro Leu Arg Leu Asn Leu Glu Glu Asn
 65                  70                  75                  80

Gln Trp Val Ser Gly Thr Thr Asp Val Ile Gly Ala Ser Asp Val Phe
                 85                  90                  95

Gly Asp Lys Leu Glu Leu Leu Ile Asp Asp Ala Pro Ala Val Thr Asn
            100                 105                 110
```

```
Ser Ser Leu Ser Ala Ala Pro Thr Phe Ala Met Glu Val Thr Gln Thr
        115                 120                 125

Asp Val Phe Phe Arg Asn Gly Ile Leu Ala Gly Gly Glu Glu Leu Arg
    130                 135                 140

Ile Phe Asp Gln Gly Thr Tyr Ala Asn Thr Glu Thr Ile Ser Thr Pro
145                 150                 155                 160

Val Pro Leu Tyr His Ile Asn Glu Asp Gly Thr Leu Thr Val Ser Val
                165                 170                 175

Tyr Ala Gly Thr Lys Ala Ala Pro Glu Ile Asp Leu Asn Glu Asn
            180                 185                 190


<210> 905
<211> 2115
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2092)
<223> RXN01945

<400> 905
agaaggacaa gaactgcgcg gcaccgtaga aattgatgcc caggcaaccg atgcgggtgc 60

gggcgtgaag agcgtcgaga cgcttctcga cggctaacgc gtg caa ctt cca cta   115
                                            Val Gln Leu Pro Leu
                                              1               5

acc acc ggt tcc atc gct ttg gat aaa ggt gaa cac acc ttg gtt atc   163
Thr Thr Gly Ser Ile Ala Leu Asp Lys Gly Glu His Thr Leu Val Ile
                 10                  15                  20

cgt gca gaa gat gaa gta gga aac cgc acc gag aaa acc atc acg ttt   211
Arg Ala Glu Asp Glu Val Gly Asn Arg Thr Glu Lys Thr Ile Thr Phe
             25                  30                  35

agc act ccg gat gaa aac ccc atc agt ggt gac tac gct cca agc aat   259
Ser Thr Pro Asp Glu Asn Pro Ile Ser Gly Asp Tyr Ala Pro Ser Asn
         40                  45                  50

ggg gcc acc gtg ggc gtc ggt gac gtt aag tta tct gca cga gca agt   307
Gly Ala Thr Val Gly Val Gly Asp Val Lys Leu Ser Ala Arg Ala Ser
     55                  60                  65

gat cca agt ggc gat act gtc aag atg acg ttc ctg gaa gcc gat tca   355
Asp Pro Ser Gly Asp Thr Val Lys Met Thr Phe Leu Glu Ala Asp Ser
 70                  75                  80                  85

cca aaa tta gat agt ggt cgc gtc cga atg tca tca gga acg gta gaa   403
Pro Lys Leu Asp Ser Gly Arg Val Arg Met Ser Ser Gly Thr Val Glu
                 90                  95                 100

gat gcc gga agt gtc tcg cgc gcc gag gcg aaa atg ttg gag agg gga   451
Asp Ala Gly Ser Val Ser Arg Ala Glu Ala Lys Met Leu Glu Arg Gly
            105                 110                 115
```

```
gac gtc gag aag cta tcc agc ctg gat ggg ctg ggc atg gaa gtt acc   499
Asp Val Glu Lys Leu Ser Ser Leu Asp Gly Leu Gly Met Glu Val Thr
        120                 125                 130

tcc gac gcc gca ctg ccg tac cag ctt ttt gaa gtc gat gcg gcg gat   547
Ser Asp Ala Ala Leu Pro Tyr Gln Leu Phe Glu Val Asp Ala Ala Asp
    135                 140                 145

gca ctc gcg gcc gac act gaa gtg cgc ctg aat tgg gcg gga tcc gcc   595
Ala Leu Ala Ala Asp Thr Glu Val Arg Leu Asn Trp Ala Gly Ser Ala
150                 155                 160                 165

gat ggt cgc gcg cag gtg atc atg tat gtt ttc gat ggc gag gcg tgg   643
Asp Gly Arg Ala Gln Val Ile Met Tyr Val Phe Asp Gly Glu Ala Trp
                170                 175                 180

gtt gag gtg gat cgt cac ttg acc ggc gat gag ctg gaa gag ttt acg   691
Val Glu Val Asp Arg His Leu Thr Gly Asp Glu Leu Glu Glu Phe Thr
            185                 190                 195

ctg cag ggc gtc gtc aat gcg gaa aaa ttt gca atc ggc ggc act gtc   739
Leu Gln Gly Val Val Asn Ala Glu Lys Phe Ala Ile Gly Gly Thr Val
        200                 205                 210

acc gta ttg att cag cac tcc gaa ggc ttc gcc ggt gcg gat cat tca   787
Thr Val Leu Ile Gln His Ser Glu Gly Phe Ala Gly Ala Asp His Ser
    215                 220                 225

act aga aat tcc gac gtg acc gca gcg cac ccg gat gat gtg gct cgc   835
Thr Arg Asn Ser Asp Val Thr Ala Ala His Pro Asp Asp Val Ala Arg
230                 235                 240                 245

tct gag tac gat ttc acc ctc gcg tgg gaa tct gac acc cag tac tac   883
Ser Glu Tyr Asp Phe Thr Leu Ala Trp Glu Ser Asp Thr Gln Tyr Tyr
                250                 255                 260

aac gag gaa ttc cac gag cac caa acc aac atc cat gac tac gtg ctc   931
Asn Glu Glu Phe His Glu His Gln Thr Asn Ile His Asp Tyr Val Leu
            265                 270                 275

gcc gaa cgg gag aac aag aat att cag ttc atg ttc cac act ggc gat   979
Ala Glu Arg Glu Asn Lys Asn Ile Gln Phe Met Phe His Thr Gly Asp
        280                 285                 290

gtt gtc gac gac tgg gat cag ccc gcg cag tgg gcc aca gcc aac ccc   1027
Val Val Asp Asp Trp Asp Gln Pro Ala Gln Trp Ala Thr Ala Asn Pro
    295                 300                 305

gaa tac cag cgc ctc gac gac gcc ggc ctg cca tat tct gtc ctt gcc   1075
Glu Tyr Gln Arg Leu Asp Asp Ala Gly Leu Pro Tyr Ser Val Leu Ala
310                 315                 320                 325

gga aac cac gat gtt ggc cac acc agc aat gac tac acc gaa ttc agc   1123
Gly Asn His Asp Val Gly His Thr Ser Asn Asp Tyr Thr Glu Phe Ser
                330                 335                 340

cga cac ttc ggc gaa cag cgc tac gta gac aac ccg tgg tac ggc gaa   1171
Arg His Phe Gly Glu Gln Arg Tyr Val Asp Asn Pro Trp Tyr Gly Glu
            345                 350                 355

tcc tac caa gac aac cga ggg cac tac gat cta ttt tct gcc ggc gga   1219
```

```
Ser Tyr Gln Asp Asn Arg Gly His Tyr Asp Leu Phe Ser Ala Gly Gly
        360                 365                 370

att gac ttc att aac gta gcg atg ggc tgg ggt cca gac gac gaa gaa   1267
Ile Asp Phe Ile Asn Val Ala Met Gly Trp Gly Pro Asp Asp Glu Glu
    375                 380                 385

atc gcg tgg atg aac gag gtc ctg gcc aag cat ccc gag cgt gtg gcg   1315
Ile Ala Trp Met Asn Glu Val Leu Ala Lys His Pro Glu Arg Val Ala
390                 395                 400                 405

atc ctc aac ctc cac gaa ttc atg ctc acc acc ggc gga ctt ggc ccg   1363
Ile Leu Asn Leu His Glu Phe Met Leu Thr Thr Gly Gly Leu Gly Pro
                410                 415                 420

atc ccg cag cgc att ctc gac gag gtc gca gcc acc aac cca aat gtc   1411
Ile Pro Gln Arg Ile Leu Asp Glu Val Ala Ala Thr Asn Pro Asn Val
            425                 430                 435

agc atg atc atg tcc ggc cac tac cac gac gca ttc caa cgc acc gac   1459
Ser Met Ile Met Ser Gly His Tyr His Asp Ala Phe Gln Arg Thr Asp
        440                 445                 450

tcc ttt gac gac gat ggt gat gga gta gat gac cgc acc gtc acc tct   1507
Ser Phe Asp Asp Asp Gly Asp Gly Val Asp Asp Arg Thr Val Thr Ser
    455                 460                 465

atg ctt ttc gat tac caa ggc cta ccg gag ggc gga cag ggg tac ctc   1555
Met Leu Phe Asp Tyr Gln Gly Leu Pro Glu Gly Gly Gln Gly Tyr Leu
470                 475                 480                 485

cga ctt ctc cac ttt gat aac caa ggc caa aag atg atg gtg cgc acc   1603
Arg Leu Leu His Phe Asp Asn Gln Gly Gln Lys Met Met Val Arg Thr
                490                 495                 500

tat tca cca tcc ctg aag gat tac aac tct gat gaa ccc tca ctg ttg   1651
Tyr Ser Pro Ser Leu Lys Asp Tyr Asn Ser Asp Glu Pro Ser Leu Leu
            505                 510                 515

ggg cct gca gaa gac ccc aac atg tat caa gaa ttc gaa gtg tcc tac   1699
Gly Pro Ala Glu Asp Pro Asn Met Tyr Gln Glu Phe Glu Val Ser Tyr
        520                 525                 530

gag cag ctc ggc atc aaa cca gag ggc cgc acc ctg atc ggc gat tcc   1747
Glu Gln Leu Gly Ile Lys Pro Glu Gly Arg Thr Leu Ile Gly Asp Ser
    535                 540                 545

ttc agc gcc gat ttc ttg acc tcc aat gaa att gga ata gtt gat gag   1795
Phe Ser Ala Asp Phe Leu Thr Ser Asn Glu Ile Gly Ile Val Asp Glu
550                 555                 560                 565

gtt cct tct gga acg atc gct ttc acg aac tgg aag gac gta acc gaa   1843
Val Pro Ser Gly Thr Ile Ala Phe Thr Asn Trp Lys Asp Val Thr Glu
                570                 575                 580

ggt cgc cac agt tgg tat gtt cgc tcc gag gat cct ttc ggc ggc gtc   1891
Gly Arg His Ser Trp Tyr Val Arg Ser Glu Asp Pro Phe Gly Gly Val
            585                 590                 595

gag att tca ccc gtg cag tcc ttc att gcc ggg gaa gag gct ggc ggg   1939
Glu Ile Ser Pro Val Gln Ser Phe Ile Ala Gly Glu Glu Ala Gly Gly
```

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        600                 605                 610

aac gcg ccc ggc act gga agc tcc aat ggc ggt tca tcc cac gga tta   1987
Asn Ala Pro Gly Thr Gly Ser Ser Asn Gly Gly Ser Ser His Gly Leu
    615                 620                 625

tgg ggt gcg ctt gcg gaa ttc ttt gcc gga gcg gca gcc ctg gct gga   2035
Trp Gly Ala Leu Ala Glu Phe Phe Ala Gly Ala Ala Ala Leu Ala Gly
630                 635                 640                 645

gct gcg atc gca ttt gtc ccc gga att tgg gac tat gtg acc aac gca   2083
Ala Ala Ile Ala Phe Val Pro Gly Ile Trp Asp Tyr Val Thr Asn Ala
                650                 655                 660

ttc aag cga taattatgga taggtaaacg ctc                            2115
Phe Lys Arg
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<210> 906
<211> 664
<212> PRT
<213> Corynebacterium glutamicum

<400> 906

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Val Gln Leu Pro Leu Thr Thr Gly Ser Ile Ala Leu Asp Lys Gly Glu
  1               5                  10                  15

His Thr Leu Val Ile Arg Ala Glu Asp Glu Val Gly Asn Arg Thr Glu
             20                  25                  30

Lys Thr Ile Thr Phe Ser Thr Pro Asp Glu Asn Pro Ile Ser Gly Asp
         35                  40                  45

Tyr Ala Pro Ser Asn Gly Ala Thr Val Gly Val Gly Asp Val Lys Leu
     50                  55                  60

Ser Ala Arg Ala Ser Asp Pro Ser Gly Asp Thr Val Lys Met Thr Phe
 65                  70                  75                  80

Leu Glu Ala Asp Ser Pro Lys Leu Asp Ser Gly Arg Val Arg Met Ser
                 85                  90                  95

Ser Gly Thr Val Glu Asp Ala Gly Ser Val Ser Arg Ala Glu Ala Lys
            100                 105                 110

Met Leu Glu Arg Gly Asp Val Glu Lys Leu Ser Ser Leu Asp Gly Leu
        115                 120                 125

Gly Met Glu Val Thr Ser Asp Ala Ala Leu Pro Tyr Gln Leu Phe Glu
    130                 135                 140

Val Asp Ala Ala Asp Ala Leu Ala Ala Asp Thr Glu Val Arg Leu Asn
145                 150                 155                 160

Trp Ala Gly Ser Ala Asp Gly Arg Ala Gln Val Ile Met Tyr Val Phe
                165                 170                 175

Asp Gly Glu Ala Trp Val Glu Val Asp Arg His Leu Thr Gly Asp Glu
            180                 185                 190
```

```
Leu Glu Glu Phe Thr Leu Gln Gly Val Val Asn Ala Glu Lys Phe Ala
        195                 200                 205

Ile Gly Gly Thr Val Thr Val Leu Ile Gln His Ser Glu Gly Phe Ala
    210                 215                 220

Gly Ala Asp His Ser Thr Arg Asn Ser Asp Val Thr Ala Ala His Pro
225                 230                 235                 240

Asp Asp Val Ala Arg Ser Glu Tyr Asp Phe Thr Leu Ala Trp Glu Ser
                245                 250                 255

Asp Thr Gln Tyr Tyr Asn Glu Glu Phe His Glu His Gln Thr Asn Ile
            260                 265                 270

His Asp Tyr Val Leu Ala Glu Arg Glu Asn Lys Asn Ile Gln Phe Met
        275                 280                 285

Phe His Thr Gly Asp Val Val Asp Asp Trp Asp Gln Pro Ala Gln Trp
    290                 295                 300

Ala Thr Ala Asn Pro Glu Tyr Gln Arg Leu Asp Asp Ala Gly Leu Pro
305                 310                 315                 320

Tyr Ser Val Leu Ala Gly Asn His Asp Val Gly His Thr Ser Asn Asp
                325                 330                 335

Tyr Thr Glu Phe Ser Arg His Phe Gly Glu Gln Arg Tyr Val Asp Asn
            340                 345                 350

Pro Trp Tyr Gly Glu Ser Tyr Gln Asp Asn Arg Gly His Tyr Asp Leu
        355                 360                 365

Phe Ser Ala Gly Gly Ile Asp Phe Ile Asn Val Ala Met Gly Trp Gly
    370                 375                 380

Pro Asp Asp Glu Glu Ile Ala Trp Met Asn Glu Val Leu Ala Lys His
385                 390                 395                 400

Pro Glu Arg Val Ala Ile Leu Asn Leu His Glu Phe Met Leu Thr Thr
                405                 410                 415

Gly Gly Leu Gly Pro Ile Pro Gln Arg Ile Leu Asp Glu Val Ala Ala
            420                 425                 430

Thr Asn Pro Asn Val Ser Met Ile Met Ser Gly His Tyr His Asp Ala
        435                 440                 445

Phe Gln Arg Thr Asp Ser Phe Asp Asp Asp Gly Asp Gly Val Asp Asp
    450                 455                 460

Arg Thr Val Thr Ser Met Leu Phe Asp Tyr Gln Gly Leu Pro Glu Gly
465                 470                 475                 480

Gly Gln Gly Tyr Leu Arg Leu Leu His Phe Asp Asn Gln Gly Gln Lys
                485                 490                 495

Met Met Val Arg Thr Tyr Ser Pro Ser Leu Lys Asp Tyr Asn Ser Asp
            500                 505                 510

Glu Pro Ser Leu Leu Gly Pro Ala Glu Asp Pro Asn Met Tyr Gln Glu
```

```
        515                 520                 525

Phe Glu Val Ser Tyr Glu Gln Leu Gly Ile Lys Pro Glu Gly Arg Thr
    530                 535                 540

Leu Ile Gly Asp Ser Phe Ser Ala Asp Phe Leu Thr Ser Asn Glu Ile
545                 550                 555                 560

Gly Ile Val Asp Glu Val Pro Ser Gly Thr Ile Ala Phe Thr Asn Trp
                565                 570                 575

Lys Asp Val Thr Glu Gly Arg His Ser Trp Tyr Val Arg Ser Glu Asp
            580                 585                 590

Pro Phe Gly Gly Val Glu Ile Ser Pro Val Gln Ser Phe Ile Ala Gly
        595                 600                 605

Glu Glu Ala Gly Gly Asn Ala Pro Gly Thr Gly Ser Ser Asn Gly Gly
    610                 615                 620

Ser Ser His Gly Leu Trp Gly Ala Leu Ala Glu Phe Phe Ala Gly Ala
625                 630                 635                 640

Ala Ala Leu Ala Gly Ala Ala Ile Ala Phe Val Pro Gly Ile Trp Asp
                645                 650                 655

Tyr Val Thr Asn Ala Phe Lys Arg
            660


<210> 907
<211> 1342
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1342)
<223> FRXA01945

<400> 907
agaaggacaa gaactgcgcg gcaccgtaga aattgatgcc caggcaaccg atgcgggtgc 60

gggcgtgaag agcgtcgaga cgcttctcga cggctaacgc gtg caa ctt cca cta   115
                                            Val Gln Leu Pro Leu
                                              1               5

acc acc ggt tcc atc gct ttg gat aaa ggt gaa cac acc ttg gtt atc   163
Thr Thr Gly Ser Ile Ala Leu Asp Lys Gly Glu His Thr Leu Val Ile
                 10                  15                  20

cgt gca gaa gat gaa gta gga aac cgc acc gag aaa acc atc acg ttt   211
Arg Ala Glu Asp Glu Val Gly Asn Arg Thr Glu Lys Thr Ile Thr Phe
             25                  30                  35

agc act ccg gat gaa aac ccc atc agt ggt gac tac gct cca agc aat   259
Ser Thr Pro Asp Glu Asn Pro Ile Ser Gly Asp Tyr Ala Pro Ser Asn
         40                  45                  50

ggg gcc acc gtg ggc gtc ggt gac gtt aag tta tct gca cga gca agt   307
Gly Ala Thr Val Gly Val Gly Asp Val Lys Leu Ser Ala Arg Ala Ser
```

```
     55                  60                  65

gat cca agt ggc gat act gtc aag atg acg ttc ctg gaa gcc gat tca   355
Asp Pro Ser Gly Asp Thr Val Lys Met Thr Phe Leu Glu Ala Asp Ser
 70                  75                  80                  85

cca aaa tta gat agt ggt cgc gtc cga atg tca tca gga acg gta gaa   403
Pro Lys Leu Asp Ser Gly Arg Val Arg Met Ser Ser Gly Thr Val Glu
                 90                  95                 100

gat gcc gga agt gtc tcg cgc gcc gag gcg aaa atg ttg gag agg gga   451
Asp Ala Gly Ser Val Ser Arg Ala Glu Ala Lys Met Leu Glu Arg Gly
            105                 110                 115

gac gtc gag aag cta tcc agc ctg gat ggg ctg ggc atg gaa gtt acc   499
Asp Val Glu Lys Leu Ser Ser Leu Asp Gly Leu Gly Met Glu Val Thr
        120                 125                 130

tcc gac gcc gca ctg ccg tac cag ctt ttt gaa gtc gat gcg gcg gat   547
Ser Asp Ala Ala Leu Pro Tyr Gln Leu Phe Glu Val Asp Ala Ala Asp
    135                 140                 145

gca ctc gcg gcc gac act gaa gtg cgc ctg aat tgg gcg gga tcc gcc   595
Ala Leu Ala Ala Asp Thr Glu Val Arg Leu Asn Trp Ala Gly Ser Ala
150                 155                 160                 165

gat ggt cgc gcg cag gtg atc atg tat gtt ttc gat ggc gag gcg tgg   643
Asp Gly Arg Ala Gln Val Ile Met Tyr Val Phe Asp Gly Glu Ala Trp
                170                 175                 180

gtt gag gtg gat cgt cac ttg acc ggc gat gag ctg gaa gag ttt acg   691
Val Glu Val Asp Arg His Leu Thr Gly Asp Glu Leu Glu Glu Phe Thr
            185                 190                 195

ctg cag ggc gtc gtc aat gcg gaa aaa ttt gca atc ggc ggc act gtc   739
Leu Gln Gly Val Val Asn Ala Glu Lys Phe Ala Ile Gly Gly Thr Val
        200                 205                 210

acc gta ttg att cag cac tcc gaa ggc ttc gcc ggt gcg gat cat tca   787
Thr Val Leu Ile Gln His Ser Glu Gly Phe Ala Gly Ala Asp His Ser
    215                 220                 225

act aga aat tcc gac gtg acc gca gcg cac ccg gat gat gtg gct cgc   835
Thr Arg Asn Ser Asp Val Thr Ala Ala His Pro Asp Asp Val Ala Arg
230                 235                 240                 245

tct gag tac gat ttc acc ctc gcg tgg gaa tct gac acc cag tac tac   883
Ser Glu Tyr Asp Phe Thr Leu Ala Trp Glu Ser Asp Thr Gln Tyr Tyr
                250                 255                 260

aac gag gaa ttc cac gag cac caa acc aac atc cat gac tac gtg ctc   931
Asn Glu Glu Phe His Glu His Gln Thr Asn Ile His Asp Tyr Val Leu
            265                 270                 275

gcc gaa cgg gag aac aag aat att cag ttc atg ttc cac act ggc gat   979
Ala Glu Arg Glu Asn Lys Asn Ile Gln Phe Met Phe His Thr Gly Asp
        280                 285                 290

gtt gtc gac gac tgg gat cag ccc gcg cag tgg gcc aca gcc aac ccc  1027
Val Val Asp Asp Trp Asp Gln Pro Ala Gln Trp Ala Thr Ala Asn Pro
    295                 300                 305
```

```
gaa tac cag cgc ctc gac gac gcc ggc ctg cca tat tct gtc ctt gcc   1075
Glu Tyr Gln Arg Leu Asp Asp Ala Gly Leu Pro Tyr Ser Val Leu Ala
310                 315                 320                 325

gga aac cac gat gtt ggc cac acc agc aat gac tac acc gaa ttc agc   1123
Gly Asn His Asp Val Gly His Thr Ser Asn Asp Tyr Thr Glu Phe Ser
                330                 335                 340

cga cac ttc ggc gaa cag cgc tac gta gac aac ccg tgg tac ggc gaa   1171
Arg His Phe Gly Glu Gln Arg Tyr Val Asp Asn Pro Trp Tyr Gly Glu
            345                 350                 355

tcc tac caa gac aac cga ggg cac tac gat cta ttt tct gcc ggc gga   1219
Ser Tyr Gln Asp Asn Arg Gly His Tyr Asp Leu Phe Ser Ala Gly Gly
        360                 365                 370

att gac ttc att aac gta gcg atg ggc tgg ggt cca gac gac gaa gaa   1267
Ile Asp Phe Ile Asn Val Ala Met Gly Trp Gly Pro Asp Asp Glu Glu
    375                 380                 385

atc gcg tgg atg aac gag gtc ctg gcc aag cat ccc gag cgt gtg gcg   1315
Ile Ala Trp Met Asn Glu Val Leu Ala Lys His Pro Glu Arg Val Ala
390                 395                 400                 405

atc ctc aac ctc cac gaa ttc atg ctc                              1342
Ile Leu Asn Leu His Glu Phe Met Leu
                410
```

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<210> 908
<211> 414
<212> PRT
<213> Corynebacterium glutamicum

<400> 908

```
Val Gln Leu Pro Leu Thr Thr Gly Ser Ile Ala Leu Asp Lys Gly Glu
  1               5                  10                  15

His Thr Leu Val Ile Arg Ala Glu Asp Glu Val Gly Asn Arg Thr Glu
             20                  25                  30

Lys Thr Ile Thr Phe Ser Thr Pro Asp Glu Asn Pro Ile Ser Gly Asp
         35                  40                  45

Tyr Ala Pro Ser Asn Gly Ala Thr Val Gly Val Gly Asp Val Lys Leu
     50                  55                  60

Ser Ala Arg Ala Ser Asp Pro Ser Gly Asp Thr Val Lys Met Thr Phe
 65                  70                  75                  80

Leu Glu Ala Asp Ser Pro Lys Leu Asp Ser Gly Arg Val Arg Met Ser
                 85                  90                  95

Ser Gly Thr Val Glu Asp Ala Gly Ser Val Ser Arg Ala Glu Ala Lys
            100                 105                 110

Met Leu Glu Arg Gly Asp Val Glu Lys Leu Ser Ser Leu Asp Gly Leu
        115                 120                 125

Gly Met Glu Val Thr Ser Asp Ala Ala Leu Pro Tyr Gln Leu Phe Glu
```

```
    130                 135                 140

Val Asp Ala Ala Asp Ala Leu Ala Ala Asp Thr Glu Val Arg Leu Asn
145                 150                 155                 160

Trp Ala Gly Ser Ala Asp Gly Arg Ala Gln Val Ile Met Tyr Val Phe
                165                 170                 175

Asp Gly Glu Ala Trp Val Glu Val Asp Arg His Leu Thr Gly Asp Glu
            180                 185                 190

Leu Glu Glu Phe Thr Leu Gln Gly Val Val Asn Ala Glu Lys Phe Ala
        195                 200                 205

Ile Gly Gly Thr Val Thr Val Leu Ile Gln His Ser Glu Gly Phe Ala
    210                 215                 220

Gly Ala Asp His Ser Thr Arg Asn Ser Asp Val Thr Ala Ala His Pro
225                 230                 235                 240

Asp Asp Val Ala Arg Ser Glu Tyr Asp Phe Thr Leu Ala Trp Glu Ser
                245                 250                 255

Asp Thr Gln Tyr Tyr Asn Glu Glu Phe His Glu His Gln Thr Asn Ile
            260                 265                 270

His Asp Tyr Val Leu Ala Glu Arg Glu Asn Lys Asn Ile Gln Phe Met
        275                 280                 285

Phe His Thr Gly Asp Val Val Asp Asp Trp Asp Gln Pro Ala Gln Trp
    290                 295                 300

Ala Thr Ala Asn Pro Glu Tyr Gln Arg Leu Asp Asp Ala Gly Leu Pro
305                 310                 315                 320

Tyr Ser Val Leu Ala Gly Asn His Asp Val Gly His Thr Ser Asn Asp
                325                 330                 335

Tyr Thr Glu Phe Ser Arg His Phe Gly Glu Gln Arg Tyr Val Asp Asn
            340                 345                 350

Pro Trp Tyr Gly Glu Ser Tyr Gln Asp Asn Arg Gly His Tyr Asp Leu
        355                 360                 365

Phe Ser Ala Gly Gly Ile Asp Phe Ile Asn Val Ala Met Gly Trp Gly
    370                 375                 380

Pro Asp Asp Glu Glu Ile Ala Trp Met Asn Glu Val Leu Ala Lys His
385                 390                 395                 400

Pro Glu Arg Val Ala Ile Leu Asn Leu His Glu Phe Met Leu
                405                 410
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<210> 909
<211> 518
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (1)..(495)
<223> FRXA01627

<400> 909
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cgc acc tat tca cca tcc ctg aag gat tac aac tct gat gaa ccc tca   48
Arg Thr Tyr Ser Pro Ser Leu Lys Asp Tyr Asn Ser Asp Glu Pro Ser
  1               5                  10                  15

ctg ttg ggg cct gca gaa gac ccc aac atg tat caa gaa ttc gaa gtg   96
Leu Leu Gly Pro Ala Glu Asp Pro Asn Met Tyr Gln Glu Phe Glu Val
             20                  25                  30

tcc tac gag cag ctc ggc atc aaa cca gag ggc cgc acc ctg atc ggc   144
Ser Tyr Glu Gln Leu Gly Ile Lys Pro Glu Gly Arg Thr Leu Ile Gly
         35                  40                  45

gat tcc ttc agc gcc gat ttc ttg acc tcc aat gaa att gga ata gtt   192
Asp Ser Phe Ser Ala Asp Phe Leu Thr Ser Asn Glu Ile Gly Ile Val
     50                  55                  60

gat gag gtt cct tct gga acg atc gct ttc acg aac tgg aag gac gta   240
Asp Glu Val Pro Ser Gly Thr Ile Ala Phe Thr Asn Trp Lys Asp Val
 65                  70                  75                  80

acc gaa ggt cgc cac agt tgg tat gtt cgc tcc gag gat cct ttc ggc   288
Thr Glu Gly Arg His Ser Trp Tyr Val Arg Ser Glu Asp Pro Phe Gly
                 85                  90                  95

ggc gtc gag att tca ccc gtg cag tcc ttc att gcc ggg gaa gag gct   336
Gly Val Glu Ile Ser Pro Val Gln Ser Phe Ile Ala Gly Glu Glu Ala
            100                 105                 110

ggc ggg aac gcg ccc ggc act gga agc tcc aat ggc ggt tca tcc cac   384
Gly Gly Asn Ala Pro Gly Thr Gly Ser Ser Asn Gly Gly Ser Ser His
        115                 120                 125

gga tta tgg ggt gcg ctt gcg gaa ttc ttt gcc gga gcg gca gcc ctg   432
Gly Leu Trp Gly Ala Leu Ala Glu Phe Phe Ala Gly Ala Ala Ala Leu
    130                 135                 140

gct gga gct gcg atc gca ttt gtc ccc gga att tgg gac tat gtg acc   480
Ala Gly Ala Ala Ile Ala Phe Val Pro Gly Ile Trp Asp Tyr Val Thr
145                 150                 155                 160

aac gca ttc aag cga taattatgga taggtaaacg ctc                    518
Asn Ala Phe Lys Arg
                165
```

<210> 910
<211> 165
<212> PRT
<213> Corynebacterium glutamicum

<400> 910
```
Arg Thr Tyr Ser Pro Ser Leu Lys Asp Tyr Asn Ser Asp Glu Pro Ser
  1               5                  10                  15

Leu Leu Gly Pro Ala Glu Asp Pro Asn Met Tyr Gln Glu Phe Glu Val
             20                  25                  30
```

```
Ser Tyr Glu Gln Leu Gly Ile Lys Pro Glu Gly Arg Thr Leu Ile Gly
         35                  40                  45

Asp Ser Phe Ser Ala Asp Phe Leu Thr Ser Asn Glu Ile Gly Ile Val
     50                  55                  60

Asp Glu Val Pro Ser Gly Thr Ile Ala Phe Thr Asn Trp Lys Asp Val
 65                  70                  75                  80

Thr Glu Gly Arg His Ser Trp Tyr Val Arg Ser Glu Asp Pro Phe Gly
                 85                  90                  95

Gly Val Glu Ile Ser Pro Val Gln Ser Phe Ile Ala Gly Glu Glu Ala
            100                 105                 110

Gly Gly Asn Ala Pro Gly Thr Gly Ser Ser Asn Gly Gly Ser Ser His
        115                 120                 125

Gly Leu Trp Gly Ala Leu Ala Glu Phe Phe Ala Gly Ala Ala Ala Leu
    130                 135                 140

Ala Gly Ala Ala Ile Ala Phe Val Pro Gly Ile Trp Asp Tyr Val Thr
145                 150                 155                 160

Asn Ala Phe Lys Arg
                165
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20050037360

<210> 911
<211> 441
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(418)
<223> RXN01960

<400> 911

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tccagattga tcgtgccaac aaagactaag ccactctagc taaaccaact taccccaccc 60

caacacccca tgaggcatct gcttcatggg gtgttttgct atg ccg caa cac ttt   115
                                              Met Pro Gln His Phe
                                                1               5

tct caa gaa aac tac aga aag gcc ccc gtc att atg tct gca ccg ctc   163
Ser Gln Glu Asn Tyr Arg Lys Ala Pro Val Ile Met Ser Ala Pro Leu
                 10                  15                  20

acc att cat gat ctg ctg tcc acc aat tcg aag ctt aac ctc aag tgg   211
Thr Ile His Asp Leu Leu Ser Thr Asn Ser Lys Leu Asn Leu Lys Trp
             25                  30                  35

ctg acc tgc act gtc ttg aac agc cca aat ctc acc gaa ccc tgc atc   259
Leu Thr Cys Thr Val Leu Asn Ser Pro Asn Leu Thr Glu Pro Cys Ile
         40                  45                  50

acg gtt tct gtg aac cac acc gaa ggc atg tcc ctg gtc tct ttc gaa   307
Thr Val Ser Val Asn His Thr Glu Gly Met Ser Leu Val Ser Phe Glu
     55                  60                  65
```

```
ggt ggt cac ggg ctc acc gag att gcc aac acc cag cta gtg cct gtg   355
Gly Gly His Gly Leu Thr Glu Ile Ala Asn Thr Gln Leu Val Pro Val
 70                  75                  80                  85

ctt gag cta cca aag ttc aat cct ttt gag gca ctt gct atc cac ctt   403
Leu Glu Leu Pro Lys Phe Asn Pro Phe Glu Ala Leu Ala Ile His Leu
                 90                  95                 100

gaa gcc gcc aac aac taagaaagca tccttcatga ctg                    441
Glu Ala Ala Asn Asn
            105
```

<210> 912
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 912

```
Met Pro Gln His Phe Ser Gln Glu Asn Tyr Arg Lys Ala Pro Val Ile
  1               5                  10                  15

Met Ser Ala Pro Leu Thr Ile His Asp Leu Leu Ser Thr Asn Ser Lys
             20                  25                  30

Leu Asn Leu Lys Trp Leu Thr Cys Thr Val Leu Asn Ser Pro Asn Leu
         35                  40                  45

Thr Glu Pro Cys Ile Thr Val Ser Val Asn His Thr Glu Gly Met Ser
     50                  55                  60

Leu Val Ser Phe Glu Gly Gly His Gly Leu Thr Glu Ile Ala Asn Thr
 65                  70                  75                  80

Gln Leu Val Pro Val Leu Glu Leu Pro Lys Phe Asn Pro Phe Glu Ala
                 85                  90                  95

Leu Ala Ile His Leu Glu Ala Ala Asn Asn
            100                 105
```

<210> 913
<211> 441
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(418)
<223> FRXA01960

<400> 913

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tccagattga tcgtgccaac aaagactaag ccactctagc taaaccaact taccccaccc 60

caacacccca tgaggcatct gcttcatggg gtgttttgct atg ccg caa cac ttt   115
                                               Met Pro Gln His Phe
                                                 1               5

tct caa gaa aac tac aga aag gcc ccc gtc att atg tct gca ccg ctc   163
Ser Gln Glu Asn Tyr Arg Lys Ala Pro Val Ile Met Ser Ala Pro Leu
                 10                  15                  20
```

```
acc att cat gat ctg ctg tcc acc aat tcg aag ctt aac ctc aag tgg   211
Thr Ile His Asp Leu Leu Ser Thr Asn Ser Lys Leu Asn Leu Lys Trp
             25                  30                  35

ctg acc tgc act gtc ttg aac agc cca aat ctc ccc gaa ccc tgc atc   259
Leu Thr Cys Thr Val Leu Asn Ser Pro Asn Leu Pro Glu Pro Cys Ile
         40                  45                  50

acg gtt tct gtg aac cac acc gaa ggc atg tcc ctg gtc tct ttc gaa   307
Thr Val Ser Val Asn His Thr Glu Gly Met Ser Leu Val Ser Phe Glu
     55                  60                  65

ggt ggt cac ggg ctc acc gag att gcc aac acc cag cta gtg cct gtg   355
Gly Gly His Gly Leu Thr Glu Ile Ala Asn Thr Gln Leu Val Pro Val
 70                  75                  80                  85

ctt gag cta cca aag ttc aat cct ttt gag gca ctt gct atc cac ctt   403
Leu Glu Leu Pro Lys Phe Asn Pro Phe Glu Ala Leu Ala Ile His Leu
                 90                  95                 100

gaa gcc gcc aac aac taagaaagca tccttcatga ctg                    441
Glu Ala Ala Asn Asn
            105
```

<210> 914
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 914

```
Met Pro Gln His Phe Ser Gln Glu Asn Tyr Arg Lys Ala Pro Val Ile
  1               5                  10                  15

Met Ser Ala Pro Leu Thr Ile His Asp Leu Leu Ser Thr Asn Ser Lys
             20                  25                  30

Leu Asn Leu Lys Trp Leu Thr Cys Thr Val Leu Asn Ser Pro Asn Leu
         35                  40                  45

Pro Glu Pro Cys Ile Thr Val Ser Val Asn His Thr Glu Gly Met Ser
     50                  55                  60

Leu Val Ser Phe Glu Gly Gly His Gly Leu Thr Glu Ile Ala Asn Thr
 65                  70                  75                  80

Gln Leu Val Pro Val Leu Glu Leu Pro Lys Phe Asn Pro Phe Glu Ala
                 85                  90                  95

Leu Ala Ile His Leu Glu Ala Ala Asn Asn
            100                 105
```

<210> 915
<211> 1173
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(1150)
<223> RXN01985

<400> 915
gacgtgagac atttcctcca atacctctcc agtgatattc tgtcgggcag cctaacctaa 60

gttattccgt tgttgttcga gaaagagaga gaaacttttc atg cgt acg tct cgc 115
Met Arg Thr Ser Arg
1 5

gtt cta gcc ggc att ctt gcc gca acc ctc acg gtg tcc ctc gcg gcc 163
Val Leu Ala Gly Ile Leu Ala Ala Thr Leu Thr Val Ser Leu Ala Ala
10 15 20

tgc tcc cag gat tct tca gaa acg tcc tcc aat tcg tct tca gca gca 211
Cys Ser Gln Asp Ser Ser Glu Thr Ser Ser Asn Ser Ser Ser Ala Ala
25 30 35

tcc caa agc tct gac gtt tcc aac gag gcg ttc cct gtc acc att gag 259
Ser Gln Ser Ser Asp Val Ser Asn Glu Ala Phe Pro Val Thr Ile Glu
40 45 50

cac gct ttc ggc gag acc acc att gag tcc aag cca gaa cgc atc gca 307
His Ala Phe Gly Glu Thr Thr Ile Glu Ser Lys Pro Glu Arg Ile Ala
55 60 65

act gtt ggc tgg tcc aac cat gaa gtc cct ctc gca ttg ggt gtg act 355
Thr Val Gly Trp Ser Asn His Glu Val Pro Leu Ala Leu Gly Val Thr
70 75 80 85

cct gtc ggc ttt gag aag gtc acg tgg ggc gac gat gac aac aac ggc 403
Pro Val Gly Phe Glu Lys Val Thr Trp Gly Asp Asp Asp Asn Asn Gly
90 95 100

atc ttg cca tgg gtg gaa gaa acc ttg agc aag ctc ggc tcc gat gag 451
Ile Leu Pro Trp Val Glu Glu Thr Leu Ser Lys Leu Gly Ser Asp Glu
105 110 115

cct gtg ctt ttc gat gcc acc gat tcc att cct ttt gag gag atc gcc 499
Pro Val Leu Phe Asp Ala Thr Asp Ser Ile Pro Phe Glu Glu Ile Ala
120 125 130

aac act gct ccg gat gtc att ttg gcg tcc tac tct ggc atc acc cag 547
Asn Thr Ala Pro Asp Val Ile Leu Ala Ser Tyr Ser Gly Ile Thr Gln
135 140 145

gaa gac tac gat cag ctg tcc cag atc gca cct gtg gtt gcc tac cca 595
Glu Asp Tyr Asp Gln Leu Ser Gln Ile Ala Pro Val Val Ala Tyr Pro
150 155 160 165

gaa atc gca tgg ggc acc tcc ctg gat gaa atg att gag atg aac tct 643
Glu Ile Ala Trp Gly Thr Ser Leu Asp Glu Met Ile Glu Met Asn Ser
170 175 180

aag gcg att ggc ttg gag caa gaa ggc aag gat ctc atc gca gat ctg 691
Lys Ala Ile Gly Leu Glu Gln Glu Gly Lys Asp Leu Ile Ala Asp Leu
185 190 195

gat gca gag gtt gct tcc gcc atc gat gcc aac cca gag ttg aag gat 739
Asp Ala Glu Val Ala Ser Ala Ile Asp Ala Asn Pro Glu Leu Lys Asp
200 205 210

```
gcg aag cct gta ttc gcg ttc ttc gat gag agc gat ttc tcg cag att   787
Ala Lys Pro Val Phe Ala Phe Phe Asp Glu Ser Asp Phe Ser Gln Ile
    215                 220                 225

ggt gtg tac acc agc att gat cct cgc atg agc ttc ttg ctt gat gcg   835
Gly Val Tyr Thr Ser Ile Asp Pro Arg Met Ser Phe Leu Leu Asp Ala
230                 235                 240                 245

ggt gtc cag gaa gct tca gtc ctc aag gag cac tcc agc cca gat agc   883
Gly Val Gln Glu Ala Ser Val Leu Lys Glu His Ser Ser Pro Asp Ser
                250                 255                 260

ttc tac gag cag gtt tct gca gaa aac cct gaa acc ttc gac gat gtt   931
Phe Tyr Glu Gln Val Ser Ala Glu Asn Pro Glu Thr Phe Asp Asp Val
            265                 270                 275

gat gtg atc atc acc tac ggc acc gaa gat gat gct gca aac gct gag   979
Asp Val Ile Ile Thr Tyr Gly Thr Glu Asp Asp Ala Ala Asn Ala Glu
        280                 285                 290

ctg ttg tcc aag atg cag gct gat cca ctg ctg tct cga atc cca gct   1027
Leu Leu Ser Lys Met Gln Ala Asp Pro Leu Leu Ser Arg Ile Pro Ala
    295                 300                 305

atc gcc gag ggc aag gtt gtg ttc ttg ggt gct aac cca ctg gct gct   1075
Ile Ala Glu Gly Lys Val Val Phe Leu Gly Ala Asn Pro Leu Ala Ala
310                 315                 320                 325

tca gcg aat gaa tcc cca cta tct att cct tgg ggt atc aac gat tac   1123
Ser Ala Asn Glu Ser Pro Leu Ser Ile Pro Trp Gly Ile Asn Asp Tyr
                330                 335                 340

ttt gca aaa ctc gcc gaa cct ctg aag taaaactgct tgatgtcaac         1170
Phe Ala Lys Leu Ala Glu Pro Leu Lys
            345                 350

aac                                                              1173
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<210> 916
<211> 350
<212> PRT
<213> Corynebacterium glutamicum

<400> 916

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Met Arg Thr Ser Arg Val Leu Ala Gly Ile Leu Ala Ala Thr Leu Thr
  1               5                  10                  15

Val Ser Leu Ala Ala Cys Ser Gln Asp Ser Ser Glu Thr Ser Ser Asn
             20                  25                  30

Ser Ser Ser Ala Ala Ser Gln Ser Ser Asp Val Ser Asn Glu Ala Phe
         35                  40                  45

Pro Val Thr Ile Glu His Ala Phe Gly Glu Thr Thr Ile Glu Ser Lys
     50                  55                  60

Pro Glu Arg Ile Ala Thr Val Gly Trp Ser Asn His Glu Val Pro Leu
 65                  70                  75                  80
```

```
Ala Leu Gly Val Thr Pro Val Gly Phe Glu Lys Val Thr Trp Gly Asp
                 85                  90                  95

Asp Asp Asn Asn Gly Ile Leu Pro Trp Val Glu Glu Thr Leu Ser Lys
            100                 105                 110

Leu Gly Ser Asp Glu Pro Val Leu Phe Asp Ala Thr Asp Ser Ile Pro
        115                 120                 125

Phe Glu Glu Ile Ala Asn Thr Ala Pro Asp Val Ile Leu Ala Ser Tyr
    130                 135                 140

Ser Gly Ile Thr Gln Glu Asp Tyr Asp Gln Leu Ser Gln Ile Ala Pro
145                 150                 155                 160

Val Val Ala Tyr Pro Glu Ile Ala Trp Gly Thr Ser Leu Asp Glu Met
                165                 170                 175

Ile Glu Met Asn Ser Lys Ala Ile Gly Leu Glu Gln Glu Gly Lys Asp
            180                 185                 190

Leu Ile Ala Asp Leu Asp Ala Glu Val Ala Ser Ala Ile Asp Ala Asn
        195                 200                 205

Pro Glu Leu Lys Asp Ala Lys Pro Val Phe Ala Phe Phe Asp Glu Ser
    210                 215                 220

Asp Phe Ser Gln Ile Gly Val Tyr Thr Ser Ile Asp Pro Arg Met Ser
225                 230                 235                 240

Phe Leu Leu Asp Ala Gly Val Gln Glu Ala Ser Val Leu Lys Glu His
                245                 250                 255

Ser Ser Pro Asp Ser Phe Tyr Glu Gln Val Ser Ala Glu Asn Pro Glu
            260                 265                 270

Thr Phe Asp Asp Val Asp Val Ile Ile Thr Tyr Gly Thr Glu Asp Asp
        275                 280                 285

Ala Ala Asn Ala Glu Leu Leu Ser Lys Met Gln Ala Asp Pro Leu Leu
    290                 295                 300

Ser Arg Ile Pro Ala Ile Ala Glu Gly Lys Val Val Phe Leu Gly Ala
305                 310                 315                 320

Asn Pro Leu Ala Ala Ser Ala Asn Glu Ser Pro Leu Ser Ile Pro Trp
                325                 330                 335

Gly Ile Asn Asp Tyr Phe Ala Lys Leu Ala Glu Pro Leu Lys
            340                 345                 350
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<210> 917
<211> 336
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> RXN01987

<400> 917
gggttaggag aggggaaatc cccgatgtgc tctaggttct tattggcgat gattgaagaa 60

gaaagaaaaa ctcaatcagc cataaaggag cttgatcccg atg act ttc cca gca 115
Met Thr Phe Pro Ala
1 5

caa tct cga cga ctc gcc cga agc acc acc gac aaa tgg atc ggc ggc 163
Gln Ser Arg Arg Leu Ala Arg Ser Thr Thr Asp Lys Trp Ile Gly Gly
10 15 20

gtc gct ggt ggc ctc gca gag acc tac ggt tgg aat ccg gcc tat gtg 211
Val Ala Gly Gly Leu Ala Glu Thr Tyr Gly Trp Asn Pro Ala Tyr Val
25 30 35

cgt ctc gcg ttc gtg gcg tcg gtt ctg ttt cca ctg cca ggt tca cag 259
Arg Leu Ala Phe Val Ala Ser Val Leu Phe Pro Leu Pro Gly Ser Gln
40 45 50

atc ctg ttc tac gcc cta gcg tgg ctg atc atc cca tcc cga gaa aat 307
Ile Leu Phe Tyr Ala Leu Ala Trp Leu Ile Ile Pro Ser Arg Glu Asn
55 60 65

cgc ttc taacgtgcgt tgcataacgc aga 336
Arg Phe
70

<210> 918
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 918
Met Thr Phe Pro Ala Gln Ser Arg Arg Leu Ala Arg Ser Thr Thr Asp
1 5 10 15

Lys Trp Ile Gly Gly Val Ala Gly Gly Leu Ala Glu Thr Tyr Gly Trp
20 25 30

Asn Pro Ala Tyr Val Arg Leu Ala Phe Val Ala Ser Val Leu Phe Pro
35 40 45

Leu Pro Gly Ser Gln Ile Leu Phe Tyr Ala Leu Ala Trp Leu Ile Ile
50 55 60

Pro Ser Arg Glu Asn Arg Phe
65 70

<210> 919
<211> 336
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> FRXA01987

<400> 919
gggttaggag aggggaaatc cccgatgtgc tctaggttct tattggcgat gattgaagaa 60

gaaagaaaaa ctcaatcagc cataaaggag cttgatcccg atg act ttc cca gca 115
Met Thr Phe Pro Ala
1 5

caa tct cga cga ctc gcc cga agc acc acc gac aaa tgg atc ggc ggc 163
Gln Ser Arg Arg Leu Ala Arg Ser Thr Thr Asp Lys Trp Ile Gly Gly
10 15 20

gtc gct ggt ggc ctc gca gag acc tac ggt tgg aat ccg gcc tat gtg 211
Val Ala Gly Gly Leu Ala Glu Thr Tyr Gly Trp Asn Pro Ala Tyr Val
25 30 35

cgt ctc gcg ttc gtg gcg tcg gtt ctg ttt cca ctg cca ggt tca cag 259
Arg Leu Ala Phe Val Ala Ser Val Leu Phe Pro Leu Pro Gly Ser Gln
40 45 50

atc ctg ttc tac gcc cta gcg tgg ctg atc atc cca tcc cga gaa aat 307
Ile Leu Phe Tyr Ala Leu Ala Trp Leu Ile Ile Pro Ser Arg Glu Asn
55 60 65

cgc ttc taacgtgcgt tgcataacgc aga 336
Arg Phe
70

<210> 920
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 920
Met Thr Phe Pro Ala Gln Ser Arg Arg Leu Ala Arg Ser Thr Thr Asp
1 5 10 15

Lys Trp Ile Gly Gly Val Ala Gly Gly Leu Ala Glu Thr Tyr Gly Trp
20 25 30

Asn Pro Ala Tyr Val Arg Leu Ala Phe Val Ala Ser Val Leu Phe Pro
35 40 45

Leu Pro Gly Ser Gln Ile Leu Phe Tyr Ala Leu Ala Trp Leu Ile Ile
50 55 60

Pro Ser Arg Glu Asn Arg Phe
65 70

<210> 921
<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(526)
<223> RXN01988

<400> 921

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ttaagaattg gattcgagtc ggtaccgctt gaaagtactt tgcgtaagtt cccaccgact 60

gcccctagtt gttgcgaata tttatagatt gttgagaaag atg aac atg aag acg   115
                                             Met Asn Met Lys Thr
                                               1               5

cac ccg gct tcc gcc aag cag acc acc gag ctt cga ctc ctg aca gcc   163
His Pro Ala Ser Ala Lys Gln Thr Thr Glu Leu Arg Leu Leu Thr Ala
                 10                  15                  20

acc gtg tac ttc aaa gca ctc aat gaa gtc cac aac gtc atg cag atg   211
Thr Val Tyr Phe Lys Ala Leu Asn Glu Val His Asn Val Met Gln Met
             25                  30                  35

atc gac cca cta act cca gtc gtt ccc atc acc acg ggc acc tca gtt   259
Ile Asp Pro Leu Thr Pro Val Val Pro Ile Thr Thr Gly Thr Ser Val
         40                  45                  50

gcc gag ctt tat gct gac gcc cgc gag cac ctc gac aat ggt gca acc   307
Ala Glu Leu Tyr Ala Asp Ala Arg Glu His Leu Asp Asn Gly Ala Thr
     55                  60                  65

cag gtg atg atc ccc gtc att tca cct tcc aac ctg acc ttg tca gta   355
Gln Val Met Ile Pro Val Ile Ser Pro Ser Asn Leu Thr Leu Ser Val
 70                  75                  80                  85

gtt gcc ctg ggc aat gaa gag gtt gac gca ctg ggc cat tcc gaa gga   403
Val Ala Leu Gly Asn Glu Glu Val Asp Ala Leu Gly His Ser Glu Gly
                 90                  95                 100

caa gca gtt cac tcc ctt ctg gaa att cat acc ccg aag cgc agc tgg   451
Gln Ala Val His Ser Leu Leu Glu Ile His Thr Pro Lys Arg Ser Trp
             105                 110                 115

cct ctt tcc gag ctt tat att gat gac aat gag ggt ttg gct cag gtg   499
Pro Leu Ser Glu Leu Tyr Ile Asp Asp Asn Glu Gly Leu Ala Gln Val
         120                 125                 130

tcg cgc tgc ttc gcc cgc ctt gtt ggc tagtcccacc ccaccaattg         546
Ser Arg Cys Phe Ala Arg Leu Val Gly
    135                 140

cat                                                               549


<210> 922
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 922
Met Asn Met Lys Thr His Pro Ala Ser Ala Lys Gln Thr Thr Glu Leu
  1               5                  10                  15

Arg Leu Leu Thr Ala Thr Val Tyr Phe Lys Ala Leu Asn Glu Val His
             20                  25                  30

Asn Val Met Gln Met Ile Asp Pro Leu Thr Pro Val Val Pro Ile Thr
         35                  40                  45

Thr Gly Thr Ser Val Ala Glu Leu Tyr Ala Asp Ala Arg Glu His Leu
```

```
     50                  55                  60

Asp Asn Gly Ala Thr Gln Val Met Ile Pro Val Ile Ser Pro Ser Asn
 65                  70                  75                  80

Leu Thr Leu Ser Val Val Ala Leu Gly Asn Glu Glu Val Asp Ala Leu
                 85                  90                  95

Gly His Ser Glu Gly Gln Ala Val His Ser Leu Leu Glu Ile His Thr
            100                 105                 110

Pro Lys Arg Ser Trp Pro Leu Ser Glu Leu Tyr Ile Asp Asp Asn Glu
        115                 120                 125

Gly Leu Ala Gln Val Ser Arg Cys Phe Ala Arg Leu Val Gly
    130                 135                 140


<210> 923
<211> 341
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(318)
<223> FRXA01988

<400> 923
atg atc gac cca cta act cca gtc gtt ccc atc acc acg ggc acc tca   48
Met Ile Asp Pro Leu Thr Pro Val Val Pro Ile Thr Thr Gly Thr Ser
  1               5                  10                  15

gtt gcc gag ctt tat gct gac gcc cgc gag cac ctc gac aat ggt gca   96
Val Ala Glu Leu Tyr Ala Asp Ala Arg Glu His Leu Asp Asn Gly Ala
             20                  25                  30

acc cag gtg atg atc ccc gtc att tca cct tcc aac ctg acc ttg tca   144
Thr Gln Val Met Ile Pro Val Ile Ser Pro Ser Asn Leu Thr Leu Ser
         35                  40                  45

gta gtt gcc ctg ggc aat caa gag gtt gac gca ctg ggc cat tcc gaa   192
Val Val Ala Leu Gly Asn Gln Glu Val Asp Ala Leu Gly His Ser Glu
     50                  55                  60

gga caa gca gtt cac tcc ctt ctg gaa att cat acc ccg aag cgc agc   240
Gly Gln Ala Val His Ser Leu Leu Glu Ile His Thr Pro Lys Arg Ser
 65                  70                  75                  80

tgg cct ctt tcc gag ctt tat att gat gac aat gag ggt ttg gct cag   288
Trp Pro Leu Ser Glu Leu Tyr Ile Asp Asp Asn Glu Gly Leu Ala Gln
                 85                  90                  95

gtg tcg cgc tgc ttc gcc cgc ctt gtt ggc tagtcccacc ccaccaattg     338
Val Ser Arg Cys Phe Ala Arg Leu Val Gly
            100                 105

cat                                                               341


<210> 924
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<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 924
Met Ile Asp Pro Leu Thr Pro Val Val Pro Ile Thr Thr Gly Thr Ser
1 5 10 15

Val Ala Glu Leu Tyr Ala Asp Ala Arg Glu His Leu Asp Asn Gly Ala
20 25 30

Thr Gln Val Met Ile Pro Val Ile Ser Pro Ser Asn Leu Thr Leu Ser
35 40 45

Val Val Ala Leu Gly Asn Gln Glu Val Asp Ala Leu Gly His Ser Glu
50 55 60

Gly Gln Ala Val His Ser Leu Leu Glu Ile His Thr Pro Lys Arg Ser
65 70 75 80

Trp Pro Leu Ser Glu Leu Tyr Ile Asp Asp Asn Glu Gly Leu Ala Gln
85 90 95

Val Ser Arg Cys Phe Ala Arg Leu Val Gly
100 105

<210> 925
<211> 996
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(973)
<223> RXN01991

<400> 925
tccggaggtg gatttgagga tttcgacgtt ttctcggaag ttcctcgggt agaggaaaca 60

tcgacgagga tcagctattc ttacaaaaat tcatttgaat atg acg aat ttg ttg 115
Met Thr Asn Leu Leu
1 5

ccg cat ttc ccg agt acc gac gta gct gcg tgg gaa cca acc gtt gtg 163
Pro His Phe Pro Ser Thr Asp Val Ala Ala Trp Glu Pro Thr Val Val
10 15 20

tat tca gcg gat aag acc aca gca aca gcg acg ttt aag aat att cct 211
Tyr Ser Ala Asp Lys Thr Thr Ala Thr Ala Thr Phe Lys Asn Ile Pro
25 30 35

tcg gat att tcc ttt agt tgg act ggt att gaa gca cta gag cca ttt 259
Ser Asp Ile Ser Phe Ser Trp Thr Gly Ile Glu Ala Leu Glu Pro Phe
40 45 50

agc cct ggt aaa acc ttc gaa cat aag gtg caa ggt tct gtt ggt gaa 307
Ser Pro Gly Lys Thr Phe Glu His Lys Val Gln Gly Ser Val Gly Glu
55 60 65

cca gcg ggg gcg ttc act agg gat aac tat ttc act gag ggt gag ctc 355

```
Pro Ala Gly Ala Phe Thr Arg Asp Asn Tyr Phe Thr Glu Gly Glu Leu
 70                  75                  80                  85

tac aaa cat cgc cac gca gac gat ctg ctt tcc ggt gat ggc ttg ttt   403
Tyr Lys His Arg His Ala Asp Asp Leu Leu Ser Gly Asp Gly Leu Phe
                 90                  95                 100

ggc ccc aac atc acc gat ggc gat ggc aac ctc ccc tct gtt gat gac   451
Gly Pro Asn Ile Thr Asp Gly Asp Gly Asn Leu Pro Ser Val Asp Asp
            105                 110                 115

ggc aag gac ggt gac gat ggg tct gat ggc tca gac ggc cga gac ggt   499
Gly Lys Asp Gly Asp Asp Gly Ser Asp Gly Ser Asp Gly Arg Asp Gly
        120                 125                 130

gtt gtc gcc att gat gtt gtt gac aat gct gac ggc acg gtg act gtc   547
Val Val Ala Ile Asp Val Val Asp Asn Ala Asp Gly Thr Val Thr Val
    135                 140                 145

acc ttg tcc gat ggc act acg ttt act ctt gat gct ggt caa gac ggc   595
Thr Leu Ser Asp Gly Thr Thr Phe Thr Leu Asp Ala Gly Gln Asp Gly
150                 155                 160                 165

aaa gat ggt ctt gac ggg ctt gat ggt act ggc cta acg ctg gaa tct   643
Lys Asp Gly Leu Asp Gly Leu Asp Gly Thr Gly Leu Thr Leu Glu Ser
                170                 175                 180

gct acc cct gat gag gac ggc aac atc acc tat gtt ctt tct gac ggt   691
Ala Thr Pro Asp Glu Asp Gly Asn Ile Thr Tyr Val Leu Ser Asp Gly
            185                 190                 195

act gag ttc act gtg cgc aac ggt gtt gat ggg tca gac ggt aag gac   739
Thr Glu Phe Thr Val Arg Asn Gly Val Asp Gly Ser Asp Gly Lys Asp
        200                 205                 210

ggc aaa gat gga gtc aat ggc aca gat ggc gta gac ggg tca gac ggt   787
Gly Lys Asp Gly Val Asn Gly Thr Asp Gly Val Asp Gly Ser Asp Gly
    215                 220                 225

aaa ggt ctg gta gag gtg tcc cga gtt acc aac gac aac ggc tca gtg   835
Lys Gly Leu Val Glu Val Ser Arg Val Thr Asn Asp Asn Gly Ser Val
230                 235                 240                 245

acc att acc tac gag gac ggt tca cag atc acc acg aag cca acg ccg   883
Thr Ile Thr Tyr Glu Asp Gly Ser Gln Ile Thr Thr Lys Pro Thr Pro
                250                 255                 260

aca aac tgg ctg tcc aag ctg ctt gat ttg ctt ctc ccg ctg ttt aat   931
Thr Asn Trp Leu Ser Lys Leu Leu Asp Leu Leu Leu Pro Leu Phe Asn
            265                 270                 275

ctg ttc ggt ctt ggt ggc ggc tcc gtc att agt tcc agt aag           973
Leu Phe Gly Leu Gly Gly Gly Ser Val Ile Ser Ser Ser Lys
        280                 285                 290

tagttttttc actccctgtt ttg                                        996
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<210> 926
<211> 291
<212> PRT

<213> Corynebacterium glutamicum

<400> 926

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Met Thr Asn Leu Leu Pro His Phe Pro Ser Thr Asp Val Ala Ala Trp
  1               5                  10                  15

Glu Pro Thr Val Val Tyr Ser Ala Asp Lys Thr Thr Ala Thr Ala Thr
             20                  25                  30

Phe Lys Asn Ile Pro Ser Asp Ile Ser Phe Ser Trp Thr Gly Ile Glu
         35                  40                  45

Ala Leu Glu Pro Phe Ser Pro Gly Lys Thr Phe Glu His Lys Val Gln
     50                  55                  60

Gly Ser Val Gly Glu Pro Ala Gly Ala Phe Thr Arg Asp Asn Tyr Phe
 65                  70                  75                  80

Thr Glu Gly Glu Leu Tyr Lys His Arg His Ala Asp Asp Leu Leu Ser
                 85                  90                  95

Gly Asp Gly Leu Phe Gly Pro Asn Ile Thr Asp Gly Asp Gly Asn Leu
            100                 105                 110

Pro Ser Val Asp Asp Gly Lys Asp Gly Asp Asp Gly Ser Asp Gly Ser
        115                 120                 125

Asp Gly Arg Asp Gly Val Val Ala Ile Asp Val Val Asp Asn Ala Asp
    130                 135                 140

Gly Thr Val Thr Val Thr Leu Ser Asp Gly Thr Thr Phe Thr Leu Asp
145                 150                 155                 160

Ala Gly Gln Asp Gly Lys Asp Gly Leu Asp Gly Leu Asp Gly Thr Gly
                165                 170                 175

Leu Thr Leu Glu Ser Ala Thr Pro Asp Glu Asp Gly Asn Ile Thr Tyr
            180                 185                 190

Val Leu Ser Asp Gly Thr Glu Phe Thr Val Arg Asn Gly Val Asp Gly
        195                 200                 205

Ser Asp Gly Lys Asp Gly Lys Asp Gly Val Asn Gly Thr Asp Gly Val
    210                 215                 220

Asp Gly Ser Asp Gly Lys Gly Leu Val Glu Val Ser Arg Val Thr Asn
225                 230                 235                 240

Asp Asn Gly Ser Val Thr Ile Thr Tyr Glu Asp Gly Ser Gln Ile Thr
                245                 250                 255

Thr Lys Pro Thr Pro Thr Asn Trp Leu Ser Lys Leu Leu Asp Leu Leu
            260                 265                 270

Leu Pro Leu Phe Asn Leu Phe Gly Leu Gly Gly Gly Ser Val Ile Ser
        275                 280                 285

Ser Ser Lys
    290
```

<210> 927
<211> 895
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(895)
<223> FRXA01991

<400> 927
tccggaggtg gatttgagga tttcgacgtt ttctcggaag ttcctcgggt agaggaaaca 60

tcgacgagga tcagctattc ttacaaaaat tcatttgaat atg acg aat ttg ttg 115
Met Thr Asn Leu Leu
1 5

ccg cat ttc ccg agt acc gac gta gct gcg tgg gaa cca acc gtt gtg 163
Pro His Phe Pro Ser Thr Asp Val Ala Ala Trp Glu Pro Thr Val Val
10 15 20

tat tca gcg gat aag acc aca gca aca gcg acg ttt aag aat att cct 211
Tyr Ser Ala Asp Lys Thr Thr Ala Thr Ala Thr Phe Lys Asn Ile Pro
25 30 35

tcg gat att tcc ttt agt tgg act ggt att gaa gca cta gag cca ttt 259
Ser Asp Ile Ser Phe Ser Trp Thr Gly Ile Glu Ala Leu Glu Pro Phe
40 45 50

agc cct ggt aaa acc ttc gaa cat aag gtg caa ggt tct gtt ggt gaa 307
Ser Pro Gly Lys Thr Phe Glu His Lys Val Gln Gly Ser Val Gly Glu
55 60 65

cca gcg ggg gcg ttc act agg gat aac tat ttc act gag ggt gag ctc 355
Pro Ala Gly Ala Phe Thr Arg Asp Asn Tyr Phe Thr Glu Gly Glu Leu
70 75 80 85

tac aaa cat cgc cac gca gac gat ctg ctt tcc ggt gat ggc ttg ttt 403
Tyr Lys His Arg His Ala Asp Asp Leu Leu Ser Gly Asp Gly Leu Phe
90 95 100

ggc ccc aac atc acc gat ggc gat ggc aac ctc ccc tct gtt gat gac 451
Gly Pro Asn Ile Thr Asp Gly Asp Gly Asn Leu Pro Ser Val Asp Asp
105 110 115

ggc aag gac ggt gac gat ggg tct gat ggc tca gac ggc cga gac ggt 499
Gly Lys Asp Gly Asp Asp Gly Ser Asp Gly Ser Asp Gly Arg Asp Gly
120 125 130

gtt gtc gcc att gat gtt gtt gac aat gct gac ggc acg gtg act gtc 547
Val Val Ala Ile Asp Val Val Asp Asn Ala Asp Gly Thr Val Thr Val
135 140 145

acc ttg tcc gat ggc act acg ttt act ctt gat gct ggt caa gac ggc 595
Thr Leu Ser Asp Gly Thr Thr Phe Thr Leu Asp Ala Gly Gln Asp Gly
150 155 160 165

aaa gat ggt ctt gac ggg ctt gat ggt act ggc cta acg ctg gaa tct 643
Lys Asp Gly Leu Asp Gly Leu Asp Gly Thr Gly Leu Thr Leu Glu Ser
170 175 180

```
gct acc cct gat gag gac ggc aac atc acc tat gtt ctt tct gac ggt   691
Ala Thr Pro Asp Glu Asp Gly Asn Ile Thr Tyr Val Leu Ser Asp Gly
            185                 190                 195

act gag ttc act gtg cgc aac ggt gtt gat ggg tca gac ggt aag gac   739
Thr Glu Phe Thr Val Arg Asn Gly Val Asp Gly Ser Asp Gly Lys Asp
        200                 205                 210

ggc aaa gat gga gtc aat ggc aca gat ggc gta gac ggg tca gac ggt   787
Gly Lys Asp Gly Val Asn Gly Thr Asp Gly Val Asp Gly Ser Asp Gly
    215                 220                 225

aaa ggt ctg gta gag gtg tcc cga gtt acc aac gac aac ggc tca gtg   835
Lys Gly Leu Val Glu Val Ser Arg Val Thr Asn Asp Asn Gly Ser Val
230                 235                 240                 245

acc att acc tac gag gac ggt tca cag atc acc acg aag cca acg ccg   883
Thr Ile Thr Tyr Glu Asp Gly Ser Gln Ile Thr Thr Lys Pro Thr Pro
                250                 255                 260

aca aac tgg ctg                                                  895
Thr Asn Trp Leu
            265
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<210> 928
<211> 265
<212> PRT
<213> Corynebacterium glutamicum

<400> 928

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Met Thr Asn Leu Leu Pro His Phe Pro Ser Thr Asp Val Ala Ala Trp
  1               5                  10                  15

Glu Pro Thr Val Val Tyr Ser Ala Asp Lys Thr Thr Ala Thr Ala Thr
             20                  25                  30

Phe Lys Asn Ile Pro Ser Asp Ile Ser Phe Ser Trp Thr Gly Ile Glu
         35                  40                  45

Ala Leu Glu Pro Phe Ser Pro Gly Lys Thr Phe Glu His Lys Val Gln
     50                  55                  60

Gly Ser Val Gly Glu Pro Ala Gly Ala Phe Thr Arg Asp Asn Tyr Phe
 65                  70                  75                  80

Thr Glu Gly Glu Leu Tyr Lys His Arg His Ala Asp Asp Leu Leu Ser
                85                  90                  95

Gly Asp Gly Leu Phe Gly Pro Asn Ile Thr Asp Gly Asp Gly Asn Leu
            100                 105                 110

Pro Ser Val Asp Asp Gly Lys Asp Gly Asp Asp Gly Ser Asp Gly Ser
        115                 120                 125

Asp Gly Arg Asp Gly Val Val Ala Ile Asp Val Val Asp Asn Ala Asp
    130                 135                 140

Gly Thr Val Thr Val Thr Leu Ser Asp Gly Thr Thr Phe Thr Leu Asp
145                 150                 155                 160
```

```
Ala Gly Gln Asp Gly Lys Asp Gly Leu Asp Gly Leu Asp Gly Thr Gly
                165                 170                 175

Leu Thr Leu Glu Ser Ala Thr Pro Asp Glu Asp Gly Asn Ile Thr Tyr
            180                 185                 190

Val Leu Ser Asp Gly Thr Glu Phe Thr Val Arg Asn Gly Val Asp Gly
        195                 200                 205

Ser Asp Gly Lys Asp Gly Lys Asp Gly Val Asn Gly Thr Asp Gly Val
    210                 215                 220

Asp Gly Ser Asp Gly Lys Gly Leu Val Glu Val Ser Arg Val Thr Asn
225                 230                 235                 240

Asp Asn Gly Ser Val Thr Ile Thr Tyr Glu Asp Gly Ser Gln Ile Thr
                245                 250                 255

Thr Lys Pro Thr Pro Thr Asn Trp Leu
            260                 265
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<210> 929
<211> 660
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(637)
<223> RXN01996

<400> 929

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ctagtataga acggaacacg gcagcgacac aaactgcaca gatgcaagag tgtcggtacc 60

gttaaaaacg aaacacactt tcaccgaaaa ggacttccca atg agc aag ttg act   115
                                              Met Ser Lys Leu Thr
                                                1               5

ggc acc tgg acc ctc gac cct gca cac acc gaa atc aag ttc gtg gct   163
Gly Thr Trp Thr Leu Asp Pro Ala His Thr Glu Ile Lys Phe Val Ala
                10                  15                  20

cgc cac gca atg gtt acc aag gtt cgc ggt gaa ttc acc gag tac acc   211
Arg His Ala Met Val Thr Lys Val Arg Gly Glu Phe Thr Glu Tyr Thr
            25                  30                  35

gac tcc att gtc gta gat gct gaa aac cca gag aac tcc tct gca aag   259
Asp Ser Ile Val Val Asp Ala Glu Asn Pro Glu Asn Ser Ser Ala Lys
        40                  45                  50

gtt gtt atc aag acc gct tcc gtt acc acc ggc aac gca gac cgc gat   307
Val Val Ile Lys Thr Ala Ser Val Thr Thr Gly Asn Ala Asp Arg Asp
    55                  60                  65

gca cac gtt aag ggc gac gac ttc ttc gca gta gac aag ttc cct gaa   355
Ala His Val Lys Gly Asp Asp Phe Phe Ala Val Asp Lys Phe Pro Glu
70                  75                  80                  85

atg act ttc gaa gct act tcc ttt gtt atc aag aac gaa aac gaa ggc   403
Met Thr Phe Glu Ala Thr Ser Phe Val Ile Lys Asn Glu Asn Glu Gly
```

```
                    90                  95                  100

acc gtt acc ggc gac ctc aca att cgt gac acc acc aag tcc gtc acc   451
Thr Val Thr Gly Asp Leu Thr Ile Arg Asp Thr Thr Lys Ser Val Thr
            105                 110                 115

ctg gac gtt gag gtt ggt ggc gtt gct gag gat cca ttc ggc aac acc   499
Leu Asp Val Glu Val Gly Gly Val Ala Glu Asp Pro Phe Gly Asn Thr
        120                 125                 130

cgc ctt ggc ttc gaa gcc tcc acc gaa atc aac cgc aag gac ttc ggc   547
Arg Leu Gly Phe Glu Ala Ser Thr Glu Ile Asn Arg Lys Asp Phe Gly
    135                 140                 145

gta gat ttc cag gct cca ctc tcc acc ggt ggc gtt ctg gtt tct gag   595
Val Asp Phe Gln Ala Pro Leu Ser Thr Gly Gly Val Leu Val Ser Glu
150                 155                 160                 165

aag atc aag atc gag atc gac ggc tcc gca atc aag gct gct           637
Lys Ile Lys Ile Glu Ile Asp Gly Ser Ala Ile Lys Ala Ala
                170                 175

taagcgccca caaacaaaaa gcc                                        660


<210> 930
<211> 179
<212> PRT
<213> Corynebacterium glutamicum

<400> 930
Met Ser Lys Leu Thr Gly Thr Trp Thr Leu Asp Pro Ala His Thr Glu
  1               5                  10                  15

Ile Lys Phe Val Ala Arg His Ala Met Val Thr Lys Val Arg Gly Glu
             20                  25                  30

Phe Thr Glu Tyr Thr Asp Ser Ile Val Val Asp Ala Glu Asn Pro Glu
         35                  40                  45

Asn Ser Ser Ala Lys Val Val Ile Lys Thr Ala Ser Val Thr Thr Gly
     50                  55                  60

Asn Ala Asp Arg Asp Ala His Val Lys Gly Asp Asp Phe Phe Ala Val
 65                  70                  75                  80

Asp Lys Phe Pro Glu Met Thr Phe Glu Ala Thr Ser Phe Val Ile Lys
                 85                  90                  95

Asn Glu Asn Glu Gly Thr Val Thr Gly Asp Leu Thr Ile Arg Asp Thr
            100                 105                 110

Thr Lys Ser Val Thr Leu Asp Val Glu Val Gly Gly Val Ala Glu Asp
        115                 120                 125

Pro Phe Gly Asn Thr Arg Leu Gly Phe Glu Ala Ser Thr Glu Ile Asn
    130                 135                 140

Arg Lys Asp Phe Gly Val Asp Phe Gln Ala Pro Leu Ser Thr Gly Gly
145                 150                 155                 160
```

```
Val Leu Val Ser Glu Lys Ile Lys Ile Glu Ile Asp Gly Ser Ala Ile
                165                 170                 175

Lys Ala Ala
```

<210> 931
<211> 647
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (88)..(624)
<223> FRXA01996

<400> 931

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gaacacggca gcgacacaaa ctgcacagat gcaagagtgt cggtaccgtt aaaaacgaaa 60

cacactttca ccgaaaagga cttcccaatg agc aag ttg act ggc acc tgg acc  114
                            Met Ser Lys Leu Thr Gly Thr Trp Thr
                              1               5

ctc gac cct gca cac acc gaa atc aag ttc gtg gct cgc cac gca atg   162
Leu Asp Pro Ala His Thr Glu Ile Lys Phe Val Ala Arg His Ala Met
 10                  15                  20                  25

gtt acc aag gtt cgc ggt gaa ttc acc gag tac acc gac tcc att gtc   210
Val Thr Lys Val Arg Gly Glu Phe Thr Glu Tyr Thr Asp Ser Ile Val
                 30                  35                  40

gta gat gct gaa aac cca gag aac tcc tct gca aag gtt gtt atc aag   258
Val Asp Ala Glu Asn Pro Glu Asn Ser Ser Ala Lys Val Val Ile Lys
             45                  50                  55

acc gct tcc gtt acc acc ggc aac gca gac cgc gat gca cac gtt aag   306
Thr Ala Ser Val Thr Thr Gly Asn Ala Asp Arg Asp Ala His Val Lys
         60                  65                  70

ggc gac gac ttc ttc gca gta gac aag ttc cct gaa atg act ttc gaa   354
Gly Asp Asp Phe Phe Ala Val Asp Lys Phe Pro Glu Met Thr Phe Glu
     75                  80                  85

gct act tcc ttt gtt atc aag aac gaa aac gaa ggc acc gtt acc ggc   402
Ala Thr Ser Phe Val Ile Lys Asn Glu Asn Glu Gly Thr Val Thr Gly
 90                  95                 100                 105

gac ctc aca att cgt gac acc acc aag tcc gtc acc ctg gac gtt gag   450
Asp Leu Thr Ile Arg Asp Thr Thr Lys Ser Val Thr Leu Asp Val Glu
                110                 115                 120

gtt ggt ggc gtt gct gag gat cca ttc ggc aac acc cgc ctt ggc ttc   498
Val Gly Gly Val Ala Glu Asp Pro Phe Gly Asn Thr Arg Leu Gly Phe
            125                 130                 135

gaa gcc tcc acc gaa atc aac cgc aag gac ttc ggc gta gat ttc cag   546
Glu Ala Ser Thr Glu Ile Asn Arg Lys Asp Phe Gly Val Asp Phe Gln
        140                 145                 150

gct cca ctc tcc acc ggt ggc gtt ctg gtt tct gag aag atc aag atc   594
```

```
Ala Pro Leu Ser Thr Gly Gly Val Leu Val Ser Glu Lys Ile Lys Ile
    155                 160                 165

gag atc gac ggc tcc gca atc aag gct gct taagcgccca caaacaaaaa     644
Glu Ile Asp Gly Ser Ala Ile Lys Ala Ala
170                 175

gcc                                                               647
```

<210> 932
<211> 179
<212> PRT
<213> Corynebacterium glutamicum

<400> 932

```
Met Ser Lys Leu Thr Gly Thr Trp Thr Leu Asp Pro Ala His Thr Glu
  1               5                  10                  15

Ile Lys Phe Val Ala Arg His Ala Met Val Thr Lys Val Arg Gly Glu
             20                  25                  30

Phe Thr Glu Tyr Thr Asp Ser Ile Val Val Asp Ala Glu Asn Pro Glu
         35                  40                  45

Asn Ser Ser Ala Lys Val Val Ile Lys Thr Ala Ser Val Thr Thr Gly
     50                  55                  60

Asn Ala Asp Arg Asp Ala His Val Lys Gly Asp Asp Phe Phe Ala Val
 65                  70                  75                  80

Asp Lys Phe Pro Glu Met Thr Phe Glu Ala Thr Ser Phe Val Ile Lys
                 85                  90                  95

Asn Glu Asn Glu Gly Thr Val Thr Gly Asp Leu Thr Ile Arg Asp Thr
            100                 105                 110

Thr Lys Ser Val Thr Leu Asp Val Glu Val Gly Gly Val Ala Glu Asp
        115                 120                 125

Pro Phe Gly Asn Thr Arg Leu Gly Phe Glu Ala Ser Thr Glu Ile Asn
    130                 135                 140

Arg Lys Asp Phe Gly Val Asp Phe Gln Ala Pro Leu Ser Thr Gly Gly
145                 150                 155                 160

Val Leu Val Ser Glu Lys Ile Lys Ile Glu Ile Asp Gly Ser Ala Ile
                165                 170                 175

Lys Ala Ala
```

<210> 933
<211> 756
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)

<223> RXN02007

<400> 933

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tggaagcccc agccgcggtc caagagacag ttgcgccgac gtccaccct taggacgctg 60

attacagacg tgtcccattt ctttactact attggaaatt atg agt tca gac gca   115
                                          Met Ser Ser Asp Ala
                                            1               5

gaa aag gca tcc gtg gag ctt tcc gaa aaa ttt cac cca gaa cgc acc   163
Glu Lys Ala Ser Val Glu Leu Ser Glu Lys Phe His Pro Glu Arg Thr
                10                  15                  20

cat att ttg ggc gcc gtt gtt ttt ggc ctg atc tca tta tta gtc atc   211
His Ile Leu Gly Ala Val Val Phe Gly Leu Ile Ser Leu Leu Val Ile
            25                  30                  35

ggc gca gcc cct cag tac ctg ttt tgg ctg ctc gcg ctc cct gtc atc   259
Gly Ala Ala Pro Gln Tyr Leu Phe Trp Leu Leu Ala Leu Pro Val Ile
        40                  45                  50

ttc ggt tac tgg gtt cta aaa tca tcc acg atc gtt gat gaa cag ggc   307
Phe Gly Tyr Trp Val Leu Lys Ser Ser Thr Ile Val Asp Glu Gln Gly
    55                  60                  65

atc acc gca aac tac gcc ttc aag ggc aaa aag gtt gtg gcc tgg gaa   355
Ile Thr Ala Asn Tyr Ala Phe Lys Gly Lys Lys Val Val Ala Trp Glu
70                  75                  80                  85

gac ctc gca gga atc gga ttc aag ggt gcc cgc act ttc gct cgc acc   403
Asp Leu Ala Gly Ile Gly Phe Lys Gly Ala Arg Thr Phe Ala Arg Thr
                90                  95                  100

acc tcc gat gca gaa gtc acc ctc ccg ggc gtc acc ttc aac tcc ctt   451
Thr Ser Asp Ala Glu Val Thr Leu Pro Gly Val Thr Phe Asn Ser Leu
            105                 110                 115

ccc cgc ctt gaa gct gct tcc cac ggc cgc atc ccc gat gcg atc acc   499
Pro Arg Leu Glu Ala Ala Ser His Gly Arg Ile Pro Asp Ala Ile Thr
        120                 125                 130

gca agc aag gaa gca gcc gac ggc aag gtt gta gtc gtt caa gaa gac   547
Ala Ser Lys Glu Ala Ala Asp Gly Lys Val Val Val Val Gln Glu Asp
    135                 140                 145

ggc tac tcc gtg atg atg tcc aag gaa gag tac ttg gag cgc caa aag   595
Gly Tyr Ser Val Met Met Ser Lys Glu Glu Tyr Leu Glu Arg Gln Lys
150                 155                 160                 165

gca ctg ggc aag cca gtt cag ttg aac ttc gat gac gac acc gat ggg   643
Ala Leu Gly Lys Pro Val Gln Leu Asn Phe Asp Asp Asp Thr Asp Gly
                170                 175                 180

aat aca aca caa aca gaa agc gtt gaa tcc caa gag acc gga caa gcc   691
Asn Thr Thr Gln Thr Glu Ser Val Glu Ser Gln Glu Thr Gly Gln Ala
            185                 190                 195

gcg tct gaa acc tca cat cgt gat aac cct gcg tca cag cac           733
Ala Ser Glu Thr Ser His Arg Asp Asn Pro Ala Ser Gln His
        200                 205                 210
```

tagagtgtaa taagccgtcc gaa 756

<210> 934
<211> 211
<212> PRT
<213> Corynebacterium glutamicum

<400> 934

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Met Ser Ser Asp Ala Glu Lys Ala Ser Val Glu Leu Ser Glu Lys Phe
  1               5                  10                  15

His Pro Glu Arg Thr His Ile Leu Gly Ala Val Val Phe Gly Leu Ile
             20                  25                  30

Ser Leu Leu Val Ile Gly Ala Ala Pro Gln Tyr Leu Phe Trp Leu Leu
         35                  40                  45

Ala Leu Pro Val Ile Phe Gly Tyr Trp Val Leu Lys Ser Ser Thr Ile
     50                  55                  60

Val Asp Glu Gln Gly Ile Thr Ala Asn Tyr Ala Phe Lys Gly Lys Lys
 65                  70                  75                  80

Val Val Ala Trp Glu Asp Leu Ala Gly Ile Gly Phe Lys Gly Ala Arg
                 85                  90                  95

Thr Phe Ala Arg Thr Thr Ser Asp Ala Glu Val Thr Leu Pro Gly Val
            100                 105                 110

Thr Phe Asn Ser Leu Pro Arg Leu Glu Ala Ala Ser His Gly Arg Ile
        115                 120                 125

Pro Asp Ala Ile Thr Ala Ser Lys Glu Ala Ala Asp Gly Lys Val Val
    130                 135                 140

Val Val Gln Glu Asp Gly Tyr Ser Val Met Met Ser Lys Glu Glu Tyr
145                 150                 155                 160

Leu Glu Arg Gln Lys Ala Leu Gly Lys Pro Val Gln Leu Asn Phe Asp
                165                 170                 175

Asp Asp Thr Asp Gly Asn Thr Thr Gln Thr Glu Ser Val Glu Ser Gln
            180                 185                 190

Glu Thr Gly Gln Ala Ala Ser Glu Thr Ser His Arg Asp Asn Pro Ala
        195                 200                 205

Ser Gln His
    210
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<210> 935
<211> 452
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(429)
<223> FRXA02007

<400> 935

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ggc atc acc gca aac tac gcc ttc aag ggc aaa aag gtt gtg gct tgg   48
Gly Ile Thr Ala Asn Tyr Ala Phe Lys Gly Lys Lys Val Val Ala Trp
  1               5                  10                  15

aaa gac ctc gca gga atc gga ttc aag ggt gcc cgc act ttc gct cgc   96
Lys Asp Leu Ala Gly Ile Gly Phe Lys Gly Ala Arg Thr Phe Ala Arg
             20                  25                  30

ccc acc tcc gat gca gaa gtc acc ctc ccg ggc gtc acc ttc aac tcc   144
Pro Thr Ser Asp Ala Glu Val Thr Leu Pro Gly Val Thr Phe Asn Ser
         35                  40                  45

ctt ccc cgc ctt gaa gct gct tcc cac ggc cgc atc ccc gat gcg atc   192
Leu Pro Arg Leu Glu Ala Ala Ser His Gly Arg Ile Pro Asp Ala Ile
     50                  55                  60

acc gca agc aag gaa gca gcc gac ggc aag gtt gta gtc gtt caa gaa   240
Thr Ala Ser Lys Glu Ala Ala Asp Gly Lys Val Val Val Val Gln Glu
 65                  70                  75                  80

gac ggc tac tcc gtg atg atg tcc aag gaa gag tac ttg gag cgc caa   288
Asp Gly Tyr Ser Val Met Met Ser Lys Glu Glu Tyr Leu Glu Arg Gln
                 85                  90                  95

aag gca ctg ggc aag cca gtt cag ttg aac ttc gat gac gac acc gat   336
Lys Ala Leu Gly Lys Pro Val Gln Leu Asn Phe Asp Asp Asp Thr Asp
            100                 105                 110

ggg aat aca aca caa aca gaa agc gtt gaa tcc caa gag acc gga caa   384
Gly Asn Thr Thr Gln Thr Glu Ser Val Glu Ser Gln Glu Thr Gly Gln
        115                 120                 125

gcc gcg tct gaa acc tca cat cgt gat aac cct gcg tca cag cac       429
Ala Ala Ser Glu Thr Ser His Arg Asp Asn Pro Ala Ser Gln His
    130                 135                 140

tagagtgtaa taagccgtcc gaa                                        452
```

<210> 936
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 936

```
Gly Ile Thr Ala Asn Tyr Ala Phe Lys Gly Lys Lys Val Val Ala Trp
  1               5                  10                  15

Lys Asp Leu Ala Gly Ile Gly Phe Lys Gly Ala Arg Thr Phe Ala Arg
             20                  25                  30

Pro Thr Ser Asp Ala Glu Val Thr Leu Pro Gly Val Thr Phe Asn Ser
         35                  40                  45

Leu Pro Arg Leu Glu Ala Ala Ser His Gly Arg Ile Pro Asp Ala Ile
     50                  55                  60

Thr Ala Ser Lys Glu Ala Ala Asp Gly Lys Val Val Val Val Gln Glu
 65                  70                  75                  80
```

```
Asp Gly Tyr Ser Val Met Met Ser Lys Glu Glu Tyr Leu Glu Arg Gln
                 85                  90                  95

Lys Ala Leu Gly Lys Pro Val Gln Leu Asn Phe Asp Asp Asp Thr Asp
            100                 105                 110

Gly Asn Thr Thr Gln Thr Glu Ser Val Glu Ser Gln Glu Thr Gly Gln
        115                 120                 125

Ala Ala Ser Glu Thr Ser His Arg Asp Asn Pro Ala Ser Gln His
    130                 135                 140
```

<210> 937
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(607)
<223> RXN02014

<400> 937

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agaggacaac aacatgagag cagacgcact aaaacgccgc gaacacatca taaccacaac 60

ctgcaatctc taccgcacac accatcacga ttcgctcacc atg gaa aac att gca   115
                                          Met Glu Asn Ile Ala
                                            1               5

gaa cag gca gga gtg ggt gtt gca act tta tac cga aac ttc ccc gat   163
Glu Gln Ala Gly Val Gly Val Ala Thr Leu Tyr Arg Asn Phe Pro Asp
                10                  15                  20

cgc ttc aca ctg gac atg gca tgc gcc caa tac ctt ttc aac gtg gtg   211
Arg Phe Thr Leu Asp Met Ala Cys Ala Gln Tyr Leu Phe Asn Val Val
            25                  30                  35

atc tcc ctc caa ctc caa gcc atc agc acc ttc ccc acc gac cca gaa   259
Ile Ser Leu Gln Leu Gln Ala Ile Ser Thr Phe Pro Thr Asp Pro Glu
        40                  45                  50

ggc gtg tgg acc tcc ttc aac caa cta ctt ttc gac cgc ggc cta ggc   307
Gly Val Trp Thr Ser Phe Asn Gln Leu Leu Phe Asp Arg Gly Leu Gly
    55                  60                  65

tcc ctc gtc cca gca ctt gcc cca gaa tcc tta gac gac ctc ccc gac   355
Ser Leu Val Pro Ala Leu Ala Pro Glu Ser Leu Asp Asp Leu Pro Asp
70                  75                  80                  85

gag gtc tcc gcc ctg cgt cgc acc aca gag aaa aac acc aca aca ctc   403
Glu Val Ser Ala Leu Arg Arg Thr Thr Glu Lys Asn Thr Thr Thr Leu
                90                  95                  100

atc aac cta gcc aag cag cac gga ctc gta cac cac gac atc gcg ccg   451
Ile Asn Leu Ala Lys Gln His Gly Leu Val His His Asp Ile Ala Pro
            105                 110                 115

ggc acc tac atc gtc ggt ttg atc acc att tcc cgc cca cct atc acc   499
Gly Thr Tyr Ile Val Gly Leu Ile Thr Ile Ser Arg Pro Pro Ile Thr
```

```
        120                 125                 130

gcg ctg gcg aca att tca gaa aac tcc cac aaa gca ctg ctt ggc ctt   547
Ala Leu Ala Thr Ile Ser Glu Asn Ser His Lys Ala Leu Leu Gly Leu
    135                 140                 145

tat ttg tcc ggt ctt aaa cac ggc atg atg gct aac atc gga gaa cat   595
Tyr Leu Ser Gly Leu Lys His Gly Met Met Ala Asn Ile Gly Glu His
150                 155                 160                 165

gac gga aag tcc tgatctagca gtttccttt tag                          630
Asp Gly Lys Ser
```

<210> 938
<211> 169
<212> PRT
<213> Corynebacterium glutamicum

<400> 938

```
Met Glu Asn Ile Ala Glu Gln Ala Gly Val Gly Val Ala Thr Leu Tyr
  1               5                  10                  15

Arg Asn Phe Pro Asp Arg Phe Thr Leu Asp Met Ala Cys Ala Gln Tyr
             20                  25                  30

Leu Phe Asn Val Val Ile Ser Leu Gln Leu Gln Ala Ile Ser Thr Phe
         35                  40                  45

Pro Thr Asp Pro Glu Gly Val Trp Thr Ser Phe Asn Gln Leu Leu Phe
     50                  55                  60

Asp Arg Gly Leu Gly Ser Leu Val Pro Ala Leu Ala Pro Glu Ser Leu
 65                  70                  75                  80

Asp Asp Leu Pro Asp Glu Val Ser Ala Leu Arg Arg Thr Thr Glu Lys
                 85                  90                  95

Asn Thr Thr Thr Leu Ile Asn Leu Ala Lys Gln His Gly Leu Val His
            100                 105                 110

His Asp Ile Ala Pro Gly Thr Tyr Ile Val Gly Leu Ile Thr Ile Ser
        115                 120                 125

Arg Pro Pro Ile Thr Ala Leu Ala Thr Ile Ser Glu Asn Ser His Lys
    130                 135                 140

Ala Leu Leu Gly Leu Tyr Leu Ser Gly Leu Lys His Gly Met Met Ala
145                 150                 155                 160

Asn Ile Gly Glu His Asp Gly Lys Ser
                165
```

<210> 939
<211> 419
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (1)..(396)
<223> FRXA02014

<400> 939

```
atc tcc ctc caa ctc caa gcc atc agc acc ttc ccc acc gac cca gaa   48
Ile Ser Leu Gln Leu Gln Ala Ile Ser Thr Phe Pro Thr Asp Pro Glu
  1               5                  10                  15

ggc gtg tgg acc tcc ttc aac caa cta ctt ttc gac cgc ggc cta ggc   96
Gly Val Trp Thr Ser Phe Asn Gln Leu Leu Phe Asp Arg Gly Leu Gly
             20                  25                  30

tcc ctc gtc cca gca ctt gcc cca gaa tcc tta gac gac ctc ccc gac   144
Ser Leu Val Pro Ala Leu Ala Pro Glu Ser Leu Asp Asp Leu Pro Asp
         35                  40                  45

gag gtc tcc gcc ctg cgt cgc acc aca gag aaa aac acc aca aca ctc   192
Glu Val Ser Ala Leu Arg Arg Thr Thr Glu Lys Asn Thr Thr Thr Leu
     50                  55                  60

atc aac cta gcc aag cag cac gga ctc gta cac cac gac atc gcg ccg   240
Ile Asn Leu Ala Lys Gln His Gly Leu Val His His Asp Ile Ala Pro
 65                  70                  75                  80

ggc acc tac atc gtc ggt ttg atc acc att tcc cgc cca cct atc acc   288
Gly Thr Tyr Ile Val Gly Leu Ile Thr Ile Ser Arg Pro Pro Ile Thr
                 85                  90                  95

gcg ctg gcg aca att tca gaa aac tcc cac aaa gca ctg ctt ggc ctt   336
Ala Leu Ala Thr Ile Ser Glu Asn Ser His Lys Ala Leu Leu Gly Leu
            100                 105                 110

tat ttg tcc ggt ctt aaa cac ggc atg atg gct aac atc gga gaa cat   384
Tyr Leu Ser Gly Leu Lys His Gly Met Met Ala Asn Ile Gly Glu His
        115                 120                 125

gac gga aag tcc tgatctagca gtttccttt tag                         419
Asp Gly Lys Ser
    130
```

<210> 940
<211> 132
<212> PRT
<213> Corynebacterium glutamicum

<400> 940

```
Ile Ser Leu Gln Leu Gln Ala Ile Ser Thr Phe Pro Thr Asp Pro Glu
  1               5                  10                  15

Gly Val Trp Thr Ser Phe Asn Gln Leu Leu Phe Asp Arg Gly Leu Gly
             20                  25                  30

Ser Leu Val Pro Ala Leu Ala Pro Glu Ser Leu Asp Asp Leu Pro Asp
         35                  40                  45

Glu Val Ser Ala Leu Arg Arg Thr Thr Glu Lys Asn Thr Thr Thr Leu
     50                  55                  60

Ile Asn Leu Ala Lys Gln His Gly Leu Val His His Asp Ile Ala Pro
```

```
 65                  70                  75                  80

Gly Thr Tyr Ile Val Gly Leu Ile Thr Ile Ser Arg Pro Pro Ile Thr
                85                  90                  95

Ala Leu Ala Thr Ile Ser Glu Asn Ser His Lys Ala Leu Leu Gly Leu
            100                 105                 110

Tyr Leu Ser Gly Leu Lys His Gly Met Met Ala Asn Ile Gly Glu His
        115                 120                 125

Asp Gly Lys Ser
    130
```

<210> 941
<211> 524
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(501)
<223> RXN02019

<400> 941

```
gaa att cct gct ggc acc aag gtt gag gcc tct gac ctt gga ctt cag   48
Glu Ile Pro Ala Gly Thr Lys Val Glu Ala Ser Asp Leu Gly Leu Gln
  1               5                  10                  15

gca atc cct act tcc cta ctg ccc agc acc tcc tac gat tcg att gac   96
Ala Ile Pro Thr Ser Leu Leu Pro Ser Thr Ser Tyr Asp Ser Ile Asp
             20                  25                  30

gat gta gtt ggg ctc gtt gcg gcc tcc aca tta agt tcc ggg gaa ata   144
Asp Val Val Gly Leu Val Ala Ala Ser Thr Leu Ser Ser Gly Glu Ile
         35                  40                  45

gcc aca aag cct cga ttc gtg ggc acc gaa ttg ata aac tcc att gcg   192
Ala Thr Lys Pro Arg Phe Val Gly Thr Glu Leu Ile Asn Ser Ile Ala
     50                  55                  60

aca aac gtc act gat agc tct ttg gtg gaa gaa att aac atg gtt cca   240
Thr Asn Val Thr Asp Ser Ser Leu Val Glu Glu Ile Asn Met Val Pro
 65                  70                  75                  80

ctc agt ttg gct gaa cct tcc gtc atc ccc cta ctg cag cat ggg gac   288
Leu Ser Leu Ala Glu Pro Ser Val Ile Pro Leu Leu Gln His Gly Asp
                85                  90                  95

acc att tcg gtt gtt tcc caa gac cca gac acc ggt ctc cca gag aac   336
Thr Ile Ser Val Val Ser Gln Asp Pro Asp Thr Gly Leu Pro Glu Asn
            100                 105                 110

att gct gca ggt gga aca gta att ctg gcg ggt ggt aca gac ccc tca   384
Ile Ala Ala Gly Gly Thr Val Ile Leu Ala Gly Gly Thr Asp Pro Ser
        115                 120                 125

acc atc ttg att gcg ctt cca caa tca atc gct gaa aag gtt gca gca   432
Thr Ile Leu Ile Ala Leu Pro Gln Ser Ile Ala Glu Lys Val Ala Ala
    130                 135                 140
```

```
caa tcg ctc aat acc cct ctg gcg gta gtc ctg acc gga gac aga gca   480
Gln Ser Leu Asn Thr Pro Leu Ala Val Val Leu Thr Gly Asp Arg Ala
145                 150                 155                 160

gat aat tac aca acc gaa gaa tagttcccta ttcaaaaaaa agg             524
Asp Asn Tyr Thr Thr Glu Glu
                165
```

<210> 942
<211> 167
<212> PRT
<213> Corynebacterium glutamicum

<400> 942

```
Glu Ile Pro Ala Gly Thr Lys Val Glu Ala Ser Asp Leu Gly Leu Gln
  1               5                  10                  15

Ala Ile Pro Thr Ser Leu Leu Pro Ser Thr Ser Tyr Asp Ser Ile Asp
             20                  25                  30

Asp Val Val Gly Leu Val Ala Ala Ser Thr Leu Ser Ser Gly Glu Ile
         35                  40                  45

Ala Thr Lys Pro Arg Phe Val Gly Thr Glu Leu Ile Asn Ser Ile Ala
     50                  55                  60

Thr Asn Val Thr Asp Ser Ser Leu Val Glu Glu Ile Asn Met Val Pro
 65                  70                  75                  80

Leu Ser Leu Ala Glu Pro Ser Val Ile Pro Leu Leu Gln His Gly Asp
                 85                  90                  95

Thr Ile Ser Val Val Ser Gln Asp Pro Asp Thr Gly Leu Pro Glu Asn
            100                 105                 110

Ile Ala Ala Gly Gly Thr Val Ile Leu Ala Gly Gly Thr Asp Pro Ser
        115                 120                 125

Thr Ile Leu Ile Ala Leu Pro Gln Ser Ile Ala Glu Lys Val Ala Ala
    130                 135                 140

Gln Ser Leu Asn Thr Pro Leu Ala Val Val Leu Thr Gly Asp Arg Ala
145                 150                 155                 160

Asp Asn Tyr Thr Thr Glu Glu
                165
```

<210> 943
<211> 515
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(492)
<223> FRXA02019

<400> 943

```
gct ggc acc aag gtt gag gcc tct gac ctt gga ctt cag gca atc cct   48
Ala Gly Thr Lys Val Glu Ala Ser Asp Leu Gly Leu Gln Ala Ile Pro
  1               5                  10                  15

act tcc cta ctg ccc agc acc tcc tac gat tcg att gac gat gta gtt   96
Thr Ser Leu Leu Pro Ser Thr Ser Tyr Asp Ser Ile Asp Asp Val Val
             20                  25                  30

ggg ctc gtt gcg gcc tcc aca tta agt tcc ggg gaa ata gcc aca aag   144
Gly Leu Val Ala Ala Ser Thr Leu Ser Ser Gly Glu Ile Ala Thr Lys
         35                  40                  45

cct cga ttc gtg ggc acc gaa ttg ata aac tcc att gcg aca aac gtc   192
Pro Arg Phe Val Gly Thr Glu Leu Ile Asn Ser Ile Ala Thr Asn Val
     50                  55                  60

act gat agc tct ttg gtg gaa gaa att aac atg gtt cca ctc agt ttg   240
Thr Asp Ser Ser Leu Val Glu Glu Ile Asn Met Val Pro Leu Ser Leu
 65                  70                  75                  80

gct gaa cct tcc gtc atc ccc cta ctg cag cat ggg gac acc att tcg   288
Ala Glu Pro Ser Val Ile Pro Leu Leu Gln His Gly Asp Thr Ile Ser
                 85                  90                  95

gtt gtt tcc caa gac cca gac acc ggt ctc cca gag aac att gct gca   336
Val Val Ser Gln Asp Pro Asp Thr Gly Leu Pro Glu Asn Ile Ala Ala
            100                 105                 110

ggt gga aca gta att ctg gcg ggt ggt aca gac ccc tca acc atc ttg   384
Gly Gly Thr Val Ile Leu Ala Gly Gly Thr Asp Pro Ser Thr Ile Leu
        115                 120                 125

att gcg ctt cca caa tca atc gct gaa aag gtt gca gca caa tcg ctc   432
Ile Ala Leu Pro Gln Ser Ile Ala Glu Lys Val Ala Ala Gln Ser Leu
    130                 135                 140

aat acc cct ctg gcg gta gtc ctg acc gga gac aga gca aat aat tac   480
Asn Thr Pro Leu Ala Val Val Leu Thr Gly Asp Arg Ala Asn Asn Tyr
145                 150                 155                 160

aca acc gaa gaa tagttcccta ttcaaaaaaa agg                        515
Thr Thr Glu Glu
```

<210> 944
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 944

```
Ala Gly Thr Lys Val Glu Ala Ser Asp Leu Gly Leu Gln Ala Ile Pro
  1               5                  10                  15

Thr Ser Leu Leu Pro Ser Thr Ser Tyr Asp Ser Ile Asp Asp Val Val
             20                  25                  30

Gly Leu Val Ala Ala Ser Thr Leu Ser Ser Gly Glu Ile Ala Thr Lys
         35                  40                  45

Pro Arg Phe Val Gly Thr Glu Leu Ile Asn Ser Ile Ala Thr Asn Val
```

```
     50                  55                  60

Thr Asp Ser Ser Leu Val Glu Glu Ile Asn Met Val Pro Leu Ser Leu
 65                  70                  75                  80

Ala Glu Pro Ser Val Ile Pro Leu Leu Gln His Gly Asp Thr Ile Ser
                 85                  90                  95

Val Val Ser Gln Asp Pro Asp Thr Gly Leu Pro Glu Asn Ile Ala Ala
            100                 105                 110

Gly Gly Thr Val Ile Leu Ala Gly Gly Thr Asp Pro Ser Thr Ile Leu
        115                 120                 125

Ile Ala Leu Pro Gln Ser Ile Ala Glu Lys Val Ala Ala Gln Ser Leu
    130                 135                 140

Asn Thr Pro Leu Ala Val Val Leu Thr Gly Asp Arg Ala Asn Asn Tyr
145                 150                 155                 160

Thr Thr Glu Glu
```

DO NOT ENTER ANY NEW MATTER IN THIS SPACE

<210> 945
<211> 891
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(868)
<223> RXN02023

<400> 945

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gatgtggcag caattttgaa gcagtacctg agcgagtaac cgcattcggg gttatcgtgg 60

gacttccgaa atgtaactag agactagagg aggaaacacg atg gct cct aaa caa   115
                                            Met Ala Pro Lys Gln
                                              1               5

act ccc agc cca gag aag aat cga aac ctg gtg gga cca gtt ctg caa   163
Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val Gly Pro Val Leu Gln
                 10                  15                  20

cgt cgg cag aca gag ggt act ttt gat caa cgc ttg cta gaa atg cgc   211
Arg Arg Gln Thr Glu Gly Thr Phe Asp Gln Arg Leu Leu Glu Met Arg
            25                  30                  35

gct gat cac aat tgg aag cac gcc gat cca tgg cgt gta ctg cgt att   259
Ala Asp His Asn Trp Lys His Ala Asp Pro Trp Arg Val Leu Arg Ile
        40                  45                  50

cag tct gag ttt gtg gcg ggt ttt gat gcc ctc cac gag atg cca aag   307
Gln Ser Glu Phe Val Ala Gly Phe Asp Ala Leu His Glu Met Pro Lys
    55                  60                  65

gcc gta acc gtc ttt ggt tcc gca cgc att aaa gag gat cac ccg tac   355
Ala Val Thr Val Phe Gly Ser Ala Arg Ile Lys Glu Asp His Pro Tyr
70                  75                  80                  85
```

```
tac aag gcg ggt gta gaa ctt ggt gaa aag ctc gtt gca gcg gac tac   403
Tyr Lys Ala Gly Val Glu Leu Gly Glu Lys Leu Val Ala Ala Asp Tyr
                 90                  95                 100

gca gtt gtc acc ggt ggc ggt cca ggt ctg atg gaa gcc ccc aat aag   451
Ala Val Val Thr Gly Gly Gly Pro Gly Leu Met Glu Ala Pro Asn Lys
            105                 110                 115

ggg gca agc gag gcc aat ggt tta tca gtt ggt ctg ggc att gag ttg   499
Gly Ala Ser Glu Ala Asn Gly Leu Ser Val Gly Leu Gly Ile Glu Leu
        120                 125                 130

cca cat gaa cag cat ctg aac cct tat gtg gat ttg ggt ctg aac ttc   547
Pro His Glu Gln His Leu Asn Pro Tyr Val Asp Leu Gly Leu Asn Phe
    135                 140                 145

cgg tac ttc ttc gca cgc aag acc atg ttc ctg aaa tac tcc cag gct   595
Arg Tyr Phe Phe Ala Arg Lys Thr Met Phe Leu Lys Tyr Ser Gln Ala
150                 155                 160                 165

ttt gtg tgt ctg cct ggt ggt ttc ggc acg ctc gat gag ctt ttc gag   643
Phe Val Cys Leu Pro Gly Gly Phe Gly Thr Leu Asp Glu Leu Phe Glu
                170                 175                 180

gtc ctc tgc atg gta caa acc ggc aag gta ccc aac ttt ccc atc gtg   691
Val Leu Cys Met Val Gln Thr Gly Lys Val Pro Asn Phe Pro Ile Val
            185                 190                 195

ctg atc ggc act gag ttc tgg gca ggt ttg gtg gat tgg atc cgt cac   739
Leu Ile Gly Thr Glu Phe Trp Ala Gly Leu Val Asp Trp Ile Arg His
        200                 205                 210

cgc ctg gta gag gaa ggc atg atc gat gag aag gat gtt gac cgg atg   787
Arg Leu Val Glu Glu Gly Met Ile Asp Glu Lys Asp Val Asp Arg Met
    215                 220                 225

ttg gtc act gat gac ctg gat cag gcc gtc aaa ttc atc gtc gat gca   835
Leu Val Thr Asp Asp Leu Asp Gln Ala Val Lys Phe Ile Val Asp Ala
230                 235                 240                 245

cac gct gga ttg gac gta gcg cgt ctc cac aat taagcagtgg ctacattagg 888
His Ala Gly Leu Asp Val Ala Arg Leu His Asn
                250                 255

tgt                                                               891


<210> 946
<211> 256
<212> PRT
<213> Corynebacterium glutamicum

<400> 946
Met Ala Pro Lys Gln Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val
  1               5                  10                  15

Gly Pro Val Leu Gln Arg Arg Gln Thr Glu Gly Thr Phe Asp Gln Arg
             20                  25                  30

Leu Leu Glu Met Arg Ala Asp His Asn Trp Lys His Ala Asp Pro Trp
         35                  40                  45
```

```
Arg Val Leu Arg Ile Gln Ser Glu Phe Val Ala Gly Phe Asp Ala Leu
     50                  55                  60

His Glu Met Pro Lys Ala Val Thr Val Phe Gly Ser Ala Arg Ile Lys
 65                  70                  75                  80

Glu Asp His Pro Tyr Tyr Lys Ala Gly Val Glu Leu Gly Glu Lys Leu
                 85                  90                  95

Val Ala Ala Asp Tyr Ala Val Val Thr Gly Gly Gly Pro Gly Leu Met
            100                 105                 110

Glu Ala Pro Asn Lys Gly Ala Ser Glu Ala Asn Gly Leu Ser Val Gly
        115                 120                 125

Leu Gly Ile Glu Leu Pro His Glu Gln His Leu Asn Pro Tyr Val Asp
    130                 135                 140

Leu Gly Leu Asn Phe Arg Tyr Phe Phe Ala Arg Lys Thr Met Phe Leu
145                 150                 155                 160

Lys Tyr Ser Gln Ala Phe Val Cys Leu Pro Gly Gly Phe Gly Thr Leu
                165                 170                 175

Asp Glu Leu Phe Glu Val Leu Cys Met Val Gln Thr Gly Lys Val Pro
            180                 185                 190

Asn Phe Pro Ile Val Leu Ile Gly Thr Glu Phe Trp Ala Gly Leu Val
        195                 200                 205

Asp Trp Ile Arg His Arg Leu Val Glu Glu Gly Met Ile Asp Glu Lys
    210                 215                 220

Asp Val Asp Arg Met Leu Val Thr Asp Asp Leu Asp Gln Ala Val Lys
225                 230                 235                 240

Phe Ile Val Asp Ala His Ala Gly Leu Asp Val Ala Arg Leu His Asn
                245                 250                 255
```

<210> 947
<211> 891
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(868)
<223> FRXA02023

<400> 947
gatgtggcag caattttgaa gcagtacctg agcgagtaac cgcattcggg gttatcgtgg 60

gacttccgaa atgtaactag agactagagg aggaaacacg atg gct cct aaa caa 115
                                                Met Ala Pro Lys Gln
                                                  1   5

```
act ccc agc cca gag aag aat cga aac ctg gtg gga cca gtt ctg caa   163
Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val Gly Pro Val Leu Gln
                10                  15                  20

cgt cgg cag aca gag ggt act ttt gat caa cgc ttg cta gaa atg cgc   211
Arg Arg Gln Thr Glu Gly Thr Phe Asp Gln Arg Leu Leu Glu Met Arg
            25                  30                  35

gct gat cac aat tgg aag cac gcc gat cca tgg cgt gta ctg cgt att   259
Ala Asp His Asn Trp Lys His Ala Asp Pro Trp Arg Val Leu Arg Ile
        40                  45                  50

cag tct gag ttt gtg gcg ggt ttt gat gcc ctc cac gag atg cca aag   307
Gln Ser Glu Phe Val Ala Gly Phe Asp Ala Leu His Glu Met Pro Lys
    55                  60                  65

gcc gta acc gtc ttt ggt tcc gca cgc att aaa gag gat cac ccg tac   355
Ala Val Thr Val Phe Gly Ser Ala Arg Ile Lys Glu Asp His Pro Tyr
70                  75                  80                  85

tac aag gcg ggt gta gaa ctt ggt gaa aag ctc gtt gct gct gac tac   403
Tyr Lys Ala Gly Val Glu Leu Gly Glu Lys Leu Val Ala Ala Asp Tyr
                90                  95                  100

gca gtt gtc acc ggt ggc ggt cca ggt ctg atg gaa gcc ccc aat aag   451
Ala Val Val Thr Gly Gly Gly Pro Gly Leu Met Glu Ala Pro Asn Lys
            105                 110                 115

ggg gca agc gag gcc aat ggt tta tca gtt ggt ctg ggc att gag ttg   499
Gly Ala Ser Glu Ala Asn Gly Leu Ser Val Gly Leu Gly Ile Glu Leu
        120                 125                 130

cca cat gaa cag cac ctg aac cct tat gtg gat ttg ggt ctg aac ttc   547
Pro His Glu Gln His Leu Asn Pro Tyr Val Asp Leu Gly Leu Asn Phe
    135                 140                 145

cgg tac ttc ttc gca cgc aag acc atg ttc ctg aaa tac tcc cag gct   595
Arg Tyr Phe Phe Ala Arg Lys Thr Met Phe Leu Lys Tyr Ser Gln Ala
150                 155                 160                 165

ttt gtg tgt ctg cct ggc ggt ttc ggc acg ctc gat gag ctt ttc gag   643
Phe Val Cys Leu Pro Gly Gly Phe Gly Thr Leu Asp Glu Leu Phe Glu
                170                 175                 180

gtc ctc tgc atg gta caa acc ggc aag gta acc aac ttt ccc atc gtg   691
Val Leu Cys Met Val Gln Thr Gly Lys Val Thr Asn Phe Pro Ile Val
            185                 190                 195

ctg atc ggc act gag ttc tgg gca ggt ttg gtg gat tgg atc cgt cac   739
Leu Ile Gly Thr Glu Phe Trp Ala Gly Leu Val Asp Trp Ile Arg His
        200                 205                 210

cgc ctg gta gag gaa ggc atg atc gat gag aag gat gtt gac cgg atg   787
Arg Leu Val Glu Glu Gly Met Ile Asp Glu Lys Asp Val Asp Arg Met
    215                 220                 225

ttg gtc act gat gac ctg gat cag gcc gtc aaa ttc atc gtc gat gca   835
Leu Val Thr Asp Asp Leu Asp Gln Ala Val Lys Phe Ile Val Asp Ala
230                 235                 240                 245

cac gct gga ttg gac gta gcg cgt ctc cac aat taagcagtgg ctacattagg 888
```

```
His Ala Gly Leu Asp Val Ala Arg Leu His Asn
                250                 255

tgt                                                                    891


<210> 948
<211> 256
<212> PRT
<213> Corynebacterium glutamicum

<400> 948
Met Ala Pro Lys Gln Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val
  1               5                  10                  15

Gly Pro Val Leu Gln Arg Arg Gln Thr Glu Gly Thr Phe Asp Gln Arg
             20                  25                  30

Leu Leu Glu Met Arg Ala Asp His Asn Trp Lys His Ala Asp Pro Trp
         35                  40                  45

Arg Val Leu Arg Ile Gln Ser Glu Phe Val Ala Gly Phe Asp Ala Leu
     50                  55                  60

His Glu Met Pro Lys Ala Val Thr Val Phe Gly Ser Ala Arg Ile Lys
 65                  70                  75                  80

Glu Asp His Pro Tyr Tyr Lys Ala Gly Val Glu Leu Gly Glu Lys Leu
                 85                  90                  95

Val Ala Ala Asp Tyr Ala Val Val Thr Gly Gly Gly Pro Gly Leu Met
            100                 105                 110

Glu Ala Pro Asn Lys Gly Ala Ser Glu Ala Asn Gly Leu Ser Val Gly
        115                 120                 125

Leu Gly Ile Glu Leu Pro His Glu Gln His Leu Asn Pro Tyr Val Asp
    130                 135                 140

Leu Gly Leu Asn Phe Arg Tyr Phe Phe Ala Arg Lys Thr Met Phe Leu
145                 150                 155                 160

Lys Tyr Ser Gln Ala Phe Val Cys Leu Pro Gly Gly Phe Gly Thr Leu
                165                 170                 175

Asp Glu Leu Phe Glu Val Leu Cys Met Val Gln Thr Gly Lys Val Thr
            180                 185                 190

Asn Phe Pro Ile Val Leu Ile Gly Thr Glu Phe Trp Ala Gly Leu Val
        195                 200                 205

Asp Trp Ile Arg His Arg Leu Val Glu Glu Gly Met Ile Asp Glu Lys
    210                 215                 220

Asp Val Asp Arg Met Leu Val Thr Asp Asp Leu Asp Gln Ala Val Lys
225                 230                 235                 240

Phe Ile Val Asp Ala His Ala Gly Leu Asp Val Ala Arg Leu His Asn
                245                 250                 255
```

<210> 949
<211> 693
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(670)
<223> RXN02032

<400> 949
cttaaaaagg ggctttatcg gttcaggcga gcgagacctt cggcgttcac acttcgccgg 60

ggtctatttt ttatgcccag gcacggctca taggagaacc atg ccc ttt cta caa 115
Met Pro Phe Leu Gln
1 5

atc tct ctg ctt tcc atc ggt gtc gcc gcc gat gcg ttt gct tgt tcc 163
Ile Ser Leu Leu Ser Ile Gly Val Ala Ala Asp Ala Phe Ala Cys Ser
10 15 20

gtt gtc cgc ggc acc gcc att caa gtc aac ctt ttc aaa cgc gca ctt 211
Val Val Arg Gly Thr Ala Ile Gln Val Asn Leu Phe Lys Arg Ala Leu
25 30 35

gtt ctc gcg ggc atc ttt ggt gtc ttc caa gcg gca atg cct tta atc 259
Val Leu Ala Gly Ile Phe Gly Val Phe Gln Ala Ala Met Pro Leu Ile
40 45 50

ggc tgg ttc att ggc cgt ttc ttt gct gga atc acc ttc atc gct gaa 307
Gly Trp Phe Ile Gly Arg Phe Phe Ala Gly Ile Thr Phe Ile Ala Glu
55 60 65

att gat cac tgg atc gct ttt gca cta ttg ggt att gtc ggc acc aaa 355
Ile Asp His Trp Ile Ala Phe Ala Leu Leu Gly Ile Val Gly Thr Lys
70 75 80 85

atg atc tgg gat gcc ttc caa cct gaa gat gat gaa acc att gtc gat 403
Met Ile Trp Asp Ala Phe Gln Pro Glu Asp Asp Glu Thr Ile Val Asp
90 95 100

gac ggc cgc gtt caa ttt aga cca gca att atc ctg ggg cta gcc acc 451
Asp Gly Arg Val Gln Phe Arg Pro Ala Ile Ile Leu Gly Leu Ala Thr
105 110 115

agc att gac gca tta gcc gta ggc atg ggc ctg gca ttc gtg gaa gtt 499
Ser Ile Asp Ala Leu Ala Val Gly Met Gly Leu Ala Phe Val Glu Val
120 125 130

tcc atc ctc aaa gtg gca ctg tcc atg ggc agc atc acc ttc gca ctt 547
Ser Ile Leu Lys Val Ala Leu Ser Met Gly Ser Ile Thr Phe Ala Leu
135 140 145

tcg ctt gct ggc gcc tgg atc gga cac cat ggt gga gga aag ttt ggc 595
Ser Leu Ala Gly Ala Trp Ile Gly His His Gly Gly Gly Lys Phe Gly
150 155 160 165

aag tgg gct acg att ctt ggc gga ata atc ttg atc gga atc ggc gca 643

```
Lys Trp Ala Thr Ile Leu Gly Gly Ile Ile Leu Ile Gly Ile Gly Ala
                170                 175                 180

aac atc gtc tac gaa cac ctc agc gcg taaccctcgg cgcattatcc         690
Asn Ile Val Tyr Glu His Leu Ser Ala
            185                 190

tca                                                               693
```

<210> 950
<211> 190
<212> PRT
<213> Corynebacterium glutamicum

<400> 950

```
Met Pro Phe Leu Gln Ile Ser Leu Leu Ser Ile Gly Val Ala Ala Asp
  1               5                  10                  15

Ala Phe Ala Cys Ser Val Val Arg Gly Thr Ala Ile Gln Val Asn Leu
             20                  25                  30

Phe Lys Arg Ala Leu Val Leu Ala Gly Ile Phe Gly Val Phe Gln Ala
         35                  40                  45

Ala Met Pro Leu Ile Gly Trp Phe Ile Gly Arg Phe Phe Ala Gly Ile
     50                  55                  60

Thr Phe Ile Ala Glu Ile Asp His Trp Ile Ala Phe Ala Leu Leu Gly
 65                  70                  75                  80

Ile Val Gly Thr Lys Met Ile Trp Asp Ala Phe Gln Pro Glu Asp Asp
                 85                  90                  95

Glu Thr Ile Val Asp Asp Gly Arg Val Gln Phe Arg Pro Ala Ile Ile
            100                 105                 110

Leu Gly Leu Ala Thr Ser Ile Asp Ala Leu Ala Val Gly Met Gly Leu
        115                 120                 125

Ala Phe Val Glu Val Ser Ile Leu Lys Val Ala Leu Ser Met Gly Ser
    130                 135                 140

Ile Thr Phe Ala Leu Ser Leu Ala Gly Ala Trp Ile Gly His His Gly
145                 150                 155                 160

Gly Gly Lys Phe Gly Lys Trp Ala Thr Ile Leu Gly Gly Ile Ile Leu
                165                 170                 175

Ile Gly Ile Gly Ala Asn Ile Val Tyr Glu His Leu Ser Ala
            180                 185                 190
```

<210> 951
<211> 693
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(670)

<223> FRXA02032

<400> 951

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cttaaaaagg ggctttatcg gttcaggcga gcgagacctt cggcgttcac acttcgccgg 60

ggtctatttt ttatgcccag gcacggctca taggagaacc atg ccc ttt cta caa   115
                                            Met Pro Phe Leu Gln
                                              1               5

atc tct ctg ctt tcc atc ggt gtc gcc gcc gat gcg ttt gct tgt tcc   163
Ile Ser Leu Leu Ser Ile Gly Val Ala Ala Asp Ala Phe Ala Cys Ser
                 10                  15                  20

gtt gtc cgc ggc acc gcc att caa gtc aac ctt ttc aaa cgc gca ctt   211
Val Val Arg Gly Thr Ala Ile Gln Val Asn Leu Phe Lys Arg Ala Leu
             25                  30                  35

gtt ctc gcg ggc atc ttt ggt gtc ttc caa gcg gca atg cct tta atc   259
Val Leu Ala Gly Ile Phe Gly Val Phe Gln Ala Ala Met Pro Leu Ile
         40                  45                  50

ggc tgg ttc att ggc cgt ttc ttt gct gga atc acc ttc atc gct gaa   307
Gly Trp Phe Ile Gly Arg Phe Phe Ala Gly Ile Thr Phe Ile Ala Glu
     55                  60                  65

att gat cac tgg atc gct ttt gca cta ttg ggt att gtc ggc acc aaa   355
Ile Asp His Trp Ile Ala Phe Ala Leu Leu Gly Ile Val Gly Thr Lys
 70                  75                  80                  85

atg atc tgg gat gcc ttc caa cct gaa gat gat gaa acc att gtc gat   403
Met Ile Trp Asp Ala Phe Gln Pro Glu Asp Asp Glu Thr Ile Val Asp
                 90                  95                 100

gac ggc cgc gtt caa ttt aga cca gca att atc ctg ggg cta gcc acc   451
Asp Gly Arg Val Gln Phe Arg Pro Ala Ile Ile Leu Gly Leu Ala Thr
             105                 110                 115

agc att gac gca tta gcc gta ggc atg ggc ctg gca ttc gtg gaa gtt   499
Ser Ile Asp Ala Leu Ala Val Gly Met Gly Leu Ala Phe Val Glu Val
         120                 125                 130

tcc atc ctc aaa gtg gca ctg tcc atg ggc agc atc acc ttc gca ctt   547
Ser Ile Leu Lys Val Ala Leu Ser Met Gly Ser Ile Thr Phe Ala Leu
     135                 140                 145

tcg ctt gct ggc gcc tgg atc gga cac cat ggt gga gga aag ttt ggc   595
Ser Leu Ala Gly Ala Trp Ile Gly His His Gly Gly Gly Lys Phe Gly
150                 155                 160                 165

aag tgg gct acg att ctt ggc gga ata atc ttg atc gga atc ggc gca   643
Lys Trp Ala Thr Ile Leu Gly Gly Ile Ile Leu Ile Gly Ile Gly Ala
                170                 175                 180

aac atc gtc tac gaa cac ctc agc gcg taaccctcgg cgcattatcc         690
Asn Ile Val Tyr Glu His Leu Ser Ala
            185                 190

tca                                                              693
```

<210> 952

<211> 190
<212> PRT
<213> Corynebacterium glutamicum

<400> 952

```
Met Pro Phe Leu Gln Ile Ser Leu Leu Ser Ile Gly Val Ala Ala Asp
  1               5                  10                  15

Ala Phe Ala Cys Ser Val Val Arg Gly Thr Ala Ile Gln Val Asn Leu
             20                  25                  30

Phe Lys Arg Ala Leu Val Leu Ala Gly Ile Phe Gly Val Phe Gln Ala
         35                  40                  45

Ala Met Pro Leu Ile Gly Trp Phe Ile Gly Arg Phe Phe Ala Gly Ile
     50                  55                  60

Thr Phe Ile Ala Glu Ile Asp His Trp Ile Ala Phe Ala Leu Leu Gly
 65                  70                  75                  80

Ile Val Gly Thr Lys Met Ile Trp Asp Ala Phe Gln Pro Glu Asp Asp
                 85                  90                  95

Glu Thr Ile Val Asp Asp Gly Arg Val Gln Phe Arg Pro Ala Ile Ile
            100                 105                 110

Leu Gly Leu Ala Thr Ser Ile Asp Ala Leu Ala Val Gly Met Gly Leu
        115                 120                 125

Ala Phe Val Glu Val Ser Ile Leu Lys Val Ala Leu Ser Met Gly Ser
    130                 135                 140

Ile Thr Phe Ala Leu Ser Leu Ala Gly Ala Trp Ile Gly His His Gly
145                 150                 155                 160

Gly Gly Lys Phe Gly Lys Trp Ala Thr Ile Leu Gly Gly Ile Ile Leu
                165                 170                 175

Ile Gly Ile Gly Ala Asn Ile Val Tyr Glu His Leu Ser Ala
            180                 185                 190
```

<210> 953
<211> 863
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(840)
<223> RXN02039

<400> 953

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aag gcg tcg ata agc aat tta agc ttt tgg acg tcc acc tcc acc acc   48
Lys Ala Ser Ile Ser Asn Leu Ser Phe Trp Thr Ser Thr Ser Thr Thr
  1               5                  10                  15

gca ccc ctt tgg ctc gtg ggc acg ctt gtg tgg ctg gcg gtg cag gcg   96
Ala Pro Leu Trp Leu Val Gly Thr Leu Val Trp Leu Ala Val Gln Ala
             20                  25                  30
```

```
gtg atg cat gac ggc gag ctt tac cat gtg gaa gtt ccc acg att gcg   144
Val Met His Asp Gly Glu Leu Tyr His Val Glu Val Pro Thr Ile Ala
         35                  40                  45

ctg gtc atc ggc ttt ggc gcg cag ctt ctg atc ggt gtg atg agt tat   192
Leu Val Ile Gly Phe Gly Ala Gln Leu Leu Ile Gly Val Met Ser Tyr
     50                  55                  60

cta ctg ccg tcg acg atg ggt ggc ggc gcg agc gcg gtg cgg act gga   240
Leu Leu Pro Ser Thr Met Gly Gly Gly Ala Ser Ala Val Arg Thr Gly
 65                  70                  75                  80

acg cac att tta aac act gcg ggg ctg ttt agg tgg acg ctg atc aac   288
Thr His Ile Leu Asn Thr Ala Gly Leu Phe Arg Trp Thr Leu Ile Asn
                 85                  90                  95

ggt ggc ctg gcg att tgg ctg ctc acc gac aat tcg tgg ctg cgc gtc   336
Gly Gly Leu Ala Ile Trp Leu Leu Thr Asp Asn Ser Trp Leu Arg Val
            100                 105                 110

gtg gtg tct ctg ctg agt atc gga gcg ttg gca gtt ttt gtc att ctg   384
Val Val Ser Leu Leu Ser Ile Gly Ala Leu Ala Val Phe Val Ile Leu
        115                 120                 125

ctg ccc aag gct gtg cgg gcg cag cgc gga gtg atc acc aaa aag cgc   432
Leu Pro Lys Ala Val Arg Ala Gln Arg Gly Val Ile Thr Lys Lys Arg
    130                 135                 140

gaa cca att act ccg ccg gag gag cct cga ctc aat caa att acc gcg   480
Glu Pro Ile Thr Pro Pro Glu Glu Pro Arg Leu Asn Gln Ile Thr Ala
145                 150                 155                 160

gga atc tct gtg ctt gcc ctg att ttg gca gca ttc ggt ggg ctc aac   528
Gly Ile Ser Val Leu Ala Leu Ile Leu Ala Ala Phe Gly Gly Leu Asn
                165                 170                 175

ccc ggt gtt gcg ccg gtg gca agc tca aat gaa gac gtc tat gct gtg   576
Pro Gly Val Ala Pro Val Ala Ser Ser Asn Glu Asp Val Tyr Ala Val
            180                 185                 190

acc att acc gca ggt gac atg gtg ttt atc cct gat gtg att gaa gtg   624
Thr Ile Thr Ala Gly Asp Met Val Phe Ile Pro Asp Val Ile Glu Val
        195                 200                 205

cct gct ggt aaa tca ctc gaa gtc acg atg ctc aac gaa gac gac atg   672
Pro Ala Gly Lys Ser Leu Glu Val Thr Met Leu Asn Glu Asp Asp Met
    210                 215                 220

gtg cac gat ctg aaa ttt gcc aac ggt gtg caa acc gga cgt gtg gcg   720
Val His Asp Leu Lys Phe Ala Asn Gly Val Gln Thr Gly Arg Val Ala
225                 230                 235                 240

cca ggt gat gaa att acg gtg acc gtc ggc gat att tcc gaa gac atg   768
Pro Gly Asp Glu Ile Thr Val Thr Val Gly Asp Ile Ser Glu Asp Met
                245                 250                 255

gac ggc tgg tgc acc atc gct ggg cac cgc gcg caa gga atg gat ctg   816
Asp Gly Trp Cys Thr Ile Ala Gly His Arg Ala Gln Gly Met Asp Leu
            260                 265                 270

gaa gta aag gtt gcg gct ccg aat taaccaaggg ctgctgaaaa act         863
```

```
Glu Val Lys Val Ala Ala Pro Asn
        275                 280


<210> 954
<211> 280
<212> PRT
<213> Corynebacterium glutamicum

<400> 954
Lys Ala Ser Ile Ser Asn Leu Ser Phe Trp Thr Ser Thr Ser Thr Thr
  1               5                  10                  15

Ala Pro Leu Trp Leu Val Gly Thr Leu Val Trp Leu Ala Val Gln Ala
             20                  25                  30

Val Met His Asp Gly Glu Leu Tyr His Val Glu Val Pro Thr Ile Ala
         35                  40                  45

Leu Val Ile Gly Phe Gly Ala Gln Leu Leu Ile Gly Val Met Ser Tyr
     50                  55                  60

Leu Leu Pro Ser Thr Met Gly Gly Gly Ala Ser Ala Val Arg Thr Gly
 65                  70                  75                  80

Thr His Ile Leu Asn Thr Ala Gly Leu Phe Arg Trp Thr Leu Ile Asn
                 85                  90                  95

Gly Gly Leu Ala Ile Trp Leu Leu Thr Asp Asn Ser Trp Leu Arg Val
            100                 105                 110

Val Val Ser Leu Leu Ser Ile Gly Ala Leu Ala Val Phe Val Ile Leu
        115                 120                 125

Leu Pro Lys Ala Val Arg Ala Gln Arg Gly Val Ile Thr Lys Lys Arg
    130                 135                 140

Glu Pro Ile Thr Pro Pro Glu Glu Pro Arg Leu Asn Gln Ile Thr Ala
145                 150                 155                 160

Gly Ile Ser Val Leu Ala Leu Ile Leu Ala Ala Phe Gly Gly Leu Asn
                165                 170                 175

Pro Gly Val Ala Pro Val Ala Ser Ser Asn Glu Asp Val Tyr Ala Val
            180                 185                 190

Thr Ile Thr Ala Gly Asp Met Val Phe Ile Pro Asp Val Ile Glu Val
        195                 200                 205

Pro Ala Gly Lys Ser Leu Glu Val Thr Met Leu Asn Glu Asp Asp Met
    210                 215                 220

Val His Asp Leu Lys Phe Ala Asn Gly Val Gln Thr Gly Arg Val Ala
225                 230                 235                 240

Pro Gly Asp Glu Ile Thr Val Thr Val Gly Asp Ile Ser Glu Asp Met
                245                 250                 255

Asp Gly Trp Cys Thr Ile Ala Gly His Arg Ala Gln Gly Met Asp Leu
            260                 265                 270
```

```
Glu Val Lys Val Ala Ala Pro Asn
        275                 280


<210> 955
<211> 833
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(810)
<223> FRXA02039

<400> 955
acg tcc acc tcc acc acc gca ccc ctt tgg ctc gtg ggc acg ctt gtg   48
Thr Ser Thr Ser Thr Thr Ala Pro Leu Trp Leu Val Gly Thr Leu Val
  1               5                  10                  15

tgg ctg gcg gtg cag gcg gtg atg cat gac ggc gag ctt tac cat gtg   96
Trp Leu Ala Val Gln Ala Val Met His Asp Gly Glu Leu Tyr His Val
             20                  25                  30

gaa gtt ccc acg att gcg ctg gtc atc ggc ttt ggc gcg cag ctt ctg   144
Glu Val Pro Thr Ile Ala Leu Val Ile Gly Phe Gly Ala Gln Leu Leu
         35                  40                  45

atc ggt gtg atg agt tat cta ctg ccg tcg acg atg ggt ggc ggc gcg   192
Ile Gly Val Met Ser Tyr Leu Leu Pro Ser Thr Met Gly Gly Gly Ala
     50                  55                  60

agc gcg gtg cgg act gga acg cac att tta aac act gcg ggg ctg ttt   240
Ser Ala Val Arg Thr Gly Thr His Ile Leu Asn Thr Ala Gly Leu Phe
 65                  70                  75                  80

agg tgg acg ctg atc aac ggt ggc ctg gcg att tgg ctg ctc acc gac   288
Arg Trp Thr Leu Ile Asn Gly Gly Leu Ala Ile Trp Leu Leu Thr Asp
                 85                  90                  95

aat tcg tgg ctg cgc gtc gtg gtg tct ctg ctg agt atc gga gcg ttg   336
Asn Ser Trp Leu Arg Val Val Val Ser Leu Leu Ser Ile Gly Ala Leu
            100                 105                 110

gca gtt ttt gtc att ctg ctg ccc aag gct gtg cgg gcg cag cgc gga   384
Ala Val Phe Val Ile Leu Leu Pro Lys Ala Val Arg Ala Gln Arg Gly
        115                 120                 125

gtg atc acc aaa aag cgc gaa cca att act ccg ccg gag gag cct cga   432
Val Ile Thr Lys Lys Arg Glu Pro Ile Thr Pro Pro Glu Glu Pro Arg
    130                 135                 140

ctc aat caa att acc gcg gga atc tct gtg ctt gcc ctg att ttg gca   480
Leu Asn Gln Ile Thr Ala Gly Ile Ser Val Leu Ala Leu Ile Leu Ala
145                 150                 155                 160

gca ttc ggt ggg ctc aac ccc ggt gtt gcg ccg gtg gca agc tca aat   528
Ala Phe Gly Gly Leu Asn Pro Gly Val Ala Pro Val Ala Ser Ser Asn
                165                 170                 175

gaa gac gtc tat gct gtg acc att acc gca ggt gac atg gtg ttt atc   576
Glu Asp Val Tyr Ala Val Thr Ile Thr Ala Gly Asp Met Val Phe Ile
```

```
            180                 185                 190

cct gat gtg att gaa gtg cct gct ggt aaa tca ctc gaa gtc acg atg   624
Pro Asp Val Ile Glu Val Pro Ala Gly Lys Ser Leu Glu Val Thr Met
        195                 200                 205

ctc aac gaa gac gac atg gtg cac gat ctg aaa ttt gcc aac ggt gtg   672
Leu Asn Glu Asp Asp Met Val His Asp Leu Lys Phe Ala Asn Gly Val
    210                 215                 220

caa acc gga cgt gtg gcg cca ggt gat gaa att acg gtg acc gtc ggc   720
Gln Thr Gly Arg Val Ala Pro Gly Asp Glu Ile Thr Val Thr Val Gly
225                 230                 235                 240

gat att tcc gaa gac atg gac ggc tgg tgc acc atc gct ggg cac cgc   768
Asp Ile Ser Glu Asp Met Asp Gly Trp Cys Thr Ile Ala Gly His Arg
                245                 250                 255

gcg caa gga atg gat ctg gaa gta aag gtt gcg gct ccg aat            810
Ala Gln Gly Met Asp Leu Glu Val Lys Val Ala Ala Pro Asn
            260                 265                 270

taaccaaggg ctgctgaaaa act                                         833


<210> 956
<211> 270
<212> PRT
<213> Corynebacterium glutamicum

<400> 956
Thr Ser Thr Ser Thr Thr Ala Pro Leu Trp Leu Val Gly Thr Leu Val
  1               5                  10                  15

Trp Leu Ala Val Gln Ala Val Met His Asp Gly Glu Leu Tyr His Val
             20                  25                  30

Glu Val Pro Thr Ile Ala Leu Val Ile Gly Phe Gly Ala Gln Leu Leu
         35                  40                  45

Ile Gly Val Met Ser Tyr Leu Leu Pro Ser Thr Met Gly Gly Gly Ala
     50                  55                  60

Ser Ala Val Arg Thr Gly Thr His Ile Leu Asn Thr Ala Gly Leu Phe
 65                  70                  75                  80

Arg Trp Thr Leu Ile Asn Gly Gly Leu Ala Ile Trp Leu Leu Thr Asp
                85                  90                  95

Asn Ser Trp Leu Arg Val Val Val Ser Leu Leu Ser Ile Gly Ala Leu
            100                 105                 110

Ala Val Phe Val Ile Leu Leu Pro Lys Ala Val Arg Ala Gln Arg Gly
        115                 120                 125

Val Ile Thr Lys Lys Arg Glu Pro Ile Thr Pro Pro Glu Glu Pro Arg
    130                 135                 140

Leu Asn Gln Ile Thr Ala Gly Ile Ser Val Leu Ala Leu Ile Leu Ala
145                 150                 155                 160
```

```
Ala Phe Gly Gly Leu Asn Pro Gly Val Ala Pro Val Ala Ser Ser Asn
                165                 170                 175

Glu Asp Val Tyr Ala Val Thr Ile Thr Ala Gly Asp Met Val Phe Ile
            180                 185                 190

Pro Asp Val Ile Glu Val Pro Ala Gly Lys Ser Leu Glu Val Thr Met
        195                 200                 205

Leu Asn Glu Asp Asp Met Val His Asp Leu Lys Phe Ala Asn Gly Val
    210                 215                 220

Gln Thr Gly Arg Val Ala Pro Gly Asp Glu Ile Thr Val Thr Val Gly
225                 230                 235                 240

Asp Ile Ser Glu Asp Met Asp Gly Trp Cys Thr Ile Ala Gly His Arg
                245                 250                 255

Ala Gln Gly Met Asp Leu Glu Val Lys Val Ala Ala Pro Asn
            260                 265                 270
```

<210> 957
<211> 1506
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1483)
<223> RXN02044

<400> 957

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ttactttctt aagtaattta acgaatttgg tctcgaaact gacctaaaac cccatgttgc 60

tagttggtgc aaaccaataa tagctatagc cccaatacaa atg gtc acc cca atc   115
                                              Met Val Thr Pro Ile
                                                1               5

atg ggg aat tcg aac tct atc ctg ggc att tac cgt cag aaa atc caa   163
Met Gly Asn Ser Asn Ser Ile Leu Gly Ile Tyr Arg Gln Lys Ile Gln
                10                  15                  20

aat cga cat ttg gtt tct acg ctt ttt agg gca tac ttc cca atc gtg   211
Asn Arg His Leu Val Ser Thr Leu Phe Arg Ala Tyr Phe Pro Ile Val
            25                  30                  35

acc gag ctg att att tta ttg att gtt atc gtg acg gcg ctc gcc ttc   259
Thr Glu Leu Ile Ile Leu Leu Ile Val Ile Val Thr Ala Leu Ala Phe
        40                  45                  50

gat ttc aca aac gga ttc cac gac acc ggc aat gcg atg gcc aca tcc   307
Asp Phe Thr Asn Gly Phe His Asp Thr Gly Asn Ala Met Ala Thr Ser
    55                  60                  65

att gcc aca ggc gct cta aaa cct aaa gtc gcc gtg gca cta tcc gcc   355
Ile Ala Thr Gly Ala Leu Lys Pro Lys Val Ala Val Ala Leu Ser Ala
70                  75                  80                  85

tca ctg aac ctt gtt ggc gca ttc ctc tct gta gaa gtt gcg aca act   403
Ser Leu Asn Leu Val Gly Ala Phe Leu Ser Val Glu Val Ala Thr Thr
```

```
                    90                  95                 100

gtt gcc aaa ggc gtt gtt gac ctc gac caa ttc gac cta agc aat gcc   451
Val Ala Lys Gly Val Val Asp Leu Asp Gln Phe Asp Leu Ser Asn Ala
            105                 110                 115

tgg gat tcc cac cag ctc ctg ctt gtc gtc ttc gcc ggc ctc att ggc   499
Trp Asp Ser His Gln Leu Leu Leu Val Val Phe Ala Gly Leu Ile Gly
        120                 125                 130

gcc atc gtc tgg aac ctt ctg acc tgg ctg cta ggc att cct tcc agc   547
Ala Ile Val Trp Asn Leu Leu Thr Trp Leu Leu Gly Ile Pro Ser Ser
    135                 140                 145

tcc tct cac gca ctt ttc ggt ggc ctc att ggc gcc gca att gct tca   595
Ser Ser His Ala Leu Phe Gly Gly Leu Ile Gly Ala Ala Ile Ala Ser
150                 155                 160                 165

ctc ggt ttc ggc gga gtg gtg tgg gaa ggt gtc ttg tcc aag atg atc   643
Leu Gly Phe Gly Gly Val Val Trp Glu Gly Val Leu Ser Lys Met Ile
                170                 175                 180

atc cca gca ttg gct gca cca gtt gtt gca ggt ctc gtg gcc gcc atc   691
Ile Pro Ala Leu Ala Ala Pro Val Val Ala Gly Leu Val Ala Ala Ile
            185                 190                 195

ggc act ttc gcc gtg tac agc atc aca aag gca gtt gga gac aac gag   739
Gly Thr Phe Ala Val Tyr Ser Ile Thr Lys Ala Val Gly Asp Asn Glu
        200                 205                 210

aag aac cgt tac ttc cgc tgg ggt cag atc ggc tcc gct tcc ttg gtt   787
Lys Asn Arg Tyr Phe Arg Trp Gly Gln Ile Gly Ser Ala Ser Leu Val
    215                 220                 225

tcc ctg gca cac ggc acc aac gat gcc cag aag acc atg ggc gtt atc   835
Ser Leu Ala His Gly Thr Asn Asp Ala Gln Lys Thr Met Gly Val Ile
230                 235                 240                 245

ttc ctt tcc ctg gtt gcc acc ggt cac ctg gga act gac gct gac atc   883
Phe Leu Ser Leu Val Ala Thr Gly His Leu Gly Thr Asp Ala Asp Ile
                250                 255                 260

cca ttc tgg gtc aag gct aca tgt gca ttg gca atc gca atc ggt acc   931
Pro Phe Trp Val Lys Ala Thr Cys Ala Leu Ala Ile Ala Ile Gly Thr
            265                 270                 275

tac ttg ggt ggt tgg cgc gtt atc cgc aca ctg ggc aaa ggc ttg gtt   979
Tyr Leu Gly Gly Trp Arg Val Ile Arg Thr Leu Gly Lys Gly Leu Val
        280                 285                 290

gag att gat tcc cct cag ggc atg gca gca gaa act tct tct gca gca   1027
Glu Ile Asp Ser Pro Gln Gly Met Ala Ala Glu Thr Ser Ser Ala Ala
    295                 300                 305

atc att ttg act tct tcc cac ttc ggt atg gca ctg tcc acc act cac   1075
Ile Ile Leu Thr Ser Ser His Phe Gly Met Ala Leu Ser Thr Thr His
310                 315                 320                 325

gtt gct act ggc tcc atc atg ggt acc ggc att gga cgt aaa ggg gcg   1123
Val Ala Thr Gly Ser Ile Met Gly Thr Gly Ile Gly Arg Lys Gly Ala
                330                 335                 340
```

```
aag gtt cgt tgg tcc gtc gca gga cgc atg gca atg gcc tgg gtt atc   1171
Lys Val Arg Trp Ser Val Ala Gly Arg Met Ala Met Ala Trp Val Ile
            345                 350                 355

acc ctc cct gcc tcc gcg atc gtt ggc gtt ttc tgc tgg tgg gta gct   1219
Thr Leu Pro Ala Ser Ala Ile Val Gly Val Phe Cys Trp Trp Val Ala
        360                 365                 370

cac gga att ggt ctt atc agc tca gac ctc ctc gga gtc ctc gtt gca   1267
His Gly Ile Gly Leu Ile Ser Ser Asp Leu Leu Gly Val Leu Val Ala
    375                 380                 385

ttc gcc att ctg gtc att ctg tct ggc tac att tac gcc cgt tcc cgt   1315
Phe Ala Ile Leu Val Ile Leu Ser Gly Tyr Ile Tyr Ala Arg Ser Arg
390                 395                 400                 405

cgc gtg cct gtt gat cca agc aac gtc aac gct gac tgg aat gaa gaa   1363
Arg Val Pro Val Asp Pro Ser Asn Val Asn Ala Asp Trp Asn Glu Glu
                410                 415                 420

tca aac agc gtg gaa cct gca aca cct tcc gcc ccg gct gct tct gag   1411
Ser Asn Ser Val Glu Pro Ala Thr Pro Ser Ala Pro Ala Ala Ser Glu
            425                 430                 435

att aca gaa gct cct gcc gct cca gcc gct caa gcc gtt caa gat ctc   1459
Ile Thr Glu Ala Pro Ala Ala Pro Ala Ala Gln Ala Val Gln Asp Leu
        440                 445                 450

aac aac gag aat gag gta acc aag taatgaactt cgctactatt ttc         1506
Asn Asn Glu Asn Glu Val Thr Lys
    455                 460
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<210> 958
<211> 461
<212> PRT
<213> Corynebacterium glutamicum

<400> 958

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Met Val Thr Pro Ile Met Gly Asn Ser Asn Ser Ile Leu Gly Ile Tyr
  1               5                  10                  15

Arg Gln Lys Ile Gln Asn Arg His Leu Val Ser Thr Leu Phe Arg Ala
             20                  25                  30

Tyr Phe Pro Ile Val Thr Glu Leu Ile Ile Leu Leu Ile Val Ile Val
         35                  40                  45

Thr Ala Leu Ala Phe Asp Phe Thr Asn Gly Phe His Asp Thr Gly Asn
     50                  55                  60

Ala Met Ala Thr Ser Ile Ala Thr Gly Ala Leu Lys Pro Lys Val Ala
 65                  70                  75                  80

Val Ala Leu Ser Ala Ser Leu Asn Leu Val Gly Ala Phe Leu Ser Val
                 85                  90                  95

Glu Val Ala Thr Thr Val Ala Lys Gly Val Val Asp Leu Asp Gln Phe
            100                 105                 110
```

```
Asp Leu Ser Asn Ala Trp Asp Ser His Gln Leu Leu Leu Val Val Phe
        115                 120                 125

Ala Gly Leu Ile Gly Ala Ile Val Trp Asn Leu Leu Thr Trp Leu Leu
    130                 135                 140

Gly Ile Pro Ser Ser Ser Ser His Ala Leu Phe Gly Gly Leu Ile Gly
145                 150                 155                 160

Ala Ala Ile Ala Ser Leu Gly Phe Gly Gly Val Val Trp Glu Gly Val
                165                 170                 175

Leu Ser Lys Met Ile Ile Pro Ala Leu Ala Ala Pro Val Val Ala Gly
            180                 185                 190

Leu Val Ala Ala Ile Gly Thr Phe Ala Val Tyr Ser Ile Thr Lys Ala
        195                 200                 205

Val Gly Asp Asn Glu Lys Asn Arg Tyr Phe Arg Trp Gly Gln Ile Gly
    210                 215                 220

Ser Ala Ser Leu Val Ser Leu Ala His Gly Thr Asn Asp Ala Gln Lys
225                 230                 235                 240

Thr Met Gly Val Ile Phe Leu Ser Leu Val Ala Thr Gly His Leu Gly
                245                 250                 255

Thr Asp Ala Asp Ile Pro Phe Trp Val Lys Ala Thr Cys Ala Leu Ala
            260                 265                 270

Ile Ala Ile Gly Thr Tyr Leu Gly Gly Trp Arg Val Ile Arg Thr Leu
        275                 280                 285

Gly Lys Gly Leu Val Glu Ile Asp Ser Pro Gln Gly Met Ala Ala Glu
    290                 295                 300

Thr Ser Ser Ala Ala Ile Ile Leu Thr Ser Ser His Phe Gly Met Ala
305                 310                 315                 320

Leu Ser Thr Thr His Val Ala Thr Gly Ser Ile Met Gly Thr Gly Ile
                325                 330                 335

Gly Arg Lys Gly Ala Lys Val Arg Trp Ser Val Ala Gly Arg Met Ala
            340                 345                 350

Met Ala Trp Val Ile Thr Leu Pro Ala Ser Ala Ile Val Gly Val Phe
        355                 360                 365

Cys Trp Trp Val Ala His Gly Ile Gly Leu Ile Ser Ser Asp Leu Leu
    370                 375                 380

Gly Val Leu Val Ala Phe Ala Ile Leu Val Ile Leu Ser Gly Tyr Ile
385                 390                 395                 400

Tyr Ala Arg Ser Arg Arg Val Pro Val Asp Pro Ser Asn Val Asn Ala
                405                 410                 415

Asp Trp Asn Glu Glu Ser Asn Ser Val Glu Pro Ala Thr Pro Ser Ala
            420                 425                 430

Pro Ala Ala Ser Glu Ile Thr Glu Ala Pro Ala Ala Pro Ala Ala Gln
```

```
        435                 440                 445

Ala Val Gln Asp Leu Asn Asn Glu Asn Glu Val Thr Lys
    450                 455                 460


<210> 959
<211> 384
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(361)
<223> RXN02045

<400> 959
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ccgttcaaga tctcaacaac gagaatgagg taaccaagta atg aac ttc gct act   115
                                            Met Asn Phe Ala Thr
                                              1               5

att ttc gga agc atc ttt gag gtc acc ctc gtg ggc att ttg ctc ggc   163
Ile Phe Gly Ser Ile Phe Glu Val Thr Leu Val Gly Ile Leu Leu Gly
                 10                  15                  20

gca ggc ctt cca gcc ctt ttt gca tta gga atc cgc ttt gct cac agc   211
Ala Gly Leu Pro Ala Leu Phe Ala Leu Gly Ile Arg Phe Ala His Ser
             25                  30                  35

cct tct tcc aac ggc acc aac gct ctt gga aaa att gct tca acc atc   259
Pro Ser Ser Asn Gly Thr Asn Ala Leu Gly Lys Ile Ala Ser Thr Ile
         40                  45                  50

tgc ttt gcc atc att gcg gtt gct atc atc gct ggc att ctc tgg gtc   307
Cys Phe Ala Ile Ile Ala Val Ala Ile Ile Ala Gly Ile Leu Trp Val
     55                  60                  65

acc aaa gca acg atc tac cag tac tct ggt ttc gac att ttc ggc act   355
Thr Lys Ala Thr Ile Tyr Gln Tyr Ser Gly Phe Asp Ile Phe Gly Thr
 70                  75                  80                  85

gaa ggc taaaagcacc agctgcgaat aac                                 384
Glu Gly


<210> 960
<211> 87
<212> PRT
<213> Corynebacterium glutamicum

<400> 960
Met Asn Phe Ala Thr Ile Phe Gly Ser Ile Phe Glu Val Thr Leu Val
  1               5                  10                  15

Gly Ile Leu Leu Gly Ala Gly Leu Pro Ala Leu Phe Ala Leu Gly Ile
             20                  25                  30

Arg Phe Ala His Ser Pro Ser Ser Asn Gly Thr Asn Ala Leu Gly Lys
```

```
         35                  40                  45

Ile Ala Ser Thr Ile Cys Phe Ala Ile Ile Ala Val Ala Ile Ile Ala
     50                  55                  60

Gly Ile Leu Trp Val Thr Lys Ala Thr Ile Tyr Gln Tyr Ser Gly Phe
 65                  70                  75                  80

Asp Ile Phe Gly Thr Glu Gly
                 85


<210> 961
<211> 384
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(361)
<223> FRXA02045

<400> 961
caccttccgc cccggctgct tctgagatta cagaagctcc tgccgctcca gccgctcaag 60

ccgttcaaga tctcaacaac gagaatgagg taaccaagta atg aac ttc gct act   115
                                            Met Asn Phe Ala Thr
                                              1               5

att ttc gga agc atc ttt gag gtc acc ctc gtg ggc att ttg ctc ggc   163
Ile Phe Gly Ser Ile Phe Glu Val Thr Leu Val Gly Ile Leu Leu Gly
                 10                  15                  20

gca ggc ctt cca gcc ctt ttt gca tta gga atc cgc ttt gct cac agc   211
Ala Gly Leu Pro Ala Leu Phe Ala Leu Gly Ile Arg Phe Ala His Ser
             25                  30                  35

cct tct tcc aac ggc acc aac gct ctt gga aaa att gct tca acc atc   259
Pro Ser Ser Asn Gly Thr Asn Ala Leu Gly Lys Ile Ala Ser Thr Ile
         40                  45                  50

tgc ttt gcc atc att gcg gtt gct atc atc gct ggc att ctc tgg gtc   307
Cys Phe Ala Ile Ile Ala Val Ala Ile Ile Ala Gly Ile Leu Trp Val
     55                  60                  65

acc aaa gca acg atc tac cag tac tct ggt ttc gac att ttc ggc act   355
Thr Lys Ala Thr Ile Tyr Gln Tyr Ser Gly Phe Asp Ile Phe Gly Thr
 70                  75                  80                  85

gaa ggc taaaagcacc agctgcgaat aac                                 384
Glu Gly


<210> 962
<211> 87
<212> PRT
<213> Corynebacterium glutamicum

<400> 962
Met Asn Phe Ala Thr Ile Phe Gly Ser Ile Phe Glu Val Thr Leu Val
```

```
  1               5                  10                  15

Gly Ile Leu Leu Gly Ala Gly Leu Pro Ala Leu Phe Ala Leu Gly Ile
            20                  25                  30

Arg Phe Ala His Ser Pro Ser Ser Asn Gly Thr Asn Ala Leu Gly Lys
        35                  40                  45

Ile Ala Ser Thr Ile Cys Phe Ala Ile Ile Ala Val Ala Ile Ile Ala
    50                  55                  60

Gly Ile Leu Trp Val Thr Lys Ala Thr Ile Tyr Gln Tyr Ser Gly Phe
65                  70                  75                  80

Asp Ile Phe Gly Thr Glu Gly
                85
```

<210> 963
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> RXN02049

<400> 963

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tctacgcagt ctccacagac cacgcagctt tagatgcagt gtggcagtcc tggcttcgcg 60

atctggagtt gccggagttt ccttctggtg gtttggacta gtg cgc tat ctg acg   115
                                        Val Arg Tyr Leu Thr
                                          1               5

ctg gcc aca atc atc gca ggt ctc tcc ggg ttc gtc gtc atc atc atc   163
Leu Ala Thr Ile Ile Ala Gly Leu Ser Gly Phe Val Val Ile Ile Ile
                10                  15                  20

gct gcc tgg gcc ctt ggt gat tcc agc caa ctt tcc gaa gaa ttc acc   211
Ala Ala Trp Ala Leu Gly Asp Ser Ser Gln Leu Ser Glu Glu Phe Thr
            25                  30                  35

gcc tac tgg ggt ctg ttc ttt gca gga acc gga gtg ctg act ggg ttg   259
Ala Tyr Trp Gly Leu Phe Phe Ala Gly Thr Gly Val Leu Thr Gly Leu
        40                  45                  50

acg cag gag acg acc cgc gcg gtg acg gcc ggt tct cgt ggt ggt tct   307
Thr Gln Glu Thr Thr Arg Ala Val Thr Ala Gly Ser Arg Gly Gly Ser
    55                  60                  65

cgt ggt ggg cgt gct ggt tct gtt gtt gga ttt agg ccg ttt ttg ttt   355
Arg Gly Gly Arg Ala Gly Ser Val Val Gly Phe Arg Pro Phe Leu Phe
70                  75                  80                  85

agc ttc gtg gtt gcg gcg ata gtg ctc gtg gtg ctt ggc gct tcg gcg   403
Ser Phe Val Val Ala Ala Ile Val Leu Val Val Leu Gly Ala Ser Ala
                90                  95                  100

ccg ctg tgg atc ggc cag ctt tta agt aat ttg caa ggt gtt ggt gtt   451
Pro Leu Trp Ile Gly Gln Leu Leu Ser Asn Leu Gln Gly Val Gly Val
```

```
            105                 110                 115

ggg cta ctt gct gta ggt ctt gct agc tac gcg atc caa gcg aca atc   499
Gly Leu Leu Ala Val Gly Leu Ala Ser Tyr Ala Ile Gln Ala Thr Ile
        120                 125                 130

tcc ggc att ttt gtc cgg ctg cca att gtg gaa aga gta tgc ctc gct   547
Ser Gly Ile Phe Val Arg Leu Pro Ile Val Glu Arg Val Cys Leu Ala
    135                 140                 145

gat ttc ttt gga cac cgg cgt gcg cat ggt ttt aac tgt tgc cgc ctg   595
Asp Phe Phe Gly His Arg Arg Ala His Gly Phe Asn Cys Cys Arg Leu
150                 155                 160                 165

gtt gct ggg tta tca att gct ggc gtt ctt gat cat cac cgt tgt ggg   643
Val Ala Gly Leu Ser Ile Ala Gly Val Leu Asp His His Arg Cys Gly
                170                 175                 180

atc aat atc ctg gct ggt cat cgt gct gtg ctt cgg ttc ggt gcg ttc   691
Ile Asn Ile Leu Ala Gly His Arg Ala Val Leu Arg Phe Gly Ala Phe
            185                 190                 195

cgt ttt ggg atc ggt tgc tgatgtttca cggggcgttt tca                732
Arg Phe Gly Ile Gly Cys
        200
```

20050090000

<210> 964
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 964

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Val Arg Tyr Leu Thr Leu Ala Thr Ile Ile Ala Gly Leu Ser Gly Phe
  1               5                  10                  15

Val Val Ile Ile Ile Ala Ala Trp Ala Leu Gly Asp Ser Ser Gln Leu
             20                  25                  30

Ser Glu Glu Phe Thr Ala Tyr Trp Gly Leu Phe Phe Ala Gly Thr Gly
         35                  40                  45

Val Leu Thr Gly Leu Thr Gln Glu Thr Thr Arg Ala Val Thr Ala Gly
     50                  55                  60

Ser Arg Gly Gly Ser Arg Gly Gly Arg Ala Gly Ser Val Val Gly Phe
 65                  70                  75                  80

Arg Pro Phe Leu Phe Ser Phe Val Val Ala Ala Ile Val Leu Val Val
                 85                  90                  95

Leu Gly Ala Ser Ala Pro Leu Trp Ile Gly Gln Leu Leu Ser Asn Leu
            100                 105                 110

Gln Gly Val Gly Val Gly Leu Leu Ala Val Gly Leu Ala Ser Tyr Ala
        115                 120                 125

Ile Gln Ala Thr Ile Ser Gly Ile Phe Val Arg Leu Pro Ile Val Glu
    130                 135                 140

Arg Val Cys Leu Ala Asp Phe Phe Gly His Arg Arg Ala His Gly Phe
```

```
145                 150                 155                 160

Asn Cys Cys Arg Leu Val Ala Gly Leu Ser Ile Ala Gly Val Leu Asp
                165                 170                 175

His His Arg Cys Gly Ile Asn Ile Leu Ala Gly His Arg Ala Val Leu
            180                 185                 190

Arg Phe Gly Ala Phe Arg Phe Gly Ile Gly Cys
        195                 200


<210> 965
<211> 570
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(547)
<223> FRXA02049

<400> 965
tctacgcagt ctccacagac cacgcagctt tagatgcagt gtggcagtcc tggcttcgcg 60

atctggagtt gccggagttt ccttctggtg gtttggacta gtg cgc tat ctg acg   115
                                              Val Arg Tyr Leu Thr
                                                1               5

ctg gcc aca atc atc gca ggt ctc tcc ggg ttc gtc gtc atc atc atc   163
Leu Ala Thr Ile Ile Ala Gly Leu Ser Gly Phe Val Val Ile Ile Ile
                10                  15                  20

gct gcc tgg gcc ctt ggt gat tcc agc caa ctt tcc gaa gaa ttc acc   211
Ala Ala Trp Ala Leu Gly Asp Ser Ser Gln Leu Ser Glu Glu Phe Thr
            25                  30                  35

gcc tac tgg ggt ctg ttc ttt gca gga acc gga gtg ctg act ggg ttg   259
Ala Tyr Trp Gly Leu Phe Phe Ala Gly Thr Gly Val Leu Thr Gly Leu
        40                  45                  50

acg cag gag acg acc cgc gcg gtg acg gcc ggt tct cgt ggt ggt tct   307
Thr Gln Glu Thr Thr Arg Ala Val Thr Ala Gly Ser Arg Gly Gly Ser
    55                  60                  65

cgt ggt ggg cgt gct ggt tct gtt gtt gga ttt agg ccg ttt ttg ttt   355
Arg Gly Gly Arg Ala Gly Ser Val Val Gly Phe Arg Pro Phe Leu Phe
70                  75                  80                  85

agc ttc gtg gtt gcg gcg ata gtg ctc gtg gtg ctt ggc gct tcg gcg   403
Ser Phe Val Val Ala Ala Ile Val Leu Val Val Leu Gly Ala Ser Ala
                90                  95                  100

ccg ctg tgg atc ggc cag ctt tta agt aat ttg caa ggt gtt ggt gtt   451
Pro Leu Trp Ile Gly Gln Leu Leu Ser Asn Leu Gln Gly Val Gly Val
            105                 110                 115

ggg cta ctt gct gta ggt ctt gct agc tac gcg atc caa gcg aca atc   499
Gly Leu Leu Ala Val Gly Leu Ala Ser Tyr Ala Ile Gln Ala Thr Ile
        120                 125                 130
```

```
tcc ggc att ttt gtc cgg ctg cca att gtg gaa aag agt atg cct cgc   547
Ser Gly Ile Phe Val Arg Leu Pro Ile Val Glu Lys Ser Met Pro Arg
    135                 140                 145

tgatttcttt ggacaccggc gtg                                        570


<210> 966
<211> 149
<212> PRT
<213> Corynebacterium glutamicum

<400> 966
Val Arg Tyr Leu Thr Leu Ala Thr Ile Ile Ala Gly Leu Ser Gly Phe
  1               5                  10                  15

Val Val Ile Ile Ile Ala Ala Trp Ala Leu Gly Asp Ser Ser Gln Leu
             20                  25                  30

Ser Glu Glu Phe Thr Ala Tyr Trp Gly Leu Phe Phe Ala Gly Thr Gly
         35                  40                  45

Val Leu Thr Gly Leu Thr Gln Glu Thr Thr Arg Ala Val Thr Ala Gly
     50                  55                  60

Ser Arg Gly Gly Ser Arg Gly Gly Arg Ala Gly Ser Val Val Gly Phe
 65                  70                  75                  80

Arg Pro Phe Leu Phe Ser Phe Val Val Ala Ala Ile Val Leu Val Val
                 85                  90                  95

Leu Gly Ala Ser Ala Pro Leu Trp Ile Gly Gln Leu Leu Ser Asn Leu
            100                 105                 110

Gln Gly Val Gly Val Gly Leu Leu Ala Val Gly Leu Ala Ser Tyr Ala
        115                 120                 125

Ile Gln Ala Thr Ile Ser Gly Ile Phe Val Arg Leu Pro Ile Val Glu
    130                 135                 140

Lys Ser Met Pro Arg
145


<210> 967
<211> 918
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(895)
<223> RXN02050

<400> 967
ctacttgctg taggtcttgc tagctacgcg atccaagcga caatctccgg cattttgtc 60

cggctgccaa ttgtggaaag agtatgcctc gctgatttct ttg gac acc ggc gtg   115
                                                Leu Asp Thr Gly Val
                                                  1               5
```

```
cgc atg gtt tta act gtt gcc gcc tgg ttg ctg ggt tat caa ttg ctg   163
Arg Met Val Leu Thr Val Ala Ala Trp Leu Leu Gly Tyr Gln Leu Leu
                 10                  15                  20

gcg ttc ttg atc atc acc gtt gtg gga tca ata tcc tgg ctg gtc atc   211
Ala Phe Leu Ile Ile Thr Val Val Gly Ser Ile Ser Trp Leu Val Ile
             25                  30                  35

gtg ctg tgc ttc ggt tcg gtg cgt tcc gtt ttg gga tcg gtt gct gat   259
Val Leu Cys Phe Gly Ser Val Arg Ser Val Leu Gly Ser Val Ala Asp
         40                  45                  50

gtt tca cgg ggc gtt ttc atc cga cag gct ctg ctt gcg atg gca gca   307
Val Ser Arg Gly Val Phe Ile Arg Gln Ala Leu Leu Ala Met Ala Ala
     55                  60                  65

tcc ggc gcc acg gca gtg ctg att act ggt ttc ccg acc ctg ctg aaa   355
Ser Gly Ala Thr Ala Val Leu Ile Thr Gly Phe Pro Thr Leu Leu Lys
 70                  75                  80                  85

ttc acg aac cct tca gcg gtt gca gga ggg gtt tcg atg gcc gct gtt   403
Phe Thr Asn Pro Ser Ala Val Ala Gly Gly Val Ser Met Ala Ala Val
                 90                  95                 100

tcc tac gcc gtc atc ctg acc cgc gct ccc ctg ctg gtt ccg ctg cag   451
Ser Tyr Ala Val Ile Leu Thr Arg Ala Pro Leu Leu Val Pro Leu Gln
             105                 110                 115

caa ttc caa tcg gcg atc atc gtt cgt ttt gtc aaa ggt acg tcc ggt   499
Gln Phe Gln Ser Ala Ile Ile Val Arg Phe Val Lys Gly Thr Ser Gly
         120                 125                 130

cca ttg aaa act ttg gcg ggt ccg ttg gca att gtg tgg gca gtc gga   547
Pro Leu Lys Thr Leu Ala Gly Pro Leu Ala Ile Val Trp Ala Val Gly
     135                 140                 145

ctt gtt gga gct ggt ctt gca tgg tta gtt ggc cca tgg atc ctg gac   595
Leu Val Gly Ala Gly Leu Ala Trp Leu Val Gly Pro Trp Ile Leu Asp
150                 155                 160                 165

gtt gta ctc caa aag gaa ctc ttc gcg gtc cct ggc tgg cta ctc gcg   643
Val Val Leu Gln Lys Glu Leu Phe Ala Val Pro Gly Trp Leu Leu Ala
                 170                 175                 180

atg ctc acc tta ggc gcc acc acc acc gct tca ttg atg gtg tcc ggc   691
Met Leu Thr Leu Gly Ala Thr Thr Thr Ala Ser Leu Met Val Ser Gly
             185                 190                 195

tgc gcg gcg atc gcc ttt gaa cgt cac ggg atc tat ctc acc gga tgg   739
Cys Ala Ala Ile Ala Phe Glu Arg His Gly Ile Tyr Leu Thr Gly Trp
         200                 205                 210

gtt gtt gcc act gtt gtt gcc gtc gga ttc ttg ctg gga cct ttt gat   787
Val Val Ala Thr Val Val Ala Val Gly Phe Leu Leu Gly Pro Phe Asp
     215                 220                 225

ttg ggc gtc gct gct ggc ctt gcg ctc att gtt ggc cca ctc tgc ggt   835
Leu Gly Val Ala Ala Gly Leu Ala Leu Ile Val Gly Pro Leu Cys Gly
230                 235                 240                 245

ttg ctg gta cac atg gga gcg ttt gtt ggt ggg gat cgg aat cgg gtt   883
```

```
Leu Leu Val His Met Gly Ala Phe Val Gly Gly Asp Arg Asn Arg Val
                250                 255                 260

ttg act gcg gga tagtttggtt tgattggggg att                          918
Leu Thr Ala Gly
            265


<210> 968
<211> 265
<212> PRT
<213> Corynebacterium glutamicum

<400> 968
Leu Asp Thr Gly Val Arg Met Val Leu Thr Val Ala Ala Trp Leu Leu
  1               5                  10                  15

Gly Tyr Gln Leu Leu Ala Phe Leu Ile Ile Thr Val Val Gly Ser Ile
             20                  25                  30

Ser Trp Leu Val Ile Val Leu Cys Phe Gly Ser Val Arg Ser Val Leu
         35                  40                  45

Gly Ser Val Ala Asp Val Ser Arg Gly Val Phe Ile Arg Gln Ala Leu
     50                  55                  60

Leu Ala Met Ala Ala Ser Gly Ala Thr Ala Val Leu Ile Thr Gly Phe
 65                  70                  75                  80

Pro Thr Leu Leu Lys Phe Thr Asn Pro Ser Ala Val Ala Gly Gly Val
                 85                  90                  95

Ser Met Ala Ala Val Ser Tyr Ala Val Ile Leu Thr Arg Ala Pro Leu
            100                 105                 110

Leu Val Pro Leu Gln Gln Phe Gln Ser Ala Ile Ile Val Arg Phe Val
        115                 120                 125

Lys Gly Thr Ser Gly Pro Leu Lys Thr Leu Ala Gly Pro Leu Ala Ile
    130                 135                 140

Val Trp Ala Val Gly Leu Val Gly Ala Gly Leu Ala Trp Leu Val Gly
145                 150                 155                 160

Pro Trp Ile Leu Asp Val Val Leu Gln Lys Glu Leu Phe Ala Val Pro
                165                 170                 175

Gly Trp Leu Leu Ala Met Leu Thr Leu Gly Ala Thr Thr Thr Ala Ser
            180                 185                 190

Leu Met Val Ser Gly Cys Ala Ala Ile Ala Phe Glu Arg His Gly Ile
        195                 200                 205

Tyr Leu Thr Gly Trp Val Val Ala Thr Val Val Ala Val Gly Phe Leu
    210                 215                 220

Leu Gly Pro Phe Asp Leu Gly Val Ala Ala Gly Leu Ala Leu Ile Val
225                 230                 235                 240

Gly Pro Leu Cys Gly Leu Leu Val His Met Gly Ala Phe Val Gly Gly
                245                 250                 255
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Asp Arg Asn Arg Val Leu Thr Ala Gly
            260                 265


<210> 969
<211> 495
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(472)
<223> FRXA02050

<400> 969
cgcgctcccc tgctggttcc gctgcagcaa ttccaatcgg cgatcatcgt tcgttttgtc 60

aaaggtaccg tccggtccat tgaaaacttt ggcgggtccg ttg gca att gtg tgg   115
                                            Leu Ala Ile Val Trp
                                              1               5

gca gtc gga ctt gtt gga gct ggt ctt gca tgg tta gtt ggc cca tgg   163
Ala Val Gly Leu Val Gly Ala Gly Leu Ala Trp Leu Val Gly Pro Trp
                 10                  15                  20

atc ctg gac gtt gta ctc caa aag gaa ctc ttc gcg gtc cct ggc tgg   211
Ile Leu Asp Val Val Leu Gln Lys Glu Leu Phe Ala Val Pro Gly Trp
             25                  30                  35

cta ctc gcg atg ctc acc tta ggc gcc acc acc acc gct tca ttg atg   259
Leu Leu Ala Met Leu Thr Leu Gly Ala Thr Thr Thr Ala Ser Leu Met
         40                  45                  50

gtg tcc ggc tgc gcg gcg atc gcc ttt gaa cgt cac ggg atc tat ctc   307
Val Ser Gly Cys Ala Ala Ile Ala Phe Glu Arg His Gly Ile Tyr Leu
     55                  60                  65

acc gga tgg gtt gtt gcc act gtt gtt gcc gtc gga ttc ttg ctg gga   355
Thr Gly Trp Val Val Ala Thr Val Val Ala Val Gly Phe Leu Leu Gly
 70                  75                  80                  85

cct ttt gat ttg ggc gtc gct gct ggc ctt gcg ctc att gtt ggc cca   403
Pro Phe Asp Leu Gly Val Ala Ala Gly Leu Ala Leu Ile Val Gly Pro
                 90                  95                 100

ctc tgc ggt ttg ctg gta cac atg gga gcg ttt gtt ggt ggg gat cgg   451
Leu Cys Gly Leu Leu Val His Met Gly Ala Phe Val Gly Gly Asp Arg
             105                 110                 115

aat cgg gtt ttg act gcg gga tagtttggtt tgattggggg att             495
Asn Arg Val Leu Thr Ala Gly
        120


<210> 970
<211> 124
<212> PRT
<213> Corynebacterium glutamicum

<400> 970
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Leu Ala Ile Val Trp Ala Val Gly Leu Val Gly Ala Gly Leu Ala Trp
  1               5                  10                  15

Leu Val Gly Pro Trp Ile Leu Asp Val Val Leu Gln Lys Glu Leu Phe
             20                  25                  30

Ala Val Pro Gly Trp Leu Leu Ala Met Leu Thr Leu Gly Ala Thr Thr
         35                  40                  45

Thr Ala Ser Leu Met Val Ser Gly Cys Ala Ala Ile Ala Phe Glu Arg
     50                  55                  60

His Gly Ile Tyr Leu Thr Gly Trp Val Val Ala Thr Val Val Ala Val
 65                  70                  75                  80

Gly Phe Leu Leu Gly Pro Phe Asp Leu Gly Val Ala Ala Gly Leu Ala
                 85                  90                  95

Leu Ile Val Gly Pro Leu Cys Gly Leu Leu Val His Met Gly Ala Phe
            100                 105                 110

Val Gly Gly Asp Arg Asn Arg Val Leu Thr Ala Gly
        115                 120
```

<210> 971
<211> 618
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(595)
<223> RXN02059

<400> 971

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tcgggaaatt ccactcatga acgcctagtc tacgggaacc atttcaccag cgtgtacgtt 60

gtaaatgtga actgaaaaag tgaaaaggaa gatgataaag atg act caa cca cgg   115
                                            Met Thr Gln Pro Arg
                                              1               5

ccc gat gcc gca tct gtg tcg ctg gaa aag aag cgc cca gaa gga tgg   163
Pro Asp Ala Ala Ser Val Ser Leu Glu Lys Lys Arg Pro Glu Gly Trp
                 10                  15                  20

cca gtg gga agc ttt gaa aca tac cca gaa gcc caa gca gca gtg gat   211
Pro Val Gly Ser Phe Glu Thr Tyr Pro Glu Ala Gln Ala Ala Val Asp
             25                  30                  35

ttg ctc agt gat aat gca ttc ccc gtc acc gaa ttg acc att gtt ggt   259
Leu Leu Ser Asp Asn Ala Phe Pro Val Thr Glu Leu Thr Ile Val Gly
         40                  45                  50

gtg gac ctg att gaa gtg gaa cgc gtt aca ggt cgt ctc acg tgg ggt   307
Val Asp Leu Ile Glu Val Glu Arg Val Thr Gly Arg Leu Thr Trp Gly
     55                  60                  65

cgt gtg att gcc gga gga atg gca tct ggc gca tgg ttg ggt ctg ttc   355
Arg Val Ile Ala Gly Gly Met Ala Ser Gly Ala Trp Leu Gly Leu Phe
 70                  75                  80                  85
```

```
ttt ggc att gtc atg gcc ttg atg tct gga ttc tgg ttc tct tcc atc   403
Phe Gly Ile Val Met Ala Leu Met Ser Gly Phe Trp Phe Ser Ser Ile
                 90                  95                 100

gca gcg gga ata ggt atg ggt ttg gtg ttt ggc att gtc ggt gca gca   451
Ala Ala Gly Ile Gly Met Gly Leu Val Phe Gly Ile Val Gly Ala Ala
            105                 110                 115

gtt cct tat gct gct tcc aaa ggc aag cgg gac ttt acc tct tca act   499
Val Pro Tyr Ala Ala Ser Lys Gly Lys Arg Asp Phe Thr Ser Ser Thr
        120                 125                 130

caa att gtg gcg ggg cgc tat gat gtg att tgt tcc cca gaa cgt gct   547
Gln Ile Val Ala Gly Arg Tyr Asp Val Ile Cys Ser Pro Glu Arg Ala
    135                 140                 145

cgg gaa gct cga gac atg att gcc ctg aaa act cga gat ctc cgc caa   595
Arg Glu Ala Arg Asp Met Ile Ala Leu Lys Thr Arg Asp Leu Arg Gln
150                 155                 160                 165

taagttaaac taacgcctat gaa                                        618
```

<210> 972
<211> 165
<212> PRT
<213> Corynebacterium glutamicum

<400> 972

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Met Thr Gln Pro Arg Pro Asp Ala Ala Ser Val Ser Leu Glu Lys Lys
  1               5                  10                  15

Arg Pro Glu Gly Trp Pro Val Gly Ser Phe Glu Thr Tyr Pro Glu Ala
             20                  25                  30

Gln Ala Ala Val Asp Leu Leu Ser Asp Asn Ala Phe Pro Val Thr Glu
         35                  40                  45

Leu Thr Ile Val Gly Val Asp Leu Ile Glu Val Glu Arg Val Thr Gly
     50                  55                  60

Arg Leu Thr Trp Gly Arg Val Ile Ala Gly Gly Met Ala Ser Gly Ala
 65                  70                  75                  80

Trp Leu Gly Leu Phe Phe Gly Ile Val Met Ala Leu Met Ser Gly Phe
                 85                  90                  95

Trp Phe Ser Ser Ile Ala Ala Gly Ile Gly Met Gly Leu Val Phe Gly
            100                 105                 110

Ile Val Gly Ala Ala Val Pro Tyr Ala Ala Ser Lys Gly Lys Arg Asp
        115                 120                 125

Phe Thr Ser Ser Thr Gln Ile Val Ala Gly Arg Tyr Asp Val Ile Cys
    130                 135                 140

Ser Pro Glu Arg Ala Arg Glu Ala Arg Asp Met Ile Ala Leu Lys Thr
145                 150                 155                 160

Arg Asp Leu Arg Gln
```

165

<210> 973
<211> 618
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(595)
<223> FRXA02059

<400> 973
tcgggaaatt ccactcatga acgcctagtc tacgggaacc atttcaccag cgtgtacgtt 60

gtaaatgtga actgaaaaag tgaaaaggaa gatgataaag atg act caa cca cgg 115
Met Thr Gln Pro Arg
1 5

ccc gat gcc gca tct gtg tcg ctg gaa aag aag cgc cca gaa gga tgg 163
Pro Asp Ala Ala Ser Val Ser Leu Glu Lys Lys Arg Pro Glu Gly Trp
10 15 20

cca gtg gga agc ttt gaa aca tac cca gaa gcc caa gca gca gtg gat 211
Pro Val Gly Ser Phe Glu Thr Tyr Pro Glu Ala Gln Ala Ala Val Asp
25 30 35

ttg ctc agt gat aat gca ttc ccc gtc acc gaa ttg acc att gtt ggt 259
Leu Leu Ser Asp Asn Ala Phe Pro Val Thr Glu Leu Thr Ile Val Gly
40 45 50

gtg gac ctg att gaa gtg gaa cgc gtt aca ggt cgt ctc acg tgg ggt 307
Val Asp Leu Ile Glu Val Glu Arg Val Thr Gly Arg Leu Thr Trp Gly
55 60 65

cgt gtg att gcc gga gga atg gca tct ggc gca tgg ttg ggt ctg ttc 355
Arg Val Ile Ala Gly Gly Met Ala Ser Gly Ala Trp Leu Gly Leu Phe
70 75 80 85

ttt ggc att gtc atg gcc ttg atg tct gga ttc tgg ttc tct tcc atc 403
Phe Gly Ile Val Met Ala Leu Met Ser Gly Phe Trp Phe Ser Ser Ile
90 95 100

gca gcg gga ata ggt atg ggt ttg gtg ttt ggc att gtc ggt gca gca 451
Ala Ala Gly Ile Gly Met Gly Leu Val Phe Gly Ile Val Gly Ala Ala
105 110 115

gtt cct tat gct gct tcc aaa ggc aag cgg gac ttt acc tct tca act 499
Val Pro Tyr Ala Ala Ser Lys Gly Lys Arg Asp Phe Thr Ser Ser Thr
120 125 130

caa att gtg gcg ggg cgc tat gat gtg att tgt tcc cca gaa cgt gct 547
Gln Ile Val Ala Gly Arg Tyr Asp Val Ile Cys Ser Pro Glu Arg Ala
135 140 145

cgg gaa gct cga gac atg att gcc ctg aaa act cga gat ctc cgc caa 595
Arg Glu Ala Arg Asp Met Ile Ala Leu Lys Thr Arg Asp Leu Arg Gln
150 155 160 165

taagttaaac taacgcctat gaa 618

<210> 974
<211> 165
<212> PRT
<213> Corynebacterium glutamicum

<400> 974
Met Thr Gln Pro Arg Pro Asp Ala Ala Ser Val Ser Leu Glu Lys Lys
1 5 10 15

Arg Pro Glu Gly Trp Pro Val Gly Ser Phe Glu Thr Tyr Pro Glu Ala
20 25 30

Gln Ala Ala Val Asp Leu Leu Ser Asp Asn Ala Phe Pro Val Thr Glu
35 40 45

Leu Thr Ile Val Gly Val Asp Leu Ile Glu Val Glu Arg Val Thr Gly
50 55 60

Arg Leu Thr Trp Gly Arg Val Ile Ala Gly Gly Met Ala Ser Gly Ala
65 70 75 80

Trp Leu Gly Leu Phe Phe Gly Ile Val Met Ala Leu Met Ser Gly Phe
85 90 95

Trp Phe Ser Ser Ile Ala Ala Gly Ile Gly Met Gly Leu Val Phe Gly
100 105 110

Ile Val Gly Ala Ala Val Pro Tyr Ala Ala Ser Lys Gly Lys Arg Asp
115 120 125

Phe Thr Ser Ser Thr Gln Ile Val Ala Gly Arg Tyr Asp Val Ile Cys
130 135 140

Ser Pro Glu Arg Ala Arg Glu Ala Arg Asp Met Ile Ala Leu Lys Thr
145 150 155 160

Arg Asp Leu Arg Gln
165

<210> 975
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(592)
<223> RXN02066

<400> 975
ggaacttatc acaggcgaca tccgttttga gtagtaggta tcttggataa gaagttaccc 60

acatccttga aagtcgagac acaggaggtc atcggaagat atg ttc aat tcc gac 115
Met Phe Asn Ser Asp
1 5

acc acc gcg aat ctc caa gct aaa agt cga gat cgt gca gga tct aaa 163
Thr Thr Ala Asn Leu Gln Ala Lys Ser Arg Asp Arg Ala Gly Ser Lys

```
                  10                  15                  20

gca aag cgc agc agg cca agt ttt gat tca gta gcg cgg gat gtt ttg   211
Ala Lys Arg Ser Arg Pro Ser Phe Asp Ser Val Ala Arg Asp Val Leu
            25                  30                  35

gat gtt cga aca aaa aca gca caa gtt aaa aac aag gct aaa gag ttt   259
Asp Val Arg Thr Lys Thr Ala Gln Val Lys Asn Lys Ala Lys Glu Phe
        40                  45                  50

tcc tct gtt gat cac ctt tca gca gac gcc gca gcc atg ttt gta gac   307
Ser Ser Val Asp His Leu Ser Ala Asp Ala Ala Ala Met Phe Val Asp
    55                  60                  65

aat gaa ctg tcc cgt ggc gcc atg cat cgc gcc agg ctg cac att gtg   355
Asn Glu Leu Ser Arg Gly Ala Met His Arg Ala Arg Leu His Ile Val
70                  75                  80                  85

cac tgc gct gaa tgt agg gaa gag att aac cgt cag cgg gaa acc gtt   403
His Cys Ala Glu Cys Arg Glu Glu Ile Asn Arg Gln Arg Glu Thr Val
                90                  95                  100

gat tat ctc cgc tca gag tgc aaa aac gaa gaa gtg tcc gcc cca atg   451
Asp Tyr Leu Arg Ser Glu Cys Lys Asn Glu Glu Val Ser Ala Pro Met
            105                 110                 115

gac ctc aaa gca cgg ctt gcc agc ctc gcc act gag tgc atg cct ggc   499
Asp Leu Lys Ala Arg Leu Ala Ser Leu Ala Thr Glu Cys Met Pro Gly
        120                 125                 130

cct ggc gca gag aat tta gca atg cag cgc cca gag tct ttt gtg gct   547
Pro Gly Ala Glu Asn Leu Ala Met Gln Arg Pro Glu Ser Phe Val Ala
    135                 140                 145

aaa gtt gag tcc gta gtg cgc gca gtt cgt aag aac caa ggc cgc       592
Lys Val Glu Ser Val Val Arg Ala Val Arg Lys Asn Gln Gly Arg
150                 155                 160

taatttttaa tccttattta cat                                        615
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<210> 976
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 976

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Met Phe Asn Ser Asp Thr Thr Ala Asn Leu Gln Ala Lys Ser Arg Asp
  1               5                  10                  15

Arg Ala Gly Ser Lys Ala Lys Arg Ser Arg Pro Ser Phe Asp Ser Val
            20                  25                  30

Ala Arg Asp Val Leu Asp Val Arg Thr Lys Thr Ala Gln Val Lys Asn
        35                  40                  45

Lys Ala Lys Glu Phe Ser Ser Val Asp His Leu Ser Ala Asp Ala Ala
    50                  55                  60

Ala Met Phe Val Asp Asn Glu Leu Ser Arg Gly Ala Met His Arg Ala
65                  70                  75                  80
```

```
Arg Leu His Ile Val His Cys Ala Glu Cys Arg Glu Glu Ile Asn Arg
                 85                  90                  95

Gln Arg Glu Thr Val Asp Tyr Leu Arg Ser Glu Cys Lys Asn Glu Glu
            100                 105                 110

Val Ser Ala Pro Met Asp Leu Lys Ala Arg Leu Ala Ser Leu Ala Thr
        115                 120                 125

Glu Cys Met Pro Gly Pro Gly Ala Glu Asn Leu Ala Met Gln Arg Pro
    130                 135                 140

Glu Ser Phe Val Ala Lys Val Glu Ser Val Val Arg Ala Val Arg Lys
145                 150                 155                 160

Asn Gln Gly Arg
```

<210> 977
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(592)
<223> FRXA02066

<400> 977

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ggaacttatc acaggcgaca tccgttttga gtagtaggta tcttggataa gaagttaccc 60

acatccttga aagtcgagac acaggaggtc atcggaagat atg ttc aat tcc gac   115
                                              Met Phe Asn Ser Asp
                                                1               5

acc acc gcg aat ctc caa gct aaa agt cga gat cgt gca gga tct aaa   163
Thr Thr Ala Asn Leu Gln Ala Lys Ser Arg Asp Arg Ala Gly Ser Lys
                10                  15                  20

gca aag cgc agc agg cca agt ttt gat tca gta gcg cgg gat gtt ttg   211
Ala Lys Arg Ser Arg Pro Ser Phe Asp Ser Val Ala Arg Asp Val Leu
            25                  30                  35

gat gtt cga aca aaa aca gca caa gtt aaa aac aag gct aaa gag ttt   259
Asp Val Arg Thr Lys Thr Ala Gln Val Lys Asn Lys Ala Lys Glu Phe
        40                  45                  50

tcc tct gtt gat cac ctt tca gca gac gcc gca gcc atg ttt gta gac   307
Ser Ser Val Asp His Leu Ser Ala Asp Ala Ala Ala Met Phe Val Asp
    55                  60                  65

aat gaa ctg tcc cgt ggc gcc atg cat cgc gcc agg ctg cac att gtg   355
Asn Glu Leu Ser Arg Gly Ala Met His Arg Ala Arg Leu His Ile Val
70                  75                  80                  85

cac tgc gct gaa tgt agg gaa gag att aac cgt cag cgg gaa acc gtt   403
His Cys Ala Glu Cys Arg Glu Glu Ile Asn Arg Gln Arg Glu Thr Val
                90                  95                  100
```

```
gat tat ctc cgc tca gag tgc aaa aac gaa gaa gtg tcc gcc cca atg   451
Asp Tyr Leu Arg Ser Glu Cys Lys Asn Glu Glu Val Ser Ala Pro Met
            105                 110                 115

gac ctc aaa gca cgg ctt gcc agc ctc gcc act gag tgc atg cct ggc   499
Asp Leu Lys Ala Arg Leu Ala Ser Leu Ala Thr Glu Cys Met Pro Gly
        120                 125                 130

cct ggc gca gag aat tta gca atg cag cgc cca gag tct ttt gtg gct   547
Pro Gly Ala Glu Asn Leu Ala Met Gln Arg Pro Glu Ser Phe Val Ala
    135                 140                 145

aaa gtt gag tcc gta gtg cgc gca gtt cgt aag aac caa ggc cgc       592
Lys Val Glu Ser Val Val Arg Ala Val Arg Lys Asn Gln Gly Arg
150                 155                 160

taatttttaa tccttattta cat                                        615
```

<210> 978
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 978

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Met Phe Asn Ser Asp Thr Thr Ala Asn Leu Gln Ala Lys Ser Arg Asp
  1               5                  10                  15

Arg Ala Gly Ser Lys Ala Lys Arg Ser Arg Pro Ser Phe Asp Ser Val
             20                  25                  30

Ala Arg Asp Val Leu Asp Val Arg Thr Lys Thr Ala Gln Val Lys Asn
         35                  40                  45

Lys Ala Lys Glu Phe Ser Ser Val Asp His Leu Ser Ala Asp Ala Ala
     50                  55                  60

Ala Met Phe Val Asp Asn Glu Leu Ser Arg Gly Ala Met His Arg Ala
 65                  70                  75                  80

Arg Leu His Ile Val His Cys Ala Glu Cys Arg Glu Glu Ile Asn Arg
                 85                  90                  95

Gln Arg Glu Thr Val Asp Tyr Leu Arg Ser Glu Cys Lys Asn Glu Glu
            100                 105                 110

Val Ser Ala Pro Met Asp Leu Lys Ala Arg Leu Ala Ser Leu Ala Thr
        115                 120                 125

Glu Cys Met Pro Gly Pro Gly Ala Glu Asn Leu Ala Met Gln Arg Pro
    130                 135                 140

Glu Ser Phe Val Ala Lys Val Glu Ser Val Val Arg Ala Val Arg Lys
145                 150                 155                 160

Asn Gln Gly Arg
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<210> 979
<211> 579

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXN02067

<400> 979
taaagttgag tccgtagtgc gcgcagttcg taagaaccaa ggccgctaat ttttaatcct 60

tatttacatt ttctgaaaga ccggtctgat gttttctagc gtg ggt tgg gga gag 115
Val Gly Trp Gly Glu
1 5

atc ttc ctc tta gtc gtt gtg ggc ctt gtt gtc atc ggc ccg gaa cgg 163
Ile Phe Leu Leu Val Val Val Gly Leu Val Val Ile Gly Pro Glu Arg
10 15 20

ttg cct cgt ttg atc cag gac gca cgc gct gcg ctg ctc gct gca cgt 211
Leu Pro Arg Leu Ile Gln Asp Ala Arg Ala Ala Leu Leu Ala Ala Arg
25 30 35

acc gct atc gac aat gca aag cag tcg ttg gac agt gat ttt ggt tcg 259
Thr Ala Ile Asp Asn Ala Lys Gln Ser Leu Asp Ser Asp Phe Gly Ser
40 45 50

gaa ttt gat gaa atc cga aag cca cta acc cag gtt gca cag tac agc 307
Glu Phe Asp Glu Ile Arg Lys Pro Leu Thr Gln Val Ala Gln Tyr Ser
55 60 65

cgg atg agc ccc aag acg gcc atc act aag gcg tta ttt gat aat gat 355
Arg Met Ser Pro Lys Thr Ala Ile Thr Lys Ala Leu Phe Asp Asn Asp
70 75 80 85

tcc tcg ttc ctg gat gac ttt gat cca aag aag atc atg gcc gaa gga 403
Ser Ser Phe Leu Asp Asp Phe Asp Pro Lys Lys Ile Met Ala Glu Gly
90 95 100

aca gaa ggc gaa gct cag cgc aac aag cag gca gct gac aac aat gcg 451
Thr Glu Gly Glu Ala Gln Arg Asn Lys Gln Ala Ala Asp Asn Asn Ala
105 110 115

aat gtg gtg gaa cgt cca gct gat ggt tcc acc gca cgc cca acg caa 499
Asn Val Val Glu Arg Pro Ala Asp Gly Ser Thr Ala Arg Pro Thr Gln
120 125 130

aac gat cca aaa gac ggc ccg aat tac tca ggt ggc gtc tct tgg acc 547
Asn Asp Pro Lys Asp Gly Pro Asn Tyr Ser Gly Gly Val Ser Trp Thr
135 140 145

gat att att tagcttttat ttaacgccaa gcc 579
Asp Ile Ile
150

<210> 980
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 980
Val Gly Trp Gly Glu Ile Phe Leu Leu Val Val Val Gly Leu Val Val
1 5 10 15

Ile Gly Pro Glu Arg Leu Pro Arg Leu Ile Gln Asp Ala Arg Ala Ala
20 25 30

Leu Leu Ala Ala Arg Thr Ala Ile Asp Asn Ala Lys Gln Ser Leu Asp
35 40 45

Ser Asp Phe Gly Ser Glu Phe Asp Glu Ile Arg Lys Pro Leu Thr Gln
50 55 60

Val Ala Gln Tyr Ser Arg Met Ser Pro Lys Thr Ala Ile Thr Lys Ala
65 70 75 80

Leu Phe Asp Asn Asp Ser Ser Phe Leu Asp Asp Phe Asp Pro Lys Lys
85 90 95

Ile Met Ala Glu Gly Thr Glu Gly Glu Ala Gln Arg Asn Lys Gln Ala
100 105 110

Ala Asp Asn Asn Ala Asn Val Val Glu Arg Pro Ala Asp Gly Ser Thr
115 120 125

Ala Arg Pro Thr Gln Asn Asp Pro Lys Asp Gly Pro Asn Tyr Ser Gly
130 135 140

Gly Val Ser Trp Thr Asp Ile Ile
145 150

<210> 981
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> FRXA02067

<400> 981
taaagttgag tccgtagtgc gcgcagttcg taagaaccaa ggccgctaat ttttaatcct 60

tatttacatt ttctgaaaga ccggtctgat gttttctagc gtg ggt tgg gga gag 115
Val Gly Trp Gly Glu
1 5

atc ttc ctc tta gtc gtt gtg ggc ctt gtt gtc atc ggc ccg gaa cgg 163
Ile Phe Leu Leu Val Val Val Gly Leu Val Val Ile Gly Pro Glu Arg
10 15 20

ttg cct cgt ttg atc cag gac gca cgc gct gcg ctg ctc gct gca cgt 211
Leu Pro Arg Leu Ile Gln Asp Ala Arg Ala Ala Leu Leu Ala Ala Arg
25 30 35

acc gct atc gac aat gca aag cag tcg ttg gac agt gat ttt ggt tcg 259
Thr Ala Ile Asp Asn Ala Lys Gln Ser Leu Asp Ser Asp Phe Gly Ser
40 45 50

```
gaa ttt gat gaa atc cga aag cca cta acc cag gtt gca cag tac agc   307
Glu Phe Asp Glu Ile Arg Lys Pro Leu Thr Gln Val Ala Gln Tyr Ser
     55                  60                  65

cgg atg agc ccc aag acg gcc atc act aag gcg tta ttt gat aat gat   355
Arg Met Ser Pro Lys Thr Ala Ile Thr Lys Ala Leu Phe Asp Asn Asp
 70                  75                  80                  85

tcc tcg ttc ctg gat gac ttt gat cca aag aag atc atg gcc gaa gga   403
Ser Ser Phe Leu Asp Asp Phe Asp Pro Lys Lys Ile Met Ala Glu Gly
                 90                  95                 100

aca gaa ggc gaa gct cag cgc aac aag cag gca gct gac aac aat gcg   451
Thr Glu Gly Glu Ala Gln Arg Asn Lys Gln Ala Ala Asp Asn Asn Ala
            105                 110                 115

aat gtg gtg gaa cgt cca gct gat ggt tcc acc gca cgc cca acg caa   499
Asn Val Val Glu Arg Pro Ala Asp Gly Ser Thr Ala Arg Pro Thr Gln
        120                 125                 130

aac gat cca aaa gac ggc ccg aat tac tca ggt ggc gtc tct tgg acc   547
Asn Asp Pro Lys Asp Gly Pro Asn Tyr Ser Gly Gly Val Ser Trp Thr
    135                 140                 145

gat att att tagcttttat ttaacgccaa gcc                            579
Asp Ile Ile
150
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<210> 982
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 982

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Val Gly Trp Gly Glu Ile Phe Leu Leu Val Val Val Gly Leu Val Val
  1               5                  10                  15

Ile Gly Pro Glu Arg Leu Pro Arg Leu Ile Gln Asp Ala Arg Ala Ala
             20                  25                  30

Leu Leu Ala Ala Arg Thr Ala Ile Asp Asn Ala Lys Gln Ser Leu Asp
         35                  40                  45

Ser Asp Phe Gly Ser Glu Phe Asp Glu Ile Arg Lys Pro Leu Thr Gln
     50                  55                  60

Val Ala Gln Tyr Ser Arg Met Ser Pro Lys Thr Ala Ile Thr Lys Ala
 65                  70                  75                  80

Leu Phe Asp Asn Asp Ser Ser Phe Leu Asp Asp Phe Asp Pro Lys Lys
                 85                  90                  95

Ile Met Ala Glu Gly Thr Glu Gly Glu Ala Gln Arg Asn Lys Gln Ala
            100                 105                 110

Ala Asp Asn Asn Ala Asn Val Val Glu Arg Pro Ala Asp Gly Ser Thr
        115                 120                 125

Ala Arg Pro Thr Gln Asn Asp Pro Lys Asp Gly Pro Asn Tyr Ser Gly
    130                 135                 140
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Gly Val Ser Trp Thr Asp Ile Ile
145 150

<210> 983
<211> 912
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(889)
<223> RXN02075

<400> 983
agttttcgaa taccgtctac gtggagcttt gcggaaaata cgcaccgaga cctaggcgcg 60

ccatacgcat ggttcacagg atttcagtac gattaacccc atg tac aag gtc ttc 115
Met Tyr Lys Val Phe
1 5

gaa gca ctg gat gat tta gtt caa gcc gtt caa cgc gca tac ggc gtt 163
Glu Ala Leu Asp Asp Leu Val Gln Ala Val Gln Arg Ala Tyr Gly Val
10 15 20

ccc atg acc gga aat tgc gtg gtt ccc cgt cag gaa gtg ctt gcg ctt 211
Pro Met Thr Gly Asn Cys Val Val Pro Arg Gln Glu Val Leu Ala Leu
25 30 35

ctc gat gat tta cgt gat gcg ctt cct gta gaa ctt gat gat gca caa 259
Leu Asp Asp Leu Arg Asp Ala Leu Pro Val Glu Leu Asp Asp Ala Gln
40 45 50

gat gtg ctg gac cac cgt gat ggt gtg atc cgt gaa gct gaa gaa aag 307
Asp Val Leu Asp His Arg Asp Gly Val Ile Arg Glu Ala Glu Glu Lys
55 60 65

gcc att gcc ttg gtc gac gat gca gaa aac gag gcc cga aac ctc ctt 355
Ala Ile Ala Leu Val Asp Asp Ala Glu Asn Glu Ala Arg Asn Leu Leu
70 75 80 85

gca cgc gca act gag gag tca gat gcc atg gtg gaa gac gcc acc aag 403
Ala Arg Ala Thr Glu Glu Ser Asp Ala Met Val Glu Asp Ala Thr Lys
90 95 100

cat gcg cat tct gtc gtt gct aag gct aat gac aca gcg gat cgc atc 451
His Ala His Ser Val Val Ala Lys Ala Asn Asp Thr Ala Asp Arg Ile
105 110 115

gtg agt gac gct cgt cga gaa gca aac agc gtc acc gag cgc gcc cag 499
Val Ser Asp Ala Arg Arg Glu Ala Asn Ser Val Thr Glu Arg Ala Gln
120 125 130

gct gaa tct gag cgc ctg gtc aac tcc ggc aat gat gcg tat cgc cgc 547
Ala Glu Ser Glu Arg Leu Val Asn Ser Gly Asn Asp Ala Tyr Arg Arg
135 140 145

gcg gtt gct gaa ggc cag gcc gag cag gat cgc ctg gtc agc gag gca 595
Ala Val Ala Glu Gly Gln Ala Glu Gln Asp Arg Leu Val Ser Glu Ala
150 155 160 165

```
gaa gtg gtg cgt cgc tcc acg gaa gaa gca cac cgc att gtg gat gca   643
Glu Val Val Arg Arg Ser Thr Glu Glu Ala His Arg Ile Val Asp Ala
                170                 175                 180

gcg cac gct gac tcc aac aag ctg cgc aat gaa tgc gat gac tac gtg   691
Ala His Ala Asp Ser Asn Lys Leu Arg Asn Glu Cys Asp Asp Tyr Val
            185                 190                 195

gat acc aag ttg gca gag ttt gaa acc tcg ctg tcc acc acg ttg cgt   739
Asp Thr Lys Leu Ala Glu Phe Glu Thr Ser Leu Ser Thr Thr Leu Arg
        200                 205                 210

tct gtc act gct gat cgt tcc gca cta cgc cga gga gct gga gct act   787
Ser Val Thr Ala Asp Arg Ser Ala Leu Arg Arg Gly Ala Gly Ala Thr
    215                 220                 225

ggc cgc gag ctg cgc gat gag caa ccg gca gcg cgt ggt gaa tat gag   835
Gly Arg Glu Leu Arg Asp Glu Gln Pro Ala Ala Arg Gly Glu Tyr Glu
230                 235                 240                 245

cgg gac tac gag cgt gat tat gaa cga ggc tac gaa cgc gac gat cga   883
Arg Asp Tyr Glu Arg Asp Tyr Glu Arg Gly Tyr Glu Arg Asp Asp Arg
                250                 255                 260

gac tac tagtttccaa gaaaccattt agg                                912
Asp Tyr
```

<210> 984
<211> 263
<212> PRT
<213> Corynebacterium glutamicum

<400> 984

```
Met Tyr Lys Val Phe Glu Ala Leu Asp Asp Leu Val Gln Ala Val Gln
  1               5                  10                  15

Arg Ala Tyr Gly Val Pro Met Thr Gly Asn Cys Val Val Pro Arg Gln
             20                  25                  30

Glu Val Leu Ala Leu Leu Asp Asp Leu Arg Asp Ala Leu Pro Val Glu
         35                  40                  45

Leu Asp Asp Ala Gln Asp Val Leu Asp His Arg Asp Gly Val Ile Arg
     50                  55                  60

Glu Ala Glu Glu Lys Ala Ile Ala Leu Val Asp Asp Ala Glu Asn Glu
 65                  70                  75                  80

Ala Arg Asn Leu Leu Ala Arg Ala Thr Glu Glu Ser Asp Ala Met Val
                 85                  90                  95

Glu Asp Ala Thr Lys His Ala His Ser Val Val Ala Lys Ala Asn Asp
            100                 105                 110

Thr Ala Asp Arg Ile Val Ser Asp Ala Arg Arg Glu Ala Asn Ser Val
        115                 120                 125

Thr Glu Arg Ala Gln Ala Glu Ser Glu Arg Leu Val Asn Ser Gly Asn
```

```
    130                 135                 140

Asp Ala Tyr Arg Arg Ala Val Ala Glu Gly Gln Ala Glu Gln Asp Arg
145                 150                 155                 160

Leu Val Ser Glu Ala Glu Val Val Arg Arg Ser Thr Glu Glu Ala His
                165                 170                 175

Arg Ile Val Asp Ala Ala His Ala Asp Ser Asn Lys Leu Arg Asn Glu
            180                 185                 190

Cys Asp Asp Tyr Val Asp Thr Lys Leu Ala Glu Phe Glu Thr Ser Leu
        195                 200                 205

Ser Thr Thr Leu Arg Ser Val Thr Ala Asp Arg Ser Ala Leu Arg Arg
    210                 215                 220

Gly Ala Gly Ala Thr Gly Arg Glu Leu Arg Asp Glu Gln Pro Ala Ala
225                 230                 235                 240

Arg Gly Glu Tyr Glu Arg Asp Tyr Glu Arg Asp Tyr Glu Arg Gly Tyr
                245                 250                 255

Glu Arg Asp Asp Arg Asp Tyr
            260
```

<210> 985
<211> 657
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(634)
<223> RXN02076

<400> 985

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tagtttccaa gaaaccattt aggctttttc acctttccgt ctagcgatcc tcatctgatg 60

tatgtagtca cgatgaggta cgagtaggat cttcctggtc atg aaa tct cca ttt   115
                                           Met Lys Ser Pro Phe
                                             1               5

att ttt gat gtc gcc gca ctc ctt cgt gga agt gcc ctt ccg gaa cac   163
Ile Phe Asp Val Ala Ala Leu Leu Arg Gly Ser Ala Leu Pro Glu His
                 10                  15                  20

ctc acc caa tca ggt cca agc ccg acc cgc att ggt ccg gaa atg atc   211
Leu Thr Gln Ser Gly Pro Ser Pro Thr Arg Ile Gly Pro Glu Met Ile
             25                  30                  35

gcg atc ccc gag ggc gga aaa gtt atc gta gaa gcc cag atc att cca   259
Ala Ile Pro Glu Gly Gly Lys Val Ile Val Glu Ala Gln Ile Ile Pro
         40                  45                  50

ctc ggt gga ggc ctg gcc gtc gaa gca gat atc gaa gcg cag ctt ctg   307
Leu Gly Gly Gly Leu Ala Val Glu Ala Asp Ile Glu Ala Gln Leu Leu
     55                  60                  65

gga cag tgc tcc cgc tgc ctc cgc gaa ctc acc cca acc aag acg ctg   355
```

```
Gly Gln Cys Ser Arg Cys Leu Arg Glu Leu Thr Pro Thr Lys Thr Leu
 70                  75                  80                  85

cac gtc tct gag gtt ttt gct gcc gat cca gac ttt gtt act ggt gaa   403
His Val Ser Glu Val Phe Ala Ala Asp Pro Asp Phe Val Thr Gly Glu
                 90                  95                 100

gat gca gca gat gac gaa gat gag ctg cca atg gtt aac caa gac cag   451
Asp Ala Ala Asp Asp Glu Asp Glu Leu Pro Met Val Asn Gln Asp Gln
            105                 110                 115

att gat ctg ctt cag tct gtc att gat gaa gct ggt ctg acc ttg ccg   499
Ile Asp Leu Leu Gln Ser Val Ile Asp Glu Ala Gly Leu Thr Leu Pro
        120                 125                 130

ttt aac cct gtc tgc gaa gaa ctt ggg tac ggc gca tgc cag gat gat   547
Phe Asn Pro Val Cys Glu Glu Leu Gly Tyr Gly Ala Cys Gln Asp Asp
    135                 140                 145

gaa acg cca gct cct gac ggt gtc tct gaa gaa gta gaa gac gag gaa   595
Glu Thr Pro Ala Pro Asp Gly Val Ser Glu Glu Val Glu Asp Glu Glu
150                 155                 160                 165

aag gtc gat ccg cgc tgg gct ggt ttg gag aag ttc ctg tgagcaggaa    644
Lys Val Asp Pro Arg Trp Ala Gly Leu Glu Lys Phe Leu
                170                 175

aaagaatcgc ctc                                                   657
```

<210> 986
<211> 178
<212> PRT
<213> Corynebacterium glutamicum

<400> 986

```
Met Lys Ser Pro Phe Ile Phe Asp Val Ala Ala Leu Leu Arg Gly Ser
  1               5                  10                  15

Ala Leu Pro Glu His Leu Thr Gln Ser Gly Pro Ser Pro Thr Arg Ile
             20                  25                  30

Gly Pro Glu Met Ile Ala Ile Pro Glu Gly Gly Lys Val Ile Val Glu
         35                  40                  45

Ala Gln Ile Ile Pro Leu Gly Gly Gly Leu Ala Val Glu Ala Asp Ile
     50                  55                  60

Glu Ala Gln Leu Leu Gly Gln Cys Ser Arg Cys Leu Arg Glu Leu Thr
 65                  70                  75                  80

Pro Thr Lys Thr Leu His Val Ser Glu Val Phe Ala Ala Asp Pro Asp
                 85                  90                  95

Phe Val Thr Gly Glu Asp Ala Ala Asp Asp Glu Asp Glu Leu Pro Met
            100                 105                 110

Val Asn Gln Asp Gln Ile Asp Leu Leu Gln Ser Val Ile Asp Glu Ala
        115                 120                 125

Gly Leu Thr Leu Pro Phe Asn Pro Val Cys Glu Glu Leu Gly Tyr Gly
```

```
    130                 135                 140

Ala Cys Gln Asp Asp Glu Thr Pro Ala Pro Asp Gly Val Ser Glu Glu
145                 150                 155                 160

Val Glu Asp Glu Glu Lys Val Asp Pro Arg Trp Ala Gly Leu Glu Lys
                165                 170                 175

Phe Leu
```

<210> 987
<211> 657
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(634)
<223> FRXA02076

<400> 987

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tagtttccaa gaaaccattt aggctttttc acctttccgt ctagcgatcc tcatctgatg 60

tatgtagtca cgatgaggta cgagtaggat cttcctggtc atg aaa tct cca ttt   115
                                        Met Lys Ser Pro Phe
                                          1               5

att ttt gat gtc gcc gca ctc ctt cgt gga agt gcc ctt ccg gaa cac   163
Ile Phe Asp Val Ala Ala Leu Leu Arg Gly Ser Ala Leu Pro Glu His
                 10                  15                  20

ctc acc caa tca ggt cca agc ccg acc cgc att ggt ccg gaa atg atc   211
Leu Thr Gln Ser Gly Pro Ser Pro Thr Arg Ile Gly Pro Glu Met Ile
             25                  30                  35

gcg atc ccc gag ggc gga aaa gtt atc gta gaa gcc cag atc att cca   259
Ala Ile Pro Glu Gly Gly Lys Val Ile Val Glu Ala Gln Ile Ile Pro
         40                  45                  50

ctc ggt gga ggc ctg gcc gtc gaa gca gat atc gaa gcg cag ctt ctg   307
Leu Gly Gly Gly Leu Ala Val Glu Ala Asp Ile Glu Ala Gln Leu Leu
     55                  60                  65

gga cag tgc tcc cgc tgc ctc cgc gaa ctc acc cca acc aag acg ctg   355
Gly Gln Cys Ser Arg Cys Leu Arg Glu Leu Thr Pro Thr Lys Thr Leu
 70                  75                  80                  85

cac gtc tct gag gtt ttt gct gcc gat cca gac ttt gtt act ggt gaa   403
His Val Ser Glu Val Phe Ala Ala Asp Pro Asp Phe Val Thr Gly Glu
                 90                  95                 100

gat gca gca gat gac gaa gat gag ctg cca atg gtt aac caa gac cag   451
Asp Ala Ala Asp Asp Glu Asp Glu Leu Pro Met Val Asn Gln Asp Gln
            105                 110                 115

att gat ctg ctt cag tct gtc att gat gaa gct ggt ctg acc ttg ccg   499
Ile Asp Leu Leu Gln Ser Val Ile Asp Glu Ala Gly Leu Thr Leu Pro
        120                 125                 130
```

```
ttt aac cct gtc tgc gaa gaa ctt ggg tac ggc gca tgc cag gat gat   547
Phe Asn Pro Val Cys Glu Glu Leu Gly Tyr Gly Ala Cys Gln Asp Asp
    135                 140                 145

gaa acg cca gct cct gac ggt gtc tct gaa gaa gta gaa gac gag gaa   595
Glu Thr Pro Ala Pro Asp Gly Val Ser Glu Glu Val Glu Asp Glu Glu
150                 155                 160                 165

aag gtc gat ccg cgc tgg gct ggt ttg gag aag ttc ctg tgagcaggaa    644
Lys Val Asp Pro Arg Trp Ala Gly Leu Glu Lys Phe Leu
                170                 175

aaagaatcgc ctc                                                   657
```

<210> 988
<211> 178
<212> PRT
<213> Corynebacterium glutamicum

<400> 988

```
Met Lys Ser Pro Phe Ile Phe Asp Val Ala Ala Leu Leu Arg Gly Ser
  1               5                  10                  15

Ala Leu Pro Glu His Leu Thr Gln Ser Gly Pro Ser Pro Thr Arg Ile
             20                  25                  30

Gly Pro Glu Met Ile Ala Ile Pro Glu Gly Gly Lys Val Ile Val Glu
         35                  40                  45

Ala Gln Ile Ile Pro Leu Gly Gly Gly Leu Ala Val Glu Ala Asp Ile
     50                  55                  60

Glu Ala Gln Leu Leu Gly Gln Cys Ser Arg Cys Leu Arg Glu Leu Thr
 65                  70                  75                  80

Pro Thr Lys Thr Leu His Val Ser Glu Val Phe Ala Ala Asp Pro Asp
                 85                  90                  95

Phe Val Thr Gly Glu Asp Ala Ala Asp Asp Glu Asp Glu Leu Pro Met
            100                 105                 110

Val Asn Gln Asp Gln Ile Asp Leu Leu Gln Ser Val Ile Asp Glu Ala
        115                 120                 125

Gly Leu Thr Leu Pro Phe Asn Pro Val Cys Glu Glu Leu Gly Tyr Gly
    130                 135                 140

Ala Cys Gln Asp Asp Glu Thr Pro Ala Pro Asp Gly Val Ser Glu Glu
145                 150                 155                 160

Val Glu Asp Glu Glu Lys Val Asp Pro Arg Trp Ala Gly Leu Glu Lys
                165                 170                 175

Phe Leu
```

<210> 989
<211> 840
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(817)
<223> RXN02094

<400> 989
ttccacctct acaccggagt tcttccaacc aacgaccaga tcattgctgc ggaggagttc 60

tccaagtaaa tttctctccc ctatttttag gaggcaccac atg gct gaa cac aac 115
Met Ala Glu His Asn
1 5

gcc atc atc acg gat gca gta cat tcc gac ccc gct gtt tta gaa gac 163
Ala Ile Ile Thr Asp Ala Val His Ser Asp Pro Ala Val Leu Glu Asp
10 15 20

aac gcc ggg ttc agc gga aag tac cta atc cgt gcc ctg gac aag gca 211
Asn Ala Gly Phe Ser Gly Lys Tyr Leu Ile Arg Ala Leu Asp Lys Ala
25 30 35

gct cat atg caa aca ggt gcc atc gag gga tac att tct tgg ctt cgg 259
Ala His Met Gln Thr Gly Ala Ile Glu Gly Tyr Ile Ser Trp Leu Arg
40 45 50

aag cac aat cct gag aaa aca ccg gcg cag ctg cag gta ctc gtc gac 307
Lys His Asn Pro Glu Lys Thr Pro Ala Gln Leu Gln Val Leu Val Asp
55 60 65

aag cat ttt atg cgc ctt gcc acc ggc tct ggc gct ggt gtg ggc atg 355
Lys His Phe Met Arg Leu Ala Thr Gly Ser Gly Ala Gly Val Gly Met
70 75 80 85

gct gcg gcc gtg cca ggc att ggc ttt gtc acg ggt gct ctt gcc gtt 403
Ala Ala Ala Val Pro Gly Ile Gly Phe Val Thr Gly Ala Leu Ala Val
90 95 100

ggt gct gaa tcg ttg gtg ttt ttg gat gct gct gcg ttt tac acc atg 451
Gly Ala Glu Ser Leu Val Phe Leu Asp Ala Ala Ala Phe Tyr Thr Met
105 110 115

gca tcc gcg cac ctg cgt ggc atc gac atc cgc cat cct gaa cgc cga 499
Ala Ser Ala His Leu Arg Gly Ile Asp Ile Arg His Pro Glu Arg Arg
120 125 130

cgt ggt ttg att ttg gtg gtt ctg ctg ggc acc gca ggc aaa gcc att 547
Arg Gly Leu Ile Leu Val Val Leu Leu Gly Thr Ala Gly Lys Ala Ile
135 140 145

gtt gac gca ggc gtc ggt gat tta tcc aag aaa aac cac gcg ccg ggc 595
Val Asp Ala Gly Val Gly Asp Leu Ser Lys Lys Asn His Ala Pro Gly
150 155 160 165

att gcg att tcc cgg ttt aat atc ggt ggc ttg atg gaa gtc aac ggc 643
Ile Ala Ile Ser Arg Phe Asn Ile Gly Gly Leu Met Glu Val Asn Gly
170 175 180

cga ctg atg cgc tac gca gtg aag gaa gta agc aag cgt ttc cgt tcg 691
Arg Leu Met Arg Tyr Ala Val Lys Glu Val Ser Lys Arg Phe Arg Ser
185 190 195

```
gca ttg att ggc aaa att ctg ccg ttt ggt atc ggt gcg gtg ctg ggc   739
Ala Leu Ile Gly Lys Ile Leu Pro Phe Gly Ile Gly Ala Val Leu Gly
        200                 205                 210

acg atg gcc aac cgc aaa att gcc aag agg act gtc gga aac gca tac   787
Thr Met Ala Asn Arg Lys Ile Ala Lys Arg Thr Val Gly Asn Ala Tyr
    215                 220                 225

gac tct ctt ggt cct ctc ccc acc cat ttt taagtactca agacccttcc     837
Asp Ser Leu Gly Pro Leu Pro Thr His Phe
230                 235

aac                                                               840
```

<210> 990
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 990

```
Met Ala Glu His Asn Ala Ile Ile Thr Asp Ala Val His Ser Asp Pro
  1               5                  10                  15

Ala Val Leu Glu Asp Asn Ala Gly Phe Ser Gly Lys Tyr Leu Ile Arg
             20                  25                  30

Ala Leu Asp Lys Ala Ala His Met Gln Thr Gly Ala Ile Glu Gly Tyr
         35                  40                  45

Ile Ser Trp Leu Arg Lys His Asn Pro Glu Lys Thr Pro Ala Gln Leu
     50                  55                  60

Gln Val Leu Val Asp Lys His Phe Met Arg Leu Ala Thr Gly Ser Gly
 65                  70                  75                  80

Ala Gly Val Gly Met Ala Ala Ala Val Pro Gly Ile Gly Phe Val Thr
                 85                  90                  95

Gly Ala Leu Ala Val Gly Ala Glu Ser Leu Val Phe Leu Asp Ala Ala
            100                 105                 110

Ala Phe Tyr Thr Met Ala Ser Ala His Leu Arg Gly Ile Asp Ile Arg
        115                 120                 125

His Pro Glu Arg Arg Arg Gly Leu Ile Leu Val Val Leu Leu Gly Thr
    130                 135                 140

Ala Gly Lys Ala Ile Val Asp Ala Gly Val Gly Asp Leu Ser Lys Lys
145                 150                 155                 160

Asn His Ala Pro Gly Ile Ala Ile Ser Arg Phe Asn Ile Gly Gly Leu
                165                 170                 175

Met Glu Val Asn Gly Arg Leu Met Arg Tyr Ala Val Lys Glu Val Ser
            180                 185                 190

Lys Arg Phe Arg Ser Ala Leu Ile Gly Lys Ile Leu Pro Phe Gly Ile
        195                 200                 205
```

```
Gly Ala Val Leu Gly Thr Met Ala Asn Arg Lys Ile Ala Lys Arg Thr
    210                 215                 220

Val Gly Asn Ala Tyr Asp Ser Leu Gly Pro Leu Pro Thr His Phe
225                 230                 235


<210> 991
<211> 840
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(817)
<223> FRXA02094

<400> 991
ttccacctct acaccggagt tcttccaacc aacgaccaga tcattgctgc ggaggagttc 60

tccaagtaaa tttctctccc ctatttttag gaggcaccac atg gct gaa cac aac   115
                                             Met Ala Glu His Asn
                                               1               5

gcc atc atc acg gat gca gta cat tcc gac ccc gct gtt tta gaa gac   163
Ala Ile Ile Thr Asp Ala Val His Ser Asp Pro Ala Val Leu Glu Asp
                 10                  15                  20

aac gcc ggg ttc agc gga aag tac cta atc cgt gcc ctg gac aag gca   211
Asn Ala Gly Phe Ser Gly Lys Tyr Leu Ile Arg Ala Leu Asp Lys Ala
             25                  30                  35

gct cat atg caa aca ggt gcc atc gag gga tac att tct tgg ctt cgg   259
Ala His Met Gln Thr Gly Ala Ile Glu Gly Tyr Ile Ser Trp Leu Arg
         40                  45                  50

aag cac aat cct gag aaa aca ccg gcg cag ctg cag gta ctc gtc gac   307
Lys His Asn Pro Glu Lys Thr Pro Ala Gln Leu Gln Val Leu Val Asp
     55                  60                  65

aag cat ttt atg cgc ctt gcc acc ggc tct ggc gct ggt gtg ggc atg   355
Lys His Phe Met Arg Leu Ala Thr Gly Ser Gly Ala Gly Val Gly Met
 70                  75                  80                  85

gct gcg gcc gtg cca ggc att ggc ttt gtc acg ggt gct ctt gcc gtt   403
Ala Ala Ala Val Pro Gly Ile Gly Phe Val Thr Gly Ala Leu Ala Val
                 90                  95                 100

ggt gct gaa tcg ttg gtg ttt ttg gat gct gct gcg ttt tac acc atg   451
Gly Ala Glu Ser Leu Val Phe Leu Asp Ala Ala Ala Phe Tyr Thr Met
            105                 110                 115

gca tcc gcg cac ctg cgt ggc atc gac atc cgc cat cct gaa cgc cga   499
Ala Ser Ala His Leu Arg Gly Ile Asp Ile Arg His Pro Glu Arg Arg
        120                 125                 130

cgt ggt ttg att ttg gtg gtt ctg ctg ggc acc gca ggc aaa gcc att   547
Arg Gly Leu Ile Leu Val Val Leu Leu Gly Thr Ala Gly Lys Ala Ile
    135                 140                 145

gtt gac gca ggc gtc ggt gat tta tcc aag aaa aac cac gcg ccg ggc   595
```

```
Val Asp Ala Gly Val Gly Asp Leu Ser Lys Lys Asn His Ala Pro Gly
150                 155                 160                 165

att gcg att tcc cgg ttt aat atc ggt ggc ttg atg gaa gtc aac ggc   643
Ile Ala Ile Ser Arg Phe Asn Ile Gly Gly Leu Met Glu Val Asn Gly
                170                 175                 180

cga ctg atg cgc tac gca gtg aag gaa gta agc aag cgt ttc cgt tcg   691
Arg Leu Met Arg Tyr Ala Val Lys Glu Val Ser Lys Arg Phe Arg Ser
            185                 190                 195

gca ttg att ggc aaa att ctg ccg ttt ggt atc ggt gcg gtg ctg ggc   739
Ala Leu Ile Gly Lys Ile Leu Pro Phe Gly Ile Gly Ala Val Leu Gly
        200                 205                 210

acg atg gcc aac cgc aaa att gcc aag agg act gtc gga aac gca tac   787
Thr Met Ala Asn Arg Lys Ile Ala Lys Arg Thr Val Gly Asn Ala Tyr
    215                 220                 225

gac tct ctt ggt cct ctc ccc acc cat ttt taagtactca agacccttcc     837
Asp Ser Leu Gly Pro Leu Pro Thr His Phe
230                 235

aac                                                               840


<210> 992
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 992
Met Ala Glu His Asn Ala Ile Ile Thr Asp Ala Val His Ser Asp Pro
  1               5                  10                  15

Ala Val Leu Glu Asp Asn Ala Gly Phe Ser Gly Lys Tyr Leu Ile Arg
             20                  25                  30

Ala Leu Asp Lys Ala Ala His Met Gln Thr Gly Ala Ile Glu Gly Tyr
         35                  40                  45

Ile Ser Trp Leu Arg Lys His Asn Pro Glu Lys Thr Pro Ala Gln Leu
     50                  55                  60

Gln Val Leu Val Asp Lys His Phe Met Arg Leu Ala Thr Gly Ser Gly
 65                  70                  75                  80

Ala Gly Val Gly Met Ala Ala Ala Val Pro Gly Ile Gly Phe Val Thr
                 85                  90                  95

Gly Ala Leu Ala Val Gly Ala Glu Ser Leu Val Phe Leu Asp Ala Ala
            100                 105                 110

Ala Phe Tyr Thr Met Ala Ser Ala His Leu Arg Gly Ile Asp Ile Arg
        115                 120                 125

His Pro Glu Arg Arg Arg Gly Leu Ile Leu Val Val Leu Leu Gly Thr
    130                 135                 140

Ala Gly Lys Ala Ile Val Asp Ala Gly Val Gly Asp Leu Ser Lys Lys
145                 150                 155                 160
```

```
Asn His Ala Pro Gly Ile Ala Ile Ser Arg Phe Asn Ile Gly Gly Leu
                165                 170                 175

Met Glu Val Asn Gly Arg Leu Met Arg Tyr Ala Val Lys Glu Val Ser
            180                 185                 190

Lys Arg Phe Arg Ser Ala Leu Ile Gly Lys Ile Leu Pro Phe Gly Ile
        195                 200                 205

Gly Ala Val Leu Gly Thr Met Ala Asn Arg Lys Ile Ala Lys Arg Thr
    210                 215                 220

Val Gly Asn Ala Tyr Asp Ser Leu Gly Pro Leu Pro Thr His Phe
225                 230                 235


<210> 993
<211> 1245
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1222)
<223> RXN02104

<400> 993
catggattcc catttggagc cttatttaca caggccacct ggcttgtttc ccaccgcgat 60

gtgccacaat aacgccataa cagaaaggca tactgacaca atg tcc aac tcc ccc   115
                                              Met Ser Asn Ser Pro
                                                1               5

acc gac gtt tca acg agc gca cct cga att atg atc gcg cca gat tcc   163
Thr Asp Val Ser Thr Ser Ala Pro Arg Ile Met Ile Ala Pro Asp Ser
                10                  15                  20

tac aaa gga acc gct acc gca tca gaa gct gcg caa tac tta ggc gaa   211
Tyr Lys Gly Thr Ala Thr Ala Ser Glu Ala Ala Gln Tyr Leu Gly Glu
            25                  30                  35

ggc gtg ttg gaa att ttg ccc aac gcc tcc att acg ttg gca ccc atg   259
Gly Val Leu Glu Ile Leu Pro Asn Ala Ser Ile Thr Leu Ala Pro Met
        40                  45                  50

gcc gac ggt ggc gaa gga aca tcc tca gtt ttc ggc ggg cag gtc ata   307
Ala Asp Gly Gly Glu Gly Thr Ser Ser Val Phe Gly Gly Gln Val Ile
    55                  60                  65

aca tta ccc acg aca aat gcc gcg gga cgc ctc acc gaa gcc agc tac   355
Thr Leu Pro Thr Thr Asn Ala Ala Gly Arg Leu Thr Glu Ala Ser Tyr
70                  75                  80                  85

acc tta gat tcc gaa aca aac act gcc tac att gac atc gcc gca gcc   403
Thr Leu Asp Ser Glu Thr Asn Thr Ala Tyr Ile Asp Ile Ala Ala Ala
                90                  95                  100

tcc ggt ttg ccc gcc gtt gca gac gat cta gtc ccc acc acc ggc gat   451
Ser Gly Leu Pro Ala Val Ala Asp Asp Leu Val Pro Thr Thr Gly Asp
            105                 110                 115
```

```
acc tac ggc acc ggc gtt ttg atc gca gac gcg gtc acc cgt ggc gca   499
Thr Tyr Gly Thr Gly Val Leu Ile Ala Asp Ala Val Thr Arg Gly Ala
        120                 125                 130

act cgc att gct tta ggc ctt ggc gga tca gcc aca act gac gcc ggc   547
Thr Arg Ile Ala Leu Gly Leu Gly Gly Ser Ala Thr Thr Asp Ala Gly
    135                 140                 145

tca gga att ctc atc gcc ctc ggc gcc gtc cca cgc aac aaa gag ggc   595
Ser Gly Ile Leu Ile Ala Leu Gly Ala Val Pro Arg Asn Lys Glu Gly
150                 155                 160                 165

tac gca cta cga acc ggt ggc gcc gac ctc atc aac ctc gat tac atc   643
Tyr Ala Leu Arg Thr Gly Gly Ala Asp Leu Ile Asn Leu Asp Tyr Ile
                170                 175                 180

gat acc gcc gaa ctc aac atc ccc gca gcc gcc gtc gaa tgg atc ctg   691
Asp Thr Ala Glu Leu Asn Ile Pro Ala Ala Ala Val Glu Trp Ile Leu
            185                 190                 195

ctc acc gat gtc gac gcc ccc gcc acc ggc ccg cag ggc gcg gcc acc   739
Leu Thr Asp Val Asp Ala Pro Ala Thr Gly Pro Gln Gly Ala Ala Thr
        200                 205                 210

gta ttc ggg ccc caa aaa ggt gcc acc gaa aaa gac att tcg ctt ctc   787
Val Phe Gly Pro Gln Lys Gly Ala Thr Glu Lys Asp Ile Ser Leu Leu
    215                 220                 225

gac gcc gcc ctc cac cac gcc tgc gcc caa ctg gaa gtt gat ggc aca   835
Asp Ala Ala Leu His His Ala Cys Ala Gln Leu Glu Val Asp Gly Thr
230                 235                 240                 245

aag cca ggt atg ggc gca gcc ggg ggc att gca atc gga ctg acg tgg   883
Lys Pro Gly Met Gly Ala Ala Gly Gly Ile Ala Ile Gly Leu Thr Trp
                250                 255                 260

ctg tcc acc ctc atg cac ggc aac gac caa cag atc cat atc ctc ccc   931
Leu Ser Thr Leu Met His Gly Asn Asp Gln Gln Ile His Ile Leu Pro
            265                 270                 275

ggc gcg cca ctg att gcc cgc tcc aac gga atc gag gat gcg ctg cca   979
Gly Ala Pro Leu Ile Ala Arg Ser Asn Gly Ile Glu Asp Ala Leu Pro
        280                 285                 290

gaa act gac ttg ttg atc acc ggt gaa ggc cga cta gat tcc caa tcg   1027
Glu Thr Asp Leu Leu Ile Thr Gly Glu Gly Arg Leu Asp Ser Gln Ser
    295                 300                 305

ttc acc gga aag gtt gtg ggc acc ctc cac ggt tta gct aaa gcc cac   1075
Phe Thr Gly Lys Val Val Gly Thr Leu His Gly Leu Ala Lys Ala His
310                 315                 320                 325

gat gtg gat ctc gct gtt gcg gcc ggc atc gtg gaa ggc ggt att ccc   1123
Asp Val Asp Leu Ala Val Ala Ala Gly Ile Val Glu Gly Gly Ile Pro
                330                 335                 340

gat gat ttc cta gcg gta gaa atg att aaa tcc tcc gac gtt gca gca   1171
Asp Asp Phe Leu Ala Val Glu Met Ile Lys Ser Ser Asp Val Ala Ala
            345                 350                 355
```

```
caa tta cgt gat gca ggc cga agg atc gct caa gaa tac gta gct caa   1219
Gln Leu Arg Asp Ala Gly Arg Arg Ile Ala Gln Glu Tyr Val Ala Gln
        360                 365                 370

aac tagcgaagga tctccacagt cca                                    1245
Asn
```

<210> 994
<211> 374
<212> PRT
<213> Corynebacterium glutamicum

<400> 994

```
Met Ser Asn Ser Pro Thr Asp Val Ser Thr Ser Ala Pro Arg Ile Met
  1               5                  10                  15

Ile Ala Pro Asp Ser Tyr Lys Gly Thr Ala Thr Ala Ser Glu Ala Ala
             20                  25                  30

Gln Tyr Leu Gly Glu Gly Val Leu Glu Ile Leu Pro Asn Ala Ser Ile
         35                  40                  45

Thr Leu Ala Pro Met Ala Asp Gly Gly Glu Gly Thr Ser Ser Val Phe
     50                  55                  60

Gly Gly Gln Val Ile Thr Leu Pro Thr Thr Asn Ala Ala Gly Arg Leu
 65                  70                  75                  80

Thr Glu Ala Ser Tyr Thr Leu Asp Ser Glu Thr Asn Thr Ala Tyr Ile
                 85                  90                  95

Asp Ile Ala Ala Ala Ser Gly Leu Pro Ala Val Ala Asp Asp Leu Val
            100                 105                 110

Pro Thr Thr Gly Asp Thr Tyr Gly Thr Gly Val Leu Ile Ala Asp Ala
        115                 120                 125

Val Thr Arg Gly Ala Thr Arg Ile Ala Leu Gly Leu Gly Gly Ser Ala
    130                 135                 140

Thr Thr Asp Ala Gly Ser Gly Ile Leu Ile Ala Leu Gly Ala Val Pro
145                 150                 155                 160

Arg Asn Lys Glu Gly Tyr Ala Leu Arg Thr Gly Gly Ala Asp Leu Ile
                165                 170                 175

Asn Leu Asp Tyr Ile Asp Thr Ala Glu Leu Asn Ile Pro Ala Ala Ala
            180                 185                 190

Val Glu Trp Ile Leu Leu Thr Asp Val Asp Ala Pro Ala Thr Gly Pro
        195                 200                 205

Gln Gly Ala Ala Thr Val Phe Gly Pro Gln Lys Gly Ala Thr Glu Lys
    210                 215                 220

Asp Ile Ser Leu Leu Asp Ala Ala Leu His His Ala Cys Ala Gln Leu
225                 230                 235                 240

Glu Val Asp Gly Thr Lys Pro Gly Met Gly Ala Ala Gly Gly Ile Ala
```

```
                245                 250                 255

Ile Gly Leu Thr Trp Leu Ser Thr Leu Met His Gly Asn Asp Gln Gln
            260                 265                 270

Ile His Ile Leu Pro Gly Ala Pro Leu Ile Ala Arg Ser Asn Gly Ile
        275                 280                 285

Glu Asp Ala Leu Pro Glu Thr Asp Leu Leu Ile Thr Gly Glu Gly Arg
    290                 295                 300

Leu Asp Ser Gln Ser Phe Thr Gly Lys Val Val Gly Thr Leu His Gly
305                 310                 315                 320

Leu Ala Lys Ala His Asp Val Asp Leu Ala Val Ala Ala Gly Ile Val
                325                 330                 335

Glu Gly Gly Ile Pro Asp Asp Phe Leu Ala Val Glu Met Ile Lys Ser
            340                 345                 350

Ser Asp Val Ala Ala Gln Leu Arg Asp Ala Gly Arg Arg Ile Ala Gln
        355                 360                 365

Glu Tyr Val Ala Gln Asn
    370


<210> 995
<211> 443
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(420)
<223> FRXA02104

<400> 995
cac gcc tgc gcc caa ctg gaa gtt gat ggc aca aag cca ggt atg ggc   48
His Ala Cys Ala Gln Leu Glu Val Asp Gly Thr Lys Pro Gly Met Gly
  1               5                  10                  15

gca gcc ggg ggc att gca atc gga ctg acg tgg ctg tcc acc ctc atg   96
Ala Ala Gly Gly Ile Ala Ile Gly Leu Thr Trp Leu Ser Thr Leu Met
             20                  25                  30

cac ggc aac gac caa cag atc cat atc ctc ccc ggc gcg cca ctg att   144
His Gly Asn Asp Gln Gln Ile His Ile Leu Pro Gly Ala Pro Leu Ile
         35                  40                  45

gcc cgc tcc aac gga atc gag gat gcg ctg cca gaa act gac ttg ttg   192
Ala Arg Ser Asn Gly Ile Glu Asp Ala Leu Pro Glu Thr Asp Leu Leu
     50                  55                  60

atc acc ggt gaa ggc cga cta gat tcc caa tcg ttc acc gga aag gtt   240
Ile Thr Gly Glu Gly Arg Leu Asp Ser Gln Ser Phe Thr Gly Lys Val
 65                  70                  75                  80

gtg ggc acc ctc cac ggt tta gct aaa gcc cac gat gtg gat ctc gct   288
Val Gly Thr Leu His Gly Leu Ala Lys Ala His Asp Val Asp Leu Ala
                 85                  90                  95
```

```
gtt gcg gcc ggc atc gtg gaa ggc ggt att ccc gat gat ttc cta gcg   336
Val Ala Ala Gly Ile Val Glu Gly Gly Ile Pro Asp Asp Phe Leu Ala
            100                 105                 110

gta gaa atg att aaa tcc tcc gac gtt gca gca caa tta cgt gat gca   384
Val Glu Met Ile Lys Ser Ser Asp Val Ala Ala Gln Leu Arg Asp Ala
        115                 120                 125

ggc cga agg atc gct caa gaa tac gta gct caa aac tagcgaagga        430
Gly Arg Arg Ile Ala Gln Glu Tyr Val Ala Gln Asn
    130                 135                 140

tctccacagt cca                                                   443
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<210> 996
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 996

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His Ala Cys Ala Gln Leu Glu Val Asp Gly Thr Lys Pro Gly Met Gly
  1               5                  10                  15

Ala Ala Gly Gly Ile Ala Ile Gly Leu Thr Trp Leu Ser Thr Leu Met
             20                  25                  30

His Gly Asn Asp Gln Gln Ile His Ile Leu Pro Gly Ala Pro Leu Ile
         35                  40                  45

Ala Arg Ser Asn Gly Ile Glu Asp Ala Leu Pro Glu Thr Asp Leu Leu
     50                  55                  60

Ile Thr Gly Glu Gly Arg Leu Asp Ser Gln Ser Phe Thr Gly Lys Val
 65                  70                  75                  80

Val Gly Thr Leu His Gly Leu Ala Lys Ala His Asp Val Asp Leu Ala
                 85                  90                  95

Val Ala Ala Gly Ile Val Glu Gly Gly Ile Pro Asp Asp Phe Leu Ala
            100                 105                 110

Val Glu Met Ile Lys Ser Ser Asp Val Ala Ala Gln Leu Arg Asp Ala
        115                 120                 125

Gly Arg Arg Ile Ala Gln Glu Tyr Val Ala Gln Asn
    130                 135                 140
```

<210> 997
<211> 553
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(553)
<223> FRXA02071

<400> 997

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catggattcc catttggagc cttatttaca caggccacct ggcttgtttc ccaccgcgat 60

gtgccacaat aacgccataa cagaaaggca tactgacaca atg tcc aac tcc ccc   115
                                              Met Ser Asn Ser Pro
                                                1               5

acc gac gtt tca acg agc gca cct cga att atg atc gcg cca gat tcc   163
Thr Asp Val Ser Thr Ser Ala Pro Arg Ile Met Ile Ala Pro Asp Ser
                 10                  15                  20

tac aaa gga acc gct acc gca tca gaa gct gcg caa tac tta ggc gaa   211
Tyr Lys Gly Thr Ala Thr Ala Ser Glu Ala Ala Gln Tyr Leu Gly Glu
             25                  30                  35

ggc gtg ttg gaa att ttg ccc aac gcc tcc att acg ttg gca ccc atg   259
Gly Val Leu Glu Ile Leu Pro Asn Ala Ser Ile Thr Leu Ala Pro Met
         40                  45                  50

gcc gac ggt ggc gaa gga aca tcc tca gtt ttc ggc ggg cag gtc ata   307
Ala Asp Gly Gly Glu Gly Thr Ser Ser Val Phe Gly Gly Gln Val Ile
     55                  60                  65

aca tta ccc acg aca aat gcc gcg gga cgc ctc acc gaa gcc agc tac   355
Thr Leu Pro Thr Thr Asn Ala Ala Gly Arg Leu Thr Glu Ala Ser Tyr
 70                  75                  80                  85

acc tta gat tcc gaa aca aac act gcc tac att gac atc gcc gca gcc   403
Thr Leu Asp Ser Glu Thr Asn Thr Ala Tyr Ile Asp Ile Ala Ala Ala
                 90                  95                 100

tcc ggt ttg ccc gcc gtt gca gac gat cta gtc ccc acc acc ggc gat   451
Ser Gly Leu Pro Ala Val Ala Asp Asp Leu Val Pro Thr Thr Gly Asp
             105                 110                 115

acc tac ggc acc ggc gtt ttg atc gca gac gcg gtc acc cgt ggc gca   499
Thr Tyr Gly Thr Gly Val Leu Ile Ala Asp Ala Val Thr Arg Gly Ala
         120                 125                 130

act cgc att gct tta ggc ctt ggc gga tca gcc aca act gac gcc ggc   547
Thr Arg Ile Ala Leu Gly Leu Gly Gly Ser Ala Thr Thr Asp Ala Gly
     135                 140                 145

tca gga                                                          553
Ser Gly
150
```

CONFIDENTIAL

<210> 998
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 998

```
Met Ser Asn Ser Pro Thr Asp Val Ser Thr Ser Ala Pro Arg Ile Met
  1               5                  10                  15

Ile Ala Pro Asp Ser Tyr Lys Gly Thr Ala Thr Ala Ser Glu Ala Ala
             20                  25                  30

Gln Tyr Leu Gly Glu Gly Val Leu Glu Ile Leu Pro Asn Ala Ser Ile
         35                  40                  45
```

```
Thr Leu Ala Pro Met Ala Asp Gly Gly Glu Gly Thr Ser Ser Val Phe
     50                  55                  60

Gly Gly Gln Val Ile Thr Leu Pro Thr Thr Asn Ala Ala Gly Arg Leu
 65                  70                  75                  80

Thr Glu Ala Ser Tyr Thr Leu Asp Ser Glu Thr Asn Thr Ala Tyr Ile
                 85                  90                  95

Asp Ile Ala Ala Ala Ser Gly Leu Pro Ala Val Ala Asp Asp Leu Val
            100                 105                 110

Pro Thr Thr Gly Asp Thr Tyr Gly Thr Gly Val Leu Ile Ala Asp Ala
        115                 120                 125

Val Thr Arg Gly Ala Thr Arg Ile Ala Leu Gly Leu Gly Gly Ser Ala
    130                 135                 140

Thr Thr Asp Ala Gly Ser Gly
145                 150


<210> 999
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXN02107

<400> 999
aagaagtaga gctcagcgat gaagatttcg cggcaggcca cgacctagta aaaaccaaat 60

acgccaccga ggagtggact aagcgagttc aatagtttct atg gat ctg cac aag   115
                                              Met Asp Leu His Lys
                                                1               5

gta gct gca gcg cac gcg gcg act ctt ccc ctg agc acc aaa gag ttt   163
Val Ala Ala Ala His Ala Ala Thr Leu Pro Leu Ser Thr Lys Glu Phe
                10                  15                  20

cct ttc gga ccc gag cac gaa gtg tac aaa gtg cgg ggc aag gta ttt   211
Pro Phe Gly Pro Glu His Glu Val Tyr Lys Val Arg Gly Lys Val Phe
            25                  30                  35

ttg ctg ctc acg ata cta aat gat gag ccg att atc acg ctg aaa tca   259
Leu Leu Leu Thr Ile Leu Asn Asp Glu Pro Ile Ile Thr Leu Lys Ser
        40                  45                  50

gac ccc gag att ggc gct tca cta cgc agt ggc ttc ccc acc atc cag   307
Asp Pro Glu Ile Gly Ala Ser Leu Arg Ser Gly Phe Pro Thr Ile Gln
    55                  60                  65

gct gga tat cac atg aac aaa gtg cac tgg ctg agc att agc gat ggt   355
Ala Gly Tyr His Met Asn Lys Val His Trp Leu Ser Ile Ser Asp Gly
70                  75                  80                  85

gaa cgg atc acg aaa gac ttc atc gaa ggt ctc gtg gaa gag tcc tat   403
```

```
Glu Arg Ile Thr Lys Asp Phe Ile Glu Gly Leu Val Glu Glu Ser Tyr
                 90                  95                 100

gaa ctg gta att tcc acc ttg ccg aag tat aaa agg cct taacttggtt    452
Glu Leu Val Ile Ser Thr Leu Pro Lys Tyr Lys Arg Pro
            105                 110

gcttgcgggt ggc                                                   465


<210> 1000
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 1000
Met Asp Leu His Lys Val Ala Ala Ala His Ala Ala Thr Leu Pro Leu
  1               5                  10                  15

Ser Thr Lys Glu Phe Pro Phe Gly Pro Glu His Glu Val Tyr Lys Val
             20                  25                  30

Arg Gly Lys Val Phe Leu Leu Leu Thr Ile Leu Asn Asp Glu Pro Ile
         35                  40                  45

Ile Thr Leu Lys Ser Asp Pro Glu Ile Gly Ala Ser Leu Arg Ser Gly
     50                  55                  60

Phe Pro Thr Ile Gln Ala Gly Tyr His Met Asn Lys Val His Trp Leu
 65                  70                  75                  80

Ser Ile Ser Asp Gly Glu Arg Ile Thr Lys Asp Phe Ile Glu Gly Leu
                 85                  90                  95

Val Glu Glu Ser Tyr Glu Leu Val Ile Ser Thr Leu Pro Lys Tyr Lys
            100                 105                 110

Arg Pro


<210> 1001
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> FRXA02107

<400> 1001
aagaagtaga gctcagcgat gaagatttcg cggcaggcca cgacctagta aaaaccaaat 60

acgccaccga ggagtggact aagcgagttc aatagtttct atg gat ctg cac aag   115
                                               Met Asp Leu His Lys
                                                 1               5

gta gct gca gcg cac gcg gcg act ctt ccc ctg agc acc aaa gag ttt   163
Val Ala Ala Ala His Ala Ala Thr Leu Pro Leu Ser Thr Lys Glu Phe
                10                  15                  20
```

```
cct ttc gga ccc gag cac gaa gtg tac aaa gtg cgg ggc aag gta ttt   211
Pro Phe Gly Pro Glu His Glu Val Tyr Lys Val Arg Gly Lys Val Phe
            25                  30                  35

ttg ctg ctc acg ata cta aat gat gag ccg att atc acg ctg aaa tca   259
Leu Leu Leu Thr Ile Leu Asn Asp Glu Pro Ile Ile Thr Leu Lys Ser
        40                  45                  50

gac ccc gag att ggc gct tca cta cgc agt ggc ttc ccc acc atc cag   307
Asp Pro Glu Ile Gly Ala Ser Leu Arg Ser Gly Phe Pro Thr Ile Gln
    55                  60                  65

gct gga tat cac atg aac aaa gtg cac tgg ctg agc att agc gat ggt   355
Ala Gly Tyr His Met Asn Lys Val His Trp Leu Ser Ile Ser Asp Gly
70                  75                  80                  85

gaa cgg atc acg aaa gac ttc atc gaa ggt ctc gtg gaa gag tcc tat   403
Glu Arg Ile Thr Lys Asp Phe Ile Glu Gly Leu Val Glu Glu Ser Tyr
                90                  95                  100

gaa ctg gta att tcc acc ttg ccg aag tat aaa agg cct taacttggtt   452
Glu Leu Val Ile Ser Thr Leu Pro Lys Tyr Lys Arg Pro
            105                 110

gcttgcgggt ggc                                                  465


<210> 1002
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 1002
Met Asp Leu His Lys Val Ala Ala Ala His Ala Ala Thr Leu Pro Leu
  1               5                  10                  15

Ser Thr Lys Glu Phe Pro Phe Gly Pro Glu His Glu Val Tyr Lys Val
            20                  25                  30

Arg Gly Lys Val Phe Leu Leu Leu Thr Ile Leu Asn Asp Glu Pro Ile
        35                  40                  45

Ile Thr Leu Lys Ser Asp Pro Glu Ile Gly Ala Ser Leu Arg Ser Gly
    50                  55                  60

Phe Pro Thr Ile Gln Ala Gly Tyr His Met Asn Lys Val His Trp Leu
65                  70                  75                  80

Ser Ile Ser Asp Gly Glu Arg Ile Thr Lys Asp Phe Ile Glu Gly Leu
                85                  90                  95

Val Glu Glu Ser Tyr Glu Leu Val Ile Ser Thr Leu Pro Lys Tyr Lys
            100                 105                 110

Arg Pro


<210> 1003
<211> 732
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> RXN02108

<400> 1003
aagacttcat cgaaggtctc gtggaagagt cctatgaact ggtaatttcc accttgccga 60

agtataaaag gccttaactt ggttgcttgc gggtggcaag atg ggt gat atg aaa 115
Met Gly Asp Met Lys
1 5

att acc cgc cac atc cat gca tgc gtt gag atc tca cag gga aac gat 163
Ile Thr Arg His Ile His Ala Cys Val Glu Ile Ser Gln Gly Asn Asp
10 15 20

cga atc att att gat ccc ggt act ttt ggc gcc cca gat tta tgt ggc 211
Arg Ile Ile Ile Asp Pro Gly Thr Phe Gly Ala Pro Asp Leu Cys Gly
25 30 35

gcg acc atc ctg gtc acc cac aat cat gcc gat cac gtt gat ccc gag 259
Ala Thr Ile Leu Val Thr His Asn His Ala Asp His Val Asp Pro Glu
40 45 50

ttg ctc aag ccc ggc atg acg att tac gcg cct cga tca gta gca cat 307
Leu Leu Lys Pro Gly Met Thr Ile Tyr Ala Pro Arg Ser Val Ala His
55 60 65

tca att cca gta gaa tgc cac atc gtg gaa cac ggc cga aac ttt acc 355
Ser Ile Pro Val Glu Cys His Ile Val Glu His Gly Arg Asn Phe Thr
70 75 80 85

gtt ggg tcc cta tcc gtt gag gtt ctt ggt tct gaa cat gcg atg ctc 403
Val Gly Ser Leu Ser Val Glu Val Leu Gly Ser Glu His Ala Met Leu
90 95 100

acc cat tcc atg ccg atc gcg gaa aac gtt gga tac tta atc aac ggc 451
Thr His Ser Met Pro Ile Ala Glu Asn Val Gly Tyr Leu Ile Asn Gly
105 110 115

cga gtg ctc cac ccc ggc gat acc ttc caa ccc att aaa gat gtc gaa 499
Arg Val Leu His Pro Gly Asp Thr Phe Gln Pro Ile Lys Asp Val Glu
120 125 130

ctc gcc ctg gtt cct gtc aac ggc ccc tgg gtg aaa atg ctg gat gtg 547
Leu Ala Leu Val Pro Val Asn Gly Pro Trp Val Lys Met Leu Asp Val
135 140 145

gaa ggc tat ttg aag aaa ttt cca cca aag cgt ttc atc ggc att cac 595
Glu Gly Tyr Leu Lys Lys Phe Pro Pro Lys Arg Phe Ile Gly Ile His
150 155 160 165

gat ggc att gtt aat gat cgc ggt ttg gcg atc aac aag aag ttc tta 643
Asp Gly Ile Val Asn Asp Arg Gly Leu Ala Ile Asn Lys Lys Phe Leu
170 175 180

acg cat ctt ggt gaa acc tat ggc tcg gaa tac tcg ccg ctt gaa gag 691
Thr His Leu Gly Glu Thr Tyr Gly Ser Glu Tyr Ser Pro Leu Glu Glu

185 190 195

gga gag tcg ttg gaa att tagattcttg gtttagattc ttg 732
Gly Glu Ser Leu Glu Ile
200

<210> 1004
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 1004
Met Gly Asp Met Lys Ile Thr Arg His Ile His Ala Cys Val Glu Ile
1 5 10 15

Ser Gln Gly Asn Asp Arg Ile Ile Ile Asp Pro Gly Thr Phe Gly Ala
20 25 30

Pro Asp Leu Cys Gly Ala Thr Ile Leu Val Thr His Asn His Ala Asp
35 40 45

His Val Asp Pro Glu Leu Leu Lys Pro Gly Met Thr Ile Tyr Ala Pro
50 55 60

Arg Ser Val Ala His Ser Ile Pro Val Glu Cys His Ile Val Glu His
65 70 75 80

Gly Arg Asn Phe Thr Val Gly Ser Leu Ser Val Glu Val Leu Gly Ser
85 90 95

Glu His Ala Met Leu Thr His Ser Met Pro Ile Ala Glu Asn Val Gly
100 105 110

Tyr Leu Ile Asn Gly Arg Val Leu His Pro Gly Asp Thr Phe Gln Pro
115 120 125

Ile Lys Asp Val Glu Leu Ala Leu Val Pro Val Asn Gly Pro Trp Val
130 135 140

Lys Met Leu Asp Val Glu Gly Tyr Leu Lys Lys Phe Pro Pro Lys Arg
145 150 155 160

Phe Ile Gly Ile His Asp Gly Ile Val Asn Asp Arg Gly Leu Ala Ile
165 170 175

Asn Lys Lys Phe Leu Thr His Leu Gly Glu Thr Tyr Gly Ser Glu Tyr
180 185 190

Ser Pro Leu Glu Glu Gly Glu Ser Leu Glu Ile
195 200

<210> 1005
<211> 558
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(535)

<223> FRXA02108

<400> 1005
ttgatcccgg tacttttggc gccccagatt tagatgggcg accatcctga tcacccacaa 60

tcatgccgat cacgttgatc ccgagttgct caagcccggc atg acg att tac gcg 115
Met Thr Ile Tyr Ala
1 5

cct cga tca gta gca cat tca att cca gta gaa tgc cac atc gtg gaa 163
Pro Arg Ser Val Ala His Ser Ile Pro Val Glu Cys His Ile Val Glu
10 15 20

cac ggc cga aac ttt acc gtt ggg tcc cta tcc gtt gag gtt ctt ggt 211
His Gly Arg Asn Phe Thr Val Gly Ser Leu Ser Val Glu Val Leu Gly
25 30 35

tct gaa cat gcg atg ctc acc cat tcc atg ccg atc gcg gaa aac gtt 259
Ser Glu His Ala Met Leu Thr His Ser Met Pro Ile Ala Glu Asn Val
40 45 50

gga tac tta atc aac ggc cga gtg ctc cac ccc ggc gat acc ttc caa 307
Gly Tyr Leu Ile Asn Gly Arg Val Leu His Pro Gly Asp Thr Phe Gln
55 60 65

ccc att aaa gat gtc gaa ctc gcc ctg gtt cct gtc aac ggc ccc tgg 355
Pro Ile Lys Asp Val Glu Leu Ala Leu Val Pro Val Asn Gly Pro Trp
70 75 80 85

gtg aaa atg ctg gat gtg gaa ggc tat ttg aag aaa ttt cca cca aag 403
Val Lys Met Leu Asp Val Glu Gly Tyr Leu Lys Lys Phe Pro Pro Lys
90 95 100

cgt ttc atc ggc att cac gat ggc att gtt aat gat cgc ggt ttg gcg 451
Arg Phe Ile Gly Ile His Asp Gly Ile Val Asn Asp Arg Gly Leu Ala
105 110 115

atc aac aag aag ttc tta acg cat ctt ggt gaa acc tat ggc tcg gaa 499
Ile Asn Lys Lys Phe Leu Thr His Leu Gly Glu Thr Tyr Gly Ser Glu
120 125 130

tac tcg ccg ctt gaa gag gga gag tcg ttg gaa att tagattcttg 545
Tyr Ser Pro Leu Glu Glu Gly Glu Ser Leu Glu Ile
135 140 145

gtttagattc ttg 558

<210> 1006
<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 1006
Met Thr Ile Tyr Ala Pro Arg Ser Val Ala His Ser Ile Pro Val Glu
1 5 10 15

Cys His Ile Val Glu His Gly Arg Asn Phe Thr Val Gly Ser Leu Ser
20 25 30

Val Glu Val Leu Gly Ser Glu His Ala Met Leu Thr His Ser Met Pro

```
         35                  40                  45

Ile Ala Glu Asn Val Gly Tyr Leu Ile Asn Gly Arg Val Leu His Pro
     50                  55                  60

Gly Asp Thr Phe Gln Pro Ile Lys Asp Val Glu Leu Ala Leu Val Pro
 65                  70                  75                  80

Val Asn Gly Pro Trp Val Lys Met Leu Asp Val Glu Gly Tyr Leu Lys
                 85                  90                  95

Lys Phe Pro Pro Lys Arg Phe Ile Gly Ile His Asp Gly Ile Val Asn
            100                 105                 110

Asp Arg Gly Leu Ala Ile Asn Lys Lys Phe Leu Thr His Leu Gly Glu
        115                 120                 125

Thr Tyr Gly Ser Glu Tyr Ser Pro Leu Glu Glu Gly Glu Ser Leu Glu
    130                 135                 140

Ile
145
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CORRECTED SHEET (RULE 91) ISA/EP

<210> 1007
<211> 509
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(486)
<223> RXN02114

<400> 1007

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tcc atc ggc tac gcc tgg acc acc gca ttt cac gca ctc aca cca ggc   48
Ser Ile Gly Tyr Ala Trp Thr Thr Ala Phe His Ala Leu Thr Pro Gly
  1               5                  10                  15

ctt ggc ggc atc gcc att ggt att tgg ctg ctc ggt ggt gtg ctc ggt   96
Leu Gly Gly Ile Ala Ile Gly Ile Trp Leu Leu Gly Gly Val Leu Gly
             20                  25                  30

ggg ttg gtt atc cgc aag ccg ggt gcc gca att ttc gtt gaa gta gtg   144
Gly Leu Val Ile Arg Lys Pro Gly Ala Ala Ile Phe Val Glu Val Val
         35                  40                  45

gcc gca tgt gtc tct gca gcg ctt gct tca cag ttt ggt atc tcc acc   192
Ala Ala Cys Val Ser Ala Ala Leu Ala Ser Gln Phe Gly Ile Ser Thr
     50                  55                  60

att tac tcc ggc ttg gcg cag gga atc ggc gct gaa atc atc ttc gcg   240
Ile Tyr Ser Gly Leu Ala Gln Gly Ile Gly Ala Glu Ile Ile Phe Ala
 65                  70                  75                  80

ctg ttc ctc tac cgt cgc tac agc ctg ccc acc acc atg ctt gca ggt   288
Leu Phe Leu Tyr Arg Arg Tyr Ser Leu Pro Thr Thr Met Leu Ala Gly
                 85                  90                  95

atg ggc gca ggt ggc ggc gca att ttc ctg gaa atg ttc ttc tac gga   336
Met Gly Ala Gly Gly Gly Ala Ile Phe Leu Glu Met Phe Phe Tyr Gly
```

```
            100                 105                 110

aac ctc gca aag acg atg tcc ttc aac atc atc tat tcc acc act gtc   384
Asn Leu Ala Lys Thr Met Ser Phe Asn Ile Ile Tyr Ser Thr Thr Val
        115                 120                 125

ctt att tcc ggt gcg atc ctt gcc ggc ctg ctc agc tgg tac ctg gtc   432
Leu Ile Ser Gly Ala Ile Leu Ala Gly Leu Leu Ser Trp Tyr Leu Val
    130                 135                 140

cgc gcg ttg gcg agg act ggt gca ctt gat cgt ttc gcc gct ggc cgc   480
Arg Ala Leu Ala Arg Thr Gly Ala Leu Asp Arg Phe Ala Ala Gly Arg
145                 150                 155                 160

gag gta taaatgacca ccgcacttgg aac                                 509
Glu Val
```

<210> 1008
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 1008

```
Ser Ile Gly Tyr Ala Trp Thr Thr Ala Phe His Ala Leu Thr Pro Gly
  1               5                  10                  15

Leu Gly Gly Ile Ala Ile Gly Ile Trp Leu Leu Gly Gly Val Leu Gly
             20                  25                  30

Gly Leu Val Ile Arg Lys Pro Gly Ala Ala Ile Phe Val Glu Val Val
         35                  40                  45

Ala Ala Cys Val Ser Ala Ala Leu Ala Ser Gln Phe Gly Ile Ser Thr
     50                  55                  60

Ile Tyr Ser Gly Leu Ala Gln Gly Ile Gly Ala Glu Ile Ile Phe Ala
 65                  70                  75                  80

Leu Phe Leu Tyr Arg Arg Tyr Ser Leu Pro Thr Thr Met Leu Ala Gly
                 85                  90                  95

Met Gly Ala Gly Gly Gly Ala Ile Phe Leu Glu Met Phe Phe Tyr Gly
            100                 105                 110

Asn Leu Ala Lys Thr Met Ser Phe Asn Ile Ile Tyr Ser Thr Thr Val
        115                 120                 125

Leu Ile Ser Gly Ala Ile Leu Ala Gly Leu Leu Ser Trp Tyr Leu Val
    130                 135                 140

Arg Ala Leu Ala Arg Thr Gly Ala Leu Asp Arg Phe Ala Ala Gly Arg
145                 150                 155                 160

Glu Val
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<210> 1009
<211> 509

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(486)
<223> FRXA02114

<400> 1009
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tcc atc ggc tac gcc tgg acc acc gca ttt cac gca ctc aca cca ggc   48
Ser Ile Gly Tyr Ala Trp Thr Thr Ala Phe His Ala Leu Thr Pro Gly
  1               5                  10                  15

ctt ggc ggc atc gcc att ggt att tgg ctg ctc ggt ggt gtg ctc ggt   96
Leu Gly Gly Ile Ala Ile Gly Ile Trp Leu Leu Gly Gly Val Leu Gly
             20                  25                  30

ggg ttg gtt atc cgc aag ccg ggt gcc gca att ttc gtt gaa gta gtg   144
Gly Leu Val Ile Arg Lys Pro Gly Ala Ala Ile Phe Val Glu Val Val
         35                  40                  45

gcc gca tgt gtc tct gca gcg ctt gct tca cag ttt ggt atc tcc acc   192
Ala Ala Cys Val Ser Ala Ala Leu Ala Ser Gln Phe Gly Ile Ser Thr
     50                  55                  60

att tac tcc ggc ttg gcg cag gga atc ggc gct gaa atc atc ttc gcg   240
Ile Tyr Ser Gly Leu Ala Gln Gly Ile Gly Ala Glu Ile Ile Phe Ala
 65                  70                  75                  80

ctg ttc ctc tac cgt cgc tac agc ctg ccc acc acc atg ctt gca ggt   288
Leu Phe Leu Tyr Arg Arg Tyr Ser Leu Pro Thr Thr Met Leu Ala Gly
                 85                  90                  95

atg ggc gca ggt ggc ggc gca att ttc ctg gaa atg ttc ttc tac gga   336
Met Gly Ala Gly Gly Gly Ala Ile Phe Leu Glu Met Phe Phe Tyr Gly
            100                 105                 110

aac ctc gca aag acg atg tcc ttc aac atc atc tat tcc acc act gtc   384
Asn Leu Ala Lys Thr Met Ser Phe Asn Ile Ile Tyr Ser Thr Thr Val
        115                 120                 125

ctt att tcc ggt gcg atc ctt gcc ggc ctg ctc agc tgg tac ctg gtc   432
Leu Ile Ser Gly Ala Ile Leu Ala Gly Leu Leu Ser Trp Tyr Leu Val
    130                 135                 140

cgc gcg ttg gcg agg act ggt gca ctt gat cgt ttc gcc gct ggc cgc   480
Arg Ala Leu Ala Arg Thr Gly Ala Leu Asp Arg Phe Ala Ala Gly Arg
145                 150                 155                 160

gag gta taaatgacca ccgcacttgg aac                                 509
Glu Val
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<210> 1010
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 1010
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Ser Ile Gly Tyr Ala Trp Thr Thr Ala Phe His Ala Leu Thr Pro Gly
```

```
  1               5                  10                  15

Leu Gly Gly Ile Ala Ile Gly Ile Trp Leu Leu Gly Gly Val Leu Gly
            20                  25                  30

Gly Leu Val Ile Arg Lys Pro Gly Ala Ala Ile Phe Val Glu Val Val
        35                  40                  45

Ala Ala Cys Val Ser Ala Ala Leu Ala Ser Gln Phe Gly Ile Ser Thr
    50                  55                  60

Ile Tyr Ser Gly Leu Ala Gln Gly Ile Gly Ala Glu Ile Ile Phe Ala
65                  70                  75                  80

Leu Phe Leu Tyr Arg Arg Tyr Ser Leu Pro Thr Thr Met Leu Ala Gly
                85                  90                  95

Met Gly Ala Gly Gly Gly Ala Ile Phe Leu Glu Met Phe Phe Tyr Gly
            100                 105                 110

Asn Leu Ala Lys Thr Met Ser Phe Asn Ile Ile Tyr Ser Thr Thr Val
        115                 120                 125

Leu Ile Ser Gly Ala Ile Leu Ala Gly Leu Leu Ser Trp Tyr Leu Val
    130                 135                 140

Arg Ala Leu Ala Arg Thr Gly Ala Leu Asp Arg Phe Ala Ala Gly Arg
145                 150                 155                 160

Glu Val
```

09/25/2003 09:50:50

<210> 1011
<211> 828
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(805)
<223> RXN02121

<400> 1011
ccgggaaatc ttcaggcgtc tcctcccata tgctgctgac aaattccaga acaggatcgt 60

tgggatacct tcgagacaaa cttccgaaag ctccgcaacc atg atc acc tca cca 115
                                              Met Ile Thr Ser Pro
                                                1   5

ttt gag cgc gag ctg aag ctg ctc aac gag ggg gaa ctg ggt att gtc 163
Phe Glu Arg Glu Leu Lys Leu Leu Asn Glu Gly Glu Leu Gly Ile Val
                10   15   20

cag cag ttg gtg gaa tca agc aac atc gga ttc atc gtc gat ctt gaa 211
Gln Gln Leu Val Glu Ser Ser Asn Ile Gly Phe Ile Val Asp Leu Glu
            25   30   35

tta gat ggc gat tat ggg tgg gcg gtc tac aaa ccg gaa ttg ggg gag 259
Leu Asp Gly Asp Tyr Gly Trp Ala Val Tyr Lys Pro Glu Leu Gly Glu
        40   45   50

```
caa ccc ctg tgg gat ttc cct cct ggc ctg tac aaa cgt gaa cgt gca   307
Gln Pro Leu Trp Asp Phe Pro Pro Gly Leu Tyr Lys Arg Glu Arg Ala
     55                  60                  65

gcc ttt gtg atc agt gag ttt ttg ggt tgg aac atc gtg cct cca acg   355
Ala Phe Val Ile Ser Glu Phe Leu Gly Trp Asn Ile Val Pro Pro Thr
 70                  75                  80                  85

gtg atc atg cac gat gcc ccg gct ggt gtg ggc tcg gtg cag tgg ttt   403
Val Ile Met His Asp Ala Pro Ala Gly Val Gly Ser Val Gln Trp Phe
                 90                  95                 100

att gaa aac aat ggc gaa cac tat ttt cca ctg ttt gac acc cgc gct   451
Ile Glu Asn Asn Gly Glu His Tyr Phe Pro Leu Phe Asp Thr Arg Ala
            105                 110                 115

gac ctg cat ccg cag ttt gtc cgc atg gct gtg ttt gat ctg ttg tgc   499
Asp Leu His Pro Gln Phe Val Arg Met Ala Val Phe Asp Leu Leu Cys
        120                 125                 130

aac aac act gac cgg aaa gcg ggc cat gtg ttg tta gac ggc gat cat   547
Asn Asn Thr Asp Arg Lys Ala Gly His Val Leu Leu Asp Gly Asp His
    135                 140                 145

att tgg ggc atc gat cac ggg ttg tgt ttt tcc gtc gaa ccg aag ctg   595
Ile Trp Gly Ile Asp His Gly Leu Cys Phe Ser Val Glu Pro Lys Leu
150                 155                 160                 165

cgc acg gtg att tgg gat ttc gca ggc tgc acc att cca gat gac ttg   643
Arg Thr Val Ile Trp Asp Phe Ala Gly Cys Thr Ile Pro Asp Asp Leu
                170                 175                 180

gtg aca gat gtt gag cag ctt ttg gag gac gtc ccg gaa gaa ctt cat   691
Val Thr Asp Val Glu Gln Leu Leu Glu Asp Val Pro Glu Glu Leu His
            185                 190                 195

cag ctt ctt cat ccc gca gaa att gat gcg ctg cag cgc cgt gcc tca   739
Gln Leu Leu His Pro Ala Glu Ile Asp Ala Leu Gln Arg Arg Ala Ser
        200                 205                 210

aga atc agc agg tta ccg ttc ctt ccg cag gcg aaa tcg cat cgt caa   787
Arg Ile Ser Arg Leu Pro Phe Leu Pro Gln Ala Lys Ser His Arg Gln
    215                 220                 225

ttc cct tgg cca ctt gtt tgagtaggct ggcgggcagg tgc                828
Phe Pro Trp Pro Leu Val
230                 235
```

CONFIDENTIAL

<210> 1012
<211> 235
<212> PRT
<213> Corynebacterium glutamicum

<400> 1012

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Met Ile Thr Ser Pro Phe Glu Arg Glu Leu Lys Leu Leu Asn Glu Gly
  1               5                  10                  15

Glu Leu Gly Ile Val Gln Gln Leu Val Glu Ser Ser Asn Ile Gly Phe
             20                  25                  30
```

```
Ile Val Asp Leu Glu Leu Asp Gly Asp Tyr Gly Trp Ala Val Tyr Lys
         35                  40                  45

Pro Glu Leu Gly Glu Gln Pro Leu Trp Asp Phe Pro Pro Gly Leu Tyr
     50                  55                  60

Lys Arg Glu Arg Ala Ala Phe Val Ile Ser Glu Phe Leu Gly Trp Asn
 65                  70                  75                  80

Ile Val Pro Pro Thr Val Ile Met His Asp Ala Pro Ala Gly Val Gly
                 85                  90                  95

Ser Val Gln Trp Phe Ile Glu Asn Asn Gly Glu His Tyr Phe Pro Leu
            100                 105                 110

Phe Asp Thr Arg Ala Asp Leu His Pro Gln Phe Val Arg Met Ala Val
        115                 120                 125

Phe Asp Leu Leu Cys Asn Asn Thr Asp Arg Lys Ala Gly His Val Leu
    130                 135                 140

Leu Asp Gly Asp His Ile Trp Gly Ile Asp His Gly Leu Cys Phe Ser
145                 150                 155                 160

Val Glu Pro Lys Leu Arg Thr Val Ile Trp Asp Phe Ala Gly Cys Thr
                165                 170                 175

Ile Pro Asp Asp Leu Val Thr Asp Val Glu Gln Leu Leu Glu Asp Val
            180                 185                 190

Pro Glu Glu Leu His Gln Leu Leu His Pro Ala Glu Ile Asp Ala Leu
        195                 200                 205

Gln Arg Arg Ala Ser Arg Ile Ser Arg Leu Pro Phe Leu Pro Gln Ala
    210                 215                 220

Lys Ser His Arg Gln Phe Pro Trp Pro Leu Val
225                 230                 235
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<210> 1013
<211> 828
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(805)
<223> FRXA02121

<400> 1013
ccgggaaatc ttcaggcgtc tcctcccata tgctgctgac aaattccaga acaggatcgt 60

tgggatacct tcgagacaaa cttccgaaag ctccgcaacc atg atc acc tca cca 115
                                              Met Ile Thr Ser Pro
                                                1   5

ttt gag cgc gag ctg aag ctg ctc aac gag ggg gaa ctg ggt att gtc 163
Phe Glu Arg Glu Leu Lys Leu Leu Asn Glu Gly Glu Leu Gly Ile Val
                10   15   20

```
cag cag ttg gtg gaa tca agc aac atc gga ttc atc gtc gat ctt gaa   211
Gln Gln Leu Val Glu Ser Ser Asn Ile Gly Phe Ile Val Asp Leu Glu
            25                  30                  35

tta gat ggc gat tat ggg tgg gcg gtc tac aaa ccg gaa ttg ggg gag   259
Leu Asp Gly Asp Tyr Gly Trp Ala Val Tyr Lys Pro Glu Leu Gly Glu
        40                  45                  50

caa ccc ctg tgg gat ttc cct cct ggc ctg tac aaa cgt gaa cgt gca   307
Gln Pro Leu Trp Asp Phe Pro Pro Gly Leu Tyr Lys Arg Glu Arg Ala
    55                  60                  65

gcc ttt gtg atc agt gag ttt ttg ggt tgg aac atc gtg cct cca acg   355
Ala Phe Val Ile Ser Glu Phe Leu Gly Trp Asn Ile Val Pro Pro Thr
70                  75                  80                  85

gtg atc atg cac gat gcc ccg gct ggt gtg ggc tcg gtg cag tgg ttt   403
Val Ile Met His Asp Ala Pro Ala Gly Val Gly Ser Val Gln Trp Phe
                90                  95                  100

att gaa aac aat ggc gaa cac tat ttt cca ctg ttt gac acc cgc gct   451
Ile Glu Asn Asn Gly Glu His Tyr Phe Pro Leu Phe Asp Thr Arg Ala
            105                 110                 115

gac ctg cat ccg cag ttt gtc cgc atg gct gtg ttt gat ctg ttg tgc   499
Asp Leu His Pro Gln Phe Val Arg Met Ala Val Phe Asp Leu Leu Cys
        120                 125                 130

aac aac act gac cgg aaa tcg ggc cat gtg ttg cta gac ggc gat cat   547
Asn Asn Thr Asp Arg Lys Ser Gly His Val Leu Leu Asp Gly Asp His
    135                 140                 145

att tgg ggc atc gat cac ggg ttg tgt ttt tcc gtc gaa ccg aag ctg   595
Ile Trp Gly Ile Asp His Gly Leu Cys Phe Ser Val Glu Pro Lys Leu
150                 155                 160                 165

cgc acg gtg att tgg gat ttc gca ggc tgc acc att cca gat gac ttg   643
Arg Thr Val Ile Trp Asp Phe Ala Gly Cys Thr Ile Pro Asp Asp Leu
                170                 175                 180

gtg aca gat gtt gag cag ctt ttg gag gac gtc ccg gaa gaa ctt cat   691
Val Thr Asp Val Glu Gln Leu Leu Glu Asp Val Pro Glu Glu Leu His
            185                 190                 195

cag ctt ctt cat ccc gca gaa att gat gcg ctg cag cgc cgt gcc tca   739
Gln Leu Leu His Pro Ala Glu Ile Asp Ala Leu Gln Arg Arg Ala Ser
        200                 205                 210

aga atc agc agg tta ccg ttc ctt ccg cag gcg aaa tcg cat cgt caa   787
Arg Ile Ser Arg Leu Pro Phe Leu Pro Gln Ala Lys Ser His Arg Gln
    215                 220                 225

ttc cct tgg cca ctt gtt tgagtaggct ggcgggcagg tgc                828
Phe Pro Trp Pro Leu Val
230                 235
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<210> 1014
<211> 235
<212> PRT

<213> Corynebacterium glutamicum

<400> 1014
Met Ile Thr Ser Pro Phe Glu Arg Glu Leu Lys Leu Leu Asn Glu Gly
1 5 10 15

Glu Leu Gly Ile Val Gln Gln Leu Val Glu Ser Ser Asn Ile Gly Phe
20 25 30

Ile Val Asp Leu Glu Leu Asp Gly Asp Tyr Gly Trp Ala Val Tyr Lys
35 40 45

Pro Glu Leu Gly Glu Gln Pro Leu Trp Asp Phe Pro Pro Gly Leu Tyr
50 55 60

Lys Arg Glu Arg Ala Ala Phe Val Ile Ser Glu Phe Leu Gly Trp Asn
65 70 75 80

Ile Val Pro Pro Thr Val Ile Met His Asp Ala Pro Ala Gly Val Gly
85 90 95

Ser Val Gln Trp Phe Ile Glu Asn Asn Gly Glu His Tyr Phe Pro Leu
100 105 110

Phe Asp Thr Arg Ala Asp Leu His Pro Gln Phe Val Arg Met Ala Val
115 120 125

Phe Asp Leu Leu Cys Asn Asn Thr Asp Arg Lys Ser Gly His Val Leu
130 135 140

Leu Asp Gly Asp His Ile Trp Gly Ile Asp His Gly Leu Cys Phe Ser
145 150 155 160

Val Glu Pro Lys Leu Arg Thr Val Ile Trp Asp Phe Ala Gly Cys Thr
165 170 175

Ile Pro Asp Asp Leu Val Thr Asp Val Glu Gln Leu Leu Glu Asp Val
180 185 190

Pro Glu Glu Leu His Gln Leu Leu His Pro Ala Glu Ile Asp Ala Leu
195 200 205

Gln Arg Arg Ala Ser Arg Ile Ser Arg Leu Pro Phe Leu Pro Gln Ala
210 215 220

Lys Ser His Arg Gln Phe Pro Trp Pro Leu Val
225 230 235

<210> 1015
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXN02138

<400> 1015
tcactcgccg gagatccgta aaaaggggag tacactgcaa gcctatgatg tcccggccta 60

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aaagtaattc aaagggccaa cagttaagga gactaaagcg atg acc gct cca tca   115
                                            Met Thr Ala Pro Ser
                                              1               5

acc aac acc ggt gtt atc ttg acc gag tcc gca gcg tcc aaa gct aag   163
Thr Asn Thr Gly Val Ile Leu Thr Glu Ser Ala Ala Ser Lys Ala Lys
                 10                  15                  20

gca ctc atc gat cag gaa ggc cgc gac gac ctc tct ctg cgt atc gcc   211
Ala Leu Ile Asp Gln Glu Gly Arg Asp Asp Leu Ser Leu Arg Ile Ala
             25                  30                  35

gtt cag cct ggc ggc tgc tct ggc ctt cgt tac cag ctt tac ttc gac   259
Val Gln Pro Gly Gly Cys Ser Gly Leu Arg Tyr Gln Leu Tyr Phe Asp
         40                  45                  50

gac cgc acc ctt gat ggc gat aag gaa gac atc gtc ggt ggc gtt cgc   307
Asp Arg Thr Leu Asp Gly Asp Lys Glu Asp Ile Val Gly Gly Val Arg
     55                  60                  65

ctt gtc gtt gac aag atg agc acc cca tac ttg ctc ggc gct cag atc   355
Leu Val Val Asp Lys Met Ser Thr Pro Tyr Leu Leu Gly Ala Gln Ile
 70                  75                  80                  85

gac ttc gct gac acc atc gag cag cag ggc ttc acc atc gac aac cca   403
Asp Phe Ala Asp Thr Ile Glu Gln Gln Gly Phe Thr Ile Asp Asn Pro
                 90                  95                 100

aac gca ggc agc tct tgc gct tgt ggt gac tcc ttc aac taaagagatt    452
Asn Ala Gly Ser Ser Cys Ala Cys Gly Asp Ser Phe Asn
            105                 110

ccgttatgta gga                                                   465


<210> 1016
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 1016
Met Thr Ala Pro Ser Thr Asn Thr Gly Val Ile Leu Thr Glu Ser Ala
  1               5                  10                  15

Ala Ser Lys Ala Lys Ala Leu Ile Asp Gln Glu Gly Arg Asp Asp Leu
             20                  25                  30

Ser Leu Arg Ile Ala Val Gln Pro Gly Gly Cys Ser Gly Leu Arg Tyr
         35                  40                  45

Gln Leu Tyr Phe Asp Asp Arg Thr Leu Asp Gly Asp Lys Glu Asp Ile
     50                  55                  60

Val Gly Gly Val Arg Leu Val Val Asp Lys Met Ser Thr Pro Tyr Leu
 65                  70                  75                  80

Leu Gly Ala Gln Ile Asp Phe Ala Asp Thr Ile Glu Gln Gln Gly Phe
                 85                  90                  95

Thr Ile Asp Asn Pro Asn Ala Gly Ser Ser Cys Ala Cys Gly Asp Ser
```

100 105 110

Phe Asn

<210> 1017
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> FRXA02138

<400> 1017
tcactcgccg gagatccgta aaaaggggag tacactgcaa gcctatgatg tcccggccta 60

aaagtaattc aaagggccaa cagttaagga gactaaagcg atg acc gct cca tca 115
Met Thr Ala Pro Ser
1 5

acc aac acc ggt gtt atc ttg acc gag tcc gca gcg tcc aaa gct aag 163
Thr Asn Thr Gly Val Ile Leu Thr Glu Ser Ala Ala Ser Lys Ala Lys
10 15 20

gca ctc atc gat cag gaa ggc cgc gac gac ctc tct ctg cgt atc gcc 211
Ala Leu Ile Asp Gln Glu Gly Arg Asp Asp Leu Ser Leu Arg Ile Ala
25 30 35

gtt cag cct ggc ggc tgc tct ggc ctt cgt tac cag ctt tac ttc gac 259
Val Gln Pro Gly Gly Cys Ser Gly Leu Arg Tyr Gln Leu Tyr Phe Asp
40 45 50

gac cgc acc ctt gat ggc gat aag gaa gac atc gtc ggt ggc gtt cgc 307
Asp Arg Thr Leu Asp Gly Asp Lys Glu Asp Ile Val Gly Gly Val Arg
55 60 65

ctt gtc gtt gac aag atg agc acc cca tac ttg ctc ggc gct cag atc 355
Leu Val Val Asp Lys Met Ser Thr Pro Tyr Leu Leu Gly Ala Gln Ile
70 75 80 85

gac ttc gct gac acc atc gag cag cag ggc ttc acc atc gac aac cca 403
Asp Phe Ala Asp Thr Ile Glu Gln Gln Gly Phe Thr Ile Asp Asn Pro
90 95 100

aac gca ggc agc tct tgc gct tgt ggt gac tcc ttc aac taaagagatt 452
Asn Ala Gly Ser Ser Cys Ala Cys Gly Asp Ser Phe Asn
105 110

ccgttatgta gga 465

<210> 1018
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 1018
Met Thr Ala Pro Ser Thr Asn Thr Gly Val Ile Leu Thr Glu Ser Ala

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  1               5                  10                  15

Ala Ser Lys Ala Lys Ala Leu Ile Asp Gln Glu Gly Arg Asp Asp Leu
             20                  25                  30

Ser Leu Arg Ile Ala Val Gln Pro Gly Gly Cys Ser Gly Leu Arg Tyr
         35                  40                  45

Gln Leu Tyr Phe Asp Asp Arg Thr Leu Asp Gly Asp Lys Glu Asp Ile
     50                  55                  60

Val Gly Gly Val Arg Leu Val Val Asp Lys Met Ser Thr Pro Tyr Leu
 65                  70                  75                  80

Leu Gly Ala Gln Ile Asp Phe Ala Asp Thr Ile Glu Gln Gln Gly Phe
                 85                  90                  95

Thr Ile Asp Asn Pro Asn Ala Gly Ser Ser Cys Ala Cys Gly Asp Ser
            100                 105                 110

Phe Asn
```

US 20090275090 A1

<210> 1019
<211> 1311
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1288)
<223> RXN02151

<400> 1019

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atgagcgcat cgtctttttt aggagttgtc cgccaccgtg aaaactggaa acttaaaccc 60

agccccacag caggtgacgg ctccccagaa caaggctcgt atg gat tgg cca gac   115
                                          Met Asp Trp Pro Asp
                                            1               5

atc gcc aag gga ata tcc atc cta ggt gtc gtg tta cta cac gtg tcg   163
Ile Ala Lys Gly Ile Ser Ile Leu Gly Val Val Leu Leu His Val Ser
                10                  15                  20

ttg gca att cca ggt ggc cag gac acc atg atg tcc cac ctg aac gca   211
Leu Ala Ile Pro Gly Gly Gln Asp Thr Met Met Ser His Leu Asn Ala
            25                  30                  35

ctg ctt gat cca ctt cgg atg cca tta ttt ttt atg gtg agt gga ttt   259
Leu Leu Asp Pro Leu Arg Met Pro Leu Phe Phe Met Val Ser Gly Phe
        40                  45                  50

ttt gca gtt aaa gtt ctg aat caa agc ttt ggt gaa ctt ttc cgc ggg   307
Phe Ala Val Lys Val Leu Asn Gln Ser Phe Gly Glu Leu Phe Arg Gly
    55                  60                  65

cga ctg tgg ttc tac ctg gtt cca tat ttg ctg tgg act cca gtg aat   355
Arg Leu Trp Phe Tyr Leu Val Pro Tyr Leu Leu Trp Thr Pro Val Asn
70                  75                  80                  85
```

```
ctt tat cta cac cgc ctc gag ggc aca gtt ttt acc ggt aga gca ccg   403
Leu Tyr Leu His Arg Leu Glu Gly Thr Val Phe Thr Gly Arg Ala Pro
                 90                  95                 100

gga aca tgg gaa tgg tac agc ggc tcg atg ctc tcg gcc acc aat atg   451
Gly Thr Trp Glu Trp Tyr Ser Gly Ser Met Leu Ser Ala Thr Asn Met
            105                 110                 115

tac tgg ttc ctc tac ttc ttg gtc atc ttc aac cta ttt tta tgg gca   499
Tyr Trp Phe Leu Tyr Phe Leu Val Ile Phe Asn Leu Phe Leu Trp Ala
        120                 125                 130

acg aga aaa ctc cca gct tgg gca att gtg gcg ttg gtg gcc tca ctg   547
Thr Arg Lys Leu Pro Ala Trp Ala Ile Val Ala Leu Val Ala Ser Leu
    135                 140                 145

tgg cta ctt atg ccg gct tat agc gag att gag att cta cgc aag tcc   595
Trp Leu Leu Met Pro Ala Tyr Ser Glu Ile Glu Ile Leu Arg Lys Ser
150                 155                 160                 165

att att tac ttg cct aca ttc ctc att ggc gct tac ttc cgc cca ctg   643
Ile Ile Tyr Leu Pro Thr Phe Leu Ile Gly Ala Tyr Phe Arg Pro Leu
                170                 175                 180

att tcg cgt ttt gca gaa gcc gca aca agg cca aaa gca ata gtg ttt   691
Ile Ser Arg Phe Ala Glu Ala Ala Thr Arg Pro Lys Ala Ile Val Phe
            185                 190                 195

gca gcg gtc ctt tat gtc tcg gga ctt gct ttg ggc gtg atc tca aat   739
Ala Ala Val Leu Tyr Val Ser Gly Leu Ala Leu Gly Val Ile Ser Asn
        200                 205                 210

ggg ctg cgc gac agc gaa aac cat ggc gca agc gtg ctg tgg ctg atg   787
Gly Leu Arg Asp Ser Glu Asn His Gly Ala Ser Val Leu Trp Leu Met
    215                 220                 225

aac ctc cgc gat act ttt gct cat gca ctc ggc ggc aac ctc act gga   835
Asn Leu Arg Asp Thr Phe Ala His Ala Leu Gly Gly Asn Leu Thr Gly
230                 235                 240                 245

ttc gat atg gat cac ctt cct gga atg atc att cgg att gtt tcc ctg   883
Phe Asp Met Asp His Leu Pro Gly Met Ile Ile Arg Ile Val Ser Leu
                250                 255                 260

cct gca gga att gtg ttg tgc gta tgg ctt ggc cga ata aag cca gta   931
Pro Ala Gly Ile Val Leu Cys Val Trp Leu Gly Arg Ile Lys Pro Val
            265                 270                 275

ggg gag ttt ttg aaa ctt att ggt agg cac acc ctt ccc atc tac att   979
Gly Glu Phe Leu Lys Leu Ile Gly Arg His Thr Leu Pro Ile Tyr Ile
        280                 285                 290

ggg cat gca aca gga cta tcg ctg att ttt ggt ttc ggc ttg cgc tgg  1027
Gly His Ala Thr Gly Leu Ser Leu Ile Phe Gly Phe Gly Leu Arg Trp
    295                 300                 305

aat ttc atg gag att gat aac ttc tct gac agt ttg tgg cac cac acc  1075
Asn Phe Met Glu Ile Asp Asn Phe Ser Asp Ser Leu Trp His His Thr
310                 315                 320                 325

aat acg tgg atg gtc atc gcg ttt gcc tgc gcg atg ctc ggc ggg tac  1123
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Asn Thr Trp Met Val Ile Ala Phe Ala Cys Ala Met Leu Gly Gly Tyr
                330                 335                 340

ctg acc tat ctg atc tcg cga gtt cca gtg ctg gga tgg act ctt gtt   1171
Leu Thr Tyr Leu Ile Ser Arg Val Pro Val Leu Gly Trp Thr Leu Val
            345                 350                 355

ccc cct aaa ctg cca gaa cca gat aaa act cca gct aaa gca caa gct   1219
Pro Pro Lys Leu Pro Glu Pro Asp Lys Thr Pro Ala Lys Ala Gln Ala
        360                 365                 370

gat tct cac gtt aaa gct cag tct gcg aag cct atg aat gct tct acc   1267
Asp Ser His Val Lys Ala Gln Ser Ala Lys Pro Met Asn Ala Ser Thr
    375                 380                 385

tct tct aag acg tac ggt ata taactgaagc ataacctgtg tga            1311
Ser Ser Lys Thr Tyr Gly Ile
390                 395


<210> 1020
<211> 396
<212> PRT
<213> Corynebacterium glutamicum

<400> 1020
Met Asp Trp Pro Asp Ile Ala Lys Gly Ile Ser Ile Leu Gly Val Val
  1               5                  10                  15

Leu Leu His Val Ser Leu Ala Ile Pro Gly Gly Gln Asp Thr Met Met
            20                  25                  30

Ser His Leu Asn Ala Leu Leu Asp Pro Leu Arg Met Pro Leu Phe Phe
        35                  40                  45

Met Val Ser Gly Phe Phe Ala Val Lys Val Leu Asn Gln Ser Phe Gly
    50                  55                  60

Glu Leu Phe Arg Gly Arg Leu Trp Phe Tyr Leu Val Pro Tyr Leu Leu
65                  70                  75                  80

Trp Thr Pro Val Asn Leu Tyr Leu His Arg Leu Glu Gly Thr Val Phe
                85                  90                  95

Thr Gly Arg Ala Pro Gly Thr Trp Glu Trp Tyr Ser Gly Ser Met Leu
            100                 105                 110

Ser Ala Thr Asn Met Tyr Trp Phe Leu Tyr Phe Leu Val Ile Phe Asn
        115                 120                 125

Leu Phe Leu Trp Ala Thr Arg Lys Leu Pro Ala Trp Ala Ile Val Ala
    130                 135                 140

Leu Val Ala Ser Leu Trp Leu Leu Met Pro Ala Tyr Ser Glu Ile Glu
145                 150                 155                 160

Ile Leu Arg Lys Ser Ile Ile Tyr Leu Pro Thr Phe Leu Ile Gly Ala
                165                 170                 175

Tyr Phe Arg Pro Leu Ile Ser Arg Phe Ala Glu Ala Ala Thr Arg Pro
            180                 185                 190
```

```
Lys Ala Ile Val Phe Ala Ala Val Leu Tyr Val Ser Gly Leu Ala Leu
        195                 200                 205

Gly Val Ile Ser Asn Gly Leu Arg Asp Ser Glu Asn His Gly Ala Ser
    210                 215                 220

Val Leu Trp Leu Met Asn Leu Arg Asp Thr Phe Ala His Ala Leu Gly
225                 230                 235                 240

Gly Asn Leu Thr Gly Phe Asp Met Asp His Leu Pro Gly Met Ile Ile
                245                 250                 255

Arg Ile Val Ser Leu Pro Ala Gly Ile Val Leu Cys Val Trp Leu Gly
            260                 265                 270

Arg Ile Lys Pro Val Gly Glu Phe Leu Lys Leu Ile Gly Arg His Thr
        275                 280                 285

Leu Pro Ile Tyr Ile Gly His Ala Thr Gly Leu Ser Leu Ile Phe Gly
    290                 295                 300

Phe Gly Leu Arg Trp Asn Phe Met Glu Ile Asp Asn Phe Ser Asp Ser
305                 310                 315                 320

Leu Trp His His Thr Asn Thr Trp Met Val Ile Ala Phe Ala Cys Ala
                325                 330                 335

Met Leu Gly Gly Tyr Leu Thr Tyr Leu Ile Ser Arg Val Pro Val Leu
            340                 345                 350

Gly Trp Thr Leu Val Pro Pro Lys Leu Pro Glu Pro Asp Lys Thr Pro
        355                 360                 365

Ala Lys Ala Gln Ala Asp Ser His Val Lys Ala Gln Ser Ala Lys Pro
    370                 375                 380

Met Asn Ala Ser Thr Ser Ser Lys Thr Tyr Gly Ile
385                 390                 395
```

<210> 1021
<211> 1311
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1288)
<223> FRXA02151

<400> 1021
atgagcgcat cgtctttttt aggagttgtc cgccaccgtg aaaactggaa acttaaaccc 60

agccccacag caggtgacgg ctccccagaa caaggctcgt atg gat tgg cca gac 115
                                                Met Asp Trp Pro Asp
                                                  1   5

atc gcc aag gga ata tcc atc cta ggt gtc gtg tta cta cac gtg tcg 163
Ile Ala Lys Gly Ile Ser Ile Leu Gly Val Val Leu Leu His Val Ser
                10   15   20

```
ttg gca att cca ggt ggc cag gac acc atg atg tcc cac ctg aac gca   211
Leu Ala Ile Pro Gly Gly Gln Asp Thr Met Met Ser His Leu Asn Ala
             25                  30                  35

ctg ctt gat cca ctt cgg atg cca tta ttt ttt atg gtg agt gga ttt   259
Leu Leu Asp Pro Leu Arg Met Pro Leu Phe Phe Met Val Ser Gly Phe
         40                  45                  50

ttt gca gtt aaa gtt ctg aat caa agc ttt ggt gaa ctt ttc cgc ggg   307
Phe Ala Val Lys Val Leu Asn Gln Ser Phe Gly Glu Leu Phe Arg Gly
     55                  60                  65

cga ctg tgg ttc tac ctg gtt cca tat ttg ctg tgg act cca gtg aat   355
Arg Leu Trp Phe Tyr Leu Val Pro Tyr Leu Leu Trp Thr Pro Val Asn
 70                  75                  80                  85

ctt tat cta cac cgc ctc gag ggc aca gtt ttt acc ggt aga gca ccg   403
Leu Tyr Leu His Arg Leu Glu Gly Thr Val Phe Thr Gly Arg Ala Pro
                 90                  95                 100

gga aca tgg gaa tgg tac agc ggc tcg atg ctc tcg gcc acc aat atg   451
Gly Thr Trp Glu Trp Tyr Ser Gly Ser Met Leu Ser Ala Thr Asn Met
             105                 110                 115

tac tgg ttc ctc tac ttc ttg gtc atc ttc aac cta ttt tta tgg gca   499
Tyr Trp Phe Leu Tyr Phe Leu Val Ile Phe Asn Leu Phe Leu Trp Ala
         120                 125                 130

acg aga aaa ctc cca gct tgg gca att gtg gcg ttg gtg gcc tca ctg   547
Thr Arg Lys Leu Pro Ala Trp Ala Ile Val Ala Leu Val Ala Ser Leu
     135                 140                 145

tgg cta ctt atg ccg gct tat agc gag att gag att cta cgc aag tcc   595
Trp Leu Leu Met Pro Ala Tyr Ser Glu Ile Glu Ile Leu Arg Lys Ser
150                 155                 160                 165

att att tac ttg cct aca ttc ctc att ggc gct tac ttc cgc cca ctg   643
Ile Ile Tyr Leu Pro Thr Phe Leu Ile Gly Ala Tyr Phe Arg Pro Leu
                170                 175                 180

att tcg cgt ttt gca gaa gcc gca aca agg cca aaa gca ata gtg ttt   691
Ile Ser Arg Phe Ala Glu Ala Ala Thr Arg Pro Lys Ala Ile Val Phe
             185                 190                 195

gca gcg gtc ctt tat gtc tcg gga ctt gct ttg ggc gtg atc tca aat   739
Ala Ala Val Leu Tyr Val Ser Gly Leu Ala Leu Gly Val Ile Ser Asn
         200                 205                 210

ggg ctg cgc gac agc gaa aac cat ggc gca agc gtg ctg tgg ctg atg   787
Gly Leu Arg Asp Ser Glu Asn His Gly Ala Ser Val Leu Trp Leu Met
     215                 220                 225

aac ctc cgc gat act ttt gct cat gca ctc ggc ggc aac ctc act gga   835
Asn Leu Arg Asp Thr Phe Ala His Ala Leu Gly Gly Asn Leu Thr Gly
230                 235                 240                 245

ttc gat atg gat cac ctt cct gga atg atc att cgg att gtt tcc ctg   883
Phe Asp Met Asp His Leu Pro Gly Met Ile Ile Arg Ile Val Ser Leu
                250                 255                 260
```

```
cct gca gga att gtg ttg tgc gta tgg ctt ggc cga ata aag cca gta   931
Pro Ala Gly Ile Val Leu Cys Val Trp Leu Gly Arg Ile Lys Pro Val
            265                 270                 275

ggg gag ttt ttg aaa ctt att ggt agg cac acc ctt ccc atc tac att   979
Gly Glu Phe Leu Lys Leu Ile Gly Arg His Thr Leu Pro Ile Tyr Ile
        280                 285                 290

ggg cat gca aca gga cta tcg ctg att ttt ggt ttc ggc ttg cgc tgg   1027
Gly His Ala Thr Gly Leu Ser Leu Ile Phe Gly Phe Gly Leu Arg Trp
    295                 300                 305

aat ttc atg gag att gat aac ttc tct gac agt ttg tgg cac cac acc   1075
Asn Phe Met Glu Ile Asp Asn Phe Ser Asp Ser Leu Trp His His Thr
310                 315                 320                 325

aat acg tgg atg gtc atc gcg ttt gcc tgc gcg atg ctc ggc ggg tac   1123
Asn Thr Trp Met Val Ile Ala Phe Ala Cys Ala Met Leu Gly Gly Tyr
                330                 335                 340

ctg acc tat ctg atc tcg cga gtt cca gtg ctg gga tgg act ctt gtt   1171
Leu Thr Tyr Leu Ile Ser Arg Val Pro Val Leu Gly Trp Thr Leu Val
            345                 350                 355

ccc cct aaa ctg cca gaa cca gat aaa act cca gct aaa gca caa gct   1219
Pro Pro Lys Leu Pro Glu Pro Asp Lys Thr Pro Ala Lys Ala Gln Ala
        360                 365                 370

gat tct cac gtt aaa gct cag tct gcg aag cct atg aat gct tct acc   1267
Asp Ser His Val Lys Ala Gln Ser Ala Lys Pro Met Asn Ala Ser Thr
    375                 380                 385

tct tct aag acg tac ggt ata taactgaagc ataacctgtg tga            1311
Ser Ser Lys Thr Tyr Gly Ile
390                 395
```

<210> 1022
<211> 396
<212> PRT
<213> Corynebacterium glutamicum

<400> 1022

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Met Asp Trp Pro Asp Ile Ala Lys Gly Ile Ser Ile Leu Gly Val Val
  1               5                  10                  15

Leu Leu His Val Ser Leu Ala Ile Pro Gly Gly Gln Asp Thr Met Met
            20                  25                  30

Ser His Leu Asn Ala Leu Leu Asp Pro Leu Arg Met Pro Leu Phe Phe
        35                  40                  45

Met Val Ser Gly Phe Phe Ala Val Lys Val Leu Asn Gln Ser Phe Gly
    50                  55                  60

Glu Leu Phe Arg Gly Arg Leu Trp Phe Tyr Leu Val Pro Tyr Leu Leu
65                  70                  75                  80

Trp Thr Pro Val Asn Leu Tyr Leu His Arg Leu Glu Gly Thr Val Phe
                85                  90                  95
```

```
Thr Gly Arg Ala Pro Gly Thr Trp Glu Trp Tyr Ser Gly Ser Met Leu
            100                 105                 110

Ser Ala Thr Asn Met Tyr Trp Phe Leu Tyr Phe Leu Val Ile Phe Asn
        115                 120                 125

Leu Phe Leu Trp Ala Thr Arg Lys Leu Pro Ala Trp Ala Ile Val Ala
    130                 135                 140

Leu Val Ala Ser Leu Trp Leu Leu Met Pro Ala Tyr Ser Glu Ile Glu
145                 150                 155                 160

Ile Leu Arg Lys Ser Ile Ile Tyr Leu Pro Thr Phe Leu Ile Gly Ala
                165                 170                 175

Tyr Phe Arg Pro Leu Ile Ser Arg Phe Ala Glu Ala Ala Thr Arg Pro
            180                 185                 190

Lys Ala Ile Val Phe Ala Ala Val Leu Tyr Val Ser Gly Leu Ala Leu
        195                 200                 205

Gly Val Ile Ser Asn Gly Leu Arg Asp Ser Glu Asn His Gly Ala Ser
    210                 215                 220

Val Leu Trp Leu Met Asn Leu Arg Asp Thr Phe Ala His Ala Leu Gly
225                 230                 235                 240

Gly Asn Leu Thr Gly Phe Asp Met Asp His Leu Pro Gly Met Ile Ile
                245                 250                 255

Arg Ile Val Ser Leu Pro Ala Gly Ile Val Leu Cys Val Trp Leu Gly
            260                 265                 270

Arg Ile Lys Pro Val Gly Glu Phe Leu Lys Leu Ile Gly Arg His Thr
        275                 280                 285

Leu Pro Ile Tyr Ile Gly His Ala Thr Gly Leu Ser Leu Ile Phe Gly
    290                 295                 300

Phe Gly Leu Arg Trp Asn Phe Met Glu Ile Asp Asn Phe Ser Asp Ser
305                 310                 315                 320

Leu Trp His His Thr Asn Thr Trp Met Val Ile Ala Phe Ala Cys Ala
                325                 330                 335

Met Leu Gly Gly Tyr Leu Thr Tyr Leu Ile Ser Arg Val Pro Val Leu
            340                 345                 350

Gly Trp Thr Leu Val Pro Pro Lys Leu Pro Glu Pro Asp Lys Thr Pro
        355                 360                 365

Ala Lys Ala Gln Ala Asp Ser His Val Lys Ala Gln Ser Ala Lys Pro
    370                 375                 380

Met Asn Ala Ser Thr Ser Ser Lys Thr Tyr Gly Ile
385                 390                 395
```

<210> 1023
<211> 969
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> RXN02169

<400> 1023
gttaaaggtc gaaaaatccc acccctagcc cttttaaatg agtgttgtta ttgttaacca 60

ctgttactgg tgggattaat acttattttt gggagaactt ttg gac atg caa ata 115
Leu Asp Met Gln Ile
1 5

aac cgc cga ggc ttc tta aaa gcc acc aca gga ctt gcc act atc ggc 163
Asn Arg Arg Gly Phe Leu Lys Ala Thr Thr Gly Leu Ala Thr Ile Gly
10 15 20

gct gcc agc atg ttt atg cca aag gcc aac gcc ctt gga gca atc aag 211
Ala Ala Ser Met Phe Met Pro Lys Ala Asn Ala Leu Gly Ala Ile Lys
25 30 35

ggc acc gtc atc gac tac gca gca ggc gtc ccc agc gca gca tcc att 259
Gly Thr Val Ile Asp Tyr Ala Ala Gly Val Pro Ser Ala Ala Ser Ile
40 45 50

aaa aat gca ggg cac ctt gga gct gtc cgt tac gtg tca cag cga cgc 307
Lys Asn Ala Gly His Leu Gly Ala Val Arg Tyr Val Ser Gln Arg Arg
55 60 65

ccc ggc act gaa tcc tgg atg atc ggc aag cca gtc aca ctg gca gaa 355
Pro Gly Thr Glu Ser Trp Met Ile Gly Lys Pro Val Thr Leu Ala Glu
70 75 80 85

acc cga gct ttt gaa caa aac ggc ctc aaa acc gca tcc gtc tat caa 403
Thr Arg Ala Phe Glu Gln Asn Gly Leu Lys Thr Ala Ser Val Tyr Gln
90 95 100

tac gga aag gca gag acc gcc gat tgg aag aac ggc gcc gca gga gcg 451
Tyr Gly Lys Ala Glu Thr Ala Asp Trp Lys Asn Gly Ala Ala Gly Ala
105 110 115

gca acc cac gct cca cag gca att gcg ctt cac gtg gca gct ggt ggc 499
Ala Thr His Ala Pro Gln Ala Ile Ala Leu His Val Ala Ala Gly Gly
120 125 130

cct aaa aat cgc ccc atc tac gtg gcg atc gac gac aac cca agc tgg 547
Pro Lys Asn Arg Pro Ile Tyr Val Ala Ile Asp Asp Asn Pro Ser Trp
135 140 145

tct gaa tac acc aat cag att cgc ccc tac ctc cag gca ttc aat gtt 595
Ser Glu Tyr Thr Asn Gln Ile Arg Pro Tyr Leu Gln Ala Phe Asn Val
150 155 160 165

gcg ctg tcc gct gcc ggc tac cag tta ggt gtc tac ggc aac tac aac 643
Ala Leu Ser Ala Ala Gly Tyr Gln Leu Gly Val Tyr Gly Asn Tyr Asn
170 175 180

gtc att aat tgg gct atc gcc gac ggc ctt gga gaa ttc ttc tgg atg 691
Val Ile Asn Trp Ala Ile Ala Asp Gly Leu Gly Glu Phe Phe Trp Met
185 190 195

```
cac aac tgg gga tca gaa gga aag atc cac cca cgc acc acc atc cac   739
His Asn Trp Gly Ser Glu Gly Lys Ile His Pro Arg Thr Thr Ile His
        200                 205                 210

cag atc cgc att gat aag gac acc ctc gac gga gtc ggc atc gac atg   787
Gln Ile Arg Ile Asp Lys Asp Thr Leu Asp Gly Val Gly Ile Asp Met
    215                 220                 225

aac aat gtc tat gca gac gac tgg ggt cag tgg acc cca ggc aac gcg   835
Asn Asn Val Tyr Ala Asp Asp Trp Gly Gln Trp Thr Pro Gly Asn Ala
230                 235                 240                 245

gtt gac gat gcc atc ccc acc att cct gga aac tcc aac acg gga aca   883
Val Asp Asp Ala Ile Pro Thr Ile Pro Gly Asn Ser Asn Thr Gly Thr
                250                 255                 260

ggt act gga att gat gct gac acc atc aac caa gta atc aag att ctt   931
Gly Thr Gly Ile Asp Ala Asp Thr Ile Asn Gln Val Ile Lys Ile Leu
            265                 270                 275

ggc acc cta tct agc taaactagcc gtgctgactc aca                    969
Gly Thr Leu Ser Ser
        280
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US20050059090A1

<210> 1024
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 1024

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Leu Asp Met Gln Ile Asn Arg Arg Gly Phe Leu Lys Ala Thr Thr Gly
  1               5                  10                  15

Leu Ala Thr Ile Gly Ala Ala Ser Met Phe Met Pro Lys Ala Asn Ala
             20                  25                  30

Leu Gly Ala Ile Lys Gly Thr Val Ile Asp Tyr Ala Ala Gly Val Pro
         35                  40                  45

Ser Ala Ala Ser Ile Lys Asn Ala Gly His Leu Gly Ala Val Arg Tyr
     50                  55                  60

Val Ser Gln Arg Arg Pro Gly Thr Glu Ser Trp Met Ile Gly Lys Pro
 65                  70                  75                  80

Val Thr Leu Ala Glu Thr Arg Ala Phe Glu Gln Asn Gly Leu Lys Thr
                 85                  90                  95

Ala Ser Val Tyr Gln Tyr Gly Lys Ala Glu Thr Ala Asp Trp Lys Asn
            100                 105                 110

Gly Ala Ala Gly Ala Ala Thr His Ala Pro Gln Ala Ile Ala Leu His
        115                 120                 125

Val Ala Ala Gly Gly Pro Lys Asn Arg Pro Ile Tyr Val Ala Ile Asp
    130                 135                 140

Asp Asn Pro Ser Trp Ser Glu Tyr Thr Asn Gln Ile Arg Pro Tyr Leu
145                 150                 155                 160
```

```
Gln Ala Phe Asn Val Ala Leu Ser Ala Ala Gly Tyr Gln Leu Gly Val
                165                 170                 175

Tyr Gly Asn Tyr Asn Val Ile Asn Trp Ala Ile Ala Asp Gly Leu Gly
            180                 185                 190

Glu Phe Phe Trp Met His Asn Trp Gly Ser Glu Gly Lys Ile His Pro
        195                 200                 205

Arg Thr Thr Ile His Gln Ile Arg Ile Asp Lys Asp Thr Leu Asp Gly
    210                 215                 220

Val Gly Ile Asp Met Asn Asn Val Tyr Ala Asp Asp Trp Gly Gln Trp
225                 230                 235                 240

Thr Pro Gly Asn Ala Val Asp Asp Ala Ile Pro Thr Ile Pro Gly Asn
                245                 250                 255

Ser Asn Thr Gly Thr Gly Thr Gly Ile Asp Ala Asp Thr Ile Asn Gln
            260                 265                 270

Val Ile Lys Ile Leu Gly Thr Leu Ser Ser
        275                 280


<210> 1025
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> FRXA02169

<400> 1025
gttaaaggtc gaaaaatccc acccctagcc cttttaaatg agtgttgtta ttgttaacca 60

ctgttactgg tgggattaat acttattttt gggagaactt ttg gac atg caa ata   115
                                              Leu Asp Met Gln Ile
                                                1               5

aac cgc cga ggc ttc tta aaa gcc acc aca gga ctt gcc act atc ggc   163
Asn Arg Arg Gly Phe Leu Lys Ala Thr Thr Gly Leu Ala Thr Ile Gly
                10                  15                  20

gct gcc agc atg ttt atg cca aag gcc aac gcc ctt gga gca atc aag   211
Ala Ala Ser Met Phe Met Pro Lys Ala Asn Ala Leu Gly Ala Ile Lys
            25                  30                  35

ggc acc gtc atc gac tac gca gca ggc gtc ccc agc gca gca tcc att   259
Gly Thr Val Ile Asp Tyr Ala Ala Gly Val Pro Ser Ala Ala Ser Ile
        40                  45                  50

aaa aat gca ggg cac ctt gga gct gtc cgt tac gtg tca cag cga cgc   307
Lys Asn Ala Gly His Leu Gly Ala Val Arg Tyr Val Ser Gln Arg Arg
    55                  60                  65

ccc ggc act gaa tcc tgg atg atc ggc aag cca gtc aca ctg gca gaa   355
Pro Gly Thr Glu Ser Trp Met Ile Gly Lys Pro Val Thr Leu Ala Glu
```

```
 70                  75                  80                  85

acc cga gct ttt gaa caa aac ggc ctc aaa acc gca tcc gtc tat caa   403
Thr Arg Ala Phe Glu Gln Asn Gly Leu Lys Thr Ala Ser Val Tyr Gln
                 90                  95                 100

tac gga aag gca gag acc gcc gat tgg aag aac ggc gcc gca gga gcg   451
Tyr Gly Lys Ala Glu Thr Ala Asp Trp Lys Asn Gly Ala Ala Gly Ala
            105                 110                 115

gca acc cac gct cca cag gca att gcg ctt cac gtg gca gct ggt ggc   499
Ala Thr His Ala Pro Gln Ala Ile Ala Leu His Val Ala Ala Gly Gly
        120                 125                 130

cct aaa aat cgc ccc atc tac gtg gcg atc gac gac aac cca agc tgg   547
Pro Lys Asn Arg Pro Ile Tyr Val Ala Ile Asp Asp Asn Pro Ser Trp
    135                 140                 145

tct gaa tac acc aat cag att cgc ccc tac ctc cag gca ttc aat gtt   595
Ser Glu Tyr Thr Asn Gln Ile Arg Pro Tyr Leu Gln Ala Phe Asn Val
150                 155                 160                 165

gcg ctg tcc gct gcc ggc tac cag tta ggt gtc tac ggc aac tac aac   643
Ala Leu Ser Ala Ala Gly Tyr Gln Leu Gly Val Tyr Gly Asn Tyr Asn
                170                 175                 180

gtc att aat tgg gct atc gcc gac ggc ctt gga gaa ttc ttc tgg atg   691
Val Ile Asn Trp Ala Ile Ala Asp Gly Leu Gly Glu Phe Phe Trp Met
            185                 190                 195

cac aac tgg gga tca gaa gga aag atc cac cca cgc acc acc atc cac   739
His Asn Trp Gly Ser Glu Gly Lys Ile His Pro Arg Thr Thr Ile His
        200                 205                 210

cag atc cgc att gat aag gac acc ctc gac gga gtc ggc atc gac atg   787
Gln Ile Arg Ile Asp Lys Asp Thr Leu Asp Gly Val Gly Ile Asp Met
    215                 220                 225

aac aat gtc tat gca gac gac tgg ggt cag tgg acc cca ggc aac gcg   835
Asn Asn Val Tyr Ala Asp Asp Trp Gly Gln Trp Thr Pro Gly Asn Ala
230                 235                 240                 245

gtt gac gat gcc atc ccc acc att cct gga aac tcc aac acg gga aca   883
Val Asp Asp Ala Ile Pro Thr Ile Pro Gly Asn Ser Asn Thr Gly Thr
                250                 255                 260

ggt act gga att gat gct gac acc atc aac caa gta atc aag att ctt   931
Gly Thr Gly Ile Asp Ala Asp Thr Ile Asn Gln Val Ile Lys Ile Leu
            265                 270                 275

ggc acc cta tct agc taaactagcc gtgctgactc aca                    969
Gly Thr Leu Ser Ser
        280
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<210> 1026
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 1026

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Leu Asp Met Gln Ile Asn Arg Arg Gly Phe Leu Lys Ala Thr Thr Gly
  1               5                  10                  15

Leu Ala Thr Ile Gly Ala Ala Ser Met Phe Met Pro Lys Ala Asn Ala
             20                  25                  30

Leu Gly Ala Ile Lys Gly Thr Val Ile Asp Tyr Ala Ala Gly Val Pro
         35                  40                  45

Ser Ala Ala Ser Ile Lys Asn Ala Gly His Leu Gly Ala Val Arg Tyr
     50                  55                  60

Val Ser Gln Arg Arg Pro Gly Thr Glu Ser Trp Met Ile Gly Lys Pro
 65                  70                  75                  80

Val Thr Leu Ala Glu Thr Arg Ala Phe Glu Gln Asn Gly Leu Lys Thr
                 85                  90                  95

Ala Ser Val Tyr Gln Tyr Gly Lys Ala Glu Thr Ala Asp Trp Lys Asn
            100                 105                 110

Gly Ala Ala Gly Ala Ala Thr His Ala Pro Gln Ala Ile Ala Leu His
        115                 120                 125

Val Ala Ala Gly Gly Pro Lys Asn Arg Pro Ile Tyr Val Ala Ile Asp
    130                 135                 140

Asp Asn Pro Ser Trp Ser Glu Tyr Thr Asn Gln Ile Arg Pro Tyr Leu
145                 150                 155                 160

Gln Ala Phe Asn Val Ala Leu Ser Ala Ala Gly Tyr Gln Leu Gly Val
                165                 170                 175

Tyr Gly Asn Tyr Asn Val Ile Asn Trp Ala Ile Ala Asp Gly Leu Gly
            180                 185                 190

Glu Phe Phe Trp Met His Asn Trp Gly Ser Glu Gly Lys Ile His Pro
        195                 200                 205

Arg Thr Thr Ile His Gln Ile Arg Ile Asp Lys Asp Thr Leu Asp Gly
    210                 215                 220

Val Gly Ile Asp Met Asn Asn Val Tyr Ala Asp Asp Trp Gly Gln Trp
225                 230                 235                 240

Thr Pro Gly Asn Ala Val Asp Asp Ala Ile Pro Thr Ile Pro Gly Asn
                245                 250                 255

Ser Asn Thr Gly Thr Gly Thr Gly Ile Asp Ala Asp Thr Ile Asn Gln
            260                 265                 270

Val Ile Lys Ile Leu Gly Thr Leu Ser Ser
        275                 280
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<210> 1027
<211> 1581
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(1558)
<223> RXN02180

<400> 1027
gtttcagcta aaagaagaat ccttgctagt ggaatcagct gagttttcca cgagttttcc 60

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agctttctca caacttgaat agaaattgag gtatccggca atg acg tca ggg aaa   115
                                              Met Thr Ser Gly Lys
                                                1               5

tca acg agt act agg gga gcc cta gac cgg tat ttc aaa atc tcg gag   163
Ser Thr Ser Thr Arg Gly Ala Leu Asp Arg Tyr Phe Lys Ile Ser Glu
                10                  15                  20

cga gga tca agc att ggc acg gaa atc cgt gca ggt gtg gtc aca ttc   211
Arg Gly Ser Ser Ile Gly Thr Glu Ile Arg Ala Gly Val Val Thr Phe
            25                  30                  35

ttc gcg atg gcc tac atc atc atc ctc aac ccc ttg atc ctt ggc acc   259
Phe Ala Met Ala Tyr Ile Ile Ile Leu Asn Pro Leu Ile Leu Gly Thr
        40                  45                  50

acc cct gac gta gag ggc aac acc cta ggc atc gca cag gtt gca gcg   307
Thr Pro Asp Val Glu Gly Asn Thr Leu Gly Ile Ala Gln Val Ala Ala
    55                  60                  65

gca aca gcg ctt gcc gct ggt gtc atg acc atc gcg ttt ggt ttg att   355
Ala Thr Ala Leu Ala Ala Gly Val Met Thr Ile Ala Phe Gly Leu Ile
70                  75                  80                  85

gcg cgt tat cca ttc ggc att gct gct ggc ctg gga att aac acc atg   403
Ala Arg Tyr Pro Phe Gly Ile Ala Ala Gly Leu Gly Ile Asn Thr Met
                90                  95                  100

gtc gcc gtg aca ctg gtt tca ggt gag ggc ctg acc tgg ccg gaa gca   451
Val Ala Val Thr Leu Val Ser Gly Glu Gly Leu Thr Trp Pro Glu Ala
            105                 110                 115

atg gga ctt gtg gtc ctt gac ggt gtg gtc att gtt att ttg gct gtg   499
Met Gly Leu Val Val Leu Asp Gly Val Val Ile Val Ile Leu Ala Val
        120                 125                 130

tcc ggc ttc cgt gtt gct gtg ttc cgt gcg atc cca gca tcc atg aag   547
Ser Gly Phe Arg Val Ala Val Phe Arg Ala Ile Pro Ala Ser Met Lys
    135                 140                 145

gcg gcc atc agc gtg ggt atc ggc ctg ttc atc gcc atg atc ggc ctc   595
Ala Ala Ile Ser Val Gly Ile Gly Leu Phe Ile Ala Met Ile Gly Leu
150                 155                 160                 165

gtg gat gca ggc ttt gtt cgc cgt att cca gat gct gcc ggt act act   643
Val Asp Ala Gly Phe Val Arg Arg Ile Pro Asp Ala Ala Gly Thr Thr
                170                 175                 180

gtg cca gtg act ttg ggc att gat ggt tcc att gcg tct tgg cca acg   691
Val Pro Val Thr Leu Gly Ile Asp Gly Ser Ile Ala Ser Trp Pro Thr
            185                 190                 195

ttc gtg ttc gtt gtc ggt gtt ctt ctc tgt ggc atc ctt gtt gtc cgt   739
Phe Val Phe Val Val Gly Val Leu Leu Cys Gly Ile Leu Val Val Arg
```

```
        200                 205                 210

cga gtt cgc ggt gga ctg ttt atc ggc att ttg gga acc acc att ttg   787
Arg Val Arg Gly Gly Leu Phe Ile Gly Ile Leu Gly Thr Thr Ile Leu
    215                 220                 225

gcg atc atc gca gaa gca atc ttt gat tcc ggt gcg tcc ttt gaa aat   835
Ala Ile Ile Ala Glu Ala Ile Phe Asp Ser Gly Ala Ser Phe Glu Asn
230                 235                 240                 245

ggt gaa gca aac gca gaa ggc tgg tca ctc gcc gtt cct ggt ctc cca   883
Gly Glu Ala Asn Ala Glu Gly Trp Ser Leu Ala Val Pro Gly Leu Pro
                250                 255                 260

gac tcc ttc ggt ggc atc ccg gat ctt tcc atc gtc ggc gca gtt gat   931
Asp Ser Phe Gly Gly Ile Pro Asp Leu Ser Ile Val Gly Ala Val Asp
            265                 270                 275

ttg atc ggt gcg ttc agc cgc atc ggt gtg gtc gcc gcg acc ttg ctg   979
Leu Ile Gly Ala Phe Ser Arg Ile Gly Val Val Ala Ala Thr Leu Leu
        280                 285                 290

atc ttt acc ctg gtc ctt gca aac ttc ttc gac gcc atg ggc acc atg   1027
Ile Phe Thr Leu Val Leu Ala Asn Phe Phe Asp Ala Met Gly Thr Met
    295                 300                 305

acc gct ctt ggt aag cag ggc aac ttg gtt gat gat gaa ggc aac ctt   1075
Thr Ala Leu Gly Lys Gln Gly Asn Leu Val Asp Asp Glu Gly Asn Leu
310                 315                 320                 325

cca gac att aag aag gca ctg gtt gtg gaa ggc gca ggt gcc att gtc   1123
Pro Asp Ile Lys Lys Ala Leu Val Val Glu Gly Ala Gly Ala Ile Val
                330                 335                 340

ggt ggt gct ttc tct gca tcc tcc aac acc gtg ttc gct gac tct tct   1171
Gly Gly Ala Phe Ser Ala Ser Ser Asn Thr Val Phe Ala Asp Ser Ser
            345                 350                 355

gca ggt gtt gca gac ggc gca cga acc ggc ctt gcc aac gtg gtc acc   1219
Ala Gly Val Ala Asp Gly Ala Arg Thr Gly Leu Ala Asn Val Val Thr
        360                 365                 370

ggc tcc ttg ttc ttg gct gcc atg ttc ttg acc cca ctg tat gaa atc   1267
Gly Ser Leu Phe Leu Ala Ala Met Phe Leu Thr Pro Leu Tyr Glu Ile
    375                 380                 385

gtc ccc atc gaa gca gca gca cca gtg ctt gta gtt gtt ggc gcg atg   1315
Val Pro Ile Glu Ala Ala Ala Pro Val Leu Val Val Val Gly Ala Met
390                 395                 400                 405

atg atg ggg cag gtt acc gag att gat ttc tcc aag ttc tac atc gca   1363
Met Met Gly Gln Val Thr Glu Ile Asp Phe Ser Lys Phe Tyr Ile Ala
                410                 415                 420

ttc cca gcg ttc ttg acc att gtg atc atg cct ttc acc tac tcc att   1411
Phe Pro Ala Phe Leu Thr Ile Val Ile Met Pro Phe Thr Tyr Ser Ile
            425                 430                 435

gca aac ggc att ggc gtt gga ttc atc atg tac gcc atc atg gct gca   1459
Ala Asn Gly Ile Gly Val Gly Phe Ile Met Tyr Ala Ile Met Ala Ala
        440                 445                 450
```

```
gcg gca ggc aaa gca aag caa gtg cac tgg ctg atg tgg ctg gtc gct   1507
Ala Ala Gly Lys Ala Lys Gln Val His Trp Leu Met Trp Leu Val Ala
    455                 460                 465

gga ctc ttc gtc gtg ttc ttc gcg att gat ccc atc atg gaa gct gtc   1555
Gly Leu Phe Val Val Phe Phe Ala Ile Asp Pro Ile Met Glu Ala Val
470                 475                 480                 485

ggc taatgacaac gcgcacggta att                                    1581
Gly
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<210> 1028
<211> 486
<212> PRT
<213> Corynebacterium glutamicum

<400> 1028

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Met Thr Ser Gly Lys Ser Thr Ser Thr Arg Gly Ala Leu Asp Arg Tyr
  1               5                  10                  15

Phe Lys Ile Ser Glu Arg Gly Ser Ser Ile Gly Thr Glu Ile Arg Ala
             20                  25                  30

Gly Val Val Thr Phe Phe Ala Met Ala Tyr Ile Ile Ile Leu Asn Pro
         35                  40                  45

Leu Ile Leu Gly Thr Thr Pro Asp Val Glu Gly Asn Thr Leu Gly Ile
     50                  55                  60

Ala Gln Val Ala Ala Ala Thr Ala Leu Ala Ala Gly Val Met Thr Ile
 65                  70                  75                  80

Ala Phe Gly Leu Ile Ala Arg Tyr Pro Phe Gly Ile Ala Ala Gly Leu
                 85                  90                  95

Gly Ile Asn Thr Met Val Ala Val Thr Leu Val Ser Gly Glu Gly Leu
            100                 105                 110

Thr Trp Pro Glu Ala Met Gly Leu Val Val Leu Asp Gly Val Val Ile
        115                 120                 125

Val Ile Leu Ala Val Ser Gly Phe Arg Val Ala Val Phe Arg Ala Ile
    130                 135                 140

Pro Ala Ser Met Lys Ala Ala Ile Ser Val Gly Ile Gly Leu Phe Ile
145                 150                 155                 160

Ala Met Ile Gly Leu Val Asp Ala Gly Phe Val Arg Arg Ile Pro Asp
                165                 170                 175

Ala Ala Gly Thr Thr Val Pro Val Thr Leu Gly Ile Asp Gly Ser Ile
            180                 185                 190

Ala Ser Trp Pro Thr Phe Val Phe Val Val Gly Val Leu Leu Cys Gly
        195                 200                 205

Ile Leu Val Val Arg Arg Val Arg Gly Gly Leu Phe Ile Gly Ile Leu
    210                 215                 220
```

```
Gly Thr Thr Ile Leu Ala Ile Ile Ala Glu Ala Ile Phe Asp Ser Gly
225                 230                 235                 240

Ala Ser Phe Glu Asn Gly Glu Ala Asn Ala Glu Gly Trp Ser Leu Ala
                245                 250                 255

Val Pro Gly Leu Pro Asp Ser Phe Gly Gly Ile Pro Asp Leu Ser Ile
            260                 265                 270

Val Gly Ala Val Asp Leu Ile Gly Ala Phe Ser Arg Ile Gly Val Val
        275                 280                 285

Ala Ala Thr Leu Leu Ile Phe Thr Leu Val Leu Ala Asn Phe Phe Asp
    290                 295                 300

Ala Met Gly Thr Met Thr Ala Leu Gly Lys Gln Gly Asn Leu Val Asp
305                 310                 315                 320

Asp Glu Gly Asn Leu Pro Asp Ile Lys Lys Ala Leu Val Val Glu Gly
                325                 330                 335

Ala Gly Ala Ile Val Gly Gly Ala Phe Ser Ala Ser Ser Asn Thr Val
            340                 345                 350

Phe Ala Asp Ser Ser Ala Gly Val Ala Asp Gly Ala Arg Thr Gly Leu
        355                 360                 365

Ala Asn Val Val Thr Gly Ser Leu Phe Leu Ala Ala Met Phe Leu Thr
    370                 375                 380

Pro Leu Tyr Glu Ile Val Pro Ile Glu Ala Ala Ala Pro Val Leu Val
385                 390                 395                 400

Val Val Gly Ala Met Met Met Gly Gln Val Thr Glu Ile Asp Phe Ser
                405                 410                 415

Lys Phe Tyr Ile Ala Phe Pro Ala Phe Leu Thr Ile Val Ile Met Pro
            420                 425                 430

Phe Thr Tyr Ser Ile Ala Asn Gly Ile Gly Val Gly Phe Ile Met Tyr
        435                 440                 445

Ala Ile Met Ala Ala Ala Ala Gly Lys Ala Lys Gln Val His Trp Leu
    450                 455                 460

Met Trp Leu Val Ala Gly Leu Phe Val Val Phe Phe Ala Ile Asp Pro
465                 470                 475                 480

Ile Met Glu Ala Val Gly
                485
```

<210> 1029
<211> 1581
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1558)

<223> FRXA02180

<400> 1029

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gtttcagcta aaagaagaat ccttgctagt ggaatcagct gagttttcca cgagttttcc 60

agctttctca caacttgaat agaaattgag gtatccggca atg acg tca ggg aaa   115
                                              Met Thr Ser Gly Lys
                                                1               5

tca acg agt act agg gga gcc cta gac cgg tat ttc aaa atc tcg gag   163
Ser Thr Ser Thr Arg Gly Ala Leu Asp Arg Tyr Phe Lys Ile Ser Glu
                   10                  15                  20

cga gga tca agc att ggc acg gaa atc cgt gca ggt gtg gtc aca ttc   211
Arg Gly Ser Ser Ile Gly Thr Glu Ile Arg Ala Gly Val Val Thr Phe
               25                  30                  35

ttc gcg atg gcc tac atc atc atc ctc aac ccc ttg atc ctt ggc acc   259
Phe Ala Met Ala Tyr Ile Ile Ile Leu Asn Pro Leu Ile Leu Gly Thr
           40                  45                  50

acc cct gac gta gag ggc aac acc cta ggc atc gca cag gtt gca gcg   307
Thr Pro Asp Val Glu Gly Asn Thr Leu Gly Ile Ala Gln Val Ala Ala
       55                  60                  65

gca aca gcg ctt gcc gct ggt gtc atg acc atc gcg ttt ggt ttg att   355
Ala Thr Ala Leu Ala Ala Gly Val Met Thr Ile Ala Phe Gly Leu Ile
   70                  75                  80                  85

gcg cgt tat cca ttc ggc att gct gct ggc ctg gga att aac acc atg   403
Ala Arg Tyr Pro Phe Gly Ile Ala Ala Gly Leu Gly Ile Asn Thr Met
                   90                  95                 100

gtc gcc gtg aca ctg gtt tca ggt gag ggc ctg acc tgg ccg gaa gca   451
Val Ala Val Thr Leu Val Ser Gly Glu Gly Leu Thr Trp Pro Glu Ala
               105                 110                 115

atg gga ctt gtg gtc ctt gac ggt gtg gtc att gtt att ttg gct gtg   499
Met Gly Leu Val Val Leu Asp Gly Val Val Ile Val Ile Leu Ala Val
           120                 125                 130

tcc ggc ttc cgt gtt gct gtg ttc cgt gcg atc cca gca tcc atg aag   547
Ser Gly Phe Arg Val Ala Val Phe Arg Ala Ile Pro Ala Ser Met Lys
       135                 140                 145

gcg gcc atc agc gtg ggt atc ggc ctg ttc atc gcc atg atc ggc ctc   595
Ala Ala Ile Ser Val Gly Ile Gly Leu Phe Ile Ala Met Ile Gly Leu
150                 155                 160                 165

gtg gat gca ggc ttt gtt cgc cgt att cca gat gct gcc ggt act act   643
Val Asp Ala Gly Phe Val Arg Arg Ile Pro Asp Ala Ala Gly Thr Thr
                   170                 175                 180

gtg cca gtg act ttg ggc att gat ggt tcc att gcg tct tgg cca acg   691
Val Pro Val Thr Leu Gly Ile Asp Gly Ser Ile Ala Ser Trp Pro Thr
               185                 190                 195

ttc gtg ttc gtt gtc ggt gtt ctt ctc tgt ggc atc ctt gtt gtc cgt   739
Phe Val Phe Val Val Gly Val Leu Leu Cys Gly Ile Leu Val Val Arg
           200                 205                 210
```

```
cga gtt cgc ggt gga ctg ttt atc ggc att ttg gga acc acc att ttg   787
Arg Val Arg Gly Gly Leu Phe Ile Gly Ile Leu Gly Thr Thr Ile Leu
    215                 220                 225

gcg atc atc gca gaa gca atc ttt gat tcc ggt gcg tcc ttt gaa aat   835
Ala Ile Ile Ala Glu Ala Ile Phe Asp Ser Gly Ala Ser Phe Glu Asn
230                 235                 240                 245

ggt gaa gca aac gca gaa ggc tgg tca ctc gcc gtt cct ggt ctc cca   883
Gly Glu Ala Asn Ala Glu Gly Trp Ser Leu Ala Val Pro Gly Leu Pro
                250                 255                 260

gac tcc ttc ggt ggc atc ccg gat ctt tcc atc gtc ggc gca gtt gat   931
Asp Ser Phe Gly Gly Ile Pro Asp Leu Ser Ile Val Gly Ala Val Asp
            265                 270                 275

ttg atc ggt gcg ttc agc cgc atc ggt gtg gtc gcc gcg acc ttg ctg   979
Leu Ile Gly Ala Phe Ser Arg Ile Gly Val Val Ala Ala Thr Leu Leu
        280                 285                 290

atc ttt acc ctg gtc ctt gca aac ttc ttc gac gcc atg ggc acc atg   1027
Ile Phe Thr Leu Val Leu Ala Asn Phe Phe Asp Ala Met Gly Thr Met
    295                 300                 305

acc gct ctt ggt aag cag ggc aac ttg gtt gat gat gaa ggc aac ctt   1075
Thr Ala Leu Gly Lys Gln Gly Asn Leu Val Asp Asp Glu Gly Asn Leu
310                 315                 320                 325

cca gac att aag aag gca ctg gtt gtg gaa ggc gca ggt gcc att gtc   1123
Pro Asp Ile Lys Lys Ala Leu Val Val Glu Gly Ala Gly Ala Ile Val
                330                 335                 340

ggt ggt gct ttc tct gca tcc tcc aac acc gtg ttc gct gac tct tct   1171
Gly Gly Ala Phe Ser Ala Ser Ser Asn Thr Val Phe Ala Asp Ser Ser
            345                 350                 355

gca ggt gtt gca gac ggc gca cga acc ggc ctt gcc aac gtg gtc acc   1219
Ala Gly Val Ala Asp Gly Ala Arg Thr Gly Leu Ala Asn Val Val Thr
        360                 365                 370

ggc tcc ttg ttc ttg gct gcc atg ttc ttg acc cca ctg tat gaa atc   1267
Gly Ser Leu Phe Leu Ala Ala Met Phe Leu Thr Pro Leu Tyr Glu Ile
    375                 380                 385

gtc ccc atc gaa gca gca gca cca gtg ctt gta gtt gtt ggc gcg atg   1315
Val Pro Ile Glu Ala Ala Ala Pro Val Leu Val Val Val Gly Ala Met
390                 395                 400                 405

atg atg ggg cag gtt acc gag att gat ttc tcc aag ttc tac atc gca   1363
Met Met Gly Gln Val Thr Glu Ile Asp Phe Ser Lys Phe Tyr Ile Ala
                410                 415                 420

ttc cca gcg ttc ttg acc att gtg atc atg cct ttc acc tac tcc att   1411
Phe Pro Ala Phe Leu Thr Ile Val Ile Met Pro Phe Thr Tyr Ser Ile
            425                 430                 435

gca aac ggc att ggc gtt gga ttc atc atg tac gcc atc atg gct gca   1459
Ala Asn Gly Ile Gly Val Gly Phe Ile Met Tyr Ala Ile Met Ala Ala
        440                 445                 450

gcg gca ggc aaa gca aag caa gtg cac tgg ctg atg tgg ctg gtc gct   1507
```

```
Ala Ala Gly Lys Ala Lys Gln Val His Trp Leu Met Trp Leu Val Ala
    455                 460                 465

gga ctc ttc gtc gtg ttc ttc gcg att gat ccc atc atg gaa gct gtc   1555
Gly Leu Phe Val Val Phe Phe Ala Ile Asp Pro Ile Met Glu Ala Val
470                 475                 480                 485

ggc taatgacaac gcgcacggta att                                   1581
Gly
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<210> 1030
<211> 486
<212> PRT
<213> Corynebacterium glutamicum

<400> 1030

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Met Thr Ser Gly Lys Ser Thr Ser Thr Arg Gly Ala Leu Asp Arg Tyr
  1               5                  10                  15

Phe Lys Ile Ser Glu Arg Gly Ser Ser Ile Gly Thr Glu Ile Arg Ala
             20                  25                  30

Gly Val Val Thr Phe Phe Ala Met Ala Tyr Ile Ile Ile Leu Asn Pro
         35                  40                  45

Leu Ile Leu Gly Thr Thr Pro Asp Val Glu Gly Asn Thr Leu Gly Ile
     50                  55                  60

Ala Gln Val Ala Ala Ala Thr Ala Leu Ala Ala Gly Val Met Thr Ile
 65                  70                  75                  80

Ala Phe Gly Leu Ile Ala Arg Tyr Pro Phe Gly Ile Ala Ala Gly Leu
                 85                  90                  95

Gly Ile Asn Thr Met Val Ala Val Thr Leu Val Ser Gly Glu Gly Leu
            100                 105                 110

Thr Trp Pro Glu Ala Met Gly Leu Val Val Leu Asp Gly Val Val Ile
        115                 120                 125

Val Ile Leu Ala Val Ser Gly Phe Arg Val Ala Val Phe Arg Ala Ile
    130                 135                 140

Pro Ala Ser Met Lys Ala Ala Ile Ser Val Gly Ile Gly Leu Phe Ile
145                 150                 155                 160

Ala Met Ile Gly Leu Val Asp Ala Gly Phe Val Arg Arg Ile Pro Asp
                165                 170                 175

Ala Ala Gly Thr Thr Val Pro Val Thr Leu Gly Ile Asp Gly Ser Ile
            180                 185                 190

Ala Ser Trp Pro Thr Phe Val Phe Val Val Gly Val Leu Leu Cys Gly
        195                 200                 205

Ile Leu Val Val Arg Arg Val Arg Gly Gly Leu Phe Ile Gly Ile Leu
    210                 215                 220

Gly Thr Thr Ile Leu Ala Ile Ile Ala Glu Ala Ile Phe Asp Ser Gly
```

225 230 235 240

Ala Ser Phe Glu Asn Gly Glu Ala Asn Ala Glu Gly Trp Ser Leu Ala
245 250 255

Val Pro Gly Leu Pro Asp Ser Phe Gly Gly Ile Pro Asp Leu Ser Ile
260 265 270

Val Gly Ala Val Asp Leu Ile Gly Ala Phe Ser Arg Ile Gly Val Val
275 280 285

Ala Ala Thr Leu Leu Ile Phe Thr Leu Val Leu Ala Asn Phe Phe Asp
290 295 300

Ala Met Gly Thr Met Thr Ala Leu Gly Lys Gln Gly Asn Leu Val Asp
305 310 315 320

Asp Glu Gly Asn Leu Pro Asp Ile Lys Lys Ala Leu Val Val Glu Gly
325 330 335

Ala Gly Ala Ile Val Gly Gly Ala Phe Ser Ala Ser Ser Asn Thr Val
340 345 350

Phe Ala Asp Ser Ser Ala Gly Val Ala Asp Gly Ala Arg Thr Gly Leu
355 360 365

Ala Asn Val Val Thr Gly Ser Leu Phe Leu Ala Ala Met Phe Leu Thr
370 375 380

Pro Leu Tyr Glu Ile Val Pro Ile Glu Ala Ala Ala Pro Val Leu Val
385 390 395 400

Val Val Gly Ala Met Met Met Gly Gln Val Thr Glu Ile Asp Phe Ser
405 410 415

Lys Phe Tyr Ile Ala Phe Pro Ala Phe Leu Thr Ile Val Ile Met Pro
420 425 430

Phe Thr Tyr Ser Ile Ala Asn Gly Ile Gly Val Gly Phe Ile Met Tyr
435 440 445

Ala Ile Met Ala Ala Ala Ala Gly Lys Ala Lys Gln Val His Trp Leu
450 455 460

Met Trp Leu Val Ala Gly Leu Phe Val Val Phe Phe Ala Ile Asp Pro
465 470 475 480

Ile Met Glu Ala Val Gly
485

<210> 1031
<211> 702
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(679)
<223> RXN02185

<400> 1031
caactccttg gggtgaagcc agacatccac tggcagagca actcctccgc tctaacccga 60

cagctaacct cgacggcgac aaatgagagg aaaacttttc atg gga cgt cac tcc 115
Met Gly Arg His Ser
1 5

act aag act agc tcc gcg ttc acc aag ctc gca gct tcc acc atc gct 163
Thr Lys Thr Ser Ser Ala Phe Thr Lys Leu Ala Ala Ser Thr Ile Ala
10 15 20

ttc ggt gct gct gca acc atc atg gct cct tct gca tct gct gca cct 211
Phe Gly Ala Ala Ala Thr Ile Met Ala Pro Ser Ala Ser Ala Ala Pro
25 30 35

gat tcc gac tgg gat cgc ctc gca cag tgc gag tcc ggt ggt aac tgg 259
Asp Ser Asp Trp Asp Arg Leu Ala Gln Cys Glu Ser Gly Gly Asn Trp
40 45 50

gca atc aac acc ggt aac ggc tac cac ggt ggt ctg cag ttc tcc gct 307
Ala Ile Asn Thr Gly Asn Gly Tyr His Gly Gly Leu Gln Phe Ser Ala
55 60 65

agc acc tgg gct gct tac ggc ggc cag gag ttc gct acc tac gca tac 355
Ser Thr Trp Ala Ala Tyr Gly Gly Gln Glu Phe Ala Thr Tyr Ala Tyr
70 75 80 85

cag gca acc cgt gag cag cag atc gct gtt gca gag cgc acc ttg gct 403
Gln Ala Thr Arg Glu Gln Gln Ile Ala Val Ala Glu Arg Thr Leu Ala
90 95 100

ggt cag ggc tgg ggc gca tgg cct gct tgc tcc gct tcc ctt gga ctg 451
Gly Gln Gly Trp Gly Ala Trp Pro Ala Cys Ser Ala Ser Leu Gly Leu
105 110 115

aac tcc gct cca acc cag cgt gac ctc tcc gct acc acc tcc acc cca 499
Asn Ser Ala Pro Thr Gln Arg Asp Leu Ser Ala Thr Thr Ser Thr Pro
120 125 130

gag cca gct gca gct gca cca gct gtt gct gag tac aac gct cct gca 547
Glu Pro Ala Ala Ala Ala Pro Ala Val Ala Glu Tyr Asn Ala Pro Ala
135 140 145

gcc aac atc gca gtt ggc tcc acc gac ttg aac acc atc aag tcc acc 595
Ala Asn Ile Ala Val Gly Ser Thr Asp Leu Asn Thr Ile Lys Ser Thr
150 155 160 165

tac ggc gct gtc acc ggc acc ctc gct cag tac ggc atc acc gtt cca 643
Tyr Gly Ala Val Thr Gly Thr Leu Ala Gln Tyr Gly Ile Thr Val Pro
170 175 180

gct gag gtt gag tct tac tac aac gct ttc gtc ggc taaatctagc 689
Ala Glu Val Glu Ser Tyr Tyr Asn Ala Phe Val Gly
185 190

tgcacttttt aaa 702

<210> 1032
<211> 193
<212> PRT

<213> Corynebacterium glutamicum

<400> 1032

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Met Gly Arg His Ser Thr Lys Thr Ser Ser Ala Phe Thr Lys Leu Ala
  1               5                  10                  15

Ala Ser Thr Ile Ala Phe Gly Ala Ala Ala Thr Ile Met Ala Pro Ser
             20                  25                  30

Ala Ser Ala Ala Pro Asp Ser Asp Trp Asp Arg Leu Ala Gln Cys Glu
         35                  40                  45

Ser Gly Gly Asn Trp Ala Ile Asn Thr Gly Asn Gly Tyr His Gly Gly
     50                  55                  60

Leu Gln Phe Ser Ala Ser Thr Trp Ala Ala Tyr Gly Gly Gln Glu Phe
 65                  70                  75                  80

Ala Thr Tyr Ala Tyr Gln Ala Thr Arg Glu Gln Gln Ile Ala Val Ala
                 85                  90                  95

Glu Arg Thr Leu Ala Gly Gln Gly Trp Gly Ala Trp Pro Ala Cys Ser
            100                 105                 110

Ala Ser Leu Gly Leu Asn Ser Ala Pro Thr Gln Arg Asp Leu Ser Ala
        115                 120                 125

Thr Thr Ser Thr Pro Glu Pro Ala Ala Ala Ala Pro Ala Val Ala Glu
    130                 135                 140

Tyr Asn Ala Pro Ala Ala Asn Ile Ala Val Gly Ser Thr Asp Leu Asn
145                 150                 155                 160

Thr Ile Lys Ser Thr Tyr Gly Ala Val Thr Gly Thr Leu Ala Gln Tyr
                165                 170                 175

Gly Ile Thr Val Pro Ala Glu Val Glu Ser Tyr Tyr Asn Ala Phe Val
            180                 185                 190

Gly
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<210> 1033
<211> 702
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(679)
<223> FRXA02185

<400> 1033

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caactccttg gggtgaagcc agacatccac tggcagagca actcctccgc tctaacccga 60

cagctaacct cgacggcgac aaatgagagg aaaacttttc atg gga cgt cac tcc   115
                                              Met Gly Arg His Ser
                                                1               5

act aag act agc tcc gcg ttc acc aag ctc gca gct tcc acc atc gct   163
```

```
Thr Lys Thr Ser Ser Ala Phe Thr Lys Leu Ala Ala Ser Thr Ile Ala
                 10                  15                  20

ttc ggt gct gct gca acc atc atg gct cct tct gca tct gct gca cct   211
Phe Gly Ala Ala Ala Thr Ile Met Ala Pro Ser Ala Ser Ala Ala Pro
             25                  30                  35

gat tcc gac tgg gat cgc ctc gca cag tgc gag tcc ggt ggt aac tgg   259
Asp Ser Asp Trp Asp Arg Leu Ala Gln Cys Glu Ser Gly Gly Asn Trp
         40                  45                  50

gca atc aac acc ggt aac ggc tac cac ggt ggt ctg cag ttc tcc gct   307
Ala Ile Asn Thr Gly Asn Gly Tyr His Gly Gly Leu Gln Phe Ser Ala
     55                  60                  65

agc acc tgg gct gct tac ggc ggc cag gag ttc gct acc tac gca tac   355
Ser Thr Trp Ala Ala Tyr Gly Gly Gln Glu Phe Ala Thr Tyr Ala Tyr
 70                  75                  80                  85

cag gca acc cgt gag cag cag atc gct gtt gca gag cgc acc ttg gct   403
Gln Ala Thr Arg Glu Gln Gln Ile Ala Val Ala Glu Arg Thr Leu Ala
                 90                  95                 100

ggt cag ggc tgg ggc gca tgg cct gct tgc tcc gct tcc ctt gga ctg   451
Gly Gln Gly Trp Gly Ala Trp Pro Ala Cys Ser Ala Ser Leu Gly Leu
             105                 110                 115

aac tcc gct cca acc cag cgt gac ctc tcc gct acc acc tcc acc cca   499
Asn Ser Ala Pro Thr Gln Arg Asp Leu Ser Ala Thr Thr Ser Thr Pro
         120                 125                 130

gag cca gct gca gct gca cca gct gtt gct gag tac aac gct cct gca   547
Glu Pro Ala Ala Ala Ala Pro Ala Val Ala Glu Tyr Asn Ala Pro Ala
     135                 140                 145

gcc aac atc gca gtt ggc tcc acc gac ttg aac acc atc aag tcc acc   595
Ala Asn Ile Ala Val Gly Ser Thr Asp Leu Asn Thr Ile Lys Ser Thr
150                 155                 160                 165

tac ggc gct gtc acc ggc acc ctc gct cag tac ggc atc acc gtt cca   643
Tyr Gly Ala Val Thr Gly Thr Leu Ala Gln Tyr Gly Ile Thr Val Pro
                170                 175                 180

gct gag gtt gag tct tac tac aac gct ttc gtc ggc taaatctagc        689
Ala Glu Val Glu Ser Tyr Tyr Asn Ala Phe Val Gly
            185                 190

tgcacttttt aaa                                                   702


<210> 1034
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 1034
Met Gly Arg His Ser Thr Lys Thr Ser Ser Ala Phe Thr Lys Leu Ala
  1               5                  10                  15

Ala Ser Thr Ile Ala Phe Gly Ala Ala Ala Thr Ile Met Ala Pro Ser
             20                  25                  30
```

```
Ala Ser Ala Ala Pro Asp Ser Asp Trp Asp Arg Leu Ala Gln Cys Glu
          35                  40                  45

Ser Gly Gly Asn Trp Ala Ile Asn Thr Gly Asn Gly Tyr His Gly Gly
      50                  55                  60

Leu Gln Phe Ser Ala Ser Thr Trp Ala Ala Tyr Gly Gly Gln Glu Phe
 65                  70                  75                  80

Ala Thr Tyr Ala Tyr Gln Ala Thr Arg Glu Gln Gln Ile Ala Val Ala
                 85                  90                  95

Glu Arg Thr Leu Ala Gly Gln Gly Trp Gly Ala Trp Pro Ala Cys Ser
            100                 105                 110

Ala Ser Leu Gly Leu Asn Ser Ala Pro Thr Gln Arg Asp Leu Ser Ala
        115                 120                 125

Thr Thr Ser Thr Pro Glu Pro Ala Ala Ala Ala Pro Ala Val Ala Glu
    130                 135                 140

Tyr Asn Ala Pro Ala Ala Asn Ile Ala Val Gly Ser Thr Asp Leu Asn
145                 150                 155                 160

Thr Ile Lys Ser Thr Tyr Gly Ala Val Thr Gly Thr Leu Ala Gln Tyr
                165                 170                 175

Gly Ile Thr Val Pro Ala Glu Val Glu Ser Tyr Tyr Asn Ala Phe Val
            180                 185                 190

Gly
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20050244934

<210> 1035
<211> 321
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(298)
<223> RXN02186

<400> 1035
tccaaccacc ccttgagggt ggggatgggg gagtcttttt tcatgatgtt gttaagttta 60

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agccttgttg aggtgacttt tgttcccaga gtttgaaaga atg tat gac atg gca   115
                                            Met Tyr Asp Met Ala
                                              1               5

aac gta gag aag aag cac ttc gtc gat ccg gca tgg ccg gag cac aat   163
Asn Val Glu Lys Lys His Phe Val Asp Pro Ala Trp Pro Glu His Asn
                  10                  15                  20

cca gct gac gga cac gtc gtt act gaa ctc atc tcc aag gtc gca ggc   211
Pro Ala Asp Gly His Val Val Thr Glu Leu Ile Ser Lys Val Ala Gly
              25                  30                  35

gcg tcc agc cca tgg ggc gat gac aag gaa ttc cca gtt tct gca gaa   259
```

```
Ala Ser Ser Pro Trp Gly Asp Asp Lys Glu Phe Pro Val Ser Ala Glu
         40                  45                  50

gag acc gga tac gtt cac ccg tac acc cgg atc aac cgc taagaaactt    308
Glu Thr Gly Tyr Val His Pro Tyr Thr Arg Ile Asn Arg
     55                  60                  65

aaaaaagagg caa                                                   321


<210> 1036
<211> 66
<212> PRT
<213> Corynebacterium glutamicum

<400> 1036
Met Tyr Asp Met Ala Asn Val Glu Lys Lys His Phe Val Asp Pro Ala
  1               5                  10                  15

Trp Pro Glu His Asn Pro Ala Asp Gly His Val Val Thr Glu Leu Ile
             20                  25                  30

Ser Lys Val Ala Gly Ala Ser Ser Pro Trp Gly Asp Asp Lys Glu Phe
         35                  40                  45

Pro Val Ser Ala Glu Glu Thr Gly Tyr Val His Pro Tyr Thr Arg Ile
     50                  55                  60

Asn Arg
 65


<210> 1037
<211> 342
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(319)
<223> FRXA02186

<400> 1037
agctgatcat cactttgagt atccaaccac cccttgaggg tggggatggg ggagtctttt 60

ttcatgatgt tgttaagttt aagccttgtt gaggtgactt ttg ttc cca gag ttt   115
                                          Leu Phe Pro Glu Phe
                                            1               5

gaa aga atg tat gac atg gca aac gta gag aag aag cac ttc gtc gat   163
Glu Arg Met Tyr Asp Met Ala Asn Val Glu Lys Lys His Phe Val Asp
                 10                  15                  20

ccg gca tgg ccg gag cac aat cca gct gac gga cac gtc gtt act gaa   211
Pro Ala Trp Pro Glu His Asn Pro Ala Asp Gly His Val Val Thr Glu
             25                  30                  35

ctc atc tcc aag gtc gca ggc gcg tcc agc cca tgg ggc gat gac aag   259
Leu Ile Ser Lys Val Ala Gly Ala Ser Ser Pro Trp Gly Asp Asp Lys
         40                  45                  50
```

```
gaa ttc cca gtt tct gca gaa gag acc gga tac gtt cac ccg tac acc   307
Glu Phe Pro Val Ser Ala Glu Glu Thr Gly Tyr Val His Pro Tyr Thr
     55                  60                  65

cgg atc aac cgc taagaaactt aaaaaagagg caa                        342
Arg Ile Asn Arg
 70
```

<210> 1038
<211> 73
<212> PRT
<213> Corynebacterium glutamicum

<400> 1038

```
Leu Phe Pro Glu Phe Glu Arg Met Tyr Asp Met Ala Asn Val Glu Lys
  1               5                  10                  15

Lys His Phe Val Asp Pro Ala Trp Pro Glu His Asn Pro Ala Asp Gly
             20                  25                  30

His Val Val Thr Glu Leu Ile Ser Lys Val Ala Gly Ala Ser Ser Pro
         35                  40                  45

Trp Gly Asp Asp Lys Glu Phe Pro Val Ser Ala Glu Glu Thr Gly Tyr
     50                  55                  60

Val His Pro Tyr Thr Arg Ile Asn Arg
 65                  70
```

<210> 1039
<211> 898
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(898)
<223> RXN02207

<400> 1039

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gaatcggtga ctttgccaac accaatcaca caagcccttg atgatgtctc cctgtgactt 60

ggtccaatta cattcactgg taatctgaaa ccttgtgaat atg cgc cgt cga tcc   115
                                              Met Arg Arg Arg Ser
                                                1               5

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca   163
Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala
                 10                  15                  20

ctt ctt tta agt gca tgt acg caa ggg gta acg gac tcc ccg gat atg   211
Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr Asp Ser Pro Asp Met
             25                  30                  35

ggc aag gca act ccc gct gtc tcc ccc gca gca agc aac ccg gat ggc   259
Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala Ser Asn Pro Asp Gly
         40                  45                  50

caa gta att gag ttc ggc aac atc act gac atg gaa gtc act gat ggt   307
```

```
Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met Glu Val Thr Asp Gly
     55                  60                  65

gac atc ctc ggt gta cgc acc gaa gac gca ctc gct att ggt aca gtc   355
Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu Ala Ile Gly Thr Val
 70                  75                  80                  85

tcc gac ttc gaa gcg ggt agc cag gtg gaa ctg gac gtc gat aag caa   403
Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu Asp Val Asp Lys Gln
                 90                  95                 100

tgc ggc gac ctg acc gca acc ggc ggc act ttc gtg ctc ccc tgc gcc   451
Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe Val Leu Pro Cys Ala
            105                 110                 115

gat ggc gtt tat ttg att gat gcc aag gac ccg gat ctg gat gag ttg   499
Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro Asp Leu Asp Glu Leu
        120                 125                 130

cgt gca act gac aag cca gtc acg gtg gca gcc ttg acc agc gat gat   547
Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala Leu Thr Ser Asp Asp
    135                 140                 145

cag ctt ctg gtg ggc aat ggt gaa gat gaa gaa ctc acc atc tac cgc   595
Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu Leu Thr Ile Tyr Arg
150                 155                 160                 165

gag ggc gaa gag cca gaa acc ttc acc gtc gcg ggt ccc aat acc cag   643
Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala Gly Pro Asn Thr Gln
                170                 175                 180

ctc atc gcc gtt cct gtc att gat cgc cac gac gcc gtt gtg cgc acc   691
Leu Ile Ala Val Pro Val Ile Asp Arg His Asp Ala Val Val Arg Thr
            185                 190                 195

tgg aac gaa aac acc acg att caa gat gtg gac tac ccc aac gac cgt   739
Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp Tyr Pro Asn Asp Arg
        200                 205                 210

gaa ggc gcg acc ctt cgc gtg gga ctc ggc gtt ggt caa atg gct ggt   787
Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val Gly Gln Met Ala Gly
    215                 220                 225

ggc gaa gac ggc ctg ctg gtg gtc tct gat gaa atg ggt ggc caa att   835
Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu Met Gly Gly Gln Ile
230                 235                 240                 245

gcc atc tac aac gct gat gat gtc atc cga ctt caa aat gac cgc ccc   883
Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu Gln Asn Asp Arg Pro
                250                 255                 260

cac cga cga gga acc                                              898
His Arg Arg Gly Thr
            265
```

<210> 1040
<211> 266
<212> PRT
<213> Corynebacterium glutamicum

<400> 1040

```
Met Arg Arg Arg Ser Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu
  1               5                  10                  15

Leu Ala Ser Thr Ala Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr
             20                  25                  30

Asp Ser Pro Asp Met Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala
         35                  40                  45

Ser Asn Pro Asp Gly Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met
     50                  55                  60

Glu Val Thr Asp Gly Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu
 65                  70                  75                  80

Ala Ile Gly Thr Val Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu
                 85                  90                  95

Asp Val Asp Lys Gln Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe
            100                 105                 110

Val Leu Pro Cys Ala Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro
        115                 120                 125

Asp Leu Asp Glu Leu Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala
    130                 135                 140

Leu Thr Ser Asp Asp Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu
145                 150                 155                 160

Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala
                165                 170                 175

Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp
            180                 185                 190

Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp
        195                 200                 205

Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val
    210                 215                 220

Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu
225                 230                 235                 240

Met Gly Gly Gln Ile Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu
                245                 250                 255

Gln Asn Asp Arg Pro His Arg Arg Gly Thr
            260                 265
```

<210> 1041
<211> 859
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(859)

<223> FRXA02207

<400> 1041

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gaatcggtga ctttgccaac accaatcaca caagcccttg atgatgtctc cctgtgactt 60

ggtccaatta cattcactgg taatctgaaa ccttgtgaat atg cgc cgt cga tcc   115
                                            Met Arg Arg Arg Ser
                                              1               5

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca   163
Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala
                 10                  15                  20

ctt ctt tta agt gca tgt acg caa ggg gta acg gac tcc ccg gat atg   211
Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr Asp Ser Pro Asp Met
             25                  30                  35

ggc aag gca act ccc gct gtc tcc ccc gca gca agc aac ccg gat ggc   259
Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala Ser Asn Pro Asp Gly
         40                  45                  50

caa gta att gag ttc ggc aac atc act gac atg gaa gtc act gat ggt   307
Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met Glu Val Thr Asp Gly
     55                  60                  65

gac atc ctc ggt gta cgc acc gaa gac gca ctc gct att ggt aca gtc   355
Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu Ala Ile Gly Thr Val
 70                  75                  80                  85

tcc gac ttc gaa gcg ggt agc cag gtg gaa ctg gac gtc gat aag caa   403
Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu Asp Val Asp Lys Gln
                 90                  95                 100

tgc ggc gac ctg acc gca acc ggc ggc act ttc gtg ctc ccc tgc gcc   451
Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe Val Leu Pro Cys Ala
             105                 110                 115

gat ggc gtt tat ttg att gat gcc aag gac ccg gat ctg gat gag ttg   499
Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro Asp Leu Asp Glu Leu
         120                 125                 130

cgt gca act gac aag cca gtc acg gtg gca gcc ttg acc agc gat gat   547
Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala Leu Thr Ser Asp Asp
     135                 140                 145

cag ctt ctg gtg ggc aat ggt gaa gat gaa gaa ctc acc atc tac cgc   595
Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu Leu Thr Ile Tyr Arg
150                 155                 160                 165

gag ggc gaa gag cca gaa acc ttc acc gtc gcg ggt ccc aat acc cag   643
Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala Gly Pro Asn Thr Gln
                 170                 175                 180

ctc atc gcc gtt cct gtc att gat cgc cac gac gcc gtt gtg cgc acc   691
Leu Ile Ala Val Pro Val Ile Asp Arg His Asp Ala Val Val Arg Thr
             185                 190                 195

tgg aac gaa aac acc acg att caa gat gtg gac tac ccc aac gac cgt   739
Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp Tyr Pro Asn Asp Arg
         200                 205                 210
```

```
gaa ggc gcg acc ctt cgc gtg gga ctc ggc gtt ggt caa atg gct ggt   787
Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val Gly Gln Met Ala Gly
    215                 220                 225

ggc gaa gac ggc ctg ctg gtg gtc tct gat gaa atg ggt ggc caa att   835
Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu Met Gly Gly Gln Ile
230                 235                 240                 245

gcc atc tac aac gct gat gat gtc                                  859
Ala Ile Tyr Asn Ala Asp Asp Val
                250
```

<210> 1042
<211> 253
<212> PRT
<213> Corynebacterium glutamicum

<400> 1042

```
Met Arg Arg Arg Ser Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu
  1               5                  10                  15

Leu Ala Ser Thr Ala Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr
             20                  25                  30

Asp Ser Pro Asp Met Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala
         35                  40                  45

Ser Asn Pro Asp Gly Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met
     50                  55                  60

Glu Val Thr Asp Gly Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu
 65                  70                  75                  80

Ala Ile Gly Thr Val Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu
                 85                  90                  95

Asp Val Asp Lys Gln Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe
            100                 105                 110

Val Leu Pro Cys Ala Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro
        115                 120                 125

Asp Leu Asp Glu Leu Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala
    130                 135                 140

Leu Thr Ser Asp Asp Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu
145                 150                 155                 160

Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala
                165                 170                 175

Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp
            180                 185                 190

Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp
        195                 200                 205

Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val
    210                 215                 220
```

```
Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu
225                 230                 235                 240

Met Gly Gly Gln Ile Ala Ile Tyr Asn Ala Asp Asp Val
                245                 250


<210> 1043
<211> 601
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(601)
<223> RXN02223

<400> 1043
cttgcttttg agggccgcta cgcgcagctg tatcaacgat ggagtgctca atagttcaaa 60

tccaccacaa actctagaga tttggggtag aaacgaagac atg agc acc tac caa   115
                                            Met Ser Thr Tyr Gln
                                              1               5

gac gat cgt ttc cca ggc cca gac ccc tac gca ccg ctt ggt gaa aag   163
Asp Asp Arg Phe Pro Gly Pro Asp Pro Tyr Ala Pro Leu Gly Glu Lys
                 10                  15                  20

cca agc ttt acc ctc acc tcc acc gac ttg gaa aac ggt gca aag ctg   211
Pro Ser Phe Thr Leu Thr Ser Thr Asp Leu Glu Asn Gly Ala Lys Leu
             25                  30                  35

gcc gaa gcc caa ctc ggt ggc acc gat att tcc cca cag ctg tcc tgg   259
Ala Glu Ala Gln Leu Gly Gly Thr Asp Ile Ser Pro Gln Leu Ser Trp
         40                  45                  50

tca gat ctt cca gaa ggc acc aaa tcc ctc gcg atc acc tgc ctc gac   307
Ser Asp Leu Pro Glu Gly Thr Lys Ser Leu Ala Ile Thr Cys Leu Asp
     55                  60                  65

cca gat gcc cca acc ggc gct ggt ttc tgg cac tgg gca gtg ttt aac   355
Pro Asp Ala Pro Thr Gly Ala Gly Phe Trp His Trp Ala Val Phe Asn
 70                  75                  80                  85

atc ccc aca act gtc acg gag atc ccc acc ggt gct ggc gat gaa acc   403
Ile Pro Thr Thr Val Thr Glu Ile Pro Thr Gly Ala Gly Asp Glu Thr
                 90                  95                 100

ctc ggc ggc atc gaa ggc gta gtt tcc ctc aag ggt gat tcc ggc aag   451
Leu Gly Gly Ile Glu Gly Val Val Ser Leu Lys Gly Asp Ser Gly Lys
            105                 110                 115

cgt ggc ttc tac gga gcg caa cct cca gct ggc cac gca ccg cac cgt   499
Arg Gly Phe Tyr Gly Ala Gln Pro Pro Ala Gly His Ala Pro His Arg
        120                 125                 130

tac ctc ttc gca gtt cat gca ctt gat gtg gaa aaa ctc gac atc gcc   547
Tyr Leu Phe Ala Val His Ala Leu Asp Val Glu Lys Leu Asp Ile Ala
    135                 140                 145

ccc gac gct acc ccc act ggt cta ggc ttc aac ctg tat ttc cac act   595
```

```
Pro Asp Ala Thr Pro Thr Gly Leu Gly Phe Asn Leu Tyr Phe His Thr
150                 155                 160                 165

ctt ggc                                                      601
Leu Gly
```

<210> 1044
<211> 167
<212> PRT
<213> Corynebacterium glutamicum

<400> 1044

```
Met Ser Thr Tyr Gln Asp Asp Arg Phe Pro Gly Pro Asp Pro Tyr Ala
  1               5                  10                  15

Pro Leu Gly Glu Lys Pro Ser Phe Thr Leu Thr Ser Thr Asp Leu Glu
            20                  25                  30

Asn Gly Ala Lys Leu Ala Glu Ala Gln Leu Gly Gly Thr Asp Ile Ser
         35                  40                  45

Pro Gln Leu Ser Trp Ser Asp Leu Pro Glu Gly Thr Lys Ser Leu Ala
     50                  55                  60

Ile Thr Cys Leu Asp Pro Asp Ala Pro Thr Gly Ala Gly Phe Trp His
 65                  70                  75                  80

Trp Ala Val Phe Asn Ile Pro Thr Thr Val Thr Glu Ile Pro Thr Gly
                 85                  90                  95

Ala Gly Asp Glu Thr Leu Gly Gly Ile Glu Gly Val Val Ser Leu Lys
            100                 105                 110

Gly Asp Ser Gly Lys Arg Gly Phe Tyr Gly Ala Gln Pro Pro Ala Gly
        115                 120                 125

His Ala Pro His Arg Tyr Leu Phe Ala Val His Ala Leu Asp Val Glu
    130                 135                 140

Lys Leu Asp Ile Ala Pro Asp Ala Thr Pro Thr Gly Leu Gly Phe Asn
145                 150                 155                 160

Leu Tyr Phe His Thr Leu Gly
                165
```

<210> 1045
<211> 520
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> FRXA02223

<400> 1045

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cttgcttttg agggccgcta cgcgcagctg tatcaacgat ggagtgctca atagttcaaa 60
```

```
tccaccacaa actctagaga tttggggtag aaacgaagac atg agc acc tac caa   115
                                              Met Ser Thr Tyr Gln
                                                1               5

gac gat cgt ttc cca ggc cca gac ccc tac gca ccg ctt ggt gaa aag   163
Asp Asp Arg Phe Pro Gly Pro Asp Pro Tyr Ala Pro Leu Gly Glu Lys
                10                  15                  20

cca agc ttt acc ctc acc tcc acc gac ttg gaa aac ggt gca aag ctg   211
Pro Ser Phe Thr Leu Thr Ser Thr Asp Leu Glu Asn Gly Ala Lys Leu
            25                  30                  35

gcc gaa gcc caa ctc ggt ggc acc gat att tcc cca cag ctg tcc tgg   259
Ala Glu Ala Gln Leu Gly Gly Thr Asp Ile Ser Pro Gln Leu Ser Trp
        40                  45                  50

tca gat ctt cca gaa ggc acc aaa tcc ctc gcg atc acc tgc ctc gac   307
Ser Asp Leu Pro Glu Gly Thr Lys Ser Leu Ala Ile Thr Cys Leu Asp
    55                  60                  65

cca gat gcc cca acc ggc gct ggt ttc tgg cac tgg gca gtg ttt aac   355
Pro Asp Ala Pro Thr Gly Ala Gly Phe Trp His Trp Ala Val Phe Asn
70                  75                  80                  85

atc ccc aca act gtc acg gag atc ccc acc ggt gct ggc gat gaa acc   403
Ile Pro Thr Thr Val Thr Glu Ile Pro Thr Gly Ala Gly Asp Glu Thr
                90                  95                  100

ctc ggc ggc atc gaa ggc gta gtt tcc ctc aag ggt gat tcc ggc aag   451
Leu Gly Gly Ile Glu Gly Val Val Ser Leu Lys Gly Asp Ser Gly Lys
            105                 110                 115

cgt ggc ttc tac gga gcg caa cct cca gct ggc cac gca ccg cac cgt   499
Arg Gly Phe Tyr Gly Ala Gln Pro Pro Ala Gly His Ala Pro His Arg
        120                 125                 130

tac ctc ttc gca gtt cat gca                                      520
Tyr Leu Phe Ala Val His Ala
    135                 140
```

Doc Code: AP.PRE.REQ Doc Description: Pre-Request Application Filed Before Examination

<210> 1046
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 1046

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Met Ser Thr Tyr Gln Asp Asp Arg Phe Pro Gly Pro Asp Pro Tyr Ala
  1               5                  10                  15

Pro Leu Gly Glu Lys Pro Ser Phe Thr Leu Thr Ser Thr Asp Leu Glu
            20                  25                  30

Asn Gly Ala Lys Leu Ala Glu Ala Gln Leu Gly Gly Thr Asp Ile Ser
        35                  40                  45

Pro Gln Leu Ser Trp Ser Asp Leu Pro Glu Gly Thr Lys Ser Leu Ala
    50                  55                  60

Ile Thr Cys Leu Asp Pro Asp Ala Pro Thr Gly Ala Gly Phe Trp His
65                  70                  75                  80
```

```
Trp Ala Val Phe Asn Ile Pro Thr Thr Val Thr Glu Ile Pro Thr Gly
                 85                  90                  95

Ala Gly Asp Glu Thr Leu Gly Gly Ile Glu Gly Val Val Ser Leu Lys
            100                 105                 110

Gly Asp Ser Gly Lys Arg Gly Phe Tyr Gly Ala Gln Pro Pro Ala Gly
        115                 120                 125

His Ala Pro His Arg Tyr Leu Phe Ala Val His Ala
    130                 135                 140


<210> 1047
<211> 1156
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1156)
<223> RXN02226

<400> 1047
ctgacacctc ctatggcacg cggtatgttt aataaacgta attcgagttt cggcggccgt 60

gtcgcgcggc caggacgacc ctagctttta aggacccacc atg act gag aac cag   115
                                           Met Thr Glu Asn Gln
                                             1               5

act ccc agc tcc acc tct gca ccg aag ccg gga cct cgc ccg ggc cca   163
Thr Pro Ser Ser Thr Ser Ala Pro Lys Pro Gly Pro Arg Pro Gly Pro
                 10                  15                  20

cgg cca gga ccc cga cct ggg gct cag gtt gct gca aag aaa gct gcg   211
Arg Pro Gly Pro Arg Pro Gly Ala Gln Val Ala Ala Lys Lys Ala Ala
             25                  30                  35

gtt gct aca cct gcg ccg atc gcc aaa act tct aac gat cct gca aag   259
Val Ala Thr Pro Ala Pro Ile Ala Lys Thr Ser Asn Asp Pro Ala Lys
         40                  45                  50

ttt ggt cgc gtt gag gca gac gga tct gca tat gtc acc acc tct gct   307
Phe Gly Arg Val Glu Ala Asp Gly Ser Ala Tyr Val Thr Thr Ser Ala
     55                  60                  65

ggc gag cgt ctg att ggt tct tgg cag gcc ggc acc cct gag gaa ggt   355
Gly Glu Arg Leu Ile Gly Ser Trp Gln Ala Gly Thr Pro Glu Glu Gly
 70                  75                  80                  85

ctt gct cac tac ggc gcc cgt ttt gat gat ctg gcc acc gaa gtt gag   403
Leu Ala His Tyr Gly Ala Arg Phe Asp Asp Leu Ala Thr Glu Val Glu
                 90                  95                 100

ctc atg gaa cag cgc cta atc tcc cac cct gat gat gcg acc tcc atc   451
Leu Met Glu Gln Arg Leu Ile Ser His Pro Asp Asp Ala Thr Ser Ile
            105                 110                 115

cgc acg aag gct gaa gaa ctc aag gca acc ctg ccc acc atc gct gcg   499
Arg Thr Lys Ala Glu Glu Leu Lys Ala Thr Leu Pro Thr Ile Ala Ala
```

```
        120                 125                 130

atc ggt gac ctt gat ggc gtt gaa gct cgc ctg tcc aag atc atc aac   547
Ile Gly Asp Leu Asp Gly Val Glu Ala Arg Leu Ser Lys Ile Ile Asn
    135                 140                 145

aac tcc gag gaa gcc aac gag cgc gcc aag gaa caa aag gct aaa aac   595
Asn Ser Glu Glu Ala Asn Glu Arg Ala Lys Glu Gln Lys Ala Lys Asn
150                 155                 160                 165

cgt gag cgc gca gta gct cgc aag gaa gag ctc gct gtt gag gct gaa   643
Arg Glu Arg Ala Val Ala Arg Lys Glu Glu Leu Ala Val Glu Ala Glu
                170                 175                 180

acc ttg gca gaa aac tcc tcc gac tgg aag gtt gct ggc gac cgc atc   691
Thr Leu Ala Glu Asn Ser Ser Asp Trp Lys Val Ala Gly Asp Arg Ile
            185                 190                 195

cgc gcc atc ctg gat gag tgg aag tcc atc cac ggc atc gac cgc aag   739
Arg Ala Ile Leu Asp Glu Trp Lys Ser Ile His Gly Ile Asp Arg Lys
        200                 205                 210

acc gat gat gaa ctg tgg aaa cgc tac tcc cgt gcg cgt gac tcc ttc   787
Thr Asp Asp Glu Leu Trp Lys Arg Tyr Ser Arg Ala Arg Asp Ser Phe
    215                 220                 225

aac cgt cgc cgc ggc gca cac ttc gca gag ctg gat cgc acc cgc gca   835
Asn Arg Arg Arg Gly Ala His Phe Ala Glu Leu Asp Arg Thr Arg Ala
230                 235                 240                 245

tct gca cgc aaa ctc aag gaa gaa ctc gtt gag cgc gcc aat gct ctc   883
Ser Ala Arg Lys Leu Lys Glu Glu Leu Val Glu Arg Ala Asn Ala Leu
                250                 255                 260

aag gaa tcc act gag tgg aac gac acc gcc cgc gca ttc cgc gat ctc   931
Lys Glu Ser Thr Glu Trp Asn Asp Thr Ala Arg Ala Phe Arg Asp Leu
            265                 270                 275

atg acc gaa tgg aaa gcc gcc ggc cgc gca cca cgc gaa atc gac gac   979
Met Thr Glu Trp Lys Ala Ala Gly Arg Ala Pro Arg Glu Ile Asp Asp
        280                 285                 290

aag ctg tgg gca gca ttc aag ggc gcc cag gac tac ttc ttt gat aag   1027
Lys Leu Trp Ala Ala Phe Lys Gly Ala Gln Asp Tyr Phe Phe Asp Lys
    295                 300                 305

cgc aac gcc gta gcc aag gaa cgc gac cag gaa ttc gaa gcc aac gca   1075
Arg Asn Ala Val Ala Lys Glu Arg Asp Gln Glu Phe Glu Ala Asn Ala
310                 315                 320                 325

acc gca aag cag cag ctc atc gac gaa tac gac gca cag atc aac ccc   1123
Thr Ala Lys Gln Gln Leu Ile Asp Glu Tyr Asp Ala Gln Ile Asn Pro
                330                 335                 340

gag cag ggc ctc gat gga gcg cgc agc aag ctc                      1156
Glu Gln Gly Leu Asp Gly Ala Arg Ser Lys Leu
            345                 350
```

<210> 1048
<211> 352

<212> PRT
<213> Corynebacterium glutamicum

<400> 1048

```
Met Thr Glu Asn Gln Thr Pro Ser Ser Thr Ser Ala Pro Lys Pro Gly
  1               5                  10                  15

Pro Arg Pro Gly Pro Arg Pro Gly Pro Arg Pro Gly Ala Gln Val Ala
             20                  25                  30

Ala Lys Lys Ala Ala Val Ala Thr Pro Ala Pro Ile Ala Lys Thr Ser
         35                  40                  45

Asn Asp Pro Ala Lys Phe Gly Arg Val Glu Ala Asp Gly Ser Ala Tyr
     50                  55                  60

Val Thr Thr Ser Ala Gly Glu Arg Leu Ile Gly Ser Trp Gln Ala Gly
 65                  70                  75                  80

Thr Pro Glu Glu Gly Leu Ala His Tyr Gly Ala Arg Phe Asp Asp Leu
                 85                  90                  95

Ala Thr Glu Val Glu Leu Met Glu Gln Arg Leu Ile Ser His Pro Asp
            100                 105                 110

Asp Ala Thr Ser Ile Arg Thr Lys Ala Glu Glu Leu Lys Ala Thr Leu
        115                 120                 125

Pro Thr Ile Ala Ala Ile Gly Asp Leu Asp Gly Val Glu Ala Arg Leu
    130                 135                 140

Ser Lys Ile Ile Asn Asn Ser Glu Glu Ala Asn Glu Arg Ala Lys Glu
145                 150                 155                 160

Gln Lys Ala Lys Asn Arg Glu Arg Ala Val Ala Arg Lys Glu Glu Leu
                165                 170                 175

Ala Val Glu Ala Glu Thr Leu Ala Glu Asn Ser Ser Asp Trp Lys Val
            180                 185                 190

Ala Gly Asp Arg Ile Arg Ala Ile Leu Asp Glu Trp Lys Ser Ile His
        195                 200                 205

Gly Ile Asp Arg Lys Thr Asp Asp Glu Leu Trp Lys Arg Tyr Ser Arg
    210                 215                 220

Ala Arg Asp Ser Phe Asn Arg Arg Arg Gly Ala His Phe Ala Glu Leu
225                 230                 235                 240

Asp Arg Thr Arg Ala Ser Ala Arg Lys Leu Lys Glu Glu Leu Val Glu
                245                 250                 255

Arg Ala Asn Ala Leu Lys Glu Ser Thr Glu Trp Asn Asp Thr Ala Arg
            260                 265                 270

Ala Phe Arg Asp Leu Met Thr Glu Trp Lys Ala Ala Gly Arg Ala Pro
        275                 280                 285

Arg Glu Ile Asp Asp Lys Leu Trp Ala Ala Phe Lys Gly Ala Gln Asp
    290                 295                 300
```

```
Tyr Phe Phe Asp Lys Arg Asn Ala Val Ala Lys Glu Arg Asp Gln Glu
305                 310                 315                 320

Phe Glu Ala Asn Ala Thr Ala Lys Gln Gln Leu Ile Asp Glu Tyr Asp
                325                 330                 335

Ala Gln Ile Asn Pro Glu Gln Gly Leu Asp Gly Ala Arg Ser Lys Leu
            340                 345                 350
```

<210> 1049
<211> 1156
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1156)
<223> FRXA02226

<400> 1049

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ctgacacctc ctatggcacg cggtatgttt aataaacgta attcgagttt cggcggccgt 60

gtcgcgcggc caggacgacc ctagctttta aggacccacc atg act gag aac cag  115
                                          Met Thr Glu Asn Gln
                                            1               5

act ccc agc tcc acc tct gca ccg aag ccg gga cct cgc ccg ggc cca  163
Thr Pro Ser Ser Thr Ser Ala Pro Lys Pro Gly Pro Arg Pro Gly Pro
                10                  15                  20

cgg cca gga ccc cga cct ggg gct cag gtt gct gca aag aaa gct gcg  211
Arg Pro Gly Pro Arg Pro Gly Ala Gln Val Ala Ala Lys Lys Ala Ala
            25                  30                  35

gtt gct aca cct gcg ccg atc gcc aaa act tct aac gat cct gca aag  259
Val Ala Thr Pro Ala Pro Ile Ala Lys Thr Ser Asn Asp Pro Ala Lys
        40                  45                  50

ttt ggt cgc gtt gag gca gac gga tct gca tat gtc acc acc tct gct  307
Phe Gly Arg Val Glu Ala Asp Gly Ser Ala Tyr Val Thr Thr Ser Ala
    55                  60                  65

ggc gag cgt ctg att ggt tct tgg cag gcc ggc acc cct gag gaa ggt  355
Gly Glu Arg Leu Ile Gly Ser Trp Gln Ala Gly Thr Pro Glu Glu Gly
70                  75                  80                  85

ctt gct cac tac ggc gcc cgt ttt gat gat ctg gcc acc gaa gtt gag  403
Leu Ala His Tyr Gly Ala Arg Phe Asp Asp Leu Ala Thr Glu Val Glu
                90                  95                  100

ctc atg gaa cag cgc cta atc tcc cac cct gat gat gcg acc tcc atc  451
Leu Met Glu Gln Arg Leu Ile Ser His Pro Asp Asp Ala Thr Ser Ile
            105                 110                 115

cgc acg aag gct gaa gaa ctc aag gca acc ctg ccc acc atc gct gcg  499
Arg Thr Lys Ala Glu Glu Leu Lys Ala Thr Leu Pro Thr Ile Ala Ala
        120                 125                 130
```

```
atc ggt gac ctt gat ggc gtt gaa gct cgc ctg tcc aag atc atc aac   547
Ile Gly Asp Leu Asp Gly Val Glu Ala Arg Leu Ser Lys Ile Ile Asn
    135                 140                 145

aac tcc gag gaa gcc aac gag cgc gcc aag gaa caa aag gct aaa aac   595
Asn Ser Glu Glu Ala Asn Glu Arg Ala Lys Glu Gln Lys Ala Lys Asn
150                 155                 160                 165

cgt gag cgc gca gta gct cgc aag gaa gag ctc gct gtt gag gct gaa   643
Arg Glu Arg Ala Val Ala Arg Lys Glu Glu Leu Ala Val Glu Ala Glu
                170                 175                 180

acc ttg gca gaa aac tcc tcc gac tgg aag gtt gct ggc gac cgc atc   691
Thr Leu Ala Glu Asn Ser Ser Asp Trp Lys Val Ala Gly Asp Arg Ile
            185                 190                 195

cgc gcc atc ctg gat gag tgg aag tcc atc cac ggc atc gac cgc aag   739
Arg Ala Ile Leu Asp Glu Trp Lys Ser Ile His Gly Ile Asp Arg Lys
        200                 205                 210

acc gat gat gaa ctg tgg aaa cgc tac tcc cgt gcg cgt gac tcc ttc   787
Thr Asp Asp Glu Leu Trp Lys Arg Tyr Ser Arg Ala Arg Asp Ser Phe
    215                 220                 225

aac cgt cgc cgc ggc gca cac ttc gca gag ctg gat cgc acc cgc gca   835
Asn Arg Arg Arg Gly Ala His Phe Ala Glu Leu Asp Arg Thr Arg Ala
230                 235                 240                 245

tct gca cgc aaa ctc aag gaa gaa ctc gtt gag cgc gcc aat gct ctc   883
Ser Ala Arg Lys Leu Lys Glu Glu Leu Val Glu Arg Ala Asn Ala Leu
                250                 255                 260

aag gaa tcc act gag tgg aac gac acc gcc cgc gca ttc cgc gat ctc   931
Lys Glu Ser Thr Glu Trp Asn Asp Thr Ala Arg Ala Phe Arg Asp Leu
            265                 270                 275

atg acc gaa tgg aaa gcc gcc ggc cgc gca cca cgc gaa atc gac gac   979
Met Thr Glu Trp Lys Ala Ala Gly Arg Ala Pro Arg Glu Ile Asp Asp
        280                 285                 290

aag ctg tgg gca gca ttc aag ggc gcc cag gac tac ttc ttt gat aag   1027
Lys Leu Trp Ala Ala Phe Lys Gly Ala Gln Asp Tyr Phe Phe Asp Lys
    295                 300                 305

cgc aac gcc gta gcc aag gaa cgc gac cag gaa ttc gaa gcc aac gca   1075
Arg Asn Ala Val Ala Lys Glu Arg Asp Gln Glu Phe Glu Ala Asn Ala
310                 315                 320                 325

acc gca aag cag cag ctc atc gac gaa tac gac gca cag atc aac ccc   1123
Thr Ala Lys Gln Gln Leu Ile Asp Glu Tyr Asp Ala Gln Ile Asn Pro
                330                 335                 340

gag cag ggc ctc gat gga gcg cgc agc aag ctc                      1156
Glu Gln Gly Leu Asp Gly Ala Arg Ser Lys Leu
            345                 350
```

<210> 1050
<211> 352
<212> PRT

<213> Corynebacterium glutamicum

<400> 1050

```
Met Thr Glu Asn Gln Thr Pro Ser Ser Thr Ser Ala Pro Lys Pro Gly
  1               5                  10                  15

Pro Arg Pro Gly Pro Arg Pro Gly Pro Arg Pro Gly Ala Gln Val Ala
             20                  25                  30

Ala Lys Lys Ala Ala Val Ala Thr Pro Ala Pro Ile Ala Lys Thr Ser
         35                  40                  45

Asn Asp Pro Ala Lys Phe Gly Arg Val Glu Ala Asp Gly Ser Ala Tyr
     50                  55                  60

Val Thr Thr Ser Ala Gly Glu Arg Leu Ile Gly Ser Trp Gln Ala Gly
 65                  70                  75                  80

Thr Pro Glu Glu Gly Leu Ala His Tyr Gly Ala Arg Phe Asp Asp Leu
                 85                  90                  95

Ala Thr Glu Val Glu Leu Met Glu Gln Arg Leu Ile Ser His Pro Asp
            100                 105                 110

Asp Ala Thr Ser Ile Arg Thr Lys Ala Glu Glu Leu Lys Ala Thr Leu
        115                 120                 125

Pro Thr Ile Ala Ala Ile Gly Asp Leu Asp Gly Val Glu Ala Arg Leu
    130                 135                 140

Ser Lys Ile Ile Asn Asn Ser Glu Glu Ala Asn Glu Arg Ala Lys Glu
145                 150                 155                 160

Gln Lys Ala Lys Asn Arg Glu Arg Ala Val Ala Arg Lys Glu Glu Leu
                165                 170                 175

Ala Val Glu Ala Glu Thr Leu Ala Glu Asn Ser Ser Asp Trp Lys Val
            180                 185                 190

Ala Gly Asp Arg Ile Arg Ala Ile Leu Asp Glu Trp Lys Ser Ile His
        195                 200                 205

Gly Ile Asp Arg Lys Thr Asp Asp Glu Leu Trp Lys Arg Tyr Ser Arg
    210                 215                 220

Ala Arg Asp Ser Phe Asn Arg Arg Arg Gly Ala His Phe Ala Glu Leu
225                 230                 235                 240

Asp Arg Thr Arg Ala Ser Ala Arg Lys Leu Lys Glu Glu Leu Val Glu
                245                 250                 255

Arg Ala Asn Ala Leu Lys Glu Ser Thr Glu Trp Asn Asp Thr Ala Arg
            260                 265                 270

Ala Phe Arg Asp Leu Met Thr Glu Trp Lys Ala Ala Gly Arg Ala Pro
        275                 280                 285

Arg Glu Ile Asp Asp Lys Leu Trp Ala Ala Phe Lys Gly Ala Gln Asp
    290                 295                 300

Tyr Phe Phe Asp Lys Arg Asn Ala Val Ala Lys Glu Arg Asp Gln Glu
```

```
305                 310                 315                 320

Phe Glu Ala Asn Ala Thr Ala Lys Gln Gln Leu Ile Asp Glu Tyr Asp
                325                 330                 335

Ala Gln Ile Asn Pro Glu Gln Gly Leu Asp Gly Ala Arg Ser Lys Leu
            340                 345                 350
```

<210> 1051
<211> 408
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> RXN02238

<400> 1051

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ggcgcttagc caaaacatag agcggtaggg tatgcttatc cgattgagca acctttcccg 60

ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc   115
                                            Val Thr Asn Val Ser
                                              1               5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att   163
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
                  10                  15                  20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac   211
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
              25                  30                  35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc   259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
          40                  45                  50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt   307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
      55                  60                  65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc   355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
  70                  75                  80                  85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca     405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
                  90                  95

cac                                                               408
```

<210> 1052
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 1052
Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
1 5 10 15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
20 25 30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
35 40 45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
50 55 60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
65 70 75 80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
85 90 95

<210> 1053
<211> 408
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> FRXA02238

<400> 1053
ggcgcttagc caaaacatag agcggtaggg tatgcttatc cgattgagca acctttcccg 60

ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115
Val Thr Asn Val Ser
1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
40 45 50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
55 60 65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
70 75 80 85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
90 95

```
cac                                                                    408


<210> 1054
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 1054
Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
  1               5                  10                  15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
             20                  25                  30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
         35                  40                  45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
     50                  55                  60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
 65                  70                  75                  80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
                 85                  90                  95


<210> 1055
<211> 800
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(777)
<223> RXN02254

<400> 1055
atc gcc gtt gcc gaa gaa ggc gga ttg tgg gaa aac ctc ctg cag cac   48
Ile Ala Val Ala Glu Glu Gly Gly Leu Trp Glu Asn Leu Leu Gln His
  1               5                  10                  15

cgc ttc ggt gga cat ggt gcg cta gct ggt cac gcc ttg gga aac ctc   96
Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu
             20                  25                  30

gtg atc gcg gcg ttg acc gac att ttg ggc acc tcc cag cat gcg ctt  144
Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu
         35                  40                  45

gat caa atc gct caa ctc gct gga gcc aaa gga cgc atc atc ccg gta  192
Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val
     50                  55                  60

tgt gct gaa cct ttg gat ctt gaa gcg gaa gta tca ggt cta gac tct  240
Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser
 65                  70                  75                  80

gat gct cga gtc atg cgt caa gtt cgt ggt caa gtg gcg gta gct gca  288
Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala
```

```
                  85                  90                  95

acc ccc ggg cag gtg cga cgc gtt cga atc att ccg gac aat cca gaa   336
Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu
            100                 105                 110

ccg aac ccc gct gcc atc gag gcc att ctc gat gca gat ttg gtc acc   384
Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr
        115                 120                 125

ctt ggc cca ggt tcc tgg ttc tcc tct gtg att cca cac att ttg gtc   432
Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val
    130                 135                 140

cca ggg atc gtt gat gcc ttg gcg cag aca aaa gca acc aaa acc gtg   480
Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val
145                 150                 155                 160

gtg tta aac ctg acg tcc gag cca ggg gag acc gcg gga ttc tct gca   528
Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala
                165                 170                 175

gaa cga cac atc cat gtg ctc cgc cag cat gct cga aac ctt cag gtt   576
Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val
            180                 185                 190

gac caa gtc att gtc gat gcc aag aca ctg tcc tca caa acc gaa cgc   624
Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg
        195                 200                 205

aat cat gta gaa cga gct gct cgc acc ctt ggt gca gaa gtc tcc ttc   672
Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe
    210                 215                 220

cat gat gtc cag gct gaa gat ggc cgt ggt cga ttc acc agt att cac   720
His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His
225                 230                 235                 240

gat cca gca aag ctg tgt gca gcg ttg ctg gca agt ttt gct gga gca   768
Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala
                245                 250                 255

cga aag cgt taaggagtag gcgtgtcact gac                            800
Arg Lys Arg
```

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<210> 1056
<211> 259
<212> PRT
<213> Corynebacterium glutamicum

<400> 1056

```
Ile Ala Val Ala Glu Glu Gly Gly Leu Trp Glu Asn Leu Leu Gln His
  1               5                  10                  15

Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu
             20                  25                  30

Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu
         35                  40                  45
```

```
Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val
     50                  55                  60

Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser
 65                  70                  75                  80

Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala
                 85                  90                  95

Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu
            100                 105                 110

Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr
        115                 120                 125

Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val
    130                 135                 140

Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val
145                 150                 155                 160

Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala
                165                 170                 175

Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val
            180                 185                 190

Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg
        195                 200                 205

Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe
    210                 215                 220

His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His
225                 230                 235                 240

Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala
                245                 250                 255

Arg Lys Arg
```

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<210> 1057
<211> 804
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(781)
<223> FRXA02254

<400> 1057
ttgatcgccg atgccgaaga aggcggattg tgggaaaacc tcctgcagca ccgcttcagg 60

tggacatggt gcgctagctg gtcacgcctt gggaaacctc gtg atc gcg gcg ttg 115
                                              Val Ile Ala Ala Leu
                                                1   5

```
acc gac att ttg ggc acc tcc cag cat gcg ctt gat caa atc gct caa   163
Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu Asp Gln Ile Ala Gln
                 10                  15                  20

ctc gct gga gcc aaa gga cgc atc atc ccg gta tgt gct gaa cct ttg   211
Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val Cys Ala Glu Pro Leu
             25                  30                  35

gat ctt gaa gcg gaa gta tca ggt cta gac tct gat gct cga gtc atg   259
Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser Asp Ala Arg Val Met
         40                  45                  50

cgt caa gtt cgt ggt caa gtg gcg gta gct gca acc ccc ggg cag gtg   307
Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala Thr Pro Gly Gln Val
     55                  60                  65

cga cgc gtt cga atc att ccg gac aat cca gaa ccg aac ccc gct gcc   355
Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu Pro Asn Pro Ala Ala
 70                  75                  80                  85

atc gag gcc att ctc gat gca gat ttg gtc acc ctt ggc cca ggt tcc   403
Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr Leu Gly Pro Gly Ser
                 90                  95                 100

tgg ttc tcc tct gtg att cca cac att ttg gtc cca ggg atc gtt gat   451
Trp Phe Ser Ser Val Ile Pro His Ile Leu Val Pro Gly Ile Val Asp
             105                 110                 115

gcc ttg gcg cag aca aaa gca acc aaa acc gtg gtg tta aac ctg acg   499
Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val Val Leu Asn Leu Thr
         120                 125                 130

tcc gag cca ggg gag acc gcg gga ttc tct gca gaa cga cac atc cat   547
Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala Glu Arg His Ile His
     135                 140                 145

gtg ctc cgc cag cat gct cga aac ctt cag gtt gac caa gtc att gtc   595
Val Leu Arg Gln His Ala Arg Asn Leu Gln Val Asp Gln Val Ile Val
150                 155                 160                 165

gat gcc aag aca ctg tcc tca caa acc gaa cgc aat cat gta gaa cga   643
Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg Asn His Val Glu Arg
                 170                 175                 180

gct gct cgc acc ctt ggt gca gaa gtc tcc ttc cat gat gtc cag gct   691
Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe His Asp Val Gln Ala
             185                 190                 195

gaa gat ggc cgt ggt cga ttc acc agt att cac gat cca gca aag ctg   739
Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His Asp Pro Ala Lys Leu
         200                 205                 210

tgt gca gcg ttg ctg gca agt ttt gct gga gca cga aag cgt           781
Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala Arg Lys Arg
     215                 220                 225

taaggagtag gcgtgtcact gac                                       804
```

<210> 1058
<211> 227

<212> PRT
<213> Corynebacterium glutamicum

<400> 1058

```
Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu
  1               5                  10                  15

Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val
             20                  25                  30

Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser
         35                  40                  45

Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala
     50                  55                  60

Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu
 65                  70                  75                  80

Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr
                 85                  90                  95

Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val
            100                 105                 110

Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val
        115                 120                 125

Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala
    130                 135                 140

Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val
145                 150                 155                 160

Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg
                165                 170                 175

Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe
            180                 185                 190

His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His
        195                 200                 205

Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala
    210                 215                 220

Arg Lys Arg
225
```

<210> 1059
<211> 681
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(658)
<223> RXN02271

<400> 1059

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cactccccta tcctaagcca catctcggtt tattaaactg ttagtgaatt ctcacccgca 60

acactggtgt atttcagtta catccgtatg gttattggtt atg agc ttt ctt aac   115
                                            Met Ser Phe Leu Asn
                                              1               5

tct gca aaa acc aag acc gta gcc ctc acc gca acc ttc gtt ggt gca   163
Ser Ala Lys Thr Lys Thr Val Ala Leu Thr Ala Thr Phe Val Gly Ala
                  10                  15                  20

gca acc ctt gca act cct gca atc gca tcc gct gac atc gtc gac aac   211
Ala Thr Leu Ala Thr Pro Ala Ile Ala Ser Ala Asp Ile Val Asp Asn
              25                  30                  35

gcc ctc gca gcc ctc cca tcc ggt gag atc agc tgc tcc cag gct gaa   259
Ala Leu Ala Ala Leu Pro Ser Gly Glu Ile Ser Cys Ser Gln Ala Glu
          40                  45                  50

aag tac tgg acc acc gaa gct gat tac aac agc aag gtt gca cag gcc   307
Lys Tyr Trp Thr Thr Glu Ala Asp Tyr Asn Ser Lys Val Ala Gln Ala
      55                  60                  65

aac gcc ttg gca atg ttt gac tcc cgc ggc cca cag atc cag gca gct   355
Asn Ala Leu Ala Met Phe Asp Ser Arg Gly Pro Gln Ile Gln Ala Ala
  70                  75                  80                  85

ctc gca cgc gtt gac gaa gca gca aac cgc tgc gga ctc aag ggc ggc   403
Leu Ala Arg Val Asp Glu Ala Ala Asn Arg Cys Gly Leu Lys Gly Gly
                  90                  95                 100

acc gta gct gcg cag gct gag gca act gag gct gcg cct gcc gct cca   451
Thr Val Ala Ala Gln Ala Glu Ala Thr Glu Ala Ala Pro Ala Ala Pro
              105                 110                 115

gca cct gca ccg cag gat aac acc ggc act tct cag act gcc cct gcc   499
Ala Pro Ala Pro Gln Asp Asn Thr Gly Thr Ser Gln Thr Ala Pro Ala
          120                 125                 130

cca gca gca cca gca gca cca gca gct acc cct gtg gtt aac ctt gca   547
Pro Ala Ala Pro Ala Ala Pro Ala Ala Thr Pro Val Val Asn Leu Ala
      135                 140                 145

cct gca gga tca cca act ttc acc att gaa gtt cca gga gtt ggc ggg   595
Pro Ala Gly Ser Pro Thr Phe Thr Ile Glu Val Pro Gly Val Gly Gly
150                 155                 160                 165

gtt cag ctg cca gat cta tac caa atc gtc caa cag ttc ttg gca cag   643
Val Gln Leu Pro Asp Leu Tyr Gln Ile Val Gln Gln Phe Leu Ala Gln
                  170                 175                 180

ttc gga atc aag atc taaatctatt cacatccctt aac                    681
Phe Gly Ile Lys Ile
              185
```

<210> 1060
<211> 186
<212> PRT
<213> Corynebacterium glutamicum

<400> 1060

```
Met Ser Phe Leu Asn Ser Ala Lys Thr Lys Thr Val Ala Leu Thr Ala
  1               5                  10                  15

Thr Phe Val Gly Ala Ala Thr Leu Ala Thr Pro Ala Ile Ala Ser Ala
             20                  25                  30

Asp Ile Val Asp Asn Ala Leu Ala Ala Leu Pro Ser Gly Glu Ile Ser
         35                  40                  45

Cys Ser Gln Ala Glu Lys Tyr Trp Thr Thr Glu Ala Asp Tyr Asn Ser
     50                  55                  60

Lys Val Ala Gln Ala Asn Ala Leu Ala Met Phe Asp Ser Arg Gly Pro
 65                  70                  75                  80

Gln Ile Gln Ala Ala Leu Ala Arg Val Asp Glu Ala Ala Asn Arg Cys
                 85                  90                  95

Gly Leu Lys Gly Gly Thr Val Ala Ala Gln Ala Glu Ala Thr Glu Ala
            100                 105                 110

Ala Pro Ala Ala Pro Ala Pro Ala Pro Gln Asp Asn Thr Gly Thr Ser
        115                 120                 125

Gln Thr Ala Pro Ala Pro Ala Ala Pro Ala Ala Pro Ala Ala Thr Pro
    130                 135                 140

Val Val Asn Leu Ala Pro Ala Gly Ser Pro Thr Phe Thr Ile Glu Val
145                 150                 155                 160

Pro Gly Val Gly Gly Val Gln Leu Pro Asp Leu Tyr Gln Ile Val Gln
                165                 170                 175

Gln Phe Leu Ala Gln Phe Gly Ile Lys Ile
            180                 185


<210> 1061
<211> 681
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(658)
<223> FRXA02271

<400> 1061
cactccccta tcctaagcca catctcggtt tattaaactg ttagtgaatt ctcacccgca 60

acactggtgt atttcagtta catccgtatg gttattggtt atg agc ttt ctt aac   115
                                              Met Ser Phe Leu Asn
                                                1               5

tct gca aaa acc aag acc gta gcc ctc acc gca acc ttc gtt ggt gca   163
Ser Ala Lys Thr Lys Thr Val Ala Leu Thr Ala Thr Phe Val Gly Ala
            10                  15                  20

gca acc ctt gca act cct gca atc gca tcc gct gac atc gtc gac aac   211
Ala Thr Leu Ala Thr Pro Ala Ile Ala Ser Ala Asp Ile Val Asp Asn
        25                  30                  35
```

```
gcc ctc gca gcc ctc cca tcc ggt gag atc agc tgc tcc cag gct gaa   259
Ala Leu Ala Ala Leu Pro Ser Gly Glu Ile Ser Cys Ser Gln Ala Glu
         40                  45                  50

aag tac tgg acc acc gaa gct gat tac aac agc aag gtt gca cag gcc   307
Lys Tyr Trp Thr Thr Glu Ala Asp Tyr Asn Ser Lys Val Ala Gln Ala
     55                  60                  65

aac gcc ttg gca atg ttt gac tcc cgc ggc cca cag atc cag gca gct   355
Asn Ala Leu Ala Met Phe Asp Ser Arg Gly Pro Gln Ile Gln Ala Ala
 70                  75                  80                  85

ctc gca cgc gtt gac gaa gca gca aac cgc tgc gga ctc aag ggc ggc   403
Leu Ala Arg Val Asp Glu Ala Ala Asn Arg Cys Gly Leu Lys Gly Gly
                 90                  95                 100

acc gta gct gcg cag gct gag gca act gag gct gcg cct gcc gct cca   451
Thr Val Ala Ala Gln Ala Glu Ala Thr Glu Ala Ala Pro Ala Ala Pro
            105                 110                 115

gca cct gca ccg cag gat aac acc ggc act tct cag act gcc cct gcc   499
Ala Pro Ala Pro Gln Asp Asn Thr Gly Thr Ser Gln Thr Ala Pro Ala
        120                 125                 130

cca gca gca cca gca gca cca gca gct acc cct gtg gtt aac ctt gca   547
Pro Ala Ala Pro Ala Ala Pro Ala Ala Thr Pro Val Val Asn Leu Ala
    135                 140                 145

cct gca gga tca cca act ttc acc att gaa gtt cca gga gtt ggc ggg   595
Pro Ala Gly Ser Pro Thr Phe Thr Ile Glu Val Pro Gly Val Gly Gly
150                 155                 160                 165

gtt cag ctg cca gat cta tac caa atc gtc caa cag ttc ttg gca cag   643
Val Gln Leu Pro Asp Leu Tyr Gln Ile Val Gln Gln Phe Leu Ala Gln
                170                 175                 180

ttc gga atc aag atc taaatctatt cacatccctt aac                    681
Phe Gly Ile Lys Ile
            185
```

<210> 1062
<211> 186
<212> PRT
<213> Corynebacterium glutamicum

<400> 1062

```
Met Ser Phe Leu Asn Ser Ala Lys Thr Lys Thr Val Ala Leu Thr Ala
  1               5                  10                  15

Thr Phe Val Gly Ala Ala Thr Leu Ala Thr Pro Ala Ile Ala Ser Ala
             20                  25                  30

Asp Ile Val Asp Asn Ala Leu Ala Ala Leu Pro Ser Gly Glu Ile Ser
         35                  40                  45

Cys Ser Gln Ala Glu Lys Tyr Trp Thr Thr Glu Ala Asp Tyr Asn Ser
     50                  55                  60

Lys Val Ala Gln Ala Asn Ala Leu Ala Met Phe Asp Ser Arg Gly Pro
```

```
 65                  70                  75                  80

Gln Ile Gln Ala Ala Leu Ala Arg Val Asp Glu Ala Ala Asn Arg Cys
                 85                  90                  95

Gly Leu Lys Gly Gly Thr Val Ala Ala Gln Ala Glu Ala Thr Glu Ala
            100                 105                 110

Ala Pro Ala Ala Pro Ala Pro Ala Pro Gln Asp Asn Thr Gly Thr Ser
        115                 120                 125

Gln Thr Ala Pro Ala Pro Ala Ala Pro Ala Ala Pro Ala Ala Thr Pro
    130                 135                 140

Val Val Asn Leu Ala Pro Ala Gly Ser Pro Thr Phe Thr Ile Glu Val
145                 150                 155                 160

Pro Gly Val Gly Gly Val Gln Leu Pro Asp Leu Tyr Gln Ile Val Gln
                165                 170                 175

Gln Phe Leu Ala Gln Phe Gly Ile Lys Ile
            180                 185
```

Sequence Listing

<210> 1063
<211> 1581
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1558)
<223> RXN02279

<400> 1063

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ggtaagaggg cattttccga tgcgcagcga ttcttgctca acgccgacga gctcgcggag 60

ctttctgatt atgagcgtct ggcttatgcc atcaccttgc ttg atc agc ctg gaa   115
                                          Leu Ile Ser Leu Glu
                                            1               5

aag aag cag aag gac gcg aac ttt ttc ctt tcg gag ctt cgc cgc cag   163
Lys Lys Gln Lys Asp Ala Asn Phe Phe Leu Ser Glu Leu Arg Arg Gln
                10                  15                  20

ggc tac cgc gct gtc gat ttc ttg gaa tcc cag act gtt gac cag ctg   211
Gly Tyr Arg Ala Val Asp Phe Leu Glu Ser Gln Thr Val Asp Gln Leu
            25                  30                  35

aat aac ccc gat gtc cag act tac ctc acc gaa gcg gaa ctg att cgc   259
Asn Asn Pro Asp Val Gln Thr Tyr Leu Thr Glu Ala Glu Leu Ile Arg
        40                  45                  50

gat gac ttg agg tct tgg gca gtc atc aat caa atg gca ttg gac aac   307
Asp Asp Leu Arg Ser Trp Ala Val Ile Asn Gln Met Ala Leu Asp Asn
    55                  60                  65

atc gat ctt gtt cca tac ggc gag gaa aac gac gag cca ctt gca atc   355
Ile Asp Leu Val Pro Tyr Gly Glu Glu Asn Asp Glu Pro Leu Ala Ile
70                  75                  80                  85
```

```
gcc cgc aag atc atc gag gaa acc gct tcc cat cct gag ctg aga ttc   403
Ala Arg Lys Ile Ile Glu Glu Thr Ala Ser His Pro Glu Leu Arg Phe
                 90                  95                 100

gaa aac ctc gag gcc cag ttc tcc gag ttc acc atc ttg ctt gct caa   451
Glu Asn Leu Glu Ala Gln Phe Ser Glu Phe Thr Ile Leu Leu Ala Gln
            105                 110                 115

agc ccg gag aac ctc gac gta gcc cgc tac cag gag ctt cgt aca cag   499
Ser Pro Glu Asn Leu Asp Val Ala Arg Tyr Gln Glu Leu Arg Thr Gln
        120                 125                 130

gga aac ttt gtt caa gaa ctc gcc ttg gac agc att ttc ggc caa cat   547
Gly Asn Phe Val Gln Glu Leu Ala Leu Asp Ser Ile Phe Gly Gln His
    135                 140                 145

gcc gtt gtt caa gac acc gga aac ggc gaa gcc atc cta gat gaa act   595
Ala Val Val Gln Asp Thr Gly Asn Gly Glu Ala Ile Leu Asp Glu Thr
150                 155                 160                 165

atc ggg tac atg atc ggc gcc ggc atg cgt gaa acc act gcc cgc acc   643
Ile Gly Tyr Met Ile Gly Ala Gly Met Arg Glu Thr Thr Ala Arg Thr
                170                 175                 180

gcc agc cag ttc gcg cag ctt tac tca ttt gtg ggc agg cag gaa cgc   691
Ala Ser Gln Phe Ala Gln Leu Tyr Ser Phe Val Gly Arg Gln Glu Arg
            185                 190                 195

tcc att gaa atg gca cga ctc gct ttc gag gaa ctt caa gcg gca gga   739
Ser Ile Glu Met Ala Arg Leu Ala Phe Glu Glu Leu Gln Ala Ala Gly
        200                 205                 210

ctt ccc cac cgt gag gaa gaa ctg cga ttg ggc atg caa ctc gcc cag   787
Leu Pro His Arg Glu Glu Glu Leu Arg Leu Gly Met Gln Leu Ala Gln
    215                 220                 225

gtt gaa cca att gaa gcc cgc gaa atc ctg gaa aag ctg ctg ctg cct   835
Val Glu Pro Ile Glu Ala Arg Glu Ile Leu Glu Lys Leu Leu Leu Pro
230                 235                 240                 245

aaa ttc gag cag aat ctg aca ctt gat gaa ctt gaa act gaa gca ctc   883
Lys Phe Glu Gln Asn Leu Thr Leu Asp Glu Leu Glu Thr Glu Ala Leu
                250                 255                 260

ctt cct ttg ggt gct acc gtt gct atc cac gac ccc cag gct gcc gca   931
Leu Pro Leu Gly Ala Thr Val Ala Ile His Asp Pro Gln Ala Ala Ala
            265                 270                 275

gca att ttg cgc cac gct cgc gaa aac gcc gca ggg ttc ggc aac ttc   979
Ala Ile Leu Arg His Ala Arg Glu Asn Ala Ala Gly Phe Gly Asn Phe
        280                 285                 290

gaa ctc gca gtc caa gcg atg acc atg atc acg gat gtc ctc tac acc   1027
Glu Leu Ala Val Gln Ala Met Thr Met Ile Thr Asp Val Leu Tyr Thr
    295                 300                 305

caa aac atg cac gag caa ctg ctg gag gag ctc aac cac tct ctc ccc   1075
Gln Asn Met His Glu Gln Leu Leu Glu Glu Leu Asn His Ser Leu Pro
310                 315                 320                 325

tat gct caa atg ctt gat gat caa cac caa gct gaa ctg aaa ctg ctg   1123
```

```
Tyr Ala Gln Met Leu Asp Asp Gln His Gln Ala Glu Leu Lys Leu Leu
                330                 335                 340

gac agc atc gcc atc gtc cag gca gac ctc ggt tcc acc gaa gcg ctg   1171
Asp Ser Ile Ala Ile Val Gln Ala Asp Leu Gly Ser Thr Glu Ala Leu
            345                 350                 355

gaa acc ctg ggc acc gca atg gga ctc gca gaa acc aca gct cag aag   1219
Glu Thr Leu Gly Thr Ala Met Gly Leu Ala Glu Thr Thr Ala Gln Lys
        360                 365                 370

cta tac gtg cag gaa tcc ctc aac cgc gca tac ttc act ttt gcc cgc   1267
Leu Tyr Val Gln Glu Ser Leu Asn Arg Ala Tyr Phe Thr Phe Ala Arg
    375                 380                 385

cct gaa gat tgc atc agc gga gca gcc gac gct tct gcc ctg gcc atg   1315
Pro Glu Asp Cys Ile Ser Gly Ala Ala Asp Ala Ser Ala Leu Ala Met
390                 395                 400                 405

caa aac gat gac cct tcc aat gca gct gcc cag ttg gag cag tgt gca   1363
Gln Asn Asp Asp Pro Ser Asn Ala Ala Ala Gln Leu Glu Gln Cys Ala
                410                 415                 420

cag tac ttg ttc caa ttg ggc cac gaa act gac ggc gca agc ctg ctg   1411
Gln Tyr Leu Phe Gln Leu Gly His Glu Thr Asp Gly Ala Ser Leu Leu
            425                 430                 435

gaa tct gca ttc agg gtt gaa ggc atc ccc act gag cag gca ctg tac   1459
Glu Ser Ala Phe Arg Val Glu Gly Ile Pro Thr Glu Gln Ala Leu Tyr
        440                 445                 450

tac gca aat gca ctg tct tcc atc tat gaa gat ttc ggc gat tcc gcg   1507
Tyr Ala Asn Ala Leu Ser Ser Ile Tyr Glu Asp Phe Gly Asp Ser Ala
    455                 460                 465

aag tcg cag tac tgg gag cag cag gcg cag gaa aag cag cag ctt ctg   1555
Lys Ser Gln Tyr Trp Glu Gln Gln Ala Gln Glu Lys Gln Gln Leu Leu
470                 475                 480                 485

gag taacggccgt ttaaagagtc gaa                                    1581
Glu
```

<210> 1064
<211> 486
<212> PRT
<213> Corynebacterium glutamicum

<400> 1064

```
Leu Ile Ser Leu Glu Lys Lys Gln Lys Asp Ala Asn Phe Phe Leu Ser
  1               5                  10                  15

Glu Leu Arg Arg Gln Gly Tyr Arg Ala Val Asp Phe Leu Glu Ser Gln
             20                  25                  30

Thr Val Asp Gln Leu Asn Asn Pro Asp Val Gln Thr Tyr Leu Thr Glu
         35                  40                  45

Ala Glu Leu Ile Arg Asp Asp Leu Arg Ser Trp Ala Val Ile Asn Gln
     50                  55                  60
```

```
Met Ala Leu Asp Asn Ile Asp Leu Val Pro Tyr Gly Glu Glu Asn Asp
 65                  70                  75                  80

Glu Pro Leu Ala Ile Ala Arg Lys Ile Ile Glu Glu Thr Ala Ser His
                 85                  90                  95

Pro Glu Leu Arg Phe Glu Asn Leu Glu Ala Gln Phe Ser Glu Phe Thr
            100                 105                 110

Ile Leu Leu Ala Gln Ser Pro Glu Asn Leu Asp Val Ala Arg Tyr Gln
        115                 120                 125

Glu Leu Arg Thr Gln Gly Asn Phe Val Gln Glu Leu Ala Leu Asp Ser
    130                 135                 140

Ile Phe Gly Gln His Ala Val Val Gln Asp Thr Gly Asn Gly Glu Ala
145                 150                 155                 160

Ile Leu Asp Glu Thr Ile Gly Tyr Met Ile Gly Ala Gly Met Arg Glu
                165                 170                 175

Thr Thr Ala Arg Thr Ala Ser Gln Phe Ala Gln Leu Tyr Ser Phe Val
            180                 185                 190

Gly Arg Gln Glu Arg Ser Ile Glu Met Ala Arg Leu Ala Phe Glu Glu
        195                 200                 205

Leu Gln Ala Ala Gly Leu Pro His Arg Glu Glu Glu Leu Arg Leu Gly
    210                 215                 220

Met Gln Leu Ala Gln Val Glu Pro Ile Glu Ala Arg Glu Ile Leu Glu
225                 230                 235                 240

Lys Leu Leu Leu Pro Lys Phe Glu Gln Asn Leu Thr Leu Asp Glu Leu
                245                 250                 255

Glu Thr Glu Ala Leu Leu Pro Leu Gly Ala Thr Val Ala Ile His Asp
            260                 265                 270

Pro Gln Ala Ala Ala Ala Ile Leu Arg His Ala Arg Glu Asn Ala Ala
        275                 280                 285

Gly Phe Gly Asn Phe Glu Leu Ala Val Gln Ala Met Thr Met Ile Thr
    290                 295                 300

Asp Val Leu Tyr Thr Gln Asn Met His Glu Gln Leu Leu Glu Glu Leu
305                 310                 315                 320

Asn His Ser Leu Pro Tyr Ala Gln Met Leu Asp Asp Gln His Gln Ala
                325                 330                 335

Glu Leu Lys Leu Leu Asp Ser Ile Ala Ile Val Gln Ala Asp Leu Gly
            340                 345                 350

Ser Thr Glu Ala Leu Glu Thr Leu Gly Thr Ala Met Gly Leu Ala Glu
        355                 360                 365

Thr Thr Ala Gln Lys Leu Tyr Val Gln Glu Ser Leu Asn Arg Ala Tyr
    370                 375                 380
```

```
Phe Thr Phe Ala Arg Pro Glu Asp Cys Ile Ser Gly Ala Ala Asp Ala
385                 390                 395                 400

Ser Ala Leu Ala Met Gln Asn Asp Asp Pro Ser Asn Ala Ala Ala Gln
                405                 410                 415

Leu Glu Gln Cys Ala Gln Tyr Leu Phe Gln Leu Gly His Glu Thr Asp
            420                 425                 430

Gly Ala Ser Leu Leu Glu Ser Ala Phe Arg Val Glu Gly Ile Pro Thr
        435                 440                 445

Glu Gln Ala Leu Tyr Tyr Ala Asn Ala Leu Ser Ser Ile Tyr Glu Asp
    450                 455                 460

Phe Gly Asp Ser Ala Lys Ser Gln Tyr Trp Glu Gln Gln Ala Gln Glu
465                 470                 475                 480

Lys Gln Gln Leu Leu Glu
                485
```

<210> 1065
<211> 1427
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1404)
<223> FRXA02279

<400> 1065

```
ncn gcc agg gct acc gcg ctt gtc gat ttc ttg gaa tcc cag act gtt   48
Xaa Ala Arg Ala Thr Ala Leu Val Asp Phe Leu Glu Ser Gln Thr Val
  1               5                  10                  15

gac cag ctg aat aac ccc gat gtc cag act tac ctc acc gaa gcg gaa   96
Asp Gln Leu Asn Asn Pro Asp Val Gln Thr Tyr Leu Thr Glu Ala Glu
            20                  25                  30

ctg att cgc gat gac ttg agg tct tgg gca gtc atc aaa tca aat ggc   144
Leu Ile Arg Asp Asp Leu Arg Ser Trp Ala Val Ile Lys Ser Asn Gly
        35                  40                  45

att gga caa cat cga tct tgt tcc ata cgg cga gga aac gac gag cca   192
Ile Gly Gln His Arg Ser Cys Ser Ile Arg Arg Gly Asn Asp Glu Pro
    50                  55                  60

ctt gca atc gcc cgc aag atc atc gag gaa acc gct tcc cat cct gag   240
Leu Ala Ile Ala Arg Lys Ile Ile Glu Glu Thr Ala Ser His Pro Glu
65                  70                  75                  80

ctg aga ttc gaa aac ctc gag gcc cag ttc tcc gag ttc acc atc ttg   288
Leu Arg Phe Glu Asn Leu Glu Ala Gln Phe Ser Glu Phe Thr Ile Leu
                85                  90                  95

ctt gct caa agc ccg gag aac ctc gac gta gcc cgc tac cag gag ctt   336
Leu Ala Gln Ser Pro Glu Asn Leu Asp Val Ala Arg Tyr Gln Glu Leu
            100                 105                 110
```

```
cgt aca cag gga aac ttt gtt caa gaa ctc gcc ttg gac agc att ttc   384
Arg Thr Gln Gly Asn Phe Val Gln Glu Leu Ala Leu Asp Ser Ile Phe
        115                 120                 125

ggc caa cat gcc gtt gtt caa gac acc gga aac ggc gaa gcc atc cta   432
Gly Gln His Ala Val Val Gln Asp Thr Gly Asn Gly Glu Ala Ile Leu
    130                 135                 140

gat gaa act atc ggg tac atg atc ggc gcc ggc atg cgt gaa acc act   480
Asp Glu Thr Ile Gly Tyr Met Ile Gly Ala Gly Met Arg Glu Thr Thr
145                 150                 155                 160

gcc cgc acc gcc agc cag ttc gcg cag ctt tac tca ttt gtg ggc agg   528
Ala Arg Thr Ala Ser Gln Phe Ala Gln Leu Tyr Ser Phe Val Gly Arg
                165                 170                 175

cag gaa cgc tcc att gaa atg gca cga ctc gct ttc gag gaa ctt caa   576
Gln Glu Arg Ser Ile Glu Met Ala Arg Leu Ala Phe Glu Glu Leu Gln
            180                 185                 190

gcg gca gga ctt ccc cac cgt gag gaa gaa ctg cga ttg ggc atg caa   624
Ala Ala Gly Leu Pro His Arg Glu Glu Glu Leu Arg Leu Gly Met Gln
        195                 200                 205

ctc gcc cag gtt gaa cca att gaa gcc cgc gaa atc ctg gaa aag ctg   672
Leu Ala Gln Val Glu Pro Ile Glu Ala Arg Glu Ile Leu Glu Lys Leu
    210                 215                 220

ctg ctg cct aaa ttc gag cag aat ctg aca ctt gat gaa ctt gaa act   720
Leu Leu Pro Lys Phe Glu Gln Asn Leu Thr Leu Asp Glu Leu Glu Thr
225                 230                 235                 240

gaa gca ctc ctt cct ttg ggt gct acc gtt gct atc cac gac ccc cag   768
Glu Ala Leu Leu Pro Leu Gly Ala Thr Val Ala Ile His Asp Pro Gln
                245                 250                 255

gct gcc gca gca att ttg cgc cac gct cgc gaa aac gcc gca ggg ttc   816
Ala Ala Ala Ala Ile Leu Arg His Ala Arg Glu Asn Ala Ala Gly Phe
            260                 265                 270

ggc aac ttc gaa ctc gca gtc caa gcg atg acc atg atc acg gat gtc   864
Gly Asn Phe Glu Leu Ala Val Gln Ala Met Thr Met Ile Thr Asp Val
        275                 280                 285

ctc tac acc caa aac atg cac gag caa ctg ctg gag gag ctc aac cac   912
Leu Tyr Thr Gln Asn Met His Glu Gln Leu Leu Glu Glu Leu Asn His
    290                 295                 300

tct ctc ccc tat gct caa atg ctt gat gat caa cac caa gct gaa ctg   960
Ser Leu Pro Tyr Ala Gln Met Leu Asp Asp Gln His Gln Ala Glu Leu
305                 310                 315                 320

aaa ctg ctg gac agc atc gcc atc gtc cag gca gac ctc ggt tcc acc   1008
Lys Leu Leu Asp Ser Ile Ala Ile Val Gln Ala Asp Leu Gly Ser Thr
                325                 330                 335

gaa gcg ctg gaa acc ctg ggc acc gca atg gga ctc gca gaa acc aca   1056
Glu Ala Leu Glu Thr Leu Gly Thr Ala Met Gly Leu Ala Glu Thr Thr
            340                 345                 350

gct cag aag cta tac gtg cag gaa tcc ctc aac cgc gca tac ttc act   1104
```

```
Ala Gln Lys Leu Tyr Val Gln Glu Ser Leu Asn Arg Ala Tyr Phe Thr
        355                 360                 365

ttt gcc cgc cct gaa gat tgc atc agc gga gca gcc gac gct tct gcc   1152
Phe Ala Arg Pro Glu Asp Cys Ile Ser Gly Ala Ala Asp Ala Ser Ala
    370                 375                 380

ctg gcc atg caa aac gat gac cct tcc aat gca gct gcc cag ttg gag   1200
Leu Ala Met Gln Asn Asp Asp Pro Ser Asn Ala Ala Ala Gln Leu Glu
385                 390                 395                 400

cag tgt gca cag tac ttg ttc caa ttg ggc cac gaa act gac ggc gca   1248
Gln Cys Ala Gln Tyr Leu Phe Gln Leu Gly His Glu Thr Asp Gly Ala
                405                 410                 415

agc ctg ctg gaa tct gca ttc agg gtt gaa ggc atc ccc act gag cag   1296
Ser Leu Leu Glu Ser Ala Phe Arg Val Glu Gly Ile Pro Thr Glu Gln
            420                 425                 430

gca ctg tac tac gca aat gca ctg tct tcc atc tat gaa gat ttc ggc   1344
Ala Leu Tyr Tyr Ala Asn Ala Leu Ser Ser Ile Tyr Glu Asp Phe Gly
        435                 440                 445

gat tcc gcg aag tcg cag tac tgg gag cag cag gcg cag gaa aag cag   1392
Asp Ser Ala Lys Ser Gln Tyr Trp Glu Gln Gln Ala Gln Glu Lys Gln
    450                 455                 460

cag ctt ctg gag taacggccgt ttaaagagtc gaa                        1427
Gln Leu Leu Glu
465
```

<210> 1066
<211> 468
<212> PRT
<213> Corynebacterium glutamicum

<400> 1066

```
Xaa Ala Arg Ala Thr Ala Leu Val Asp Phe Leu Glu Ser Gln Thr Val
  1               5                  10                  15

Asp Gln Leu Asn Asn Pro Asp Val Gln Thr Tyr Leu Thr Glu Ala Glu
            20                  25                  30

Leu Ile Arg Asp Asp Leu Arg Ser Trp Ala Val Ile Lys Ser Asn Gly
        35                  40                  45

Ile Gly Gln His Arg Ser Cys Ser Ile Arg Arg Gly Asn Asp Glu Pro
    50                  55                  60

Leu Ala Ile Ala Arg Lys Ile Ile Glu Glu Thr Ala Ser His Pro Glu
65                  70                  75                  80

Leu Arg Phe Glu Asn Leu Glu Ala Gln Phe Ser Glu Phe Thr Ile Leu
                85                  90                  95

Leu Ala Gln Ser Pro Glu Asn Leu Asp Val Ala Arg Tyr Gln Glu Leu
            100                 105                 110

Arg Thr Gln Gly Asn Phe Val Gln Glu Leu Ala Leu Asp Ser Ile Phe
        115                 120                 125
```

```
Gly Gln His Ala Val Val Gln Asp Thr Gly Asn Gly Glu Ala Ile Leu
    130                 135                 140

Asp Glu Thr Ile Gly Tyr Met Ile Gly Ala Gly Met Arg Glu Thr Thr
145                 150                 155                 160

Ala Arg Thr Ala Ser Gln Phe Ala Gln Leu Tyr Ser Phe Val Gly Arg
                165                 170                 175

Gln Glu Arg Ser Ile Glu Met Ala Arg Leu Ala Phe Glu Glu Leu Gln
            180                 185                 190

Ala Ala Gly Leu Pro His Arg Glu Glu Glu Leu Arg Leu Gly Met Gln
        195                 200                 205

Leu Ala Gln Val Glu Pro Ile Glu Ala Arg Glu Ile Leu Glu Lys Leu
    210                 215                 220

Leu Leu Pro Lys Phe Glu Gln Asn Leu Thr Leu Asp Glu Leu Glu Thr
225                 230                 235                 240

Glu Ala Leu Leu Pro Leu Gly Ala Thr Val Ala Ile His Asp Pro Gln
                245                 250                 255

Ala Ala Ala Ala Ile Leu Arg His Ala Arg Glu Asn Ala Ala Gly Phe
            260                 265                 270

Gly Asn Phe Glu Leu Ala Val Gln Ala Met Thr Met Ile Thr Asp Val
        275                 280                 285

Leu Tyr Thr Gln Asn Met His Glu Gln Leu Leu Glu Glu Leu Asn His
    290                 295                 300

Ser Leu Pro Tyr Ala Gln Met Leu Asp Asp Gln His Gln Ala Glu Leu
305                 310                 315                 320

Lys Leu Leu Asp Ser Ile Ala Ile Val Gln Ala Asp Leu Gly Ser Thr
                325                 330                 335

Glu Ala Leu Glu Thr Leu Gly Thr Ala Met Gly Leu Ala Glu Thr Thr
            340                 345                 350

Ala Gln Lys Leu Tyr Val Gln Glu Ser Leu Asn Arg Ala Tyr Phe Thr
        355                 360                 365

Phe Ala Arg Pro Glu Asp Cys Ile Ser Gly Ala Ala Asp Ala Ser Ala
    370                 375                 380

Leu Ala Met Gln Asn Asp Asp Pro Ser Asn Ala Ala Ala Gln Leu Glu
385                 390                 395                 400

Gln Cys Ala Gln Tyr Leu Phe Gln Leu Gly His Glu Thr Asp Gly Ala
                405                 410                 415

Ser Leu Leu Glu Ser Ala Phe Arg Val Glu Gly Ile Pro Thr Glu Gln
            420                 425                 430

Ala Leu Tyr Tyr Ala Asn Ala Leu Ser Ser Ile Tyr Glu Asp Phe Gly
        435                 440                 445
```

```
Asp Ser Ala Lys Ser Gln Tyr Trp Glu Gln Gln Ala Gln Glu Lys Gln
    450                 455                 460

Gln Leu Leu Glu
465
```

<210> 1067
<211> 612
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(589)
<223> RXN02296

<400> 1067

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gcatcatttg tgttgtttaa agtatatggc tgttgaagtg ccattttcgc ggattagcat 60

gggaatcacc agtatttctg gacggttaag gatgattcat atg cgt aat caa aca   115
                                            Met Arg Asn Gln Thr
                                              1               5

atc gct gcg gtc gca gct ttg gtc ctg ctc acc gcc gcc acg ccc gcg   163
Ile Ala Ala Val Ala Ala Leu Val Leu Leu Thr Ala Ala Thr Pro Ala
                 10                  15                  20

atc gct gcc acc ccg gcg aca gct gga aac gga ctc tat tcc att gac   211
Ile Ala Ala Thr Pro Ala Thr Ala Gly Asn Gly Leu Tyr Ser Ile Asp
             25                  30                  35

atg ggc gac gag caa aag ctt acc tgc gtg ctt ttc gat gag ccc tcc   259
Met Gly Asp Glu Gln Lys Leu Thr Cys Val Leu Phe Asp Glu Pro Ser
         40                  45                  50

acc gaa gcg cac gtc gtc gcc agc tgt gct gcg act ttc ccg gtg acc   307
Thr Glu Ala His Val Val Ala Ser Cys Ala Ala Thr Phe Pro Val Thr
     55                  60                  65

tgg aag ctt ctc gac ggc gct cac gaa caa gcc gcg aaa ctt gaa atc   355
Trp Lys Leu Leu Asp Gly Ala His Glu Gln Ala Ala Lys Leu Glu Ile
 70                  75                  80                  85

acc cag gct caa gac ggt gaa ctc tcg gtg aca gcc agc aag cag ccg   403
Thr Gln Ala Gln Asp Gly Glu Leu Ser Val Thr Ala Ser Lys Gln Pro
                 90                  95                 100

ttg atc acc acg atg att gcg ccc acc agc atc act aag ccc atc act   451
Leu Ile Thr Thr Met Ile Ala Pro Thr Ser Ile Thr Lys Pro Ile Thr
            105                 110                 115

gtc aat agg ctt gtg gtt gtt cct ggt gag aat gag gtt cgc ttt tat   499
Val Asn Arg Leu Val Val Val Pro Gly Glu Asn Glu Val Arg Phe Tyr
        120                 125                 130

gct acc gat cct gat gtt tta cca gtg ctg atc acg cct gac tcc tat   547
Ala Thr Asp Pro Asp Val Leu Pro Val Leu Ile Thr Pro Asp Ser Tyr
    135                 140                 145

gaa gtg ttg acc gat tcc gct gct aaa gtg aaa gcg aca tta           589
```

```
Glu Val Leu Thr Asp Ser Ala Ala Lys Val Lys Ala Thr Leu
150                 155                 160

tgaaataaac gtggatcaag gag                                          612


<210> 1068
<211> 163
<212> PRT
<213> Corynebacterium glutamicum

<400> 1068
Met Arg Asn Gln Thr Ile Ala Ala Val Ala Ala Leu Val Leu Leu Thr
  1               5                  10                  15

Ala Ala Thr Pro Ala Ile Ala Ala Thr Pro Ala Thr Ala Gly Asn Gly
             20                  25                  30

Leu Tyr Ser Ile Asp Met Gly Asp Glu Gln Lys Leu Thr Cys Val Leu
         35                  40                  45

Phe Asp Glu Pro Ser Thr Glu Ala His Val Val Ala Ser Cys Ala Ala
     50                  55                  60

Thr Phe Pro Val Thr Trp Lys Leu Leu Asp Gly Ala His Glu Gln Ala
 65                  70                  75                  80

Ala Lys Leu Glu Ile Thr Gln Ala Gln Asp Gly Glu Leu Ser Val Thr
                 85                  90                  95

Ala Ser Lys Gln Pro Leu Ile Thr Thr Met Ile Ala Pro Thr Ser Ile
            100                 105                 110

Thr Lys Pro Ile Thr Val Asn Arg Leu Val Val Val Pro Gly Glu Asn
        115                 120                 125

Glu Val Arg Phe Tyr Ala Thr Asp Pro Asp Val Leu Pro Val Leu Ile
    130                 135                 140

Thr Pro Asp Ser Tyr Glu Val Leu Thr Asp Ser Ala Ala Lys Val Lys
145                 150                 155                 160

Ala Thr Leu


<210> 1069
<211> 612
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(589)
<223> FRXA02296

<400> 1069
gcatcatttg tgttgtttaa agtatatggc tgttgaagtg ccattttcgc ggattagcat 60

gggaatcacc agtatttctg gacggttaag gatgattcat atg cgt aat caa aca   115
                                                Met Arg Asn Gln Thr
```

```
                                                    1               5

atc gct gcg gtc gca gct ttg gtc ctg ctc acc gcc gcc acg ccc gcg   163
Ile Ala Ala Val Ala Ala Leu Val Leu Leu Thr Ala Ala Thr Pro Ala
                 10                  15                  20

atc gct gcc acc ccg gcg aca gct gga aac gga ctc tat tcc att gac   211
Ile Ala Ala Thr Pro Ala Thr Ala Gly Asn Gly Leu Tyr Ser Ile Asp
             25                  30                  35

atg ggc gac gag caa aag ctt acc tgc gtg ctt ttc gat gag ccc tcc   259
Met Gly Asp Glu Gln Lys Leu Thr Cys Val Leu Phe Asp Glu Pro Ser
         40                  45                  50

acc gaa gcg cac gtc gtc gcc agc tgt gct gcg act ttc ccg gtg acc   307
Thr Glu Ala His Val Val Ala Ser Cys Ala Ala Thr Phe Pro Val Thr
     55                  60                  65

tgg aag ctt ctc gac ggc gct cac gaa caa gcc gcg aaa ctt gaa atc   355
Trp Lys Leu Leu Asp Gly Ala His Glu Gln Ala Ala Lys Leu Glu Ile
 70                  75                  80                  85

acc cag gct caa gac ggt gaa ctc tcg gtg aca gcc agc aag cag ccg   403
Thr Gln Ala Gln Asp Gly Glu Leu Ser Val Thr Ala Ser Lys Gln Pro
                 90                  95                 100

ttg atc acc acg atg att gcg ccc acc agc atc act aag ccc atc act   451
Leu Ile Thr Thr Met Ile Ala Pro Thr Ser Ile Thr Lys Pro Ile Thr
            105                 110                 115

gtc aat agg ctt gtg gtt gtt cct ggt gag aat gag gtt cgc ttt tat   499
Val Asn Arg Leu Val Val Val Pro Gly Glu Asn Glu Val Arg Phe Tyr
        120                 125                 130

gct acc gat cct gat gtt tta cca gtg ctg atc acg cct gac tcc tat   547
Ala Thr Asp Pro Asp Val Leu Pro Val Leu Ile Thr Pro Asp Ser Tyr
    135                 140                 145

gaa gtg ttg acc gat tcc gct gct aaa gtg aaa gcg aca tta            589
Glu Val Leu Thr Asp Ser Ala Ala Lys Val Lys Ala Thr Leu
150                 155                 160

tgaaataaac gtggatcaag gag                                         612


<210> 1070
<211> 163
<212> PRT
<213> Corynebacterium glutamicum

<400> 1070
Met Arg Asn Gln Thr Ile Ala Ala Val Ala Ala Leu Val Leu Leu Thr
  1               5                  10                  15

Ala Ala Thr Pro Ala Ile Ala Ala Thr Pro Ala Thr Ala Gly Asn Gly
             20                  25                  30

Leu Tyr Ser Ile Asp Met Gly Asp Glu Gln Lys Leu Thr Cys Val Leu
         35                  40                  45

Phe Asp Glu Pro Ser Thr Glu Ala His Val Val Ala Ser Cys Ala Ala
```

```
     50                  55                  60

Thr Phe Pro Val Thr Trp Lys Leu Leu Asp Gly Ala His Glu Gln Ala
 65                  70                  75                  80

Ala Lys Leu Glu Ile Thr Gln Ala Gln Asp Gly Glu Leu Ser Val Thr
                 85                  90                  95

Ala Ser Lys Gln Pro Leu Ile Thr Thr Met Ile Ala Pro Thr Ser Ile
            100                 105                 110

Thr Lys Pro Ile Thr Val Asn Arg Leu Val Val Val Pro Gly Glu Asn
        115                 120                 125

Glu Val Arg Phe Tyr Ala Thr Asp Pro Asp Val Leu Pro Val Leu Ile
    130                 135                 140

Thr Pro Asp Ser Tyr Glu Val Leu Thr Asp Ser Ala Ala Lys Val Lys
145                 150                 155                 160

Ala Thr Leu
```

CN 1670208 A 2005.09.21

<210> 1071
<211> 456
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(433)
<223> RXN02300

<400> 1071

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gggtcattcc ggtgaacacg gatttcgcgc cggtgaatct gacggtcagc caattgcggg 60

caatgctgtc caaagcggag cgtaaagata aggatcagaa atg aaa act tat gca   115
                                          Met Lys Thr Tyr Ala
                                            1               5

gta cta att gcg gtg gca ggg ttg gca ctt gct ggg tgt agc tcg tcg   163
Val Leu Ile Ala Val Ala Gly Leu Ala Leu Ala Gly Cys Ser Ser Ser
                10                  15                  20

gct cct gga atc tgg cgt gcc act gaa ccc gca gat gcc tac ctt gaa   211
Ala Pro Gly Ile Trp Arg Ala Thr Glu Pro Ala Asp Ala Tyr Leu Glu
            25                  30                  35

ata gcc gat gac ggc acg ctg tcc gga acc gac ggc tgc aac aga ctt   259
Ile Ala Asp Asp Gly Thr Leu Ser Gly Thr Asp Gly Cys Asn Arg Leu
        40                  45                  50

ttt ggt ggc tgg gaa aaa gac ggc tct acc atc act ttc ggc gcc atc   307
Phe Gly Gly Trp Glu Lys Asp Gly Ser Thr Ile Thr Phe Gly Ala Ile
    55                  60                  65

ggt atg aca gaa atg tac tgc gaa ggc gtc aac gat tgg ctg tcc cag   355
Gly Met Thr Glu Met Tyr Cys Glu Gly Val Asn Asp Trp Leu Ser Gln
70                  75                  80                  85
```

```
atg cac acc gcc acc gtc acc gat gcc acc atg acc att ttc aac gag   403
Met His Thr Ala Thr Val Thr Asp Ala Thr Met Thr Ile Phe Asn Glu
                 90                  95                 100

gcc ggc agc aat att ggc gag cta aaa cgc taaatgcttc tcgacgtcaa     453
Ala Gly Ser Asn Ile Gly Glu Leu Lys Arg
            105                 110

aag                                                               456
```

<210> 1072
<211> 111
<212> PRT
<213> Corynebacterium glutamicum

<400> 1072

```
Met Lys Thr Tyr Ala Val Leu Ile Ala Val Ala Gly Leu Ala Leu Ala
  1               5                  10                  15

Gly Cys Ser Ser Ser Ala Pro Gly Ile Trp Arg Ala Thr Glu Pro Ala
             20                  25                  30

Asp Ala Tyr Leu Glu Ile Ala Asp Asp Gly Thr Leu Ser Gly Thr Asp
         35                  40                  45

Gly Cys Asn Arg Leu Phe Gly Gly Trp Glu Lys Asp Gly Ser Thr Ile
     50                  55                  60

Thr Phe Gly Ala Ile Gly Met Thr Glu Met Tyr Cys Glu Gly Val Asn
 65                  70                  75                  80

Asp Trp Leu Ser Gln Met His Thr Ala Thr Val Thr Asp Ala Thr Met
                 85                  90                  95

Thr Ile Phe Asn Glu Ala Gly Ser Asn Ile Gly Glu Leu Lys Arg
            100                 105                 110
```

<210> 1073
<211> 456
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(433)
<223> FRXA02300

<400> 1073

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gggtcattcc ggtgaacacg gatttcgcgc cggtgaatct gacggtcagc caattgcggg 60

caatgctgtc caaagcggag cgtaaagata aggatcagaa atg aaa act tat gca   115
                                              Met Lys Thr Tyr Ala
                                                1               5

gta cta att gcg gtg gca ggg ttg gca ctt gct ggg tgt agc tcg tcg   163
Val Leu Ile Ala Val Ala Gly Leu Ala Leu Ala Gly Cys Ser Ser Ser
            10                  15                  20

gct cct gga atc tgg cgt gcc act gaa ccc gca gat gcc tac ctt gaa   211
```

```
Ala Pro Gly Ile Trp Arg Ala Thr Glu Pro Ala Asp Ala Tyr Leu Glu
             25                  30                  35

ata gcc gat gac ggc acg ctg tcc gga acc gac ggc tgc aac aga ctt   259
Ile Ala Asp Asp Gly Thr Leu Ser Gly Thr Asp Gly Cys Asn Arg Leu
         40                  45                  50

ttt ggt ggc tgg gaa aaa gac ggc tct acc atc act ttc ggc gcc atc   307
Phe Gly Gly Trp Glu Lys Asp Gly Ser Thr Ile Thr Phe Gly Ala Ile
     55                  60                  65

ggt atg aca gaa atg tac tgc gaa ggc gtc aac gat tgg ctg tcc cag   355
Gly Met Thr Glu Met Tyr Cys Glu Gly Val Asn Asp Trp Leu Ser Gln
 70                  75                  80                  85

atg cac acc gcc acc gtc acc gat gcc acc atg acc att ttc aac gag   403
Met His Thr Ala Thr Val Thr Asp Ala Thr Met Thr Ile Phe Asn Glu
                 90                  95                 100

gcc ggc agc aat att ggc gag cta aaa cgc taaatgcttc tcgacgtcaa     453
Ala Gly Ser Asn Ile Gly Glu Leu Lys Arg
            105                 110

aag                                                               456


<210> 1074
<211> 111
<212> PRT
<213> Corynebacterium glutamicum

<400> 1074
Met Lys Thr Tyr Ala Val Leu Ile Ala Val Ala Gly Leu Ala Leu Ala
  1               5                  10                  15

Gly Cys Ser Ser Ser Ala Pro Gly Ile Trp Arg Ala Thr Glu Pro Ala
             20                  25                  30

Asp Ala Tyr Leu Glu Ile Ala Asp Asp Gly Thr Leu Ser Gly Thr Asp
         35                  40                  45

Gly Cys Asn Arg Leu Phe Gly Gly Trp Glu Lys Asp Gly Ser Thr Ile
     50                  55                  60

Thr Phe Gly Ala Ile Gly Met Thr Glu Met Tyr Cys Glu Gly Val Asn
 65                  70                  75                  80

Asp Trp Leu Ser Gln Met His Thr Ala Thr Val Thr Asp Ala Thr Met
                 85                  90                  95

Thr Ile Phe Asn Glu Ala Gly Ser Asn Ile Gly Glu Leu Lys Arg
            100                 105                 110


<210> 1075
<211> 840
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
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<222> (101)..(817)
<223> RXN02301

<400> 1075
gcttcgcata tgtctggatc ttattggatg tatgagtcag agatcaggga gatcgcgcac 60

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taaccgaacc tggccagtgc aacaggatta tgtttaaagc atg gat ctt gca ctg   115
                                            Met Asp Leu Ala Leu
                                              1               5

gct cag gtt gat tcc acc gtt tcg ggg ctt tat gac gcc ctc gat ctc   163
Ala Gln Val Asp Ser Thr Val Ser Gly Leu Tyr Asp Ala Leu Asp Leu
                 10                  15                  20

atc ggc gtg ctg ctg aac gga ata atc ggt gga acg atc gcc agg caa   211
Ile Gly Val Leu Leu Asn Gly Ile Ile Gly Gly Thr Ile Ala Arg Gln
             25                  30                  35

cga ggc tat gac atc att ggc ttt ctg ttc ctg gcg tta ttt tct gcg   259
Arg Gly Tyr Asp Ile Ile Gly Phe Leu Phe Leu Ala Leu Phe Ser Ala
         40                  45                  50

ctg ggt ggc gga atg atc cgt gac atg ctg att cag cag ggg act gtc   307
Leu Gly Gly Gly Met Ile Arg Asp Met Leu Ile Gln Gln Gly Thr Val
     55                  60                  65

gcg gcg atc gat aat cag atc tac ctt gcg ctc gcg ttt tct ggc gcg   355
Ala Ala Ile Asp Asn Gln Ile Tyr Leu Ala Leu Ala Phe Ser Gly Ala
 70                  75                  80                  85

ctg att gcc atg gcg gtg aac ttt aaa ggc agg gtg tgg gag ctg ttt   403
Leu Ile Ala Met Ala Val Asn Phe Lys Gly Arg Val Trp Glu Leu Phe
                 90                  95                 100

aaa gtt cac ggc gat gcc att gtg ttg ggc gtc tgg gcg gtg acg ggt   451
Lys Val His Gly Asp Ala Ile Val Leu Gly Val Trp Ala Val Thr Gly
             105                 110                 115

tcc gtg aag gcg atg aat gcg ggg gtg gct ccg ctg ccg agt att ttc   499
Ser Val Lys Ala Met Asn Ala Gly Val Ala Pro Leu Pro Ser Ile Phe
         120                 125                 130

atg ggc gtg ctc acc gcg gtg ggt ggt ggc atg gtg cgt gat gtg gct   547
Met Gly Val Leu Thr Ala Val Gly Gly Gly Met Val Arg Asp Val Ala
     135                 140                 145

act ggc cag acg ccg acg att ttt ggt ggc gga act ctt tac gct gtg   595
Thr Gly Gln Thr Pro Thr Ile Phe Gly Gly Gly Thr Leu Tyr Ala Val
150                 155                 160                 165

cct gcg acg ctt tct gcc acg tca atg gtt att ttt cat agc ttt gac   643
Pro Ala Thr Leu Ser Ala Thr Ser Met Val Ile Phe His Ser Phe Asp
                170                 175                 180

cag gta att ctg ggt atg att att tca ccg ttc ttg ggt atc gcg ttg   691
Gln Val Ile Leu Gly Met Ile Ile Ser Pro Phe Leu Gly Ile Ala Leu
            185                 190                 195

gcg gtt act gcg tat tgg tgc ggt tgg gtc att ccg gtg aac acg gat   739
Ala Val Thr Ala Tyr Trp Cys Gly Trp Val Ile Pro Val Asn Thr Asp
        200                 205                 210
```

```
ttc gcg ccg gtg aat ctg acg gtc agc caa ttg cgg gca atg ctg tcc   787
Phe Ala Pro Val Asn Leu Thr Val Ser Gln Leu Arg Ala Met Leu Ser
    215                 220                 225

aaa gcg gag cgt aaa gat aag gat cag aaa tgaaaactta tgcagtacta     837
Lys Ala Glu Arg Lys Asp Lys Asp Gln Lys
230                 235

att                                                               840
```

<210> 1076
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 1076

```
Met Asp Leu Ala Leu Ala Gln Val Asp Ser Thr Val Ser Gly Leu Tyr
  1               5                  10                  15

Asp Ala Leu Asp Leu Ile Gly Val Leu Leu Asn Gly Ile Ile Gly Gly
             20                  25                  30

Thr Ile Ala Arg Gln Arg Gly Tyr Asp Ile Ile Gly Phe Leu Phe Leu
         35                  40                  45

Ala Leu Phe Ser Ala Leu Gly Gly Gly Met Ile Arg Asp Met Leu Ile
     50                  55                  60

Gln Gln Gly Thr Val Ala Ala Ile Asp Asn Gln Ile Tyr Leu Ala Leu
 65                  70                  75                  80

Ala Phe Ser Gly Ala Leu Ile Ala Met Ala Val Asn Phe Lys Gly Arg
                 85                  90                  95

Val Trp Glu Leu Phe Lys Val His Gly Asp Ala Ile Val Leu Gly Val
            100                 105                 110

Trp Ala Val Thr Gly Ser Val Lys Ala Met Asn Ala Gly Val Ala Pro
        115                 120                 125

Leu Pro Ser Ile Phe Met Gly Val Leu Thr Ala Val Gly Gly Gly Met
    130                 135                 140

Val Arg Asp Val Ala Thr Gly Gln Thr Pro Thr Ile Phe Gly Gly Gly
145                 150                 155                 160

Thr Leu Tyr Ala Val Pro Ala Thr Leu Ser Ala Thr Ser Met Val Ile
                165                 170                 175

Phe His Ser Phe Asp Gln Val Ile Leu Gly Met Ile Ile Ser Pro Phe
            180                 185                 190

Leu Gly Ile Ala Leu Ala Val Thr Ala Tyr Trp Cys Gly Trp Val Ile
        195                 200                 205

Pro Val Asn Thr Asp Phe Ala Pro Val Asn Leu Thr Val Ser Gln Leu
    210                 215                 220

Arg Ala Met Leu Ser Lys Ala Glu Arg Lys Asp Lys Asp Gln Lys
```

225 230 235

<210> 1077
<211> 840
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(817)
<223> FRXA02301

<400> 1077
gcttcgcata tgtctggatc ttattggatg tatgagtcag agatcaggga gatcgcgcac 60

```
taaccgaacc tggccagtgc aacaggatta tgtttaaagc atg gat ctt gca ctg   115
                                            Met Asp Leu Ala Leu
                                              1               5

gct cag gtt gat tcc acc gtt tcg ggg ctt tat gac gcc ctc gat ctc   163
Ala Gln Val Asp Ser Thr Val Ser Gly Leu Tyr Asp Ala Leu Asp Leu
                  10                  15                  20

atc ggc gtg ctg ctg aac gga ata atc ggt gga acg atc gcc agg caa   211
Ile Gly Val Leu Leu Asn Gly Ile Ile Gly Gly Thr Ile Ala Arg Gln
              25                  30                  35

cga ggc tat gac atc att ggc ttt ctg ttc ctg gcg tta ttt tct gcg   259
Arg Gly Tyr Asp Ile Ile Gly Phe Leu Phe Leu Ala Leu Phe Ser Ala
          40                  45                  50

ctg ggt ggc gga atg atc cgt gac atg ctg att cag cag ggg act gtc   307
Leu Gly Gly Gly Met Ile Arg Asp Met Leu Ile Gln Gln Gly Thr Val
      55                  60                  65

gcg gcg atc gat aat cag atc tac ctt gcg ctc gcg ttt tct ggc gcg   355
Ala Ala Ile Asp Asn Gln Ile Tyr Leu Ala Leu Ala Phe Ser Gly Ala
  70                  75                  80                  85

ctg att gcc atg gcg gtg aac ttt aaa ggc agg gtg tgg gag ctg ttt   403
Leu Ile Ala Met Ala Val Asn Phe Lys Gly Arg Val Trp Glu Leu Phe
                  90                  95                 100

aaa gtt cac ggc gat gcc att gtg ttg ggc gtc tgg gcg gtg acg ggt   451
Lys Val His Gly Asp Ala Ile Val Leu Gly Val Trp Ala Val Thr Gly
              105                 110                 115

tcc gtg aag gcg atg aat gcg ggg gtg gct ccg ctg ccg agt att ttc   499
Ser Val Lys Ala Met Asn Ala Gly Val Ala Pro Leu Pro Ser Ile Phe
          120                 125                 130

atg ggc gtg ctc acc gcg gtg ggt ggt ggc atg gtg cgt gat gtg gct   547
Met Gly Val Leu Thr Ala Val Gly Gly Gly Met Val Arg Asp Val Ala
      135                 140                 145

act ggc cag acg ccg acg att ttt ggt ggc gga act ctt tac gct gtg   595
Thr Gly Gln Thr Pro Thr Ile Phe Gly Gly Gly Thr Leu Tyr Ala Val
150                 155                 160                 165

cct gcg acg ctt tct gcc acg tca atg gtt att ttt cat agc ttt gac   643
```

```
Pro Ala Thr Leu Ser Ala Thr Ser Met Val Ile Phe His Ser Phe Asp
                 170                 175                 180

cag gta att ctg ggt atg att att tca ccg ttc ttg ggt atc gcg ttg   691
Gln Val Ile Leu Gly Met Ile Ile Ser Pro Phe Leu Gly Ile Ala Leu
            185                 190                 195

gcg gtt act gcg tat tgg tgc ggt tgg gtc att ccg gtg aac acg gat   739
Ala Val Thr Ala Tyr Trp Cys Gly Trp Val Ile Pro Val Asn Thr Asp
        200                 205                 210

ttc gcg ccg gtg aat ctg acg gtc agc caa ttg cgg gca atg ctg tcc   787
Phe Ala Pro Val Asn Leu Thr Val Ser Gln Leu Arg Ala Met Leu Ser
    215                 220                 225

aaa gcg gag cgt aaa gat aag gat cag aaa tgaaaactta tgcagtacta     837
Lys Ala Glu Arg Lys Asp Lys Asp Gln Lys
230                 235

att                                                               840
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09650650 = 09650650

<210> 1078
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 1078

```
Met Asp Leu Ala Leu Ala Gln Val Asp Ser Thr Val Ser Gly Leu Tyr
  1               5                  10                  15

Asp Ala Leu Asp Leu Ile Gly Val Leu Leu Asn Gly Ile Ile Gly Gly
             20                  25                  30

Thr Ile Ala Arg Gln Arg Gly Tyr Asp Ile Ile Gly Phe Leu Phe Leu
         35                  40                  45

Ala Leu Phe Ser Ala Leu Gly Gly Gly Met Ile Arg Asp Met Leu Ile
     50                  55                  60

Gln Gln Gly Thr Val Ala Ala Ile Asp Asn Gln Ile Tyr Leu Ala Leu
 65                  70                  75                  80

Ala Phe Ser Gly Ala Leu Ile Ala Met Ala Val Asn Phe Lys Gly Arg
                 85                  90                  95

Val Trp Glu Leu Phe Lys Val His Gly Asp Ala Ile Val Leu Gly Val
            100                 105                 110

Trp Ala Val Thr Gly Ser Val Lys Ala Met Asn Ala Gly Val Ala Pro
        115                 120                 125

Leu Pro Ser Ile Phe Met Gly Val Leu Thr Ala Val Gly Gly Gly Met
    130                 135                 140

Val Arg Asp Val Ala Thr Gly Gln Thr Pro Thr Ile Phe Gly Gly Gly
145                 150                 155                 160

Thr Leu Tyr Ala Val Pro Ala Thr Leu Ser Ala Thr Ser Met Val Ile
                165                 170                 175
```

```
Phe His Ser Phe Asp Gln Val Ile Leu Gly Met Ile Ile Ser Pro Phe
            180                 185                 190

Leu Gly Ile Ala Leu Ala Val Thr Ala Tyr Trp Cys Gly Trp Val Ile
        195                 200                 205

Pro Val Asn Thr Asp Phe Ala Pro Val Asn Leu Thr Val Ser Gln Leu
    210                 215                 220

Arg Ala Met Leu Ser Lys Ala Glu Arg Lys Asp Lys Asp Gln Lys
225                 230                 235
```

<210> 1079
<211> 1002
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(979)
<223> RXN02302

<400> 1079

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ggccaggttc ggttagtgcg cgatctccct gatctctgac tcatacatcc aataagatcc 60

agacatatgc gaagctaatg aaggaaacga ggagctgata gtg gca aca aat cgt   115
                                          Val Ala Thr Asn Arg
                                            1               5

aca tct tcc gct ggt gtc atc acg tct gtt ctc gca tcc gct ttg ttc   163
Thr Ser Ser Ala Gly Val Ile Thr Ser Val Leu Ala Ser Ala Leu Phe
                10                  15                  20

gga gcg atc ttt ttc atc tct ggg gcg att gag gca aag gcg gaa aca   211
Gly Ala Ile Phe Phe Ile Ser Gly Ala Ile Glu Ala Lys Ala Glu Thr
            25                  30                  35

ctt gtt gct tgg cgt gtc ctt cta aca gcg gca tgc tat ttg ctt gcc   259
Leu Val Ala Trp Arg Val Leu Leu Thr Ala Ala Cys Tyr Leu Leu Ala
        40                  45                  50

ctt ctg cac cct gct ggt cgg aag gtg ttt aag gaa ttt tgg gac aca   307
Leu Leu His Pro Ala Gly Arg Lys Val Phe Lys Glu Phe Trp Asp Thr
    55                  60                  65

cta agg tcc caa cct cgt caa att ctg tac ttt atc ttc ctc gtt gta   355
Leu Arg Ser Gln Pro Arg Gln Ile Leu Tyr Phe Ile Phe Leu Val Val
70                  75                  80                  85

ctc atc acg ctt cag ctg tgg ctg ttt tct tgg tcg cct aag agt cat   403
Leu Ile Thr Leu Gln Leu Trp Leu Phe Ser Trp Ser Pro Lys Ser His
                90                  95                  100

gct tta gat gcc tca ctt ggt tac ctg tta ctg ccc att ttc cta gta   451
Ala Leu Asp Ala Ser Leu Gly Tyr Leu Leu Leu Pro Ile Phe Leu Val
            105                 110                 115

att gtg ggg cgg ttt ttc ttc gct gat tac atc acc agg ctg cag tgg   499
Ile Val Gly Arg Phe Phe Phe Ala Asp Tyr Ile Thr Arg Leu Gln Trp
        120                 125                 130
```

```
att gcg gtg gga atc gcg ctg atc gca gta acc ttg aaa ttt gtc att   547
Ile Ala Val Gly Ile Ala Leu Ile Ala Val Thr Leu Lys Phe Val Ile
    135                 140                 145

agt gcg caa tta tcg tgg gta act ttt gcc atc gct gcg ggt tat gca   595
Ser Ala Gln Leu Ser Trp Val Thr Phe Ala Ile Ala Ala Gly Tyr Ala
150                 155                 160                 165

ctg tat ttt gcg ctt cgt aaa tac tcg ggg ctg aac aac gct ttt gct   643
Leu Tyr Phe Ala Leu Arg Lys Tyr Ser Gly Leu Asn Asn Ala Phe Ala
                170                 175                 180

tac ggc gca gaa gtt tta gcg tta agt ccc ctg gca ttt ttc atg ctc   691
Tyr Gly Ala Glu Val Leu Ala Leu Ser Pro Leu Ala Phe Phe Met Leu
            185                 190                 195

gcc act gtc gag gat ccg ctg tct aac gcc atg ttg tca atg gtt att   739
Ala Thr Val Glu Asp Pro Leu Ser Asn Ala Met Leu Ser Met Val Ile
        200                 205                 210

ctg gcg ggc ctc gct ggc gca tta gct atg gcg ttg tat cta gcc gcc   787
Leu Ala Gly Leu Ala Gly Ala Leu Ala Met Ala Leu Tyr Leu Ala Ala
    215                 220                 225

tca act ctg ctt agt atg ccg atg ttt ggc ctg ctc agt tat ggt gaa   835
Ser Thr Leu Leu Ser Met Pro Met Phe Gly Leu Leu Ser Tyr Gly Glu
230                 235                 240                 245

cca atc ttg ctg ttt gtt gca gca cta tta ctt ggt gaa acg ttg aat   883
Pro Ile Leu Leu Phe Val Ala Ala Leu Leu Leu Gly Glu Thr Leu Asn
                250                 255                 260

ctc agc gac gcc att gtc tac tca cta ctg gcg tgc gcc ctg gcg tta   931
Leu Ser Asp Ala Ile Val Tyr Ser Leu Leu Ala Cys Ala Leu Ala Leu
            265                 270                 275

ctg gga ttt gat ggg ata cga agg tct cga aaa aac ctc gag acc gat   979
Leu Gly Phe Asp Gly Ile Arg Arg Ser Arg Lys Asn Leu Glu Thr Asp
        280                 285                 290

taacttctgc tcaacttccc acc                                        1002
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Doc code: AP.GRNP

<210> 1080
<211> 293
<212> PRT
<213> Corynebacterium glutamicum

<400> 1080

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Val Ala Thr Asn Arg Thr Ser Ser Ala Gly Val Ile Thr Ser Val Leu
  1               5                  10                  15

Ala Ser Ala Leu Phe Gly Ala Ile Phe Phe Ile Ser Gly Ala Ile Glu
             20                  25                  30

Ala Lys Ala Glu Thr Leu Val Ala Trp Arg Val Leu Leu Thr Ala Ala
         35                  40                  45

Cys Tyr Leu Leu Ala Leu Leu His Pro Ala Gly Arg Lys Val Phe Lys
     50                  55                  60
```

```
Glu Phe Trp Asp Thr Leu Arg Ser Gln Pro Arg Gln Ile Leu Tyr Phe
 65                  70                  75                  80

Ile Phe Leu Val Val Leu Ile Thr Leu Gln Leu Trp Leu Phe Ser Trp
                 85                  90                  95

Ser Pro Lys Ser His Ala Leu Asp Ala Ser Leu Gly Tyr Leu Leu Leu
            100                 105                 110

Pro Ile Phe Leu Val Ile Val Gly Arg Phe Phe Phe Ala Asp Tyr Ile
        115                 120                 125

Thr Arg Leu Gln Trp Ile Ala Val Gly Ile Ala Leu Ile Ala Val Thr
    130                 135                 140

Leu Lys Phe Val Ile Ser Ala Gln Leu Ser Trp Val Thr Phe Ala Ile
145                 150                 155                 160

Ala Ala Gly Tyr Ala Leu Tyr Phe Ala Leu Arg Lys Tyr Ser Gly Leu
                165                 170                 175

Asn Asn Ala Phe Ala Tyr Gly Ala Glu Val Leu Ala Leu Ser Pro Leu
            180                 185                 190

Ala Phe Phe Met Leu Ala Thr Val Glu Asp Pro Leu Ser Asn Ala Met
        195                 200                 205

Leu Ser Met Val Ile Leu Ala Gly Leu Ala Gly Ala Leu Ala Met Ala
    210                 215                 220

Leu Tyr Leu Ala Ala Ser Thr Leu Leu Ser Met Pro Met Phe Gly Leu
225                 230                 235                 240

Leu Ser Tyr Gly Glu Pro Ile Leu Leu Phe Val Ala Ala Leu Leu Leu
                245                 250                 255

Gly Glu Thr Leu Asn Leu Ser Asp Ala Ile Val Tyr Ser Leu Leu Ala
            260                 265                 270

Cys Ala Leu Ala Leu Leu Gly Phe Asp Gly Ile Arg Arg Ser Arg Lys
        275                 280                 285

Asn Leu Glu Thr Asp
    290


<210> 1081
<211> 865
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(865)
<223> FRXA02302

<400> 1081
ggccaggttc ggttagtgcg cgatctccct gatctctgac tcatacatcc aataagatcc 60

agacatatgc gaagctaatg aaggaaacga ggagctgata gtg gca aca aat cgt   115
```

```
                                                  Val Ala Thr Asn Arg
                                                    1               5

aca tct tcc gct ggt gtc atc acg tct gtt ctc gca tcc gct ttg ttc   163
Thr Ser Ser Ala Gly Val Ile Thr Ser Val Leu Ala Ser Ala Leu Phe
                10                  15                  20

gga gcg atc ttt ttc atc tct ggg gcg att gag gca aag gcg gaa aca   211
Gly Ala Ile Phe Phe Ile Ser Gly Ala Ile Glu Ala Lys Ala Glu Thr
            25                  30                  35

ctt gtt gct tgg cgt gtc ctt cta aca gcg gca tgc tat ttg ctt gcc   259
Leu Val Ala Trp Arg Val Leu Leu Thr Ala Ala Cys Tyr Leu Leu Ala
        40                  45                  50

ctt ctg cac cct gct ggt cgg aag gtg ttt aag gaa ttt tgg gac aca   307
Leu Leu His Pro Ala Gly Arg Lys Val Phe Lys Glu Phe Trp Asp Thr
    55                  60                  65

cta agg tcc caa cct cgt caa att ctg tac ttt atc ttc ctc gtt gta   355
Leu Arg Ser Gln Pro Arg Gln Ile Leu Tyr Phe Ile Phe Leu Val Val
70                  75                  80                  85

ctc atc acg ctt cag ctg tgg ctg ttt tct tgg tcg cct aag agt cat   403
Leu Ile Thr Leu Gln Leu Trp Leu Phe Ser Trp Ser Pro Lys Ser His
                90                  95                  100

gct tta gat gcc tca ctt ggt tac ctg tta ctg ccc att ttc cta gta   451
Ala Leu Asp Ala Ser Leu Gly Tyr Leu Leu Leu Pro Ile Phe Leu Val
            105                 110                 115

att gtg ggg cgg ttt ttc ttc gct gat tac atc acc agg ctg cag tgg   499
Ile Val Gly Arg Phe Phe Phe Ala Asp Tyr Ile Thr Arg Leu Gln Trp
        120                 125                 130

att gcg gtg gga atc gcg ctg atc gca gta acc ttg aaa ttt gtc att   547
Ile Ala Val Gly Ile Ala Leu Ile Ala Val Thr Leu Lys Phe Val Ile
    135                 140                 145

agt gcg caa tta tcg tgg gta act ttt gcc atc gct gcg ggt tat gca   595
Ser Ala Gln Leu Ser Trp Val Thr Phe Ala Ile Ala Ala Gly Tyr Ala
150                 155                 160                 165

ctg tat ttt gcg ctt cgt aaa tac tcg ggg ctg aac aac gct ttt gct   643
Leu Tyr Phe Ala Leu Arg Lys Tyr Ser Gly Leu Asn Asn Ala Phe Ala
                170                 175                 180

tac ggc gca gaa gtt tta gcg tta agt ccc ctg gca ttt ttc atg ctc   691
Tyr Gly Ala Glu Val Leu Ala Leu Ser Pro Leu Ala Phe Phe Met Leu
            185                 190                 195

gcc act gtc gag gat ccg ctg tct aac gcc atg ttg tca atg gtt att   739
Ala Thr Val Glu Asp Pro Leu Ser Asn Ala Met Leu Ser Met Val Ile
        200                 205                 210

ctg gcg ggc ctc gct ggc gca tta gct atg gcg ttg tat cta gcc gcc   787
Leu Ala Gly Leu Ala Gly Ala Leu Ala Met Ala Leu Tyr Leu Ala Ala
    215                 220                 225

tca act ctg ctt agt atg ccg atg ttt ggc ctg ctc agt tat ggt gaa   835
Ser Thr Leu Leu Ser Met Pro Met Phe Gly Leu Leu Ser Tyr Gly Glu
```

```
230                 235                 240                 245

cca atc ttg ctg ttt gtt gca gca cta tta                             865
Pro Ile Leu Leu Phe Val Ala Ala Leu Leu
                250                 255


<210> 1082
<211> 255
<212> PRT
<213> Corynebacterium glutamicum

<400> 1082
Val Ala Thr Asn Arg Thr Ser Ser Ala Gly Val Ile Thr Ser Val Leu
  1               5                  10                  15

Ala Ser Ala Leu Phe Gly Ala Ile Phe Phe Ile Ser Gly Ala Ile Glu
             20                  25                  30

Ala Lys Ala Glu Thr Leu Val Ala Trp Arg Val Leu Leu Thr Ala Ala
         35                  40                  45

Cys Tyr Leu Leu Ala Leu Leu His Pro Ala Gly Arg Lys Val Phe Lys
     50                  55                  60

Glu Phe Trp Asp Thr Leu Arg Ser Gln Pro Arg Gln Ile Leu Tyr Phe
 65                  70                  75                  80

Ile Phe Leu Val Val Leu Ile Thr Leu Gln Leu Trp Leu Phe Ser Trp
                 85                  90                  95

Ser Pro Lys Ser His Ala Leu Asp Ala Ser Leu Gly Tyr Leu Leu Leu
            100                 105                 110

Pro Ile Phe Leu Val Ile Val Gly Arg Phe Phe Phe Ala Asp Tyr Ile
        115                 120                 125

Thr Arg Leu Gln Trp Ile Ala Val Gly Ile Ala Leu Ile Ala Val Thr
    130                 135                 140

Leu Lys Phe Val Ile Ser Ala Gln Leu Ser Trp Val Thr Phe Ala Ile
145                 150                 155                 160

Ala Ala Gly Tyr Ala Leu Tyr Phe Ala Leu Arg Lys Tyr Ser Gly Leu
                165                 170                 175

Asn Asn Ala Phe Ala Tyr Gly Ala Glu Val Leu Ala Leu Ser Pro Leu
            180                 185                 190

Ala Phe Phe Met Leu Ala Thr Val Glu Asp Pro Leu Ser Asn Ala Met
        195                 200                 205

Leu Ser Met Val Ile Leu Ala Gly Leu Ala Gly Ala Leu Ala Met Ala
    210                 215                 220

Leu Tyr Leu Ala Ala Ser Thr Leu Leu Ser Met Pro Met Phe Gly Leu
225                 230                 235                 240

Leu Ser Tyr Gly Glu Pro Ile Leu Leu Phe Val Ala Ala Leu Leu
                245                 250                 255
```

<210> 1083
<211> 1029
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1006)
<223> RXN02303

<400> 1083
gcccgggccg aaatcattcc aatctcaccc ccacccaaaa cactgttgat attttcactt 60

tccaaccagc gacgtgagcg cacgcactaa ggttgtgccc atg gct gaa aac aac 115
Met Ala Glu Asn Asn
1 5

acc cca caa gaa act gaa caa gat cag gaa gca cgc ttc cgt gag gag 163
Thr Pro Gln Glu Thr Glu Gln Asp Gln Glu Ala Arg Phe Arg Glu Glu
10 15 20

ttc gag gtt ggc ggt aag gat cgt cag ctt tct gaa gaa gaa cag ctg 211
Phe Glu Val Gly Gly Lys Asp Arg Gln Leu Ser Glu Glu Glu Gln Leu
25 30 35

gag cag ctc gga tcg tat att gat gcg cac tac cct gtt cca gat ttc 259
Glu Gln Leu Gly Ser Tyr Ile Asp Ala His Tyr Pro Val Pro Asp Phe
40 45 50

acg ccc cct tgg gca ggt ggc gcc ggc gat cct gat cca gca gac cgc 307
Thr Pro Pro Trp Ala Gly Gly Ala Gly Asp Pro Asp Pro Ala Asp Arg
55 60 65

tat att gca cat ctt ccc gat cgc acc acg cat act gcg atg atc atg 355
Tyr Ile Ala His Leu Pro Asp Arg Thr Thr His Thr Ala Met Ile Met
70 75 80 85

ttg ggt tct ggc ctt gat cat tcc atg ccg ggt gtc gca ttt atc ggt 403
Leu Gly Ser Gly Leu Asp His Ser Met Pro Gly Val Ala Phe Ile Gly
90 95 100

ggt gtg agc gtc gat gac gtc ccg gag gtc gga ggc gcg att ttc cac 451
Gly Val Ser Val Asp Asp Val Pro Glu Val Gly Gly Ala Ile Phe His
105 110 115

ccg tcg aat ccg acg ggc cgc tgg gct gta tcg ttc cac agc ggt ggt 499
Pro Ser Asn Pro Thr Gly Arg Trp Ala Val Ser Phe His Ser Gly Gly
120 125 130

tgg tgg cgc ggt tcc ggt gat gcg ttg gag ttc cag tgg cgt cca gag 547
Trp Trp Arg Gly Ser Gly Asp Ala Leu Glu Phe Gln Trp Arg Pro Glu
135 140 145

gtc gcg gca gct gcg gaa ttg tcc ggc aca acc atc ctt gac ctg gac 595
Val Ala Ala Ala Ala Glu Leu Ser Gly Thr Thr Ile Leu Asp Leu Asp
150 155 160 165

tat ccg ctg gcc cca ggc cat aac ctc cac gat atg aat gag gtt gtg 643
Tyr Pro Leu Ala Pro Gly His Asn Leu His Asp Met Asn Glu Val Val
170 175 180

```
ggc aag gcg gtc ggt tac gcc cgc cac cat aat ccg gtg tcg atc acg   691
Gly Lys Ala Val Gly Tyr Ala Arg His His Asn Pro Val Ser Ile Thr
            185                 190                 195

ggt tgg ggt tat tcc tcg ggc gcg gcg tta gcc gcg att aat gca tcg   739
Gly Trp Gly Tyr Ser Ser Gly Ala Ala Leu Ala Ala Ile Asn Ala Ser
        200                 205                 210

ctt ttc gac gcc ctg gtc ctc acc ttt ccg gac ctg ggt agc gtc gag   787
Leu Phe Asp Ala Leu Val Leu Thr Phe Pro Asp Leu Gly Ser Val Glu
    215                 220                 225

aag ctc cct gcc gaa att cgt gga gac gct gta gtg ccc gcg gcg gct   835
Lys Leu Pro Ala Glu Ile Arg Gly Asp Ala Val Val Pro Ala Ala Ala
230                 235                 240                 245

gcg tgg ccg acg acc ttt gtg cag atc gcg gcg cag gat gag atc gcg   883
Ala Trp Pro Thr Thr Phe Val Gln Ile Ala Ala Gln Asp Glu Ile Ala
                250                 255                 260

gag cgg cca gga gag ctt ggc gac gcg acc gtg aag gaa tac gtt tcc   931
Glu Arg Pro Gly Glu Leu Gly Asp Ala Thr Val Lys Glu Tyr Val Ser
            265                 270                 275

cgc cac cgt att tcc aca ccg aag gtc gcg cgc gaa aaa atc acc gac   979
Arg His Arg Ile Ser Thr Pro Lys Val Ala Arg Glu Lys Ile Thr Asp
        280                 285                 290

gtg gcg gag ttc ctt aaa act gtt tgc taatgtgcca gcaggttgta        1026
Val Ala Glu Phe Leu Lys Thr Val Cys
    295                 300

aat                                                             1029


<210> 1084
<211> 302
<212> PRT
<213> Corynebacterium glutamicum

<400> 1084
Met Ala Glu Asn Asn Thr Pro Gln Glu Thr Glu Gln Asp Gln Glu Ala
  1               5                  10                  15

Arg Phe Arg Glu Glu Phe Glu Val Gly Gly Lys Asp Arg Gln Leu Ser
             20                  25                  30

Glu Glu Glu Gln Leu Glu Gln Leu Gly Ser Tyr Ile Asp Ala His Tyr
         35                  40                  45

Pro Val Pro Asp Phe Thr Pro Pro Trp Ala Gly Gly Ala Gly Asp Pro
     50                  55                  60

Asp Pro Ala Asp Arg Tyr Ile Ala His Leu Pro Asp Arg Thr Thr His
 65                  70                  75                  80

Thr Ala Met Ile Met Leu Gly Ser Gly Leu Asp His Ser Met Pro Gly
                 85                  90                  95

Val Ala Phe Ile Gly Gly Val Ser Val Asp Asp Val Pro Glu Val Gly
```

```
            100                 105                 110

Gly Ala Ile Phe His Pro Ser Asn Pro Thr Gly Arg Trp Ala Val Ser
        115                 120                 125

Phe His Ser Gly Gly Trp Trp Arg Gly Ser Gly Asp Ala Leu Glu Phe
    130                 135                 140

Gln Trp Arg Pro Glu Val Ala Ala Ala Ala Glu Leu Ser Gly Thr Thr
145                 150                 155                 160

Ile Leu Asp Leu Asp Tyr Pro Leu Ala Pro Gly His Asn Leu His Asp
                165                 170                 175

Met Asn Glu Val Val Gly Lys Ala Val Gly Tyr Ala Arg His His Asn
            180                 185                 190

Pro Val Ser Ile Thr Gly Trp Gly Tyr Ser Ser Gly Ala Ala Leu Ala
        195                 200                 205

Ala Ile Asn Ala Ser Leu Phe Asp Ala Leu Val Leu Thr Phe Pro Asp
    210                 215                 220

Leu Gly Ser Val Glu Lys Leu Pro Ala Glu Ile Arg Gly Asp Ala Val
225                 230                 235                 240

Val Pro Ala Ala Ala Ala Trp Pro Thr Thr Phe Val Gln Ile Ala Ala
                245                 250                 255

Gln Asp Glu Ile Ala Glu Arg Pro Gly Glu Leu Gly Asp Ala Thr Val
            260                 265                 270

Lys Glu Tyr Val Ser Arg His Arg Ile Ser Thr Pro Lys Val Ala Arg
        275                 280                 285

Glu Lys Ile Thr Asp Val Ala Glu Phe Leu Lys Thr Val Cys
    290                 295                 300
```

US 6,962,805 B2

<210> 1085
<211> 743
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(720)
<223> FRXA02303

<400> 1085

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gat cct gat cca gca gac cgc tat att gca cat ctt ccc gat cgc acc   48
Asp Pro Asp Pro Ala Asp Arg Tyr Ile Ala His Leu Pro Asp Arg Thr
  1               5                  10                  15

acg cat act gcg atg atc atg ttg ggt tct ggc ctt gat cat tcc atg   96
Thr His Thr Ala Met Ile Met Leu Gly Ser Gly Leu Asp His Ser Met
             20                  25                  30

ccg ggt gtc gca ttt atc ggt ggt gtg agc gtc gat gac gtc ccg gag   144
Pro Gly Val Ala Phe Ile Gly Gly Val Ser Val Asp Asp Val Pro Glu
         35                  40                  45
```

```
gtc gga ggc gcg att ttc cac ccg tcg aat ccg acg ggc cgc tgg gct   192
Val Gly Gly Ala Ile Phe His Pro Ser Asn Pro Thr Gly Arg Trp Ala
     50                  55                  60

gta tcg ttc cac agc ggt ggt tgg tgg cgc ggt tcc ggt gat gcg ttg   240
Val Ser Phe His Ser Gly Gly Trp Trp Arg Gly Ser Gly Asp Ala Leu
 65                  70                  75                  80

gag ttc cag tgg cgt cca gag gtc gcg gca gct gcg gaa ttg tcc ggc   288
Glu Phe Gln Trp Arg Pro Glu Val Ala Ala Ala Ala Glu Leu Ser Gly
                 85                  90                  95

aca acc atc ctt gac ctg gac tat ccg ctg gcc cca ggc cat aac ctc   336
Thr Thr Ile Leu Asp Leu Asp Tyr Pro Leu Ala Pro Gly His Asn Leu
            100                 105                 110

cac gat atg aat gag gtt gtg ggc aag gcg gtc ggt tac gcc cgc cac   384
His Asp Met Asn Glu Val Val Gly Lys Ala Val Gly Tyr Ala Arg His
        115                 120                 125

cat aat ccg gtg tcg atc acg ggt tgg ggt tat tcc tcg ggc gcg gcg   432
His Asn Pro Val Ser Ile Thr Gly Trp Gly Tyr Ser Ser Gly Ala Ala
    130                 135                 140

tta gcc gcg att aat gca tcg ctt ttc gac gcc ctg gtc ctc acc ttt   480
Leu Ala Ala Ile Asn Ala Ser Leu Phe Asp Ala Leu Val Leu Thr Phe
145                 150                 155                 160

ccg gac ctg ggt agc gtc gag aag ctc cct gcc gaa att cgt gga gac   528
Pro Asp Leu Gly Ser Val Glu Lys Leu Pro Ala Glu Ile Arg Gly Asp
                165                 170                 175

gct gta gtg ccc gcg gcg gct gcg tgg ccg acg acc ttt gtg cag atc   576
Ala Val Val Pro Ala Ala Ala Ala Trp Pro Thr Thr Phe Val Gln Ile
            180                 185                 190

gcg gcg cag gat gag atc gcg gag cgg cca gga gag ctt ggc gac gcg   624
Ala Ala Gln Asp Glu Ile Ala Glu Arg Pro Gly Glu Leu Gly Asp Ala
        195                 200                 205

acc gtg aag gaa tac gtt tcc cgc cac cgt att tcc aca ccg aag gtc   672
Thr Val Lys Glu Tyr Val Ser Arg His Arg Ile Ser Thr Pro Lys Val
    210                 215                 220

gcg cgc gaa aaa atc acc gac gtg gcg gag ttc ctt aaa act gtt tgc   720
Ala Arg Glu Lys Ile Thr Asp Val Ala Glu Phe Leu Lys Thr Val Cys
225                 230                 235                 240

taatgtgcca gcaggttgta aat                                        743
```

<210> 1086
<211> 240
<212> PRT
<213> Corynebacterium glutamicum

<400> 1086

```
Asp Pro Asp Pro Ala Asp Arg Tyr Ile Ala His Leu Pro Asp Arg Thr
  1               5                  10                  15
```

```
Thr His Thr Ala Met Ile Met Leu Gly Ser Gly Leu Asp His Ser Met
            20                  25                  30

Pro Gly Val Ala Phe Ile Gly Gly Val Ser Val Asp Asp Val Pro Glu
        35                  40                  45

Val Gly Gly Ala Ile Phe His Pro Ser Asn Pro Thr Gly Arg Trp Ala
    50                  55                  60

Val Ser Phe His Ser Gly Gly Trp Trp Arg Gly Ser Gly Asp Ala Leu
65                  70                  75                  80

Glu Phe Gln Trp Arg Pro Glu Val Ala Ala Ala Ala Glu Leu Ser Gly
                85                  90                  95

Thr Thr Ile Leu Asp Leu Asp Tyr Pro Leu Ala Pro Gly His Asn Leu
            100                 105                 110

His Asp Met Asn Glu Val Val Gly Lys Ala Val Gly Tyr Ala Arg His
        115                 120                 125

His Asn Pro Val Ser Ile Thr Gly Trp Gly Tyr Ser Ser Gly Ala Ala
    130                 135                 140

Leu Ala Ala Ile Asn Ala Ser Leu Phe Asp Ala Leu Val Leu Thr Phe
145                 150                 155                 160

Pro Asp Leu Gly Ser Val Glu Lys Leu Pro Ala Glu Ile Arg Gly Asp
                165                 170                 175

Ala Val Val Pro Ala Ala Ala Ala Trp Pro Thr Thr Phe Val Gln Ile
            180                 185                 190

Ala Ala Gln Asp Glu Ile Ala Glu Arg Pro Gly Glu Leu Gly Asp Ala
        195                 200                 205

Thr Val Lys Glu Tyr Val Ser Arg His Arg Ile Ser Thr Pro Lys Val
    210                 215                 220

Ala Arg Glu Lys Ile Thr Asp Val Ala Glu Phe Leu Lys Thr Val Cys
225                 230                 235                 240
```

09605 = 09605 = 09605 = 09605

<210> 1087
<211> 744
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(721)
<223> RXN02307

<400> 1087
ttttgcatta accccaggta ggggcattgt cgcaaagccc aactacagca aggtgcgtac 60

gctggtggcc aactgaatac gtttgaggag aaggttttct atg agt ggc acc gcc 115
Met Ser Gly Thr Ala

```
                                                    1               5

atc atg tac gac acg aca gtt gtt cca tcg aag aaa gaa atc gcg cag   163
Ile Met Tyr Asp Thr Thr Val Val Pro Ser Lys Lys Glu Ile Ala Gln
                  10                  15                  20

gct tgg act ggt tat gtg gat ctt cag gga agc tac cgc ctg gta gat   211
Ala Trp Thr Gly Tyr Val Asp Leu Gln Gly Ser Tyr Arg Leu Val Asp
             25                  30                  35

acg gtg gat ggg gaa gtt ggc gtt gag gtg ctg att tcc aag gat cgg   259
Thr Val Asp Gly Glu Val Gly Val Glu Val Leu Ile Ser Lys Asp Arg
         40                  45                  50

gag ggg cgt tta ctc cag att ccg ttt agt tat cgt tcg gca gag att   307
Glu Gly Arg Leu Leu Gln Ile Pro Phe Ser Tyr Arg Ser Ala Glu Ile
     55                  60                  65

aac cca gag cag aca ctt tcc aca ttg gag cat ggt gtg ttg ggc aag   355
Asn Pro Glu Gln Thr Leu Ser Thr Leu Glu His Gly Val Leu Gly Lys
 70                  75                  80                  85

cgt tgg gtg act aat gcg ttg ggt gac ccg gtg gca gtg cgg gag ttt   403
Arg Trp Val Thr Asn Ala Leu Gly Asp Pro Val Ala Val Arg Glu Phe
                 90                  95                 100

att cgc act att ttg acg ggc gat gat ggt gca gct cgt agc gat ggc   451
Ile Arg Thr Ile Leu Thr Gly Asp Asp Gly Ala Ala Arg Ser Asp Gly
            105                 110                 115

gtg aag ggc tat ctg gat att aaa ggt tcc ggc gat gct gag tcg gtg   499
Val Lys Gly Tyr Leu Asp Ile Lys Gly Ser Gly Asp Ala Glu Ser Val
        120                 125                 130

gat tta cag gat gta aag ctt act gag gtt aca agg cag cgt gcg att   547
Asp Leu Gln Asp Val Lys Leu Thr Glu Val Thr Arg Gln Arg Ala Ile
    135                 140                 145

ggt tcg gta acc atc aac ggt gag cga aag caa ttc tcg ctg cgg ttg   595
Gly Ser Val Thr Ile Asn Gly Glu Arg Lys Gln Phe Ser Leu Arg Leu
150                 155                 160                 165

cct cag ttg ctg aag aat ttc agg gag aca gcc gcg ggc cat aca gct   643
Pro Gln Leu Leu Lys Asn Phe Arg Glu Thr Ala Ala Gly His Thr Ala
                170                 175                 180

acg act ctt cgt att gtg gcg act cat ccg gaa aag gac gat gtt gag   691
Thr Thr Leu Arg Ile Val Ala Thr His Pro Glu Lys Asp Asp Val Glu
            185                 190                 195

ctg ctg gtc gct gag ttc aac tgg atg gaa taatccgaga cagctcctga     741
Leu Leu Val Ala Glu Phe Asn Trp Met Glu
        200                 205

aag                                                               744
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<210> 1088
<211> 207
<212> PRT
<213> Corynebacterium glutamicum

<400> 1088
Met Ser Gly Thr Ala Ile Met Tyr Asp Thr Thr Val Val Pro Ser Lys
1 5 10 15

Lys Glu Ile Ala Gln Ala Trp Thr Gly Tyr Val Asp Leu Gln Gly Ser
20 25 30

Tyr Arg Leu Val Asp Thr Val Asp Gly Glu Val Gly Val Glu Val Leu
35 40 45

Ile Ser Lys Asp Arg Glu Gly Arg Leu Leu Gln Ile Pro Phe Ser Tyr
50 55 60

Arg Ser Ala Glu Ile Asn Pro Glu Gln Thr Leu Ser Thr Leu Glu His
65 70 75 80

Gly Val Leu Gly Lys Arg Trp Val Thr Asn Ala Leu Gly Asp Pro Val
85 90 95

Ala Val Arg Glu Phe Ile Arg Thr Ile Leu Thr Gly Asp Asp Gly Ala
100 105 110

Ala Arg Ser Asp Gly Val Lys Gly Tyr Leu Asp Ile Lys Gly Ser Gly
115 120 125

Asp Ala Glu Ser Val Asp Leu Gln Asp Val Lys Leu Thr Glu Val Thr
130 135 140

Arg Gln Arg Ala Ile Gly Ser Val Thr Ile Asn Gly Glu Arg Lys Gln
145 150 155 160

Phe Ser Leu Arg Leu Pro Gln Leu Leu Lys Asn Phe Arg Glu Thr Ala
165 170 175

Ala Gly His Thr Ala Thr Thr Leu Arg Ile Val Ala Thr His Pro Glu
180 185 190

Lys Asp Asp Val Glu Leu Leu Val Ala Glu Phe Asn Trp Met Glu
195 200 205

<210> 1089
<211> 490
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(490)
<223> FRXA02307

<400> 1089
ttttgcatta accccaggta ggggcattgt cgcaaagccc aactacagca aggtgcgtac 60

gctggtggcc aactgaatac gtttgaggag aaggttttct atg agt ggc acc gcc 115
Met Ser Gly Thr Ala
1 5

atc atg tac gac acg aca gtt gtt cca tcg aag aaa gaa atc gcg cag 163
Ile Met Tyr Asp Thr Thr Val Val Pro Ser Lys Lys Glu Ile Ala Gln

```
                  10                  15                  20

gct tgg act ggt tat gtg gat ctt cag gga agc tac cgc ctg gta gat   211
Ala Trp Thr Gly Tyr Val Asp Leu Gln Gly Ser Tyr Arg Leu Val Asp
             25                  30                  35

acg gtg gat ggg gaa gtt ggc gtt gag gtg ctg att tcc aag gat cgg   259
Thr Val Asp Gly Glu Val Gly Val Glu Val Leu Ile Ser Lys Asp Arg
         40                  45                  50

gag ggg cgt tta ctc cag att ccg ttt agt tat cgt tcg gca gag att   307
Glu Gly Arg Leu Leu Gln Ile Pro Phe Ser Tyr Arg Ser Ala Glu Ile
     55                  60                  65

aac cca gag cag aca ctt tcc aca ttg gag cat ggt gtg ttg ggc aag   355
Asn Pro Glu Gln Thr Leu Ser Thr Leu Glu His Gly Val Leu Gly Lys
 70                  75                  80                  85

cgt tgg gtg act aat gcg ttg ggt gac ccg gtg gca gtg cgg gag ttt   403
Arg Trp Val Thr Asn Ala Leu Gly Asp Pro Val Ala Val Arg Glu Phe
                 90                  95                 100

att cgc act att ttg acg ggc gat gat ggt gca gct cgt agc gat ggc   451
Ile Arg Thr Ile Leu Thr Gly Asp Asp Gly Ala Ala Arg Ser Asp Gly
            105                 110                 115

gtg aag ggc tat ctg gat att aaa ggt tcc ggc gat gct               490
Val Lys Gly Tyr Leu Asp Ile Lys Gly Ser Gly Asp Ala
        120                 125                 130


<210> 1090
<211> 130
<212> PRT
<213> Corynebacterium glutamicum

<400> 1090
Met Ser Gly Thr Ala Ile Met Tyr Asp Thr Thr Val Val Pro Ser Lys
  1               5                  10                  15

Lys Glu Ile Ala Gln Ala Trp Thr Gly Tyr Val Asp Leu Gln Gly Ser
             20                  25                  30

Tyr Arg Leu Val Asp Thr Val Asp Gly Glu Val Gly Val Glu Val Leu
         35                  40                  45

Ile Ser Lys Asp Arg Glu Gly Arg Leu Leu Gln Ile Pro Phe Ser Tyr
     50                  55                  60

Arg Ser Ala Glu Ile Asn Pro Glu Gln Thr Leu Ser Thr Leu Glu His
 65                  70                  75                  80

Gly Val Leu Gly Lys Arg Trp Val Thr Asn Ala Leu Gly Asp Pro Val
                 85                  90                  95

Ala Val Arg Glu Phe Ile Arg Thr Ile Leu Thr Gly Asp Asp Gly Ala
            100                 105                 110

Ala Arg Ser Asp Gly Val Lys Gly Tyr Leu Asp Ile Lys Gly Ser Gly
        115                 120                 125
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```
Asp Ala
    130


<210> 1091
<211> 564
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(541)
<223> RXN02314

<400> 1091
tgataccacc gaagtatccg gattcaccat tattgaagct tcgaccgtcc gagatacccg 60

ccgtgcacaa cagcaagctc tcatggacac ggtgcactaa atg gag tgg tac caa   115
                                              Met Glu Trp Tyr Gln
                                                1               5

gtg cgc cga cgg gcc cga caa ctg ctc att gtc ctt ttt ata gca gcg   163
Val Arg Arg Arg Ala Arg Gln Leu Leu Ile Val Leu Phe Ile Ala Ala
                  10                  15                  20

atg ctc gga gca gcc tcc atg gtg atc ggg cca ttc ctt aac gac cgc   211
Met Leu Gly Ala Ala Ser Met Val Ile Gly Pro Phe Leu Asn Asp Arg
              25                  30                  35

act atc gaa ggc aac tcc ggg cgc gcc ttg gca caa gta acc aac gtc   259
Thr Ile Glu Gly Asn Ser Gly Arg Ala Leu Ala Gln Val Thr Asn Val
          40                  45                  50

ggc agc tac cgc aca acg gtg gat ttc caa gat gaa aac ggc atc tat   307
Gly Ser Tyr Arg Thr Thr Val Asp Phe Gln Asp Glu Asn Gly Ile Tyr
      55                  60                  65

cac tca cca gcc acc ggc ctg ttg ttc ccc acg gga ctg ggc gag ggg   355
His Ser Pro Ala Thr Gly Leu Leu Phe Pro Thr Gly Leu Gly Glu Gly
  70                  75                  80                  85

caa cgc gtg tgg gtg aac tac gcc aaa tca gat cca gac ctg gtc aaa   403
Gln Arg Val Trp Val Asn Tyr Ala Lys Ser Asp Pro Asp Leu Val Lys
                  90                  95                 100

gta gaa ggc cgc aag tgg aca ctg tcc atc atc cca gcg ctt agt gtc   451
Val Glu Gly Arg Lys Trp Thr Leu Ser Ile Ile Pro Ala Leu Ser Val
             105                 110                 115

gca gct gtc gcc acc gct acc tgg tca gta cta tgg ctg gga gtg ggc   499
Ala Ala Val Ala Thr Ala Thr Trp Ser Val Leu Trp Leu Gly Val Gly
         120                 125                 130

aga ttc gga aga cga tcc gac gac gcc aac gaa acc aca gtg           541
Arg Phe Gly Arg Arg Ser Asp Asp Ala Asn Glu Thr Thr Val
     135                 140                 145

taaagctcta tgccgggagc att                                        564


<210> 1092
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<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 1092
Met Glu Trp Tyr Gln Val Arg Arg Arg Ala Arg Gln Leu Leu Ile Val
1 5 10 15

Leu Phe Ile Ala Ala Met Leu Gly Ala Ala Ser Met Val Ile Gly Pro
20 25 30

Phe Leu Asn Asp Arg Thr Ile Glu Gly Asn Ser Gly Arg Ala Leu Ala
35 40 45

Gln Val Thr Asn Val Gly Ser Tyr Arg Thr Thr Val Asp Phe Gln Asp
50 55 60

Glu Asn Gly Ile Tyr His Ser Pro Ala Thr Gly Leu Leu Phe Pro Thr
65 70 75 80

Gly Leu Gly Glu Gly Gln Arg Val Trp Val Asn Tyr Ala Lys Ser Asp
85 90 95

Pro Asp Leu Val Lys Val Glu Gly Arg Lys Trp Thr Leu Ser Ile Ile
100 105 110

Pro Ala Leu Ser Val Ala Ala Val Ala Thr Ala Thr Trp Ser Val Leu
115 120 125

Trp Leu Gly Val Gly Arg Phe Gly Arg Arg Ser Asp Asp Ala Asn Glu
130 135 140

Thr Thr Val
145

<210> 1093
<211> 564
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(541)
<223> FRXA02314

<400> 1093
tgataccacc gaagtatccg gattcaccat tattgaagct tcgaccgtcc gagatacccg 60

ccgtgcacaa cagcaagctc tcatggacac ggtgcactaa atg gag tgg tac caa 115
Met Glu Trp Tyr Gln
1 5

gtg cgc cga cgg gcc cga caa ctg ctc att gtc ctt ttt ata gca gcg 163
Val Arg Arg Arg Ala Arg Gln Leu Leu Ile Val Leu Phe Ile Ala Ala
10 15 20

atg ctc gga gca gcc tcc atg gtg atc ggg cca ttc ctt aac gac cgc 211
Met Leu Gly Ala Ala Ser Met Val Ile Gly Pro Phe Leu Asn Asp Arg
25 30 35

```
act atc gaa ggc aac tcc ggg cgc gcc ttg gca caa gta acc aac gtc   259
Thr Ile Glu Gly Asn Ser Gly Arg Ala Leu Ala Gln Val Thr Asn Val
         40                  45                  50

ggc agc tac cgc aca acg gtg gat ttc caa gat gaa aac ggc atc tat   307
Gly Ser Tyr Arg Thr Thr Val Asp Phe Gln Asp Glu Asn Gly Ile Tyr
     55                  60                  65

cac tca cca gcc acc ggc ctg ttg ttc ccc acg gga ctg ggc gag ggg   355
His Ser Pro Ala Thr Gly Leu Leu Phe Pro Thr Gly Leu Gly Glu Gly
 70                  75                  80                  85

caa cgc gtg tgg gtg aac tac gcc aaa tca gat cca gac ctg gtc aaa   403
Gln Arg Val Trp Val Asn Tyr Ala Lys Ser Asp Pro Asp Leu Val Lys
                 90                  95                 100

gta gaa ggc cgc aag tgg aca ctg tcc atc atc cca gcg ctt agt gtc   451
Val Glu Gly Arg Lys Trp Thr Leu Ser Ile Ile Pro Ala Leu Ser Val
            105                 110                 115

gca gct gtc gcc acc gct acc tgg tca gta cta tgg ctg gga gtg ggc   499
Ala Ala Val Ala Thr Ala Thr Trp Ser Val Leu Trp Leu Gly Val Gly
        120                 125                 130

aga ttc gga aga cga tcc gac gac gcc aac gaa acc aca gtg           541
Arg Phe Gly Arg Arg Ser Asp Asp Ala Asn Glu Thr Thr Val
    135                 140                 145

taaagctcta tgccgggagc att                                        564


<210> 1094
<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 1094
Met Glu Trp Tyr Gln Val Arg Arg Arg Ala Arg Gln Leu Leu Ile Val
  1               5                  10                  15

Leu Phe Ile Ala Ala Met Leu Gly Ala Ala Ser Met Val Ile Gly Pro
            20                  25                  30

Phe Leu Asn Asp Arg Thr Ile Glu Gly Asn Ser Gly Arg Ala Leu Ala
        35                  40                  45

Gln Val Thr Asn Val Gly Ser Tyr Arg Thr Thr Val Asp Phe Gln Asp
    50                  55                  60

Glu Asn Gly Ile Tyr His Ser Pro Ala Thr Gly Leu Leu Phe Pro Thr
65                  70                  75                  80

Gly Leu Gly Glu Gly Gln Arg Val Trp Val Asn Tyr Ala Lys Ser Asp
                85                  90                  95

Pro Asp Leu Val Lys Val Glu Gly Arg Lys Trp Thr Leu Ser Ile Ile
            100                 105                 110

Pro Ala Leu Ser Val Ala Ala Val Ala Thr Ala Thr Trp Ser Val Leu
        115                 120                 125
```

```
Trp Leu Gly Val Gly Arg Phe Gly Arg Arg Ser Asp Asp Ala Asn Glu
    130                 135                 140

Thr Thr Val
145
```

<210> 1095
<211> 1446
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1423)
<223> RXN02337

<400> 1095

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cacaaggtaa aatttgtgta attgtgtcgt gtggatttga aggtttttgt aaatctagtt 60

aaatcatgag gtcataagct tttcgggagg ttgtcaaagg atg tcg aag ctt tac   115
                                              Met Ser Lys Leu Tyr
                                                1               5

gcg ggg gca agg atc aat gca ctg cgc cga acc cat cag ctc acc caa   163
Ala Gly Ala Arg Ile Asn Ala Leu Arg Arg Thr His Gln Leu Thr Gln
                10                  15                  20

tca gca ttg gcc gac aag ctt gat ctc tcc acc agc tat ctc aac cag   211
Ser Ala Leu Ala Asp Lys Leu Asp Leu Ser Thr Ser Tyr Leu Asn Gln
            25                  30                  35

ttg gaa aat gac gga cgg cca ctc act gcc acg gtg ctt ctg cag ctg   259
Leu Glu Asn Asp Gly Arg Pro Leu Thr Ala Thr Val Leu Leu Gln Leu
        40                  45                  50

atg aaa gtg ttc gat gtt gag gcc agt tac ttc tcc cct gac cgg ggt   307
Met Lys Val Phe Asp Val Glu Ala Ser Tyr Phe Ser Pro Asp Arg Gly
    55                  60                  65

acg gcc act gct acc cga ctg gct gaa acc ttg gcg atg aat cag ggt   355
Thr Ala Thr Ala Thr Arg Leu Ala Glu Thr Leu Ala Met Asn Gln Gly
70                  75                  80                  85

ccg acg atg tcg atg gat gat ctt tta gat ttc gcg gat cgt ttc cct   403
Pro Thr Met Ser Met Asp Asp Leu Leu Asp Phe Ala Asp Arg Phe Pro
                90                  95                  100

cag tta gcg cag cat att atc cag cct gct gag gtt gat ccc acg cat   451
Gln Leu Ala Gln His Ile Ile Gln Pro Ala Glu Val Asp Pro Thr His
            105                 110                 115

agt tct gcg cat gat ttt gtt cgg gat tat ttt gcc acc cac aaa aac   499
Ser Ser Ala His Asp Phe Val Arg Asp Tyr Phe Ala Thr His Lys Asn
        120                 125                 130

tac att gat tcg ctc gat cgc ctt gga gag gag ttg gca act gcc att   547
Tyr Ile Asp Ser Leu Asp Arg Leu Gly Glu Glu Leu Ala Thr Ala Ile
    135                 140                 145

ggt cag ccg gga ctt cgg gtt act agg ctc gcg cag ttg ctt gat gcg   595
```

```
Gly Gln Pro Gly Leu Arg Val Thr Arg Leu Ala Gln Leu Leu Asp Ala
150                 155                 160                 165

gag tac aac atc acg gtg cgt ttc cgg gcg ccg gat att act ggc cgg   643
Glu Tyr Asn Ile Thr Val Arg Phe Arg Ala Pro Asp Ile Thr Gly Arg
                170                 175                 180

agg cac ttt gat ccc caa tcg cgt cag att ctg ctg cgg caa gat ctc   691
Arg His Phe Asp Pro Gln Ser Arg Gln Ile Leu Leu Arg Gln Asp Leu
            185                 190                 195

agc gag gcg cag cag tgt ttc cag ttg gcg gag gaa ttg acg ttt ctt   739
Ser Glu Ala Gln Gln Cys Phe Gln Leu Ala Glu Glu Leu Thr Phe Leu
        200                 205                 210

gct cat gca gag ctc ttg gat acc ctg acc aca gat caa ccg gat ctc   787
Ala His Ala Glu Leu Leu Asp Thr Leu Thr Thr Asp Gln Pro Asp Leu
    215                 220                 225

cct tct gag gca gct atc cgc ctg gct aag gtg ggt ctc tcc caa tat   835
Pro Ser Glu Ala Ala Ile Arg Leu Ala Lys Val Gly Leu Ser Gln Tyr
230                 235                 240                 245

ttc gcg gct gct gtt gtc atg ccg tac acc cgc ttt ttg gaa ttc gcc   883
Phe Ala Ala Ala Val Val Met Pro Tyr Thr Arg Phe Leu Glu Phe Ala
                250                 255                 260

cag gat aag cac tat gac atc gag ttg atc tct gag gcg ttt gga gtg   931
Gln Asp Lys His Tyr Asp Ile Glu Leu Ile Ser Glu Ala Phe Gly Val
            265                 270                 275

tct ttc gag tct gca tgc cac cgc ctg tct act ctg cag cgt tcg ggg   979
Ser Phe Glu Ser Ala Cys His Arg Leu Ser Thr Leu Gln Arg Ser Gly
        280                 285                 290

gcg tca ggg gtg ccg ttt ttc ttt gtg cgc tcg gat cgt gca gga aat   1027
Ala Ser Gly Val Pro Phe Phe Phe Val Arg Ser Asp Arg Ala Gly Asn
    295                 300                 305

atc tcc aag cgg caa tct gca gct acg ttc cac ttc tcg cga aca gac   1075
Ile Ser Lys Arg Gln Ser Ala Ala Thr Phe His Phe Ser Arg Thr Asp
310                 315                 320                 325

ggc act tgt cct ttg tgg gcg ctg cat cgt gct ttt gaa cgt cag gga   1123
Gly Thr Cys Pro Leu Trp Ala Leu His Arg Ala Phe Glu Arg Gln Gly
                330                 335                 340

aac atc acc cgc cag gtt gct cgc atg ccg gat ggc cgg acc tat ttg   1171
Asn Ile Thr Arg Gln Val Ala Arg Met Pro Asp Gly Arg Thr Tyr Leu
            345                 350                 355

tgg ctc gca cgc gcg gtg aaa ggt cga act cat ggt ttc ggg tat cct   1219
Trp Leu Ala Arg Ala Val Lys Gly Arg Thr His Gly Phe Gly Tyr Pro
        360                 365                 370

gct gcg gaa ttc gcc atc ggc ctg ggc tgc gat atc agc gag gca cca   1267
Ala Ala Glu Phe Ala Ile Gly Leu Gly Cys Asp Ile Ser Glu Ala Pro
    375                 380                 385

ggc ttg gtg tat tcc caa ggc ctt aat ttg gat ccc gag tcc gcc gca   1315
Gly Leu Val Tyr Ser Gln Gly Leu Asn Leu Asp Pro Glu Ser Ala Ala
```

```
390                 395                 400                 405

gag atc ggc cct ggt tgt cgg atc tgt cct cgg gag aac tgt gtg cag   1363
Glu Ile Gly Pro Gly Cys Arg Ile Cys Pro Arg Glu Asn Cys Val Gln
                410                 415                 420

cgt gca ttc cca cca tcg ggt caa gaa tct atc cgc cca gcc cct gtc   1411
Arg Ala Phe Pro Pro Ser Gly Gln Glu Ser Ile Arg Pro Ala Pro Val
            425                 430                 435

caa ctc ctc aac taaaaaggca gcacttaaaa aac                        1446
Gln Leu Leu Asn
        440
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<210> 1096
<211> 441
<212> PRT
<213> Corynebacterium glutamicum

<400> 1096

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Met Ser Lys Leu Tyr Ala Gly Ala Arg Ile Asn Ala Leu Arg Arg Thr
  1               5                  10                  15

His Gln Leu Thr Gln Ser Ala Leu Ala Asp Lys Leu Asp Leu Ser Thr
            20                  25                  30

Ser Tyr Leu Asn Gln Leu Glu Asn Asp Gly Arg Pro Leu Thr Ala Thr
        35                  40                  45

Val Leu Leu Gln Leu Met Lys Val Phe Asp Val Glu Ala Ser Tyr Phe
    50                  55                  60

Ser Pro Asp Arg Gly Thr Ala Thr Ala Thr Arg Leu Ala Glu Thr Leu
65                  70                  75                  80

Ala Met Asn Gln Gly Pro Thr Met Ser Met Asp Asp Leu Leu Asp Phe
                85                  90                  95

Ala Asp Arg Phe Pro Gln Leu Ala Gln His Ile Ile Gln Pro Ala Glu
            100                 105                 110

Val Asp Pro Thr His Ser Ser Ala His Asp Phe Val Arg Asp Tyr Phe
        115                 120                 125

Ala Thr His Lys Asn Tyr Ile Asp Ser Leu Asp Arg Leu Gly Glu Glu
    130                 135                 140

Leu Ala Thr Ala Ile Gly Gln Pro Gly Leu Arg Val Thr Arg Leu Ala
145                 150                 155                 160

Gln Leu Leu Asp Ala Glu Tyr Asn Ile Thr Val Arg Phe Arg Ala Pro
                165                 170                 175

Asp Ile Thr Gly Arg Arg His Phe Asp Pro Gln Ser Arg Gln Ile Leu
            180                 185                 190

Leu Arg Gln Asp Leu Ser Glu Ala Gln Gln Cys Phe Gln Leu Ala Glu
        195                 200                 205

Glu Leu Thr Phe Leu Ala His Ala Glu Leu Leu Asp Thr Leu Thr Thr
```

```
    210                 215                 220

Asp Gln Pro Asp Leu Pro Ser Glu Ala Ala Ile Arg Leu Ala Lys Val
225                 230                 235                 240

Gly Leu Ser Gln Tyr Phe Ala Ala Ala Val Val Met Pro Tyr Thr Arg
                245                 250                 255

Phe Leu Glu Phe Ala Gln Asp Lys His Tyr Asp Ile Glu Leu Ile Ser
            260                 265                 270

Glu Ala Phe Gly Val Ser Phe Glu Ser Ala Cys His Arg Leu Ser Thr
        275                 280                 285

Leu Gln Arg Ser Gly Ala Ser Gly Val Pro Phe Phe Phe Val Arg Ser
    290                 295                 300

Asp Arg Ala Gly Asn Ile Ser Lys Arg Gln Ser Ala Ala Thr Phe His
305                 310                 315                 320

Phe Ser Arg Thr Asp Gly Thr Cys Pro Leu Trp Ala Leu His Arg Ala
                325                 330                 335

Phe Glu Arg Gln Gly Asn Ile Thr Arg Gln Val Ala Arg Met Pro Asp
            340                 345                 350

Gly Arg Thr Tyr Leu Trp Leu Ala Arg Ala Val Lys Gly Arg Thr His
        355                 360                 365

Gly Phe Gly Tyr Pro Ala Ala Glu Phe Ala Ile Gly Leu Gly Cys Asp
    370                 375                 380

Ile Ser Glu Ala Pro Gly Leu Val Tyr Ser Gln Gly Leu Asn Leu Asp
385                 390                 395                 400

Pro Glu Ser Ala Ala Glu Ile Gly Pro Gly Cys Arg Ile Cys Pro Arg
                405                 410                 415

Glu Asn Cys Val Gln Arg Ala Phe Pro Pro Ser Gly Gln Glu Ser Ile
            420                 425                 430

Arg Pro Ala Pro Val Gln Leu Leu Asn
        435                 440
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<210> 1097
<211> 1024
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1024)
<223> FRXA02337

<400> 1097
cacaaggtaa aatttgtgta attgtgtcgt gtggatttga aggtttttgt aaatctagtt 60

aaatcatgag gtcataagct tttcgggagg ttgtcaaagg atg tcg aag ctt tac 115
                                                Met Ser Lys Leu Tyr
                                                  1   5

```
gcg ggg gca agg atc aat gca ctg cgc cga acc cat cag ctc acc caa   163
Ala Gly Ala Arg Ile Asn Ala Leu Arg Arg Thr His Gln Leu Thr Gln
                 10                  15                  20

tca gca ttg gcc gac aag ctt gat ctc tcc acc agc tat ctc aac cag   211
Ser Ala Leu Ala Asp Lys Leu Asp Leu Ser Thr Ser Tyr Leu Asn Gln
             25                  30                  35

ttg gaa aat gac gga cgg cca ctc act gcc acg gtg ctt ctg cag ctg   259
Leu Glu Asn Asp Gly Arg Pro Leu Thr Ala Thr Val Leu Leu Gln Leu
         40                  45                  50

atg aaa gtg ttc gat gtt gag gcc agt tac ttc tcc cct gac cgg ggt   307
Met Lys Val Phe Asp Val Glu Ala Ser Tyr Phe Ser Pro Asp Arg Gly
     55                  60                  65

acg gcc act gct acc cga ctg gct gaa acc ttg gcg atg aat cag ggt   355
Thr Ala Thr Ala Thr Arg Leu Ala Glu Thr Leu Ala Met Asn Gln Gly
 70                  75                  80                  85

ccg acg atg tcg atg gat gat ctt tta gat ttc gcg gat cgt ttc cct   403
Pro Thr Met Ser Met Asp Asp Leu Leu Asp Phe Ala Asp Arg Phe Pro
                 90                  95                 100

cag tta gcg cag cat att atc cag cct gct gag gtt gat ccc acg cat   451
Gln Leu Ala Gln His Ile Ile Gln Pro Ala Glu Val Asp Pro Thr His
             105                 110                 115

agt tct gcg cat gat ttt gtt cgg gat tat ttt gcc acc cac aaa aac   499
Ser Ser Ala His Asp Phe Val Arg Asp Tyr Phe Ala Thr His Lys Asn
         120                 125                 130

tac att gat tcg ctc gat cgc ctt gga gag gag ttg gca act gcc att   547
Tyr Ile Asp Ser Leu Asp Arg Leu Gly Glu Glu Leu Ala Thr Ala Ile
     135                 140                 145

ggt cag ccg gga ctt cgg gtt act agg ctc gcg cag ttg ctt gat gcg   595
Gly Gln Pro Gly Leu Arg Val Thr Arg Leu Ala Gln Leu Leu Asp Ala
150                 155                 160                 165

gag tac aac atc acg gtg cgt ttc cgg gcg ccg gat att act ggc cgg   643
Glu Tyr Asn Ile Thr Val Arg Phe Arg Ala Pro Asp Ile Thr Gly Arg
                 170                 175                 180

agg cac ttt gat ccc caa tcg cgt cag att ctg ctg cgg caa gat ctc   691
Arg His Phe Asp Pro Gln Ser Arg Gln Ile Leu Leu Arg Gln Asp Leu
             185                 190                 195

agc gag gcg cag cag tgt ttc cag ttg gcg gag gaa ttg acg ttt ctt   739
Ser Glu Ala Gln Gln Cys Phe Gln Leu Ala Glu Glu Leu Thr Phe Leu
         200                 205                 210

gct cat gca gag ctc ttg gat acc ctg acc aca gat caa ccg gat ctc   787
Ala His Ala Glu Leu Leu Asp Thr Leu Thr Thr Asp Gln Pro Asp Leu
     215                 220                 225

cct tct gag gca gct atc cgc ctg gct aag gtg ggt ctc tcc caa tat   835
Pro Ser Glu Ala Ala Ile Arg Leu Ala Lys Val Gly Leu Ser Gln Tyr
230                 235                 240                 245
```

```
ttc gcg gct gct gtt gtc atg ccg tac acc cgc ttt ttg gaa ttc gcc   883
Phe Ala Ala Ala Val Val Met Pro Tyr Thr Arg Phe Leu Glu Phe Ala
                250                 255                 260

cag gat aag cac tat gac atc gag ttg atc tct gag gcg ttt gga gtg   931
Gln Asp Lys His Tyr Asp Ile Glu Leu Ile Ser Glu Ala Phe Gly Val
            265                 270                 275

tct ttc gag tct gca tgc cac cgc ctg tct act ctg cag cgt tcg ggg   979
Ser Phe Glu Ser Ala Cys His Arg Leu Ser Thr Leu Gln Arg Ser Gly
        280                 285                 290

gcg tca ggg gtg ccg ttt ttc ttt gtg cgc tcg gat cgt gca gga       1024
Ala Ser Gly Val Pro Phe Phe Phe Val Arg Ser Asp Arg Ala Gly
    295                 300                 305


<210> 1098
<211> 308
<212> PRT
<213> Corynebacterium glutamicum

<400> 1098
Met Ser Lys Leu Tyr Ala Gly Ala Arg Ile Asn Ala Leu Arg Arg Thr
  1               5                  10                  15

His Gln Leu Thr Gln Ser Ala Leu Ala Asp Lys Leu Asp Leu Ser Thr
             20                  25                  30

Ser Tyr Leu Asn Gln Leu Glu Asn Asp Gly Arg Pro Leu Thr Ala Thr
         35                  40                  45

Val Leu Leu Gln Leu Met Lys Val Phe Asp Val Glu Ala Ser Tyr Phe
     50                  55                  60

Ser Pro Asp Arg Gly Thr Ala Thr Ala Thr Arg Leu Ala Glu Thr Leu
 65                  70                  75                  80

Ala Met Asn Gln Gly Pro Thr Met Ser Met Asp Asp Leu Leu Asp Phe
                 85                  90                  95

Ala Asp Arg Phe Pro Gln Leu Ala Gln His Ile Ile Gln Pro Ala Glu
            100                 105                 110

Val Asp Pro Thr His Ser Ser Ala His Asp Phe Val Arg Asp Tyr Phe
        115                 120                 125

Ala Thr His Lys Asn Tyr Ile Asp Ser Leu Asp Arg Leu Gly Glu Glu
    130                 135                 140

Leu Ala Thr Ala Ile Gly Gln Pro Gly Leu Arg Val Thr Arg Leu Ala
145                 150                 155                 160

Gln Leu Leu Asp Ala Glu Tyr Asn Ile Thr Val Arg Phe Arg Ala Pro
                165                 170                 175

Asp Ile Thr Gly Arg Arg His Phe Asp Pro Gln Ser Arg Gln Ile Leu
            180                 185                 190

Leu Arg Gln Asp Leu Ser Glu Ala Gln Gln Cys Phe Gln Leu Ala Glu
        195                 200                 205
```

```
Glu Leu Thr Phe Leu Ala His Ala Glu Leu Leu Asp Thr Leu Thr Thr
    210                 215                 220

Asp Gln Pro Asp Leu Pro Ser Glu Ala Ala Ile Arg Leu Ala Lys Val
225                 230                 235                 240

Gly Leu Ser Gln Tyr Phe Ala Ala Ala Val Val Met Pro Tyr Thr Arg
                245                 250                 255

Phe Leu Glu Phe Ala Gln Asp Lys His Tyr Asp Ile Glu Leu Ile Ser
            260                 265                 270

Glu Ala Phe Gly Val Ser Phe Glu Ser Ala Cys His Arg Leu Ser Thr
        275                 280                 285

Leu Gln Arg Ser Gly Ala Ser Gly Val Pro Phe Phe Phe Val Arg Ser
    290                 295                 300

Asp Arg Ala Gly
305
```

0000000000

```
gtc ccc ttc tct cat gag cca aac cag gga gtg ttg cgg gct atc gct   384
Val Pro Phe Ser His Glu Pro Asn Gln Gly Val Leu Arg Ala Ile Ala
        115                 120                 125

tcc cta gct ctt gct gcg aag ctg att ggt gag gac aac gaa tac gat   432
Ser Leu Ala Leu Ala Ala Lys Leu Ile Gly Glu Asp Asn Glu Tyr Asp
    130                 135                 140

cgt tgc cgc cag atg ctc tct gat gcg gat cca gag tcc gtc gca gtc   480
Arg Cys Arg Gln Met Leu Ser Asp Ala Asp Pro Glu Ser Val Ala Val
145                 150                 155                 160

cta ctc gac aaa taaaccacca aaaataaaac aat                        515
Leu Leu Asp Lys
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<210> 1100
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 1100

```
Pro Thr Asp Asn Leu Phe Ser Tyr Pro Ala Gln Arg Tyr Asp Leu Leu
  1               5                  10                  15

Thr Leu Ala Phe Glu Val Arg Ile Gly Asp Met Val Gln Ile Asn Asp
             20                  25                  30

Met Leu Ala Pro Pro Pro Val Lys Leu Pro Glu Asp Pro Ala Leu Gly
         35                  40                  45

Ala Asp Pro Thr Leu Thr Ser Thr Ala Ile Ala His Pro Asp Ser Pro
     50                  55                  60

Leu Val Trp Ala Tyr Arg Ala Glu Asn Leu Ile Lys Ser Ala Ser Asn
 65                  70                  75                  80

Asp Glu Glu Lys Ile Gln Ala Tyr Ala Phe Ala Arg Thr Gly Tyr His
                 85                  90                  95

Arg Ser Leu Asp Arg Leu Arg Ala Asn Gly Trp Lys Gly Trp Gly Pro
            100                 105                 110

Val Pro Phe Ser His Glu Pro Asn Gln Gly Val Leu Arg Ala Ile Ala
        115                 120                 125

Ser Leu Ala Leu Ala Ala Lys Leu Ile Gly Glu Asp Asn Glu Tyr Asp
    130                 135                 140

Arg Cys Arg Gln Met Leu Ser Asp Ala Asp Pro Glu Ser Val Ala Val
145                 150                 155                 160

Leu Leu Asp Lys
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<210> 1101
<211> 515
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(492)
<223> FRXA02339

<400> 1101

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ccc acc gac aac ctc ttt tca tat cct gca caa cgc tat gat ctt ctc   48
Pro Thr Asp Asn Leu Phe Ser Tyr Pro Ala Gln Arg Tyr Asp Leu Leu
  1               5                  10                  15

aca ctt gcc ttt gaa gtt agg att ggg gac atg gtt caa att aat gac   96
Thr Leu Ala Phe Glu Val Arg Ile Gly Asp Met Val Gln Ile Asn Asp
             20                  25                  30

atg ctt gcc cct cct cca gta aaa ctt ccg gaa gat cct gcc ctc ggc   144
Met Leu Ala Pro Pro Pro Val Lys Leu Pro Glu Asp Pro Ala Leu Gly
         35                  40                  45

gcc gat cca act ttg acc tcg aca gcg att gcg cat cct gac agc cca   192
Ala Asp Pro Thr Leu Thr Ser Thr Ala Ile Ala His Pro Asp Ser Pro
     50                  55                  60

ttg gtg tgg gcg tac cga gct gaa aat ctt atc aaa tct gca tca aat   240
Leu Val Trp Ala Tyr Arg Ala Glu Asn Leu Ile Lys Ser Ala Ser Asn
 65                  70                  75                  80

gat gaa gag aag att cag gcc tac gct ttt gcg cgc acg ggt tac cac   288
Asp Glu Glu Lys Ile Gln Ala Tyr Ala Phe Ala Arg Thr Gly Tyr His
                 85                  90                  95

cgc agt ctc gat cgt ctg cgt gcc aat ggt tgg aag ggt tgg ggt cct   336
Arg Ser Leu Asp Arg Leu Arg Ala Asn Gly Trp Lys Gly Trp Gly Pro
            100                 105                 110

gtc ccc ttc tct cat gag cca aac cag gga gtg ttg cgg gct atc gct   384
Val Pro Phe Ser His Glu Pro Asn Gln Gly Val Leu Arg Ala Ile Ala
        115                 120                 125

tcc cta gct ctt gct gcg aag ctg att ggt gag gac aac gaa tac gat   432
Ser Leu Ala Leu Ala Ala Lys Leu Ile Gly Glu Asp Asn Glu Tyr Asp
    130                 135                 140

cgt tgc cgc cag atg ctc tct gat gcg gat cca gag tcc gtc gca gtc   480
Arg Cys Arg Gln Met Leu Ser Asp Ala Asp Pro Glu Ser Val Ala Val
145                 150                 155                 160

cta ctc gac aaa taaaccacca aaaataaaac aat                        515
Leu Leu Asp Lys
```

<210> 1102
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 1102

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Pro Thr Asp Asn Leu Phe Ser Tyr Pro Ala Gln Arg Tyr Asp Leu Leu
  1               5                  10                  15
```

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Thr Leu Ala Phe Glu Val Arg Ile Gly Asp Met Val Gln Ile Asn Asp
             20                  25                  30

Met Leu Ala Pro Pro Pro Val Lys Leu Pro Glu Asp Pro Ala Leu Gly
         35                  40                  45

Ala Asp Pro Thr Leu Thr Ser Thr Ala Ile Ala His Pro Asp Ser Pro
     50                  55                  60

Leu Val Trp Ala Tyr Arg Ala Glu Asn Leu Ile Lys Ser Ala Ser Asn
 65                  70                  75                  80

Asp Glu Glu Lys Ile Gln Ala Tyr Ala Phe Ala Arg Thr Gly Tyr His
                 85                  90                  95

Arg Ser Leu Asp Arg Leu Arg Ala Asn Gly Trp Lys Gly Trp Gly Pro
            100                 105                 110

Val Pro Phe Ser His Glu Pro Asn Gln Gly Val Leu Arg Ala Ile Ala
        115                 120                 125

Ser Leu Ala Leu Ala Ala Lys Leu Ile Gly Glu Asp Asn Glu Tyr Asp
    130                 135                 140

Arg Cys Arg Gln Met Leu Ser Asp Ala Asp Pro Glu Ser Val Ala Val
145                 150                 155                 160

Leu Leu Asp Lys
```

US20070020738A1

<210> 1103
<211> 1188
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1165)
<223> RXN02340

<400> 1103

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aaaacgtgtc taaaaattca gtttttattg ctgctgatca cctcttgaag aactcaaccc 60

aaaagtgctt caagttatga gaaagtgaaa tccaacaccc atg aaa aag agc atc   115
                                            Met Lys Lys Ser Ile
                                              1               5

gtt gta ttt gaa gtc gaa ggc ggc tcc gac aag cac ttc gac ggt cac   163
Val Val Phe Glu Val Glu Gly Gly Ser Asp Lys His Phe Asp Gly His
                 10                  15                  20

cgt aaa gac acc atg cct atc gtc aac tcc ata aat gat gct ggc tgg   211
Arg Lys Asp Thr Met Pro Ile Val Asn Ser Ile Asn Asp Ala Gly Trp
             25                  30                  35

cag gca gag gtt gtg tac tac cgc cca gag tgg acc gaa ggt ctc ttt   259
Gln Ala Glu Val Val Tyr Tyr Arg Pro Glu Trp Thr Glu Gly Leu Phe
         40                  45                  50
```

```
gag tac gta tct gaa aac ttc gac ggc tac atc tca cgt gtc aac cca   307
Glu Tyr Val Ser Glu Asn Phe Asp Gly Tyr Ile Ser Arg Val Asn Pro
     55                  60                  65

ggc aac atc cca ggc ggc gag cgc ggc tac ttt gac ctg ctc acc cgc   355
Gly Asn Ile Pro Gly Gly Glu Arg Gly Tyr Phe Asp Leu Leu Thr Arg
 70                  75                  80                  85

ctg tcc gaa gca ggg ctc gtg ggc atg tcc acc cct gag gaa atg atg   403
Leu Ser Glu Ala Gly Leu Val Gly Met Ser Thr Pro Glu Glu Met Met
                 90                  95                 100

gca tac ggc gcg aaa gat gcg ctg gtc aag cta tcc caa acc gac ctg   451
Ala Tyr Gly Ala Lys Asp Ala Leu Val Lys Leu Ser Gln Thr Asp Leu
            105                 110                 115

gtg cca tcc gac acc gag gcg tac tac gac gtg gag acc ttc cac aag   499
Val Pro Ser Asp Thr Glu Ala Tyr Tyr Asp Val Glu Thr Phe His Lys
        120                 125                 130

gtt ttc cca acc tcc ctg tcc ttc ggt gag cgc gtg ctc aag caa aac   547
Val Phe Pro Thr Ser Leu Ser Phe Gly Glu Arg Val Leu Lys Gln Asn
    135                 140                 145

cgt ggc tcc acc ggc tcc ggc att tgg cgc gtc cag ttg gta gac aag   595
Arg Gly Ser Thr Gly Ser Gly Ile Trp Arg Val Gln Leu Val Asp Lys
150                 155                 160                 165

gaa ctg gct gca tcc atc gag cca ggc acc gca ctg cca ttg gac act   643
Glu Leu Ala Ala Ser Ile Glu Pro Gly Thr Ala Leu Pro Leu Asp Thr
                170                 175                 180

gaa atc aag tgc acc gaa gca gtc gac aac cac act gaa gtc cgc aag   691
Glu Ile Lys Cys Thr Glu Ala Val Asp Asn His Thr Glu Val Arg Lys
            185                 190                 195

ctc ggc gag ttc atg gat ttc tgt gac cag tac atc atc ggc gac aac   739
Leu Gly Glu Phe Met Asp Phe Cys Asp Gln Tyr Ile Ile Gly Asp Asn
        200                 205                 210

ggc atg ctc gtt gat atg cgt ttc atg cca cgc atc gtc gaa ggc gaa   787
Gly Met Leu Val Asp Met Arg Phe Met Pro Arg Ile Val Glu Gly Glu
    215                 220                 225

atc cgc atc ctt ctc gtc gga cca cac cca gtg ttc gtc gtg cac aag   835
Ile Arg Ile Leu Leu Val Gly Pro His Pro Val Phe Val Val His Lys
230                 235                 240                 245

aag cca gca gaa ggc ggc gac aac ttc tcc gca acc ctg ttc tcc ggc   883
Lys Pro Ala Glu Gly Gly Asp Asn Phe Ser Ala Thr Leu Phe Ser Gly
                250                 255                 260

gcg aag tac acc tac gac aag cca gag cag tgg cag gaa ctg att gac   931
Ala Lys Tyr Thr Tyr Asp Lys Pro Glu Gln Trp Gln Glu Leu Ile Asp
            265                 270                 275

ctc ttc gca gac gct cgc cca gtc atc gca gaa aag ctc ggc ggc gac   979
Leu Phe Ala Asp Ala Arg Pro Val Ile Ala Glu Lys Leu Gly Gly Asp
        280                 285                 290

aac atc cca ttg atc tgg acc gca gac ttc atg ctc ggc gat gtc gtt   1027
```

```
Asn Ile Pro Leu Ile Trp Thr Ala Asp Phe Met Leu Gly Asp Val Val
    295                 300                 305

gac ggc aag gac acc tac gtg ctc ggt gaa atc aac tgc tcc tgc gtc   1075
Asp Gly Lys Asp Thr Tyr Val Leu Gly Glu Ile Asn Cys Ser Cys Val
310                 315                 320                 325

ggc ttc acc tcc gag ctg gac atg ggc atc cag cag ctt gtg gca tca   1123
Gly Phe Thr Ser Glu Leu Asp Met Gly Ile Gln Gln Leu Val Ala Ser
                330                 335                 340

gag gcc atc aag cgc atc gag gaa ttc gcg cag ctt act gtt           1165
Glu Ala Ile Lys Arg Ile Glu Glu Phe Ala Gln Leu Thr Val
            345                 350                 355

taaaactttg cttctcgacg tct                                        1188


<210> 1104
<211> 355
<212> PRT
<213> Corynebacterium glutamicum

<400> 1104
Met Lys Lys Ser Ile Val Val Phe Glu Val Glu Gly Gly Ser Asp Lys
  1               5                  10                  15

His Phe Asp Gly His Arg Lys Asp Thr Met Pro Ile Val Asn Ser Ile
            20                  25                  30

Asn Asp Ala Gly Trp Gln Ala Glu Val Val Tyr Tyr Arg Pro Glu Trp
        35                  40                  45

Thr Glu Gly Leu Phe Glu Tyr Val Ser Glu Asn Phe Asp Gly Tyr Ile
    50                  55                  60

Ser Arg Val Asn Pro Gly Asn Ile Pro Gly Gly Glu Arg Gly Tyr Phe
65                  70                  75                  80

Asp Leu Leu Thr Arg Leu Ser Glu Ala Gly Leu Val Gly Met Ser Thr
                85                  90                  95

Pro Glu Glu Met Met Ala Tyr Gly Ala Lys Asp Ala Leu Val Lys Leu
            100                 105                 110

Ser Gln Thr Asp Leu Val Pro Ser Asp Thr Glu Ala Tyr Tyr Asp Val
        115                 120                 125

Glu Thr Phe His Lys Val Phe Pro Thr Ser Leu Ser Phe Gly Glu Arg
    130                 135                 140

Val Leu Lys Gln Asn Arg Gly Ser Thr Gly Ser Gly Ile Trp Arg Val
145                 150                 155                 160

Gln Leu Val Asp Lys Glu Leu Ala Ala Ser Ile Glu Pro Gly Thr Ala
                165                 170                 175

Leu Pro Leu Asp Thr Glu Ile Lys Cys Thr Glu Ala Val Asp Asn His
            180                 185                 190

Thr Glu Val Arg Lys Leu Gly Glu Phe Met Asp Phe Cys Asp Gln Tyr
```

```
        195                 200                 205

Ile Ile Gly Asp Asn Gly Met Leu Val Asp Met Arg Phe Met Pro Arg
    210                 215                 220

Ile Val Glu Gly Glu Ile Arg Ile Leu Leu Val Gly Pro His Pro Val
225                 230                 235                 240

Phe Val Val His Lys Lys Pro Ala Glu Gly Gly Asp Asn Phe Ser Ala
                245                 250                 255

Thr Leu Phe Ser Gly Ala Lys Tyr Thr Tyr Asp Lys Pro Glu Gln Trp
            260                 265                 270

Gln Glu Leu Ile Asp Leu Phe Ala Asp Ala Arg Pro Val Ile Ala Glu
        275                 280                 285

Lys Leu Gly Gly Asp Asn Ile Pro Leu Ile Trp Thr Ala Asp Phe Met
    290                 295                 300

Leu Gly Asp Val Val Asp Gly Lys Asp Thr Tyr Val Leu Gly Glu Ile
305                 310                 315                 320

Asn Cys Ser Cys Val Gly Phe Thr Ser Glu Leu Asp Met Gly Ile Gln
                325                 330                 335

Gln Leu Val Ala Ser Glu Ala Ile Lys Arg Ile Glu Glu Phe Ala Gln
            340                 345                 350

Leu Thr Val
        355


<210> 1105
<211> 580
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> FRXA02338

<400> 1105
aaaacgtgtc taaaaattca gtttttattg ctgctgatca cctcttgaag aactcaaccc 60

aaaagtgctt caagttatga gaaagtgaaa tccaacaccc atg aaa aag agc atc   115
                                              Met Lys Lys Ser Ile
                                                1               5

gtt gta ttt gaa gtc gaa ggc ggc tcc gac aag cac ttc gac ggt cac   163
Val Val Phe Glu Val Glu Gly Gly Ser Asp Lys His Phe Asp Gly His
               10                  15                  20

cgt aaa gac acc atg cct atc gtc aac tcc ata aat gat gct ggc tgg   211
Arg Lys Asp Thr Met Pro Ile Val Asn Ser Ile Asn Asp Ala Gly Trp
            25                  30                  35

cag gca gag gtt gtg tac tac cgc cca gag tgg acc gaa ggt ctc ttt   259
Gln Ala Glu Val Val Tyr Tyr Arg Pro Glu Trp Thr Glu Gly Leu Phe
        40                  45                  50
```

```
gag tac gta tct gaa aac ttc gac ggc tac atc tca cgt gtc aac cca   307
Glu Tyr Val Ser Glu Asn Phe Asp Gly Tyr Ile Ser Arg Val Asn Pro
     55                  60                  65

ggc aac atc cca ggc ggc gag cgc ggc tac ttt gac ctg ctc acc cgc   355
Gly Asn Ile Pro Gly Gly Glu Arg Gly Tyr Phe Asp Leu Leu Thr Arg
 70                  75                  80                  85

ctg tcc gaa gca ggg ctc gtg ggc atg tcc acc cct gag gaa atg atg   403
Leu Ser Glu Ala Gly Leu Val Gly Met Ser Thr Pro Glu Glu Met Met
                 90                  95                 100

gca tac ggc gcg aaa gat gcg ctg gtc aag cta tcc caa acc gac ctg   451
Ala Tyr Gly Ala Lys Asp Ala Leu Val Lys Leu Ser Gln Thr Asp Leu
            105                 110                 115

gtg cca tcc gac acc gag gcg tac tac gac gtg gag acc ttc cac aag   499
Val Pro Ser Asp Thr Glu Ala Tyr Tyr Asp Val Glu Thr Phe His Lys
        120                 125                 130

gtt ttc cca acc tcc ctg tcc ttc ggt gaa gcg cgt gct caa gca aaa   547
Val Phe Pro Thr Ser Leu Ser Phe Gly Glu Ala Arg Ala Gln Ala Lys
    135                 140                 145

acc tgg ctt cac cgg ctt ccg cat ttg gcg cgt                      580
Thr Trp Leu His Arg Leu Pro His Leu Ala Arg
150                 155                 160
```

5'GAC TGC AGA GGA TCC 3'

<210> 1106
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 1106

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Met Lys Lys Ser Ile Val Val Phe Glu Val Glu Gly Gly Ser Asp Lys
  1               5                  10                  15

His Phe Asp Gly His Arg Lys Asp Thr Met Pro Ile Val Asn Ser Ile
             20                  25                  30

Asn Asp Ala Gly Trp Gln Ala Glu Val Val Tyr Tyr Arg Pro Glu Trp
         35                  40                  45

Thr Glu Gly Leu Phe Glu Tyr Val Ser Glu Asn Phe Asp Gly Tyr Ile
     50                  55                  60

Ser Arg Val Asn Pro Gly Asn Ile Pro Gly Gly Glu Arg Gly Tyr Phe
 65                  70                  75                  80

Asp Leu Leu Thr Arg Leu Ser Glu Ala Gly Leu Val Gly Met Ser Thr
                 85                  90                  95

Pro Glu Glu Met Met Ala Tyr Gly Ala Lys Asp Ala Leu Val Lys Leu
            100                 105                 110

Ser Gln Thr Asp Leu Val Pro Ser Asp Thr Glu Ala Tyr Tyr Asp Val
        115                 120                 125

Glu Thr Phe His Lys Val Phe Pro Thr Ser Leu Ser Phe Gly Glu Ala
```

```
    130                 135                 140

Arg Ala Gln Ala Lys Thr Trp Leu His Arg Leu Pro His Leu Ala Arg
145                 150                 155                 160
```

<210> 1107
<211> 662
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(639)
<223> FRXA02340

<400> 1107

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gag cgc gtg ctc aag caa aac cgt ggc tcc acc ggc tcc ggc att tgg   48
Glu Arg Val Leu Lys Gln Asn Arg Gly Ser Thr Gly Ser Gly Ile Trp
  1               5                  10                  15

cgc gtc cag ttg gta gac aag gaa ctg gct gca tcc atc gag cca ggc   96
Arg Val Gln Leu Val Asp Lys Glu Leu Ala Ala Ser Ile Glu Pro Gly
             20                  25                  30

acc gca ctg cca ttg gac act gaa atc aag tgc acc gaa gca gtc gac   144
Thr Ala Leu Pro Leu Asp Thr Glu Ile Lys Cys Thr Glu Ala Val Asp
         35                  40                  45

aac cac act gaa gtc cgc aag ctc ggc gag ttc atg gat ttc tgt gac   192
Asn His Thr Glu Val Arg Lys Leu Gly Glu Phe Met Asp Phe Cys Asp
     50                  55                  60

cag tac atc atc ggc gac aac ggc atg ctc gtt gat atg cgt ttc atg   240
Gln Tyr Ile Ile Gly Asp Asn Gly Met Leu Val Asp Met Arg Phe Met
 65                  70                  75                  80

cca cgc atc gtc gaa ggc gaa atc cgc atc ctt ctc gtc gga cca cac   288
Pro Arg Ile Val Glu Gly Glu Ile Arg Ile Leu Leu Val Gly Pro His
                 85                  90                  95

cca gtg ttc gtc gtg cac aag aag cca gca gaa ggc ggc gac aac ttc   336
Pro Val Phe Val Val His Lys Lys Pro Ala Glu Gly Gly Asp Asn Phe
            100                 105                 110

tcc gca acc ctg ttc tcc ggc gcg aag tac acc tac gac aag cca gag   384
Ser Ala Thr Leu Phe Ser Gly Ala Lys Tyr Thr Tyr Asp Lys Pro Glu
        115                 120                 125

cag tgg cag gaa ctg att gac ctc ttc gca gac gct cgc cca gtc atc   432
Gln Trp Gln Glu Leu Ile Asp Leu Phe Ala Asp Ala Arg Pro Val Ile
    130                 135                 140

gca gaa aag ctc ggc ggc gac aac atc cca ttg atc tgg acc gca gac   480
Ala Glu Lys Leu Gly Gly Asp Asn Ile Pro Leu Ile Trp Thr Ala Asp
145                 150                 155                 160

ttc atg ctc ggc gat gtc gtt gac ggc aag gac acc tac gtg ctc ggt   528
```

```
Phe Met Leu Gly Asp Val Val Asp Gly Lys Asp Thr Tyr Val Leu Gly
                165                 170                 175

gaa atc aac tgc tcc tgc gtc ggc ttc acc tcc gag ctg gac atg ggc   576
Glu Ile Asn Cys Ser Cys Val Gly Phe Thr Ser Glu Leu Asp Met Gly
            180                 185                 190

atc cag cag ctt gtg gca tca gag gcc atc aag cgc atc gag gaa ttc   624
Ile Gln Gln Leu Val Ala Ser Glu Ala Ile Lys Arg Ile Glu Glu Phe
        195                 200                 205

gcg cag ctt act gtt taaaactttg cttctcgacg tct                     662
Ala Gln Leu Thr Val
    210


<210> 1108
<211> 213
<212> PRT
<213> Corynebacterium glutamicum

<400> 1108
Glu Arg Val Leu Lys Gln Asn Arg Gly Ser Thr Gly Ser Gly Ile Trp
  1               5                  10                  15

Arg Val Gln Leu Val Asp Lys Glu Leu Ala Ala Ser Ile Glu Pro Gly
            20                  25                  30

Thr Ala Leu Pro Leu Asp Thr Glu Ile Lys Cys Thr Glu Ala Val Asp
        35                  40                  45

Asn His Thr Glu Val Arg Lys Leu Gly Glu Phe Met Asp Phe Cys Asp
    50                  55                  60

Gln Tyr Ile Ile Gly Asp Asn Gly Met Leu Val Asp Met Arg Phe Met
65                  70                  75                  80

Pro Arg Ile Val Glu Gly Glu Ile Arg Ile Leu Leu Val Gly Pro His
                85                  90                  95

Pro Val Phe Val Val His Lys Lys Pro Ala Glu Gly Gly Asp Asn Phe
            100                 105                 110

Ser Ala Thr Leu Phe Ser Gly Ala Lys Tyr Thr Tyr Asp Lys Pro Glu
        115                 120                 125

Gln Trp Gln Glu Leu Ile Asp Leu Phe Ala Asp Ala Arg Pro Val Ile
    130                 135                 140

Ala Glu Lys Leu Gly Gly Asp Asn Ile Pro Leu Ile Trp Thr Ala Asp
145                 150                 155                 160

Phe Met Leu Gly Asp Val Val Asp Gly Lys Asp Thr Tyr Val Leu Gly
                165                 170                 175

Glu Ile Asn Cys Ser Cys Val Gly Phe Thr Ser Glu Leu Asp Met Gly
            180                 185                 190

Ile Gln Gln Leu Val Ala Ser Glu Ala Ile Lys Arg Ile Glu Glu Phe
        195                 200                 205
```

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Ala Gln Leu Thr Val
    210


<210> 1109
<211> 609
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(586)
<223> RXN02341

<400> 1109
cgcgactggc ggagaaattc gtgttcgcga tgcttcgggc accgttcaca ccctcaacgc 60

cggtgaaatt acgcaccttc gcctgcagta aggtgacggt atg ggg aat tca ctt   115
                                            Met Gly Asn Ser Leu
                                              1               5

gag aaa cat att gca gag gga gac cgg atc cac gtc gat ctg aca tct   163
Glu Lys His Ile Ala Glu Gly Asp Arg Ile His Val Asp Leu Thr Ser
                 10                  15                  20

cct tta tcc gca atg ttg ttc ccc att ttt gaa ctc att gtg att act   211
Pro Leu Ser Ala Met Leu Phe Pro Ile Phe Glu Leu Ile Val Ile Thr
             25                  30                  35

gga atc tgt tgg atg ggc atc ggc ttt ttg gat cag ctt cca gga atc   259
Gly Ile Cys Trp Met Gly Ile Gly Phe Leu Asp Gln Leu Pro Gly Ile
         40                  45                  50

gat ggc acc aac ccc gcc gat agc ttc ccc gaa ggc acc cgc aat ctt   307
Asp Gly Thr Asn Pro Ala Asp Ser Phe Pro Glu Gly Thr Arg Asn Leu
     55                  60                  65

cta gtg ggt gtg tgg gca gta ctt gct gca tgg cgt ttc ggt ctt cct   355
Leu Val Gly Val Trp Ala Val Leu Ala Ala Trp Arg Phe Gly Leu Pro
 70                  75                  80                  85

tta ata agg caa cgt cga ctc cgc gtg atc ttg agc gac cgc aaa ctg   403
Leu Ile Arg Gln Arg Arg Leu Arg Val Ile Leu Ser Asp Arg Lys Leu
                 90                  95                 100

ctg gtc cga cgc gcg ggt ctg cgc acc ggg ttc gat tcc att cca ctg   451
Leu Val Arg Arg Ala Gly Leu Arg Thr Gly Phe Asp Ser Ile Pro Leu
             105                 110                 115

agc tac att cag cga gtc caa cgt cgg cga aac acc ctg gtc tta ggt   499
Ser Tyr Ile Gln Arg Val Gln Arg Arg Arg Asn Thr Leu Val Leu Gly
         120                 125                 130

gtt ggt gga cac cac cga ccc tat gta atc aac cag gtt ccc aag gct   547
Val Gly Gly His His Arg Pro Tyr Val Ile Asn Gln Val Pro Lys Ala
     135                 140                 145

cga aaa gtg gaa gcg ctg ctc aaa gat ctt aca ttt tgg tgaaggcgtt    596
Arg Lys Val Glu Ala Leu Leu Lys Asp Leu Thr Phe Trp
150                 155                 160
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atagttagga ctt 609

<210> 1110
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 1110
Met Gly Asn Ser Leu Glu Lys His Ile Ala Glu Gly Asp Arg Ile His
1 5 10 15

Val Asp Leu Thr Ser Pro Leu Ser Ala Met Leu Phe Pro Ile Phe Glu
20 25 30

Leu Ile Val Ile Thr Gly Ile Cys Trp Met Gly Ile Gly Phe Leu Asp
35 40 45

Gln Leu Pro Gly Ile Asp Gly Thr Asn Pro Ala Asp Ser Phe Pro Glu
50 55 60

Gly Thr Arg Asn Leu Leu Val Gly Val Trp Ala Val Leu Ala Ala Trp
65 70 75 80

Arg Phe Gly Leu Pro Leu Ile Arg Gln Arg Arg Leu Arg Val Ile Leu
85 90 95

Ser Asp Arg Lys Leu Leu Val Arg Arg Ala Gly Leu Arg Thr Gly Phe
100 105 110

Asp Ser Ile Pro Leu Ser Tyr Ile Gln Arg Val Gln Arg Arg Arg Asn
115 120 125

Thr Leu Val Leu Gly Val Gly Gly His His Arg Pro Tyr Val Ile Asn
130 135 140

Gln Val Pro Lys Ala Arg Lys Val Glu Ala Leu Leu Lys Asp Leu Thr
145 150 155 160

Phe Trp

<210> 1111
<211> 511
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> FRXA02341

<400> 1111
cgcgactggc ggagaaattc gtgttcgcga tgcttcgggc accgttcaca ccctcaacgc 60

cggtgaaatt acgcaccttc gcctgcagta aggtgacggt atg ggg aat tca ctt 115
Met Gly Asn Ser Leu
1 5

gag aaa cat att gca gag gga gac cgg atc cac gtc gat ctg aca tct 163

```
Glu Lys His Ile Ala Glu Gly Asp Arg Ile His Val Asp Leu Thr Ser
                 10                  15                  20

cct tta tcc gca atg ttg ttc ccc att ttt gaa ctc att gtg att act   211
Pro Leu Ser Ala Met Leu Phe Pro Ile Phe Glu Leu Ile Val Ile Thr
             25                  30                  35

gga atc tgt tgg atg ggc atc ggc ttt ttg gat cag ctt cca gga atc   259
Gly Ile Cys Trp Met Gly Ile Gly Phe Leu Asp Gln Leu Pro Gly Ile
         40                  45                  50

gat ggc acc aac ccc gcc gat agc ttc ccc gaa ggc acc cgc aat ctt   307
Asp Gly Thr Asn Pro Ala Asp Ser Phe Pro Glu Gly Thr Arg Asn Leu
     55                  60                  65

cta gtg ggt gtg tgg gca gta ctt gct gca tgg cgt ttc ggt ctt cct   355
Leu Val Gly Val Trp Ala Val Leu Ala Ala Trp Arg Phe Gly Leu Pro
 70                  75                  80                  85

tta ata agg caa cgt cga ctc cgc gtg atc ttg agc gac cgc aaa ctg   403
Leu Ile Arg Gln Arg Arg Leu Arg Val Ile Leu Ser Asp Arg Lys Leu
                 90                  95                 100

ctg gtc cga cgc gcg ggt ctg cgc acc ggg ttc gat tcc att cca ctg   451
Leu Val Arg Arg Ala Gly Leu Arg Thr Gly Phe Asp Ser Ile Pro Leu
             105                 110                 115

agc tac att cag cga gtc caa cgt cgg cga aac acc ctg gtc tta ggt   499
Ser Tyr Ile Gln Arg Val Gln Arg Arg Arg Asn Thr Leu Val Leu Gly
         120                 125                 130

gtt ggt gga cac                                                  511
Val Gly Gly His
    135


<210> 1112
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 1112
Met Gly Asn Ser Leu Glu Lys His Ile Ala Glu Gly Asp Arg Ile His
  1               5                  10                  15

Val Asp Leu Thr Ser Pro Leu Ser Ala Met Leu Phe Pro Ile Phe Glu
             20                  25                  30

Leu Ile Val Ile Thr Gly Ile Cys Trp Met Gly Ile Gly Phe Leu Asp
         35                  40                  45

Gln Leu Pro Gly Ile Asp Gly Thr Asn Pro Ala Asp Ser Phe Pro Glu
     50                  55                  60

Gly Thr Arg Asn Leu Leu Val Gly Val Trp Ala Val Leu Ala Ala Trp
 65                  70                  75                  80

Arg Phe Gly Leu Pro Leu Ile Arg Gln Arg Arg Leu Arg Val Ile Leu
                 85                  90                  95

Ser Asp Arg Lys Leu Leu Val Arg Arg Ala Gly Leu Arg Thr Gly Phe
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            100                 105                 110

Asp Ser Ile Pro Leu Ser Tyr Ile Gln Arg Val Gln Arg Arg Arg Asn
        115                 120                 125

Thr Leu Val Leu Gly Val Gly Gly His
    130                 135


<210> 1113
<211> 2556
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2533)
<223> RXN02360

<400> 1113
aagtaactaa agttcgaaag tatttccgaa cggtgtcggc ctctgcgcat acactgtatt 60

tttaaagaaa attcttctca attctaaggg tgaatatcca atg cgt ggt gac gtt   115
                                            Met Arg Gly Asp Val
                                              1               5

caa aaa ata acc aag gtt tat gac ggc aag cac cga acc ttg gaa atc   163
Gln Lys Ile Thr Lys Val Tyr Asp Gly Lys His Arg Thr Leu Glu Ile
                10                  15                  20

ccg gtt tat caa cgc aat tac gac tgg act gaa aag caa tgt tca cgc   211
Pro Val Tyr Gln Arg Asn Tyr Asp Trp Thr Glu Lys Gln Cys Ser Arg
            25                  30                  35

ctc ttt gat gac ctc agc gaa gtg gtc aaa gaa aac cac cgt caa cat   259
Leu Phe Asp Asp Leu Ser Glu Val Val Lys Glu Asn His Arg Gln His
        40                  45                  50

ttt ttt gga gct gtg gtt ggt aag cct caa ggc agc tgg acc tgg gtt   307
Phe Phe Gly Ala Val Val Gly Lys Pro Gln Gly Ser Trp Thr Trp Val
    55                  60                  65

gtc atc gat gga cag cag cgt ctt aca aca atc agc ttg ttc atg ctt   355
Val Ile Asp Gly Gln Gln Arg Leu Thr Thr Ile Ser Leu Phe Met Leu
70                  75                  80                  85

gcg ctg gta cat tcc ttg cgc gca tct gaa gtt gaa gaa ggt gag ttt   403
Ala Leu Val His Ser Leu Arg Ala Ser Glu Val Glu Glu Gly Glu Phe
                90                  95                  100

aat gct ggc tac aac att gat cta gcc aca ttg att gag gat gac tac   451
Asn Ala Gly Tyr Asn Ile Asp Leu Ala Thr Leu Ile Glu Asp Asp Tyr
            105                 110                 115

ctc cga tcc ggc aat gag gga aac ctc aag ttc aag ctc aag cca gtt   499
Leu Arg Ser Gly Asn Glu Gly Asn Leu Lys Phe Lys Leu Lys Pro Val
        120                 125                 130

aaa aac gat aat gag gct tat caa aag ctc ttc ggc cca gaa tct gaa   547
Lys Asn Asp Asn Glu Ala Tyr Gln Lys Leu Phe Gly Pro Glu Ser Glu
    135                 140                 145
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ttc ata gag tcc tca aac ctc act gct aat tat cgc tac ttc cgc aat   595
Phe Ile Glu Ser Ser Asn Leu Thr Ala Asn Tyr Arg Tyr Phe Arg Asn
150                 155                 160                 165

gtc ctt aag gca acc gat ctc acc gca gct caa cta tgg gaa gct atc   643
Val Leu Lys Ala Thr Asp Leu Thr Ala Ala Gln Leu Trp Glu Ala Ile
                170                 175                 180

gag aaa ctc agg gtc atg tat ctt gac ctt gag gaa ttt gat gat ccg   691
Glu Lys Leu Arg Val Met Tyr Leu Asp Leu Glu Glu Phe Asp Asp Pro
            185                 190                 195

cag cga atc ttt gaa agt ctc aac tcc acg gga tta gag ctc agt gaa   739
Gln Arg Ile Phe Glu Ser Leu Asn Ser Thr Gly Leu Glu Leu Ser Glu
        200                 205                 210

gct gat aag gta cgc aac ttg gtt ctt atg gat cag gag ctc aaa acc   787
Ala Asp Lys Val Arg Asn Leu Val Leu Met Asp Gln Glu Leu Lys Thr
    215                 220                 225

caa gaa aag ctc tat gag cag cgt tgg aat ccc att gaa gtc tgc gtg   835
Gln Glu Lys Leu Tyr Glu Gln Arg Trp Asn Pro Ile Glu Val Cys Val
230                 235                 240                 245

aaa ttt gat acc gac aat ttc att cgc tgg tac tta act ctc aaa acc   883
Lys Phe Asp Thr Asp Asn Phe Ile Arg Trp Tyr Leu Thr Leu Lys Thr
                250                 255                 260

gcg cgc acc cca aga aag caa gat gtt tat gag gaa ttc aag aaa ttc   931
Ala Arg Thr Pro Arg Lys Gln Asp Val Tyr Glu Glu Phe Lys Lys Phe
            265                 270                 275

atc cgt aac tcc aag ctc ccg gtc gaa ttc atc ctc gac gat atg tac   979
Ile Arg Asn Ser Lys Leu Pro Val Glu Phe Ile Leu Asp Asp Met Tyr
        280                 285                 290

gag tac gcg aag ctg tac cga gat ctc tta ggt gcc act act ggg ttt   1027
Glu Tyr Ala Lys Leu Tyr Arg Asp Leu Leu Gly Ala Thr Thr Gly Phe
    295                 300                 305

ata gct gcc gat agg tgt ctt aag cgt ttt gtc cct gtc atg ggc gat   1075
Ile Ala Ala Asp Arg Cys Leu Lys Arg Phe Val Pro Val Met Gly Asp
310                 315                 320                 325

gtg gtt ttg cct ttt ctg ctg cct gtt ctc aaa gat gct aaa gac ggc   1123
Val Val Leu Pro Phe Leu Leu Pro Val Leu Lys Asp Ala Lys Asp Gly
                330                 335                 340

atc atc acc gaa tca gac ttc ctc gga gtt cta aaa gtt ctg gaa tcc   1171
Ile Ile Thr Glu Ser Asp Phe Leu Gly Val Leu Lys Val Leu Glu Ser
            345                 350                 355

tat tta ttc cgc cgt ttt gca gtc ggg gtt gct agt aac gcc tta agc   1219
Tyr Leu Phe Arg Arg Phe Ala Val Gly Val Ala Ser Asn Ala Leu Ser
        360                 365                 370

aag atc ttc tcc act gct tat agc gac atc aag aaa ttc tgg act cca   1267
Lys Ile Phe Ser Thr Ala Tyr Ser Asp Ile Lys Lys Phe Trp Thr Pro
    375                 380                 385
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ggg caa agt tat agc tca ctg ctg gcc tac att ctg aaa cgt cgc gat   1315
Gly Gln Ser Tyr Ser Ser Leu Leu Ala Tyr Ile Leu Lys Arg Arg Asp
390                 395                 400                 405

ggt tcc ggg cgt ttt ccc tcc gac agt gaa ttc cgt gag aac ttc gca   1363
Gly Ser Gly Arg Phe Pro Ser Asp Ser Glu Phe Arg Glu Asn Phe Ala
                410                 415                 420

acc aaa aat ttc tgg aat att cat aac gaa aac agg cgt tac tta ttt   1411
Thr Lys Asn Phe Trp Asn Ile His Asn Glu Asn Arg Arg Tyr Leu Phe
            425                 430                 435

gat tgt cta gaa aat gcc gat tcc aat gat gtt cgt gac atc caa aca   1459
Asp Cys Leu Glu Asn Ala Asp Ser Asn Asp Val Arg Asp Ile Gln Thr
        440                 445                 450

agt ctg gat gaa gga tct ctc tcc att gaa cac atc atg cca cgt agc   1507
Ser Leu Asp Glu Gly Ser Leu Ser Ile Glu His Ile Met Pro Arg Ser
    455                 460                 465

cta aac gat cag tgg aga gct gaa ctc ggc cct gaa tat gct cga att   1555
Leu Asn Asp Gln Trp Arg Ala Glu Leu Gly Pro Glu Tyr Ala Arg Ile
470                 475                 480                 485

cat gag act tgg att aat aga att ggt aac ctc acc atc acc ggc tac   1603
His Glu Thr Trp Ile Asn Arg Ile Gly Asn Leu Thr Ile Thr Gly Tyr
                490                 495                 500

aac tcc gcc tat tca aat tct tcc tat gag cgc aag cgg acg atg gaa   1651
Asn Ser Ala Tyr Ser Asn Ser Ser Tyr Glu Arg Lys Arg Thr Met Glu
            505                 510                 515

aat gga ttt ttg gta tcc ccc tat cgc atc aat aat ttc atc aaa aag   1699
Asn Gly Phe Leu Val Ser Pro Tyr Arg Ile Asn Asn Phe Ile Lys Lys
        520                 525                 530

cag aag cat tgg tct gaa gaa cag cta att gag cga acc gag ctg ctc   1747
Gln Lys His Trp Ser Glu Glu Gln Leu Ile Glu Arg Thr Glu Leu Leu
    535                 540                 545

act caa gca gcg ctg gac tac tgg ccc ctt cca aaa gaa acc ttc cag   1795
Thr Gln Ala Ala Leu Asp Tyr Trp Pro Leu Pro Lys Glu Thr Phe Gln
550                 555                 560                 565

cca cca caa gct gtg ctt cct aca gaa tcc tta gat agt gat ctt tct   1843
Pro Pro Gln Ala Val Leu Pro Thr Glu Ser Leu Asp Ser Asp Leu Ser
                570                 575                 580

ttc cgc gga cgc gaa att gtc gcc ttt gaa tat gag gac tac aag gaa   1891
Phe Arg Gly Arg Glu Ile Val Ala Phe Glu Tyr Glu Asp Tyr Lys Glu
            585                 590                 595

acg gta acg tcc tgg gca gac atg ctc cag agc gtt cta aaa gtc ttg   1939
Thr Val Thr Ser Trp Ala Asp Met Leu Gln Ser Val Leu Lys Val Leu
        600                 605                 610

aac caa tcc ttc cgc cag gaa ctc ata gct ttg acc aat gaa gaa atc   1987
Asn Gln Ser Phe Arg Gln Glu Leu Ile Ala Leu Thr Asn Glu Glu Ile
    615                 620                 625

tgc ctg gca act tca aac aac agt aac agc agt ctc cgt gaa att gac   2035
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Cys Leu Ala Thr Ser Asn Asn Ser Asn Ser Ser Leu Arg Glu Ile Asp
630                 635                 640                 645

cac ggg ctt ttt gta gac act ggc tct agt acg agt gta aag att ggc   2083
His Gly Leu Phe Val Asp Thr Gly Ser Ser Thr Ser Val Lys Ile Gly
                650                 655                 660

ttc ctc cgc aga gtt ttt act caa ctg ggg cta gag cag gaa gca ttg   2131
Phe Leu Arg Arg Val Phe Thr Gln Leu Gly Leu Glu Gln Glu Ala Leu
            665                 670                 675

gtt ttc acc ctt cga cca ctg gca aat gat gta gaa ccc cga gat gat   2179
Val Phe Thr Leu Arg Pro Leu Ala Asn Asp Val Glu Pro Arg Asp Asp
        680                 685                 690

gaa ctc gag gta gag gta gaa aag aaa tat tcc gat ttg act aaa ttc   2227
Glu Leu Glu Val Glu Val Glu Lys Lys Tyr Ser Asp Leu Thr Lys Phe
    695                 700                 705

atc cca cag tta gaa gaa gct gag aat ctc gag ggg gcg gat aca gag   2275
Ile Pro Gln Leu Glu Glu Ala Glu Asn Leu Glu Gly Ala Asp Thr Glu
710                 715                 720                 725

gtt att cct ctc ctc tca aag ctc aag gaa caa ctg aca gcc ttt agc   2323
Val Ile Pro Leu Leu Ser Lys Leu Lys Glu Gln Leu Thr Ala Phe Ser
                730                 735                 740

ccg gag aat cct caa gca gcc cta ggg ggc cta cct gtt cca gaa ttc   2371
Pro Glu Asn Pro Gln Ala Ala Leu Gly Gly Leu Pro Val Pro Glu Phe
            745                 750                 755

ctc aaa caa aat gtg att gaa caa cta agc gca gag cac atc ctt gct   2419
Leu Lys Gln Asn Val Ile Glu Gln Leu Ser Ala Glu His Ile Leu Ala
        760                 765                 770

gta ctc act caa cac ttt aat atc gca tcc atg atg ggt gat gac tat   2467
Val Leu Thr Gln His Phe Asn Ile Ala Ser Met Met Gly Asp Asp Tyr
    775                 780                 785

ttg ctc gaa gag ctc agg tca ggc cgc tta agg gaa tta ctg cag cgt   2515
Leu Leu Glu Glu Leu Arg Ser Gly Arg Leu Arg Glu Leu Leu Gln Arg
790                 795                 800                 805

tta gag gaa ttg gat agc taatagccgt agtcggtggt caa                2556
Leu Glu Glu Leu Asp Ser
                810
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<210> 1114
<211> 811
<212> PRT
<213> Corynebacterium glutamicum

<400> 1114

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Met Arg Gly Asp Val Gln Lys Ile Thr Lys Val Tyr Asp Gly Lys His
  1               5                  10                  15

Arg Thr Leu Glu Ile Pro Val Tyr Gln Arg Asn Tyr Asp Trp Thr Glu
             20                  25                  30

Lys Gln Cys Ser Arg Leu Phe Asp Asp Leu Ser Glu Val Val Lys Glu
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         35                  40                  45

Asn His Arg Gln His Phe Phe Gly Ala Val Val Gly Lys Pro Gln Gly
     50                  55                  60

Ser Trp Thr Trp Val Val Ile Asp Gly Gln Gln Arg Leu Thr Thr Ile
 65                  70                  75                  80

Ser Leu Phe Met Leu Ala Leu Val His Ser Leu Arg Ala Ser Glu Val
                 85                  90                  95

Glu Glu Gly Glu Phe Asn Ala Gly Tyr Asn Ile Asp Leu Ala Thr Leu
            100                 105                 110

Ile Glu Asp Asp Tyr Leu Arg Ser Gly Asn Glu Gly Asn Leu Lys Phe
        115                 120                 125

Lys Leu Lys Pro Val Lys Asn Asp Asn Glu Ala Tyr Gln Lys Leu Phe
    130                 135                 140

Gly Pro Glu Ser Glu Phe Ile Glu Ser Ser Asn Leu Thr Ala Asn Tyr
145                 150                 155                 160

Arg Tyr Phe Arg Asn Val Leu Lys Ala Thr Asp Leu Thr Ala Ala Gln
                165                 170                 175

Leu Trp Glu Ala Ile Glu Lys Leu Arg Val Met Tyr Leu Asp Leu Glu
            180                 185                 190

Glu Phe Asp Asp Pro Gln Arg Ile Phe Glu Ser Leu Asn Ser Thr Gly
        195                 200                 205

Leu Glu Leu Ser Glu Ala Asp Lys Val Arg Asn Leu Val Leu Met Asp
    210                 215                 220

Gln Glu Leu Lys Thr Gln Glu Lys Leu Tyr Glu Gln Arg Trp Asn Pro
225                 230                 235                 240

Ile Glu Val Cys Val Lys Phe Asp Thr Asp Asn Phe Ile Arg Trp Tyr
                245                 250                 255

Leu Thr Leu Lys Thr Ala Arg Thr Pro Arg Lys Gln Asp Val Tyr Glu
            260                 265                 270

Glu Phe Lys Lys Phe Ile Arg Asn Ser Lys Leu Pro Val Glu Phe Ile
        275                 280                 285

Leu Asp Asp Met Tyr Glu Tyr Ala Lys Leu Tyr Arg Asp Leu Leu Gly
    290                 295                 300

Ala Thr Thr Gly Phe Ile Ala Ala Asp Arg Cys Leu Lys Arg Phe Val
305                 310                 315                 320

Pro Val Met Gly Asp Val Val Leu Pro Phe Leu Leu Pro Val Leu Lys
                325                 330                 335

Asp Ala Lys Asp Gly Ile Ile Thr Glu Ser Asp Phe Leu Gly Val Leu
            340                 345                 350

Lys Val Leu Glu Ser Tyr Leu Phe Arg Arg Phe Ala Val Gly Val Ala
        355                 360                 365
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Ser Asn Ala Leu Ser Lys Ile Phe Ser Thr Ala Tyr Ser Asp Ile Lys
    370                 375                 380

Lys Phe Trp Thr Pro Gly Gln Ser Tyr Ser Ser Leu Leu Ala Tyr Ile
385                 390                 395                 400

Leu Lys Arg Arg Asp Gly Ser Gly Arg Phe Pro Ser Asp Ser Glu Phe
                405                 410                 415

Arg Glu Asn Phe Ala Thr Lys Asn Phe Trp Asn Ile His Asn Glu Asn
            420                 425                 430

Arg Arg Tyr Leu Phe Asp Cys Leu Glu Asn Ala Asp Ser Asn Asp Val
        435                 440                 445

Arg Asp Ile Gln Thr Ser Leu Asp Glu Gly Ser Leu Ser Ile Glu His
    450                 455                 460

Ile Met Pro Arg Ser Leu Asn Asp Gln Trp Arg Ala Glu Leu Gly Pro
465                 470                 475                 480

Glu Tyr Ala Arg Ile His Glu Thr Trp Ile Asn Arg Ile Gly Asn Leu
                485                 490                 495

Thr Ile Thr Gly Tyr Asn Ser Ala Tyr Ser Asn Ser Ser Tyr Glu Arg
            500                 505                 510

Lys Arg Thr Met Glu Asn Gly Phe Leu Val Ser Pro Tyr Arg Ile Asn
        515                 520                 525

Asn Phe Ile Lys Lys Gln Lys His Trp Ser Glu Glu Gln Leu Ile Glu
    530                 535                 540

Arg Thr Glu Leu Leu Thr Gln Ala Ala Leu Asp Tyr Trp Pro Leu Pro
545                 550                 555                 560

Lys Glu Thr Phe Gln Pro Pro Gln Ala Val Leu Pro Thr Glu Ser Leu
                565                 570                 575

Asp Ser Asp Leu Ser Phe Arg Gly Arg Glu Ile Val Ala Phe Glu Tyr
            580                 585                 590

Glu Asp Tyr Lys Glu Thr Val Thr Ser Trp Ala Asp Met Leu Gln Ser
        595                 600                 605

Val Leu Lys Val Leu Asn Gln Ser Phe Arg Gln Glu Leu Ile Ala Leu
    610                 615                 620

Thr Asn Glu Glu Ile Cys Leu Ala Thr Ser Asn Asn Ser Asn Ser Ser
625                 630                 635                 640

Leu Arg Glu Ile Asp His Gly Leu Phe Val Asp Thr Gly Ser Ser Thr
                645                 650                 655

Ser Val Lys Ile Gly Phe Leu Arg Arg Val Phe Thr Gln Leu Gly Leu
            660                 665                 670

Glu Gln Glu Ala Leu Val Phe Thr Leu Arg Pro Leu Ala Asn Asp Val
        675                 680                 685
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Glu Pro Arg Asp Asp Glu Leu Glu Val Glu Val Glu Lys Lys Tyr Ser
    690                 695                 700

Asp Leu Thr Lys Phe Ile Pro Gln Leu Glu Glu Ala Glu Asn Leu Glu
705                 710                 715                 720

Gly Ala Asp Thr Glu Val Ile Pro Leu Leu Ser Lys Leu Lys Glu Gln
                725                 730                 735

Leu Thr Ala Phe Ser Pro Glu Asn Pro Gln Ala Ala Leu Gly Gly Leu
            740                 745                 750

Pro Val Pro Glu Phe Leu Lys Gln Asn Val Ile Glu Gln Leu Ser Ala
        755                 760                 765

Glu His Ile Leu Ala Val Leu Thr Gln His Phe Asn Ile Ala Ser Met
    770                 775                 780

Met Gly Asp Asp Tyr Leu Leu Glu Glu Leu Arg Ser Gly Arg Leu Arg
785                 790                 795                 800

Glu Leu Leu Gln Arg Leu Glu Glu Leu Asp Ser
                805                 810
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CD 3D CD CD CD

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gcg ctg gta cat tcc ttg cgc gca tct gaa gtt gaa gaa ggt gag ttt   403
Ala Leu Val His Ser Leu Arg Ala Ser Glu Val Glu Glu Gly Glu Phe
                 90                  95                 100

aat gct ggc tac aac att gat cta gcc aca ttg att gag gat gac tac   451
Asn Ala Gly Tyr Asn Ile Asp Leu Ala Thr Leu Ile Glu Asp Asp Tyr
            105                 110                 115

ctc cga tcc ggc aat gag gga aac ctc aag ttc aag ctc aag cca gtt   499
Leu Arg Ser Gly Asn Glu Gly Asn Leu Lys Phe Lys Leu Lys Pro Val
        120                 125                 130

aaa aac gat aat gag gct tat caa aag ctc ttc ggc cca gaa tct gaa   547
Lys Asn Asp Asn Glu Ala Tyr Gln Lys Leu Phe Gly Pro Glu Ser Glu
    135                 140                 145

ttc ata gag tcc tca aac ctc act gct aat tat cgc tac ttc cgc aat   595
Phe Ile Glu Ser Ser Asn Leu Thr Ala Asn Tyr Arg Tyr Phe Arg Asn
150                 155                 160                 165

gtc ctt aag gca acc gat ctc acc gca gct caa cta tgg gaa gct atc   643
Val Leu Lys Ala Thr Asp Leu Thr Ala Ala Gln Leu Trp Glu Ala Ile
                170                 175                 180

gag aaa ctc agg gtc atg tat ctt gac ctt gag gaa ttt gat gat ccg   691
Glu Lys Leu Arg Val Met Tyr Leu Asp Leu Glu Glu Phe Asp Asp Pro
            185                 190                 195

cag cga atc ttt gaa agt ctc aac tcc acg gga tta gag ctc agt gaa   739
Gln Arg Ile Phe Glu Ser Leu Asn Ser Thr Gly Leu Glu Leu Ser Glu
        200                 205                 210

gct gat aag gta cgc aac ttg gtt ctt atg gat cag gag ctc aaa acc   787
Ala Asp Lys Val Arg Asn Leu Val Leu Met Asp Gln Glu Leu Lys Thr
    215                 220                 225

caa gaa aag ctc tat gag cag cgt tgg aat ccc att gaa gtc tgc gtg   835
Gln Glu Lys Leu Tyr Glu Gln Arg Trp Asn Pro Ile Glu Val Cys Val
230                 235                 240                 245

aaa ttt gat acc gac aat ttc att cgc tgg tac tta act ctc aaa acc   883
Lys Phe Asp Thr Asp Asn Phe Ile Arg Trp Tyr Leu Thr Leu Lys Thr
                250                 255                 260

gcg cgc acc cca aga aag caa gat gtt tat gag gaa ttc aag aaa ttc   931
Ala Arg Thr Pro Arg Lys Gln Asp Val Tyr Glu Glu Phe Lys Lys Phe
            265                 270                 275

atc cgt aac tcc aag ctc ccg gtc gaa ttc atc ctc gac gat atg tac   979
Ile Arg Asn Ser Lys Leu Pro Val Glu Phe Ile Leu Asp Asp Met Tyr
        280                 285                 290

gag tac gcg aag ctg tac cga gat ctc tta ggt gcc act act ggg ttt   1027
Glu Tyr Ala Lys Leu Tyr Arg Asp Leu Leu Gly Ala Thr Thr Gly Phe
    295                 300                 305

ata gct gcc gat agg tgt ctt aag cgt ttt gtc cct gtc atg ggc gat   1075
Ile Ala Ala Asp Arg Cys Leu Lys Arg Phe Val Pro Val Met Gly Asp
310                 315                 320                 325
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gtg gtt ttg cct ttt ctg ctg cct gtt ctc aaa gat gct aaa gac ggc   1123
Val Val Leu Pro Phe Leu Leu Pro Val Leu Lys Asp Ala Lys Asp Gly
                330                 335                 340

atc atc acc gaa tca gac ttc ctc gga gtt cta aaa gtt ctg gaa tcc   1171
Ile Ile Thr Glu Ser Asp Phe Leu Gly Val Leu Lys Val Leu Glu Ser
            345                 350                 355

tat tta ttc cgc cgt ttt gca gtc ggg gtt gct agt aac gcc tta agc   1219
Tyr Leu Phe Arg Arg Phe Ala Val Gly Val Ala Ser Asn Ala Leu Ser
        360                 365                 370

aag atc ttc tcc act gct tat agc gac atc aag aaa ttc tgg act cca   1267
Lys Ile Phe Ser Thr Ala Tyr Ser Asp Ile Lys Lys Phe Trp Thr Pro
    375                 380                 385

ggg caa agt tat agc tca ctg ctg gcc tac att ctg aaa cgt cgc gat   1315
Gly Gln Ser Tyr Ser Ser Leu Leu Ala Tyr Ile Leu Lys Arg Arg Asp
390                 395                 400                 405

ggt tcc ggg cgt ttt ccc tcc gac agt gaa ttc cgt gag aac ttc gca   1363
Gly Ser Gly Arg Phe Pro Ser Asp Ser Glu Phe Arg Glu Asn Phe Ala
                410                 415                 420

acc aaa aat ttc tgg aat att cat aac gaa aac agg cgt tac tta ttt   1411
Thr Lys Asn Phe Trp Asn Ile His Asn Glu Asn Arg Arg Tyr Leu Phe
            425                 430                 435

gat tgt cta gaa aat gcc gat tcc aat gat gtt cgt gac atc caa aca   1459
Asp Cys Leu Glu Asn Ala Asp Ser Asn Asp Val Arg Asp Ile Gln Thr
        440                 445                 450

agt ctg gat gaa gga tct ctc tcc att gaa cac atc atg cca cgt agc   1507
Ser Leu Asp Glu Gly Ser Leu Ser Ile Glu His Ile Met Pro Arg Ser
    455                 460                 465

cta aac gat cag tgg aga gct gaa ctc ggc cct gaa tat gct cga att   1555
Leu Asn Asp Gln Trp Arg Ala Glu Leu Gly Pro Glu Tyr Ala Arg Ile
470                 475                 480                 485

cat gag act tgg att aat aga att ggt aac ctc acc atc acc ggc tac   1603
His Glu Thr Trp Ile Asn Arg Ile Gly Asn Leu Thr Ile Thr Gly Tyr
                490                 495                 500

aac tcc gcc tat tca aat tct tcc tat gag cgc aag cgg acg atg gaa   1651
Asn Ser Ala Tyr Ser Asn Ser Ser Tyr Glu Arg Lys Arg Thr Met Glu
            505                 510                 515

aat gga ttt ttg gta tcc ccc tat cgc atc aat aat ttc atc aaa aag   1699
Asn Gly Phe Leu Val Ser Pro Tyr Arg Ile Asn Asn Phe Ile Lys Lys
        520                 525                 530

cag aag cat tgg tct gaa gaa cag cta att gag cga acc gag ctg ctc   1747
Gln Lys His Trp Ser Glu Glu Gln Leu Ile Glu Arg Thr Glu Leu Leu
    535                 540                 545

act caa gca gcg ctg gac tac tgg ccc ctt cca aaa gaa acc ttc cag   1795
Thr Gln Ala Ala Leu Asp Tyr Trp Pro Leu Pro Lys Glu Thr Phe Gln
550                 555                 560                 565

cca cca caa gct gtg ctt cct aca gaa tcc tta gat agt gat ctt tct   1843
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Pro Pro Gln Ala Val Leu Pro Thr Glu Ser Leu Asp Ser Asp Leu Ser
                570                 575                 580

ttc cgc gga cgc gaa att gtc gcc ttt gaa tat gag gac tac aag gaa   1891
Phe Arg Gly Arg Glu Ile Val Ala Phe Glu Tyr Glu Asp Tyr Lys Glu
            585                 590                 595

acg gta acg tcc tgg gca gac atg ctc cag agc gtt cta aaa gtc ttg   1939
Thr Val Thr Ser Trp Ala Asp Met Leu Gln Ser Val Leu Lys Val Leu
        600                 605                 610

aac caa tcc ttc cgc cag gaa ctc ata gct ttg acc aat gaa gaa atc   1987
Asn Gln Ser Phe Arg Gln Glu Leu Ile Ala Leu Thr Asn Glu Glu Ile
    615                 620                 625

tgc ctg gca act tca aac aac agt aac agc agt ctc cgt gaa att gac   2035
Cys Leu Ala Thr Ser Asn Asn Ser Asn Ser Ser Leu Arg Glu Ile Asp
630                 635                 640                 645

cac ggg ctt ttt gta gac act ggc tct agt acg agt gta aag att ggc   2083
His Gly Leu Phe Val Asp Thr Gly Ser Ser Thr Ser Val Lys Ile Gly
                650                 655                 660

ttc ctc cgc aga gtt ttt act caa ctg ggg cta gag cag gaa gca ttg   2131
Phe Leu Arg Arg Val Phe Thr Gln Leu Gly Leu Glu Gln Glu Ala Leu
            665                 670                 675

gtt ttc acc ctt cga cca ctg gca aat gat gta gaa ccc cga gat gat   2179
Val Phe Thr Leu Arg Pro Leu Ala Asn Asp Val Glu Pro Arg Asp Asp
        680                 685                 690

gaa ctc gag gta gag gta gaa aag aaa tat tcc gat ttg act aaa ttc   2227
Glu Leu Glu Val Glu Val Glu Lys Lys Tyr Ser Asp Leu Thr Lys Phe
    695                 700                 705

atc cca cag tta gaa gaa gct gag aat ctc gag ggg gcg gat aca gag   2275
Ile Pro Gln Leu Glu Glu Ala Glu Asn Leu Glu Gly Ala Asp Thr Glu
710                 715                 720                 725

gtt att cct ctc ctc tca aag ctc aag gaa caa ctg aca gcc ttt agc   2323
Val Ile Pro Leu Leu Ser Lys Leu Lys Glu Gln Leu Thr Ala Phe Ser
                730                 735                 740

ccg gag aat cct caa gca gcc cta ggg ggc cta cct gtt cca gaa ttc   2371
Pro Glu Asn Pro Gln Ala Ala Leu Gly Gly Leu Pro Val Pro Glu Phe
            745                 750                 755

ctc aaa caa aat gtg att gaa caa cta agc gca gag cac atc ctt gct   2419
Leu Lys Gln Asn Val Ile Glu Gln Leu Ser Ala Glu His Ile Leu Ala
        760                 765                 770

gta ctc act caa cac ttt aat atc gca tcc atg atg ggt gat gac tat   2467
Val Leu Thr Gln His Phe Asn Ile Ala Ser Met Met Gly Asp Asp Tyr
    775                 780                 785

ttg ctc gaa gag ctc agg tca ggc cgc tta agg gaa tta ctg cag cgt   2515
Leu Leu Glu Glu Leu Arg Ser Gly Arg Leu Arg Glu Leu Leu Gln Arg
790                 795                 800                 805

tta gag gaa ttg gat agc taatagccgt agtcggtggt caa                 2556
Leu Glu Glu Leu Asp Ser
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810

<210> 1116
<211> 811
<212> PRT
<213> Corynebacterium glutamicum

<400> 1116

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Met Arg Gly Asp Val Gln Lys Ile Thr Lys Val Tyr Asp Gly Lys His
  1               5                  10                  15

Arg Thr Leu Glu Ile Pro Val Tyr Gln Arg Asn Tyr Asp Trp Thr Glu
             20                  25                  30

Lys Gln Cys Ser Arg Leu Phe Asp Asp Leu Ser Glu Val Val Lys Glu
         35                  40                  45

Asn His Arg Gln His Phe Phe Gly Ala Val Val Gly Lys Pro Gln Gly
     50                  55                  60

Ser Trp Thr Trp Val Val Ile Asp Gly Gln Gln Arg Leu Thr Thr Ile
 65                  70                  75                  80

Ser Leu Phe Met Leu Ala Leu Val His Ser Leu Arg Ala Ser Glu Val
                 85                  90                  95

Glu Glu Gly Glu Phe Asn Ala Gly Tyr Asn Ile Asp Leu Ala Thr Leu
            100                 105                 110

Ile Glu Asp Asp Tyr Leu Arg Ser Gly Asn Glu Gly Asn Leu Lys Phe
        115                 120                 125

Lys Leu Lys Pro Val Lys Asn Asp Asn Glu Ala Tyr Gln Lys Leu Phe
    130                 135                 140

Gly Pro Glu Ser Glu Phe Ile Glu Ser Ser Asn Leu Thr Ala Asn Tyr
145                 150                 155                 160

Arg Tyr Phe Arg Asn Val Leu Lys Ala Thr Asp Leu Thr Ala Ala Gln
                165                 170                 175

Leu Trp Glu Ala Ile Glu Lys Leu Arg Val Met Tyr Leu Asp Leu Glu
            180                 185                 190

Glu Phe Asp Asp Pro Gln Arg Ile Phe Glu Ser Leu Asn Ser Thr Gly
        195                 200                 205

Leu Glu Leu Ser Glu Ala Asp Lys Val Arg Asn Leu Val Leu Met Asp
    210                 215                 220

Gln Glu Leu Lys Thr Gln Glu Lys Leu Tyr Glu Gln Arg Trp Asn Pro
225                 230                 235                 240

Ile Glu Val Cys Val Lys Phe Asp Thr Asp Asn Phe Ile Arg Trp Tyr
                245                 250                 255

Leu Thr Leu Lys Thr Ala Arg Thr Pro Arg Lys Gln Asp Val Tyr Glu
            260                 265                 270

Glu Phe Lys Lys Phe Ile Arg Asn Ser Lys Leu Pro Val Glu Phe Ile
```

```
        275                 280                 285

Leu Asp Asp Met Tyr Glu Tyr Ala Lys Leu Tyr Arg Asp Leu Leu Gly
    290                 295                 300

Ala Thr Thr Gly Phe Ile Ala Ala Asp Arg Cys Leu Lys Arg Phe Val
305                 310                 315                 320

Pro Val Met Gly Asp Val Val Leu Pro Phe Leu Leu Pro Val Leu Lys
                325                 330                 335

Asp Ala Lys Asp Gly Ile Ile Thr Glu Ser Asp Phe Leu Gly Val Leu
            340                 345                 350

Lys Val Leu Glu Ser Tyr Leu Phe Arg Arg Phe Ala Val Gly Val Ala
        355                 360                 365

Ser Asn Ala Leu Ser Lys Ile Phe Ser Thr Ala Tyr Ser Asp Ile Lys
    370                 375                 380

Lys Phe Trp Thr Pro Gly Gln Ser Tyr Ser Ser Leu Leu Ala Tyr Ile
385                 390                 395                 400

Leu Lys Arg Arg Asp Gly Ser Gly Arg Phe Pro Ser Asp Ser Glu Phe
                405                 410                 415

Arg Glu Asn Phe Ala Thr Lys Asn Phe Trp Asn Ile His Asn Glu Asn
            420                 425                 430

Arg Arg Tyr Leu Phe Asp Cys Leu Glu Asn Ala Asp Ser Asn Asp Val
        435                 440                 445

Arg Asp Ile Gln Thr Ser Leu Asp Glu Gly Ser Leu Ser Ile Glu His
    450                 455                 460

Ile Met Pro Arg Ser Leu Asn Asp Gln Trp Arg Ala Glu Leu Gly Pro
465                 470                 475                 480

Glu Tyr Ala Arg Ile His Glu Thr Trp Ile Asn Arg Ile Gly Asn Leu
                485                 490                 495

Thr Ile Thr Gly Tyr Asn Ser Ala Tyr Ser Asn Ser Ser Tyr Glu Arg
            500                 505                 510

Lys Arg Thr Met Glu Asn Gly Phe Leu Val Ser Pro Tyr Arg Ile Asn
        515                 520                 525

Asn Phe Ile Lys Lys Gln Lys His Trp Ser Glu Glu Gln Leu Ile Glu
    530                 535                 540

Arg Thr Glu Leu Leu Thr Gln Ala Ala Leu Asp Tyr Trp Pro Leu Pro
545                 550                 555                 560

Lys Glu Thr Phe Gln Pro Pro Gln Ala Val Leu Pro Thr Glu Ser Leu
                565                 570                 575

Asp Ser Asp Leu Ser Phe Arg Gly Arg Glu Ile Val Ala Phe Glu Tyr
            580                 585                 590

Glu Asp Tyr Lys Glu Thr Val Thr Ser Trp Ala Asp Met Leu Gln Ser
        595                 600                 605
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```
Val Leu Lys Val Leu Asn Gln Ser Phe Arg Gln Glu Leu Ile Ala Leu
    610                 615                 620

Thr Asn Glu Glu Ile Cys Leu Ala Thr Ser Asn Asn Ser Asn Ser Ser
625                 630                 635                 640

Leu Arg Glu Ile Asp His Gly Leu Phe Val Asp Thr Gly Ser Ser Thr
                645                 650                 655

Ser Val Lys Ile Gly Phe Leu Arg Arg Val Phe Thr Gln Leu Gly Leu
            660                 665                 670

Glu Gln Glu Ala Leu Val Phe Thr Leu Arg Pro Leu Ala Asn Asp Val
        675                 680                 685

Glu Pro Arg Asp Asp Glu Leu Glu Val Glu Val Glu Lys Lys Tyr Ser
    690                 695                 700

Asp Leu Thr Lys Phe Ile Pro Gln Leu Glu Glu Ala Glu Asn Leu Glu
705                 710                 715                 720

Gly Ala Asp Thr Glu Val Ile Pro Leu Leu Ser Lys Leu Lys Glu Gln
                725                 730                 735

Leu Thr Ala Phe Ser Pro Glu Asn Pro Gln Ala Ala Leu Gly Gly Leu
            740                 745                 750

Pro Val Pro Glu Phe Leu Lys Gln Asn Val Ile Glu Gln Leu Ser Ala
        755                 760                 765

Glu His Ile Leu Ala Val Leu Thr Gln His Phe Asn Ile Ala Ser Met
    770                 775                 780

Met Gly Asp Asp Tyr Leu Leu Glu Glu Leu Arg Ser Gly Arg Leu Arg
785                 790                 795                 800

Glu Leu Leu Gln Arg Leu Glu Glu Leu Asp Ser
                805                 810
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<210> 1117
<211> 774
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> RXN02361

<400> 1117
tagaggaatt ggatagctaa tagccgtagt cggtggtcaa actttgacca ccggactccc 60

ctttaagcac aatctctagc ttttatttag gcttggagtt atg gaa ctt ctc tcc 115
                                              Met Glu Leu Leu Ser
                                                1   5

cac ttg ctt gct ctt gat cct gcc tcc cct cgt ttg act gtt tat aac 163
His Leu Leu Ala Leu Asp Pro Ala Ser Pro Arg Leu Thr Val Tyr Asn
                10   15   20

```
gag tcc acg ggt gcg cgt ttg gat ttc tcc gcc atc act ctt gat aac   211
Glu Ser Thr Gly Ala Arg Leu Asp Phe Ser Ala Ile Thr Leu Asp Asn
             25                  30                  35

tgg gcg tcc aag gtt ggc aat atg ctc ctt gag gaa ttg gat ctg gag   259
Trp Ala Ser Lys Val Gly Asn Met Leu Leu Glu Glu Leu Asp Leu Glu
         40                  45                  50

gaa ggc tcg ctc atc act att gat ttg ccg gtg agc tgg cag gcc gca   307
Glu Gly Ser Leu Ile Thr Ile Asp Leu Pro Val Ser Trp Gln Ala Ala
     55                  60                  65

atg att atg ctc ggc gct tta gca act agt gtt gag gtc tct ttt gat   355
Met Ile Met Leu Gly Ala Leu Ala Thr Ser Val Glu Val Ser Phe Asp
 70                  75                  80                  85

gat ccc gag gca gat gcc atc ttt acc tcc ctc gat aga ttt tcc cac   403
Asp Pro Glu Ala Asp Ala Ile Phe Thr Ser Leu Asp Arg Phe Ser His
                 90                  95                 100

tac aag ggc cat agt gat gtg ctg att gtc agc gag gat cct ttt ggt   451
Tyr Lys Gly His Ser Asp Val Leu Ile Val Ser Glu Asp Pro Phe Gly
            105                 110                 115

cgt gga gtt gtt gaa ggt ggc ggt gaa ctg cct aat ggt gcc atc gat   499
Arg Gly Val Val Glu Gly Gly Gly Glu Leu Pro Asn Gly Ala Ile Asp
        120                 125                 130

ttt ggc ccc aca gtg cgt ttt tat ggc gat caa ttc ttc cag cct acc   547
Phe Gly Pro Thr Val Arg Phe Tyr Gly Asp Gln Phe Phe Gln Pro Thr
    135                 140                 145

cgc aca ttg ccg gaa atc atc cag cat tct gat gtt ccg gtt ggc gcc   595
Arg Thr Leu Pro Glu Ile Ile Gln His Ser Asp Val Pro Val Gly Ala
150                 155                 160                 165

aga gtt ctt gca act ggt tgg tca gat atc gag tcc ttc aat cac cag   643
Arg Val Leu Ala Thr Gly Trp Ser Asp Ile Glu Ser Phe Asn His Gln
                170                 175                 180

gtt tta gaa cca ctc gca gtg ggt ggc tct gca gta att gtg acc gga   691
Val Leu Glu Pro Leu Ala Val Gly Gly Ser Ala Val Ile Val Thr Gly
            185                 190                 195

ctg gct gat att gag cgt tta aac cag att gca acc aat gag aag aca   739
Leu Ala Asp Ile Glu Arg Leu Asn Gln Ile Ala Thr Asn Glu Lys Thr
        200                 205                 210

acc cac cgt atc taggcaaatt tcggttacta cta                        774
Thr His Arg Ile
    215
```

CONFIDENTIAL

<210> 1118
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 1118

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Met Glu Leu Leu Ser His Leu Leu Ala Leu Asp Pro Ala Ser Pro Arg
```

```
  1               5                  10                  15

Leu Thr Val Tyr Asn Glu Ser Thr Gly Ala Arg Leu Asp Phe Ser Ala
             20                  25                  30

Ile Thr Leu Asp Asn Trp Ala Ser Lys Val Gly Asn Met Leu Leu Glu
         35                  40                  45

Glu Leu Asp Leu Glu Glu Gly Ser Leu Ile Thr Ile Asp Leu Pro Val
     50                  55                  60

Ser Trp Gln Ala Ala Met Ile Met Leu Gly Ala Leu Ala Thr Ser Val
 65                  70                  75                  80

Glu Val Ser Phe Asp Asp Pro Glu Ala Asp Ala Ile Phe Thr Ser Leu
                 85                  90                  95

Asp Arg Phe Ser His Tyr Lys Gly His Ser Asp Val Leu Ile Val Ser
            100                 105                 110

Glu Asp Pro Phe Gly Arg Gly Val Val Glu Gly Gly Gly Glu Leu Pro
        115                 120                 125

Asn Gly Ala Ile Asp Phe Gly Pro Thr Val Arg Phe Tyr Gly Asp Gln
    130                 135                 140

Phe Phe Gln Pro Thr Arg Thr Leu Pro Glu Ile Ile Gln His Ser Asp
145                 150                 155                 160

Val Pro Val Gly Ala Arg Val Leu Ala Thr Gly Trp Ser Asp Ile Glu
                165                 170                 175

Ser Phe Asn His Gln Val Leu Glu Pro Leu Ala Val Gly Gly Ser Ala
            180                 185                 190

Val Ile Val Thr Gly Leu Ala Asp Ile Glu Arg Leu Asn Gln Ile Ala
        195                 200                 205

Thr Asn Glu Lys Thr Thr His Arg Ile
    210                 215
```

09/09/2003 09:09:09 PM

<210> 1119
<211> 774
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> FRXA02361

<400> 1119
tagaggaatt ggatagctaa tagccgtagt cggtggtcaa actttgacca ccggactccc 60

ctttaagcac aatctctagc ttttatttag gcttggagtt atg gaa ctt ctc tcc 115
                                              Met Glu Leu Leu Ser
                                                1   5

cac ttg ctt gct ctt gat cct gcc tcc cct cgt ttg act gtt tat aac 163
His Leu Leu Ala Leu Asp Pro Ala Ser Pro Arg Leu Thr Val Tyr Asn

```
                10                  15                  20

gag tcc acg ggt gcg cgt ttg gat ttc tcc gcc atc act ctt gat aac   211
Glu Ser Thr Gly Ala Arg Leu Asp Phe Ser Ala Ile Thr Leu Asp Asn
            25                  30                  35

tgg gcg tcc aag gtt ggc aat atg ctc ctt gag gaa ttg gat ctg gag   259
Trp Ala Ser Lys Val Gly Asn Met Leu Leu Glu Glu Leu Asp Leu Glu
        40                  45                  50

gaa ggc tcg ctc atc act att gat ttg ccg gtg agc tgg cag gcc gca   307
Glu Gly Ser Leu Ile Thr Ile Asp Leu Pro Val Ser Trp Gln Ala Ala
    55                  60                  65

atg att atg ctc ggc gct tta gca act agt gtt gag gtc tct ttt gat   355
Met Ile Met Leu Gly Ala Leu Ala Thr Ser Val Glu Val Ser Phe Asp
70                  75                  80                  85

gat ccc gag gca gat gcc atc ttt acc tcc ctc gat aga ttt tcc cac   403
Asp Pro Glu Ala Asp Ala Ile Phe Thr Ser Leu Asp Arg Phe Ser His
                90                  95                  100

tac aag ggc cat agt gat gtg ctg att gtc agc gag gat cct ttt ggt   451
Tyr Lys Gly His Ser Asp Val Leu Ile Val Ser Glu Asp Pro Phe Gly
            105                 110                 115

cgt gga gtt gtt gaa ggt ggc ggt gaa ctg cct aat ggt gcc atc gat   499
Arg Gly Val Val Glu Gly Gly Gly Glu Leu Pro Asn Gly Ala Ile Asp
        120                 125                 130

ttt ggc ccc aca gtg cgt ttt tat ggc gat caa ttc ttc cag cct acc   547
Phe Gly Pro Thr Val Arg Phe Tyr Gly Asp Gln Phe Phe Gln Pro Thr
    135                 140                 145

cgc aca ttg ccg gaa atc atc cag cat tct gat gtt ccg gtt ggc gcc   595
Arg Thr Leu Pro Glu Ile Ile Gln His Ser Asp Val Pro Val Gly Ala
150                 155                 160                 165

aga gtt ctt gca act ggt tgg tca gat atc gag tcc ttc aat cac cag   643
Arg Val Leu Ala Thr Gly Trp Ser Asp Ile Glu Ser Phe Asn His Gln
                170                 175                 180

gtt tta gaa cca ctc gca gtg ggt ggc tct gca gta att gtg acc gga   691
Val Leu Glu Pro Leu Ala Val Gly Gly Ser Ala Val Ile Val Thr Gly
            185                 190                 195

ctg gct gat att gag cgt tta aac cag att gca acc aat gag aag aca   739
Leu Ala Asp Ile Glu Arg Leu Asn Gln Ile Ala Thr Asn Glu Lys Thr
        200                 205                 210

acc cac cgt atc taggcaaatt tcggttacta cta                        774
Thr His Arg Ile
    215
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Sequence Listing - 09/09/2009 09:09:09

<210> 1120
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 1120

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Met Glu Leu Leu Ser His Leu Leu Ala Leu Asp Pro Ala Ser Pro Arg
  1               5                  10                  15

Leu Thr Val Tyr Asn Glu Ser Thr Gly Ala Arg Leu Asp Phe Ser Ala
             20                  25                  30

Ile Thr Leu Asp Asn Trp Ala Ser Lys Val Gly Asn Met Leu Leu Glu
         35                  40                  45

Glu Leu Asp Leu Glu Glu Gly Ser Leu Ile Thr Ile Asp Leu Pro Val
     50                  55                  60

Ser Trp Gln Ala Ala Met Ile Met Leu Gly Ala Leu Ala Thr Ser Val
 65                  70                  75                  80

Glu Val Ser Phe Asp Asp Pro Glu Ala Asp Ala Ile Phe Thr Ser Leu
                 85                  90                  95

Asp Arg Phe Ser His Tyr Lys Gly His Ser Asp Val Leu Ile Val Ser
            100                 105                 110

Glu Asp Pro Phe Gly Arg Gly Val Val Glu Gly Gly Gly Glu Leu Pro
        115                 120                 125

Asn Gly Ala Ile Asp Phe Gly Pro Thr Val Arg Phe Tyr Gly Asp Gln
    130                 135                 140

Phe Phe Gln Pro Thr Arg Thr Leu Pro Glu Ile Ile Gln His Ser Asp
145                 150                 155                 160

Val Pro Val Gly Ala Arg Val Leu Ala Thr Gly Trp Ser Asp Ile Glu
                165                 170                 175

Ser Phe Asn His Gln Val Leu Glu Pro Leu Ala Val Gly Gly Ser Ala
            180                 185                 190

Val Ile Val Thr Gly Leu Ala Asp Ile Glu Arg Leu Asn Gln Ile Ala
        195                 200                 205

Thr Asn Glu Lys Thr Thr His Arg Ile
    210                 215
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09/25/2003 09:56:50

<210> 1121
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> RXN02367

<400> 1121
ggcacttgaa tccggacgct aagttgttga tacatcaact tatttcttgg ctatacttga 60

ggtcacgttt cctcagctca ggagaagttc ggagaagtcc atg tca aac gca gaa 115
Met Ser Asn Ala Glu
1 5

att aat ccc gtt gaa tat gaa atc aac aac cac gcc cct ggt acc gcg 163

```
Ile Asn Pro Val Glu Tyr Glu Ile Asn Asn His Ala Pro Gly Thr Ala
                 10                  15                  20

cta aac cca cag tgc gaa gac ggc gcc aac gta gaa atc atc acc tcc   211
Leu Asn Pro Gln Cys Glu Asp Gly Ala Asn Val Glu Ile Ile Thr Ser
             25                  30                  35

cgt gaa gtc ccc ctc ggc gga cca cgc gcc atg acc gtg cac cgc aca   259
Arg Glu Val Pro Leu Gly Gly Pro Arg Ala Met Thr Val His Arg Thr
         40                  45                  50

ctc ccc caa cgc cag cgc tcc ctc atc ggt gcc tgg tgt ttt gtg gat   307
Leu Pro Gln Arg Gln Arg Ser Leu Ile Gly Ala Trp Cys Phe Val Asp
     55                  60                  65

cat tac ggc ccc gat gat gtc tca cta acc ggt ggc atg gat atg gcc   355
His Tyr Gly Pro Asp Asp Val Ser Leu Thr Gly Gly Met Asp Met Ala
 70                  75                  80                  85

tcc cac ccg cac acc gga ttg caa aca gtc acg tgg ctt ttt gaa ggc   403
Ser His Pro His Thr Gly Leu Gln Thr Val Thr Trp Leu Phe Glu Gly
                 90                  95                 100

gaa gtc acc cac cat gat tcc ggc gga aat cac gca gtc gtg ctt cct   451
Glu Val Thr His His Asp Ser Gly Gly Asn His Ala Val Val Leu Pro
             105                 110                 115

ggc gaa gtc aac ctc atg acc gcc ggc gca ggc atc tgt cac acc gaa   499
Gly Glu Val Asn Leu Met Thr Ala Gly Ala Gly Ile Cys His Thr Glu
         120                 125                 130

gtt tcc gcc acc tcc acc acg att ctg cat ggt ctg cag ttg tgg aca   547
Val Ser Ala Thr Ser Thr Thr Ile Leu His Gly Leu Gln Leu Trp Thr
     135                 140                 145

gtt ctt ccc gac aaa gac cgc gaa gga cca cgc cgc ttt gat cac tac   595
Val Leu Pro Asp Lys Asp Arg Glu Gly Pro Arg Arg Phe Asp His Tyr
150                 155                 160                 165

gct cca gaa gaa atc aca ctc gaa ggc gga agt gca cgc gtt ttc cta   643
Ala Pro Glu Glu Ile Thr Leu Glu Gly Gly Ser Ala Arg Val Phe Leu
                 170                 175                 180

ggt tcg cta ttt ggt caa acc tcc cct gtt cat acg ttt act ggc tct   691
Gly Ser Leu Phe Gly Gln Thr Ser Pro Val His Thr Phe Thr Gly Ser
             185                 190                 195

tcc tgt ttt aga gtg cat tgatcttatg gaccaactgc cct                 732
Ser Cys Phe Arg Val His
         200


<210> 1122
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 1122
Met Ser Asn Ala Glu Ile Asn Pro Val Glu Tyr Glu Ile Asn Asn His
  1               5                  10                  15
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```
Ala Pro Gly Thr Ala Leu Asn Pro Gln Cys Glu Asp Gly Ala Asn Val
             20                  25                  30

Glu Ile Ile Thr Ser Arg Glu Val Pro Leu Gly Gly Pro Arg Ala Met
         35                  40                  45

Thr Val His Arg Thr Leu Pro Gln Arg Gln Arg Ser Leu Ile Gly Ala
     50                  55                  60

Trp Cys Phe Val Asp His Tyr Gly Pro Asp Asp Val Ser Leu Thr Gly
 65                  70                  75                  80

Gly Met Asp Met Ala Ser His Pro His Thr Gly Leu Gln Thr Val Thr
                 85                  90                  95

Trp Leu Phe Glu Gly Glu Val Thr His His Asp Ser Gly Gly Asn His
            100                 105                 110

Ala Val Val Leu Pro Gly Glu Val Asn Leu Met Thr Ala Gly Ala Gly
        115                 120                 125

Ile Cys His Thr Glu Val Ser Ala Thr Ser Thr Thr Ile Leu His Gly
    130                 135                 140

Leu Gln Leu Trp Thr Val Leu Pro Asp Lys Asp Arg Glu Gly Pro Arg
145                 150                 155                 160

Arg Phe Asp His Tyr Ala Pro Glu Glu Ile Thr Leu Glu Gly Gly Ser
                165                 170                 175

Ala Arg Val Phe Leu Gly Ser Leu Phe Gly Gln Thr Ser Pro Val His
            180                 185                 190

Thr Phe Thr Gly Ser Ser Cys Phe Arg Val His
        195                 200
```

<210> 1123
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> FRXA02367

<400> 1123

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ggcacttgaa tccggacgct aagttgttga tacatcaact tatttcttgg ctatacttga 60

ggtcacgttt cctcagctca ggagaagttc ggagaagtcc atg tca aac gca gaa   115
                                              Met Ser Asn Ala Glu
                                                1               5

att aat ccc gtt gaa tat gaa atc aac aac cac gcc cct ggt acc gcg   163
Ile Asn Pro Val Glu Tyr Glu Ile Asn Asn His Ala Pro Gly Thr Ala
                10                  15                  20

cta aac cca cag tgc gaa gac ggc gcc aac gta gaa atc atc acc tcc   211
Leu Asn Pro Gln Cys Glu Asp Gly Ala Asn Val Glu Ile Ile Thr Ser
            25                  30                  35
```

```
cgt gaa gtc ccc ctc ggc gga cca cgc gcc atg acc gtg cac cgc aca   259
Arg Glu Val Pro Leu Gly Gly Pro Arg Ala Met Thr Val His Arg Thr
         40                  45                  50

ctc ccc caa cgc cag cgc tcc ctc atc ggt gcc tgg tgt ttt gtg gat   307
Leu Pro Gln Arg Gln Arg Ser Leu Ile Gly Ala Trp Cys Phe Val Asp
     55                  60                  65

cat tac ggc ccc gat gat gtc tca cta acc ggt ggc atg gat atg gcc   355
His Tyr Gly Pro Asp Asp Val Ser Leu Thr Gly Gly Met Asp Met Ala
 70                  75                  80                  85

tcc cac ccg cac acc gga ttg caa aca gtc acg tgg ctt ttt gaa ggc   403
Ser His Pro His Thr Gly Leu Gln Thr Val Thr Trp Leu Phe Glu Gly
                 90                  95                 100

gaa gtc acc cac cat gat tcc ggc gga aat cac gca gtc gtg ctt cct   451
Glu Val Thr His His Asp Ser Gly Gly Asn His Ala Val Val Leu Pro
            105                 110                 115

ggc gaa gtc aac ctc atg acc gcc ggc gca ggc atc tgt cac acc gaa   499
Gly Glu Val Asn Leu Met Thr Ala Gly Ala Gly Ile Cys His Thr Glu
        120                 125                 130

gtt tcc gcc acc tcc acc acg att ctg cat ggt ctg cag ttg tgg aca   547
Val Ser Ala Thr Ser Thr Thr Ile Leu His Gly Leu Gln Leu Trp Thr
    135                 140                 145

gtt ctt ccc gac aaa gac cgc gaa gga cca cgc cgc ttt gat cac tac   595
Val Leu Pro Asp Lys Asp Arg Glu Gly Pro Arg Arg Phe Asp His Tyr
150                 155                 160                 165

gct cca gaa gaa atc aca ctc gaa ggc gga agt gca cgc gtt ttc cta   643
Ala Pro Glu Glu Ile Thr Leu Glu Gly Gly Ser Ala Arg Val Phe Leu
                170                 175                 180

ggt tcg cta ttt ggt caa acc tcc cct gtt cat acg ttt act ggc tct   691
Gly Ser Leu Phe Gly Gln Thr Ser Pro Val His Thr Phe Thr Gly Ser
            185                 190                 195

tcc tgt ttt aga gtg cat tgatcttatg gaccaactgc cct                732
Ser Cys Phe Arg Val His
        200
```

<210> 1124
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 1124

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Met Ser Asn Ala Glu Ile Asn Pro Val Glu Tyr Glu Ile Asn Asn His
  1               5                  10                  15

Ala Pro Gly Thr Ala Leu Asn Pro Gln Cys Glu Asp Gly Ala Asn Val
             20                  25                  30

Glu Ile Ile Thr Ser Arg Glu Val Pro Leu Gly Gly Pro Arg Ala Met
         35                  40                  45
```

```
Thr Val His Arg Thr Leu Pro Gln Arg Gln Arg Ser Leu Ile Gly Ala
     50                  55                  60

Trp Cys Phe Val Asp His Tyr Gly Pro Asp Asp Val Ser Leu Thr Gly
 65                  70                  75                  80

Gly Met Asp Met Ala Ser His Pro His Thr Gly Leu Gln Thr Val Thr
                 85                  90                  95

Trp Leu Phe Glu Gly Glu Val Thr His His Asp Ser Gly Gly Asn His
            100                 105                 110

Ala Val Val Leu Pro Gly Glu Val Asn Leu Met Thr Ala Gly Ala Gly
        115                 120                 125

Ile Cys His Thr Glu Val Ser Ala Thr Ser Thr Thr Ile Leu His Gly
    130                 135                 140

Leu Gln Leu Trp Thr Val Leu Pro Asp Lys Asp Arg Glu Gly Pro Arg
145                 150                 155                 160

Arg Phe Asp His Tyr Ala Pro Glu Glu Ile Thr Leu Glu Gly Gly Ser
                165                 170                 175

Ala Arg Val Phe Leu Gly Ser Leu Phe Gly Gln Thr Ser Pro Val His
            180                 185                 190

Thr Phe Thr Gly Ser Ser Cys Phe Arg Val His
        195                 200
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09/25/2003 09:55 AM

<210> 1125
<211> 798
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> RXN02368

<400> 1125

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cttaggtcaa gcttgcattt attggctagt gtcggaaatc atgggagatt tagcaaagca 60

catgggcagt gaaccaccag catggtggaa gtttttaccg atg att gtc ctc gct   115
                                            Met Ile Val Leu Ala
                                              1               5

gga gcc act cga gtt acc tat gaa gta gaa cct tgg ctg gcg atc cca   163
Gly Ala Thr Arg Val Thr Tyr Glu Val Glu Pro Trp Leu Ala Ile Pro
                 10                  15                  20

tta ttc att ttg gct ttt gca tcg ata ttg atc cca ttc ccg atc tct   211
Leu Phe Ile Leu Ala Phe Ala Ser Ile Leu Ile Pro Phe Pro Ile Ser
             25                  30                  35

aag aca aaa gga ctc cgt gat atc gat gcc tgg aaa atc cac acc acg   259
Lys Thr Lys Gly Leu Arg Asp Ile Asp Ala Trp Lys Ile His Thr Thr
         40                  45                  50

caa ggc gat aaa aag cgt gcc atc cgc caa ctg atc att ccg gct acg   307
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```
Gln Gly Asp Lys Lys Arg Ala Ile Arg Gln Leu Ile Ile Pro Ala Thr
     55                  60                  65

gct ttg gcc atc gac atc att ggg ctg ccg aca tta ttt aat gcc cct   355
Ala Leu Ala Ile Asp Ile Ile Gly Leu Pro Thr Leu Phe Asn Ala Pro
 70                  75                  80                  85

ccc ctt gct tcc gct gca ctt ttt ggc ggt gtt tac ggc gct tcc cta   403
Pro Leu Ala Ser Ala Ala Leu Phe Gly Gly Val Tyr Gly Ala Ser Leu
                 90                  95                 100

gct tgg gct gcg tac aga gct gat cag ctt cca cgc att cga acg aag   451
Ala Trp Ala Ala Tyr Arg Ala Asp Gln Leu Pro Arg Ile Arg Thr Lys
            105                 110                 115

gaa cgc ctc gca gaa ctt tca caa aat gca tct ctg gat gat gtg cgc   499
Glu Arg Leu Ala Glu Leu Ser Gln Asn Ala Ser Leu Asp Asp Val Arg
        120                 125                 130

tca gat gac tta gat gtt cta gag cag ccg gaa tcc cgt gaa tta gtg   547
Ser Asp Asp Leu Asp Val Leu Glu Gln Pro Glu Ser Arg Glu Leu Val
    135                 140                 145

cgc tgt ctg ctt gcc cac ggt gcg atg gat ggc act cgg gtg atg gcc   595
Arg Cys Leu Leu Ala His Gly Ala Met Asp Gly Thr Arg Val Met Ala
150                 155                 160                 165

aga cag gtc gcg cga gta ctg gat acc gag gta gac gaa gta cat cag   643
Arg Gln Val Ala Arg Val Leu Asp Thr Glu Val Asp Glu Val His Gln
                170                 175                 180

gta gca cgc tca cta gaa cag cat ggt ttg gtt agt cgc tcc acc atc   691
Val Ala Arg Ser Leu Glu Gln His Gly Leu Val Ser Arg Ser Thr Ile
            185                 190                 195

atg ccg ggt ggg gat cca gga aaa gta ttc atc gaa gtt tcc ctg aaa   739
Met Pro Gly Gly Asp Pro Gly Lys Val Phe Ile Glu Val Ser Leu Lys
        200                 205                 210

ggg atc tca gcc atc aag gca ctt gaa tcc gga cgc taagttgttg        785
Gly Ile Ser Ala Ile Lys Ala Leu Glu Ser Gly Arg
    215                 220                 225

atacatcaac tta                                                   798


<210> 1126
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 1126
Met Ile Val Leu Ala Gly Ala Thr Arg Val Thr Tyr Glu Val Glu Pro
  1               5                  10                  15

Trp Leu Ala Ile Pro Leu Phe Ile Leu Ala Phe Ala Ser Ile Leu Ile
             20                  25                  30

Pro Phe Pro Ile Ser Lys Thr Lys Gly Leu Arg Asp Ile Asp Ala Trp
         35                  40                  45
```

```
Lys Ile His Thr Thr Gln Gly Asp Lys Lys Arg Ala Ile Arg Gln Leu
     50                  55                  60

Ile Ile Pro Ala Thr Ala Leu Ala Ile Asp Ile Ile Gly Leu Pro Thr
 65                  70                  75                  80

Leu Phe Asn Ala Pro Pro Leu Ala Ser Ala Ala Leu Phe Gly Gly Val
                 85                  90                  95

Tyr Gly Ala Ser Leu Ala Trp Ala Ala Tyr Arg Ala Asp Gln Leu Pro
            100                 105                 110

Arg Ile Arg Thr Lys Glu Arg Leu Ala Glu Leu Ser Gln Asn Ala Ser
        115                 120                 125

Leu Asp Asp Val Arg Ser Asp Asp Leu Asp Val Leu Glu Gln Pro Glu
    130                 135                 140

Ser Arg Glu Leu Val Arg Cys Leu Leu Ala His Gly Ala Met Asp Gly
145                 150                 155                 160

Thr Arg Val Met Ala Arg Gln Val Ala Arg Val Leu Asp Thr Glu Val
                165                 170                 175

Asp Glu Val His Gln Val Ala Arg Ser Leu Glu Gln His Gly Leu Val
            180                 185                 190

Ser Arg Ser Thr Ile Met Pro Gly Gly Asp Pro Gly Lys Val Phe Ile
        195                 200                 205

Glu Val Ser Leu Lys Gly Ile Ser Ala Ile Lys Ala Leu Glu Ser Gly
    210                 215                 220

Arg
225
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09625759.1

<210> 1127
<211> 798
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> FRXA02368

<400> 1127

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cttaggtcaa gcttgcattt attggctagt gtcggaaatc atgggagatt tagcaaagca 60

catgggcagt gaaccaccag catggtggaa gtttttaccg atg att gtc ctc gct   115
                                            Met Ile Val Leu Ala
                                              1               5

gga gcc act cga gtt acc tat gaa gta gaa cct tgg ctg gcg atc cca   163
Gly Ala Thr Arg Val Thr Tyr Glu Val Glu Pro Trp Leu Ala Ile Pro
                  10                  15                  20

tta ttc att ttg gct ttt gca tcg ata ttg atc cca ttc ccg atc tct   211
Leu Phe Ile Leu Ala Phe Ala Ser Ile Leu Ile Pro Phe Pro Ile Ser
             25                  30                  35
```

```
aag aca aaa gga ctc cgt gat atc gat gcc tgg aaa atc cac acc acg   259
Lys Thr Lys Gly Leu Arg Asp Ile Asp Ala Trp Lys Ile His Thr Thr
         40                  45                  50

caa ggc gat aaa aag cgt gcc atc cgc caa ctg atc att ccg gct acg   307
Gln Gly Asp Lys Lys Arg Ala Ile Arg Gln Leu Ile Ile Pro Ala Thr
     55                  60                  65

gct ttg gcc atc gac atc att ggg ctg ccg aca tta ttt aat gcc cct   355
Ala Leu Ala Ile Asp Ile Ile Gly Leu Pro Thr Leu Phe Asn Ala Pro
 70                  75                  80                  85

ccc ctt gct tcc gct gca ctt ttt ggc ggt gtt tac ggc gct tcc cta   403
Pro Leu Ala Ser Ala Ala Leu Phe Gly Gly Val Tyr Gly Ala Ser Leu
                 90                  95                 100

gct tgg gct gcg tac aga gct gat cag ctt cca cgc att cga acg aag   451
Ala Trp Ala Ala Tyr Arg Ala Asp Gln Leu Pro Arg Ile Arg Thr Lys
            105                 110                 115

gaa cgc ctc gca gaa ctt tca caa aat gca tct ctg gat gat gtg cgc   499
Glu Arg Leu Ala Glu Leu Ser Gln Asn Ala Ser Leu Asp Asp Val Arg
        120                 125                 130

tca gat gac tta gat gtt cta gag cag ccg gaa tcc cgt gaa tta gtg   547
Ser Asp Asp Leu Asp Val Leu Glu Gln Pro Glu Ser Arg Glu Leu Val
    135                 140                 145

cgc tgt ctg ctt gcc cac ggt gcg atg gat ggc act cgg gtg atg gcc   595
Arg Cys Leu Leu Ala His Gly Ala Met Asp Gly Thr Arg Val Met Ala
150                 155                 160                 165

aga cag gtc gcg cga gta ctg gat acc gag gta gac gaa gta cat cag   643
Arg Gln Val Ala Arg Val Leu Asp Thr Glu Val Asp Glu Val His Gln
                170                 175                 180

gta gca cgc tca cta gaa cag cat ggt ttg gtt agt cgc tcc acc atc   691
Val Ala Arg Ser Leu Glu Gln His Gly Leu Val Ser Arg Ser Thr Ile
            185                 190                 195

atg ccg ggt ggg gat cca gga aaa gta ttc atc gaa gtt tcc ctg aaa   739
Met Pro Gly Gly Asp Pro Gly Lys Val Phe Ile Glu Val Ser Leu Lys
        200                 205                 210

ggg atc tca gcc atc aag gca ctt gaa tcc gga cgc taagttgttg        785
Gly Ile Ser Ala Ile Lys Ala Leu Glu Ser Gly Arg
    215                 220                 225

atacatcaac tta                                                   798
```

<210> 1128
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 1128

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Met Ile Val Leu Ala Gly Ala Thr Arg Val Thr Tyr Glu Val Glu Pro
  1               5                  10                  15
```

```
Trp Leu Ala Ile Pro Leu Phe Ile Leu Ala Phe Ala Ser Ile Leu Ile
            20                  25                  30

Pro Phe Pro Ile Ser Lys Thr Lys Gly Leu Arg Asp Ile Asp Ala Trp
        35                  40                  45

Lys Ile His Thr Thr Gln Gly Asp Lys Lys Arg Ala Ile Arg Gln Leu
    50                  55                  60

Ile Ile Pro Ala Thr Ala Leu Ala Ile Asp Ile Ile Gly Leu Pro Thr
65                  70                  75                  80

Leu Phe Asn Ala Pro Pro Leu Ala Ser Ala Ala Leu Phe Gly Gly Val
                85                  90                  95

Tyr Gly Ala Ser Leu Ala Trp Ala Ala Tyr Arg Ala Asp Gln Leu Pro
            100                 105                 110

Arg Ile Arg Thr Lys Glu Arg Leu Ala Glu Leu Ser Gln Asn Ala Ser
        115                 120                 125

Leu Asp Asp Val Arg Ser Asp Asp Leu Asp Val Leu Glu Gln Pro Glu
    130                 135                 140

Ser Arg Glu Leu Val Arg Cys Leu Leu Ala His Gly Ala Met Asp Gly
145                 150                 155                 160

Thr Arg Val Met Ala Arg Gln Val Ala Arg Val Leu Asp Thr Glu Val
                165                 170                 175

Asp Glu Val His Gln Val Ala Arg Ser Leu Glu Gln His Gly Leu Val
            180                 185                 190

Ser Arg Ser Thr Ile Met Pro Gly Gly Asp Pro Gly Lys Val Phe Ile
        195                 200                 205

Glu Val Ser Leu Lys Gly Ile Ser Ala Ile Lys Ala Leu Glu Ser Gly
    210                 215                 220

Arg
225
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US20050153417A1

<210> 1129
<211> 1146
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1123)
<223> RXN02381

<400> 1129
aagtttgaag aagtaatcaa gctcccctgt gaggactcgt tgtagtcttt tatttagtta 60

ataaaagatt tcataccaac ttgtcagcag gggagctttc atg tct gtc aca aac 115
                                                Met Ser Val Thr Asn
                                                  1   5

ttc cgt cgg ttt ctt gct ggc ata gcg gtc atc gcg gcg tgt gtt gct 163

```
Phe Arg Arg Phe Leu Ala Gly Ile Ala Val Ile Ala Ala Cys Val Ala
                 10                  15                  20

gcg act cca aca gct cag gca caa agc agt ggc tct tct gga tcc tct   211
Ala Thr Pro Thr Ala Gln Ala Gln Ser Ser Gly Ser Ser Gly Ser Ser
             25                  30                  35

ggt tct tca gcg gga tct agc ggg ctg tgg gat tta ctt ttt cca gaa   259
Gly Ser Ser Ala Gly Ser Ser Gly Leu Trp Asp Leu Leu Phe Pro Glu
         40                  45                  50

tcc cat gag tct ttt atc gag cgg ctt ctt gat cct ttg gat gac agc   307
Ser His Glu Ser Phe Ile Glu Arg Leu Leu Asp Pro Leu Asp Asp Ser
     55                  60                  65

cat ata tct att cac cct gac ctc acc cca gac ctg tat gaa gag gtg   355
His Ile Ser Ile His Pro Asp Leu Thr Pro Asp Leu Tyr Glu Glu Val
 70                  75                  80                  85

ttt gat cca ccg caa att ggt gaa tgc cca gcc gtt gtt gct gtg gtc   403
Phe Asp Pro Pro Gln Ile Gly Glu Cys Pro Ala Val Val Ala Val Val
                 90                  95                 100

gca cga ggc agt gaa caa aac ctt caa atc cga ccc gcg cga tac agc   451
Ala Arg Gly Ser Glu Gln Asn Leu Gln Ile Arg Pro Ala Arg Tyr Ser
             105                 110                 115

gag gaa tct cca tgg aca tcc aat gga ttt gag gaa aaa aac ttt cgt   499
Glu Glu Ser Pro Trp Thr Ser Asn Gly Phe Glu Glu Lys Asn Phe Arg
         120                 125                 130

agt ttc ttt ggc cga atg gaa aaa cac tac cgt gaa tcg act ggc gag   547
Ser Phe Phe Gly Arg Met Glu Lys His Tyr Arg Glu Ser Thr Gly Glu
     135                 140                 145

tcg ttg atg aaa gac gtc tac gtg atg ggt ctg aat aat atc gaa tac   595
Ser Leu Met Lys Asp Val Tyr Val Met Gly Leu Asn Asn Ile Glu Tyr
150                 155                 160                 165

cct gct tct ttg cca ctg tct tcg gag gga agc agc gcc att gaa ttg   643
Pro Ala Ser Leu Pro Leu Ser Ser Glu Gly Ser Ser Ala Ile Glu Leu
                 170                 175                 180

ggc act tcc att tct agt ggt cgc gac aat gtc atc agc gcg att gat   691
Gly Thr Ser Ile Ser Ser Gly Arg Asp Asn Val Ile Ser Ala Ile Asp
             185                 190                 195

cgc ttt gaa tca gcg aca ggg tgc acg ccg aag tac ctg ttg gcg ggt   739
Arg Phe Glu Ser Ala Thr Gly Cys Thr Pro Lys Tyr Leu Leu Ala Gly
         200                 205                 210

tat tct caa ggt gtc ctc atc gtt gat ggc tat gaa gag gag ttg att   787
Tyr Ser Gln Gly Val Leu Ile Val Asp Gly Tyr Glu Glu Glu Leu Ile
     215                 220                 225

gcg agg gat cag tac ctc ggc acc ctg cac atc gcg aat cca gcg caa   835
Ala Arg Asp Gln Tyr Leu Gly Thr Leu His Ile Ala Asn Pro Ala Gln
230                 235                 240                 245

caa gtt gat gat cca aca ctt gtt ggg cat gaa gta acc acg gga ggc   883
Gln Val Asp Asp Pro Thr Leu Val Gly His Glu Val Thr Thr Gly Gly
```

```
                250                 255                 260

ttg gct agt tcc gtg gag ccc gtc gag gac aat cct ttc aag gtg agc   931
Leu Ala Ser Ser Val Glu Pro Val Glu Asp Asn Pro Phe Lys Val Ser
            265                 270                 275

tac tgc ctg cct gga gac atc gtg tgc gat cgt tct ttt gaa cag ttc   979
Tyr Cys Leu Pro Gly Asp Ile Val Cys Asp Arg Ser Phe Glu Gln Phe
        280                 285                 290

tct gct gcg gga tcc tct ata gca gct gcg caa ttg agc acc gga aat   1027
Ser Ala Ala Gly Ser Ser Ile Ala Ala Ala Gln Leu Ser Thr Gly Asn
    295                 300                 305

atc cgt cca ggt cga gta cac gtg caa tac ttc gtt acc acc caa ccg   1075
Ile Arg Pro Gly Arg Val His Val Gln Tyr Phe Val Thr Thr Gln Pro
310                 315                 320                 325

tgg gat gag cag att ttt gac gaa gtc gca tcg tgg att gaa gct gcc   1123
Trp Asp Glu Gln Ile Phe Asp Glu Val Ala Ser Trp Ile Glu Ala Ala
                330                 335                 340

taaaaactcg cgaggacgca tgc                                       1146


<210> 1130
<211> 341
<212> PRT
<213> Corynebacterium glutamicum

<400> 1130
Met Ser Val Thr Asn Phe Arg Arg Phe Leu Ala Gly Ile Ala Val Ile
  1               5                  10                  15

Ala Ala Cys Val Ala Ala Thr Pro Thr Ala Gln Ala Gln Ser Ser Gly
            20                  25                  30

Ser Ser Gly Ser Ser Gly Ser Ser Ala Gly Ser Ser Gly Leu Trp Asp
        35                  40                  45

Leu Leu Phe Pro Glu Ser His Glu Ser Phe Ile Glu Arg Leu Leu Asp
    50                  55                  60

Pro Leu Asp Asp Ser His Ile Ser Ile His Pro Asp Leu Thr Pro Asp
65                  70                  75                  80

Leu Tyr Glu Glu Val Phe Asp Pro Pro Gln Ile Gly Glu Cys Pro Ala
                85                  90                  95

Val Val Ala Val Val Ala Arg Gly Ser Glu Gln Asn Leu Gln Ile Arg
            100                 105                 110

Pro Ala Arg Tyr Ser Glu Glu Ser Pro Trp Thr Ser Asn Gly Phe Glu
        115                 120                 125

Glu Lys Asn Phe Arg Ser Phe Phe Gly Arg Met Glu Lys His Tyr Arg
    130                 135                 140

Glu Ser Thr Gly Glu Ser Leu Met Lys Asp Val Tyr Val Met Gly Leu
145                 150                 155                 160
```

```
Asn Asn Ile Glu Tyr Pro Ala Ser Leu Pro Leu Ser Ser Glu Gly Ser
                165                 170                 175

Ser Ala Ile Glu Leu Gly Thr Ser Ile Ser Ser Gly Arg Asp Asn Val
            180                 185                 190

Ile Ser Ala Ile Asp Arg Phe Glu Ser Ala Thr Gly Cys Thr Pro Lys
        195                 200                 205

Tyr Leu Leu Ala Gly Tyr Ser Gln Gly Val Leu Ile Val Asp Gly Tyr
    210                 215                 220

Glu Glu Glu Leu Ile Ala Arg Asp Gln Tyr Leu Gly Thr Leu His Ile
225                 230                 235                 240

Ala Asn Pro Ala Gln Gln Val Asp Asp Pro Thr Leu Val Gly His Glu
                245                 250                 255

Val Thr Thr Gly Gly Leu Ala Ser Ser Val Glu Pro Val Glu Asp Asn
            260                 265                 270

Pro Phe Lys Val Ser Tyr Cys Leu Pro Gly Asp Ile Val Cys Asp Arg
        275                 280                 285

Ser Phe Glu Gln Phe Ser Ala Ala Gly Ser Ser Ile Ala Ala Ala Gln
    290                 295                 300

Leu Ser Thr Gly Asn Ile Arg Pro Gly Arg Val His Val Gln Tyr Phe
305                 310                 315                 320

Val Thr Thr Gln Pro Trp Asp Glu Gln Ile Phe Asp Glu Val Ala Ser
                325                 330                 335

Trp Ile Glu Ala Ala
            340


<210> 1131
<211> 1146
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1123)
<223> FRXA02381

<400> 1131
aagtttgaag aagtaatcaa gctcccctgt gaggactcgt tgtagtcttt tatttagtta 60

ataaaagatt tcataccaac ttgtcagcag gggagctttc atg tct gtc aca aac   115
                                              Met Ser Val Thr Asn
                                                1               5

ttc cgt cgg ttt ctt gct ggc ata gcg gtc atc gcg gcg tgt gtt gct   163
Phe Arg Arg Phe Leu Ala Gly Ile Ala Val Ile Ala Ala Cys Val Ala
                 10                  15                  20

gcg act cca aca gct cag gca caa agc agt ggc tct tct gga tcc tct   211
Ala Thr Pro Thr Ala Gln Ala Gln Ser Ser Gly Ser Ser Gly Ser Ser
             25                  30                  35
```

```
ggt tct tca gcg gga tct agc ggg ctg tgg gat tta ctt ttt cca gaa   259
Gly Ser Ser Ala Gly Ser Ser Gly Leu Trp Asp Leu Leu Phe Pro Glu
         40                  45                  50

tcc cat gag tct ttt atc gag cgg ctt ctt gat cct ttg gat gac agc   307
Ser His Glu Ser Phe Ile Glu Arg Leu Leu Asp Pro Leu Asp Asp Ser
     55                  60                  65

cat ata tct att cac cct gac ctc acc cca gac ctg tat gaa gag gtg   355
His Ile Ser Ile His Pro Asp Leu Thr Pro Asp Leu Tyr Glu Glu Val
 70                  75                  80                  85

ttt gat cca ccg caa att ggt gaa tgc cca gcc gtt gtt gct gtg gtc   403
Phe Asp Pro Pro Gln Ile Gly Glu Cys Pro Ala Val Val Ala Val Val
                90                  95                 100

gca cga ggc agt gaa caa aac ctt caa atc cga ccc gcg cga tac agc   451
Ala Arg Gly Ser Glu Gln Asn Leu Gln Ile Arg Pro Ala Arg Tyr Ser
            105                 110                 115

gag gaa tct cca tgg aca tcc aat gga ttt gag gaa aaa aac ttt cgt   499
Glu Glu Ser Pro Trp Thr Ser Asn Gly Phe Glu Glu Lys Asn Phe Arg
        120                 125                 130

agt ttc ttt ggc cga atg gaa aaa cac tac cgt gaa tcg act ggc gag   547
Ser Phe Phe Gly Arg Met Glu Lys His Tyr Arg Glu Ser Thr Gly Glu
    135                 140                 145

tcg ttg atg aaa gac gtc tac gtg atg ggt ctg aat aat atc gaa tac   595
Ser Leu Met Lys Asp Val Tyr Val Met Gly Leu Asn Asn Ile Glu Tyr
150                 155                 160                 165

cct gct tct ttg cca ctg tct tcg gag gga agc agc gcc att gaa ttg   643
Pro Ala Ser Leu Pro Leu Ser Ser Glu Gly Ser Ser Ala Ile Glu Leu
                170                 175                 180

ggc act tcc att tct agt ggt cgc gac aat gtc atc agc gcg att gat   691
Gly Thr Ser Ile Ser Ser Gly Arg Asp Asn Val Ile Ser Ala Ile Asp
            185                 190                 195

cgc ttt gaa tca gcg aca ggg tgc acg ccg aag tac ctg ttg gcg ggt   739
Arg Phe Glu Ser Ala Thr Gly Cys Thr Pro Lys Tyr Leu Leu Ala Gly
        200                 205                 210

tat tct caa ggt gtc ctc atc gtt gat ggc tat gaa gag gag ttg att   787
Tyr Ser Gln Gly Val Leu Ile Val Asp Gly Tyr Glu Glu Glu Leu Ile
    215                 220                 225

gcg agg gat cag tac ctc ggc acc ctg cac atc gcg aat cca gcg caa   835
Ala Arg Asp Gln Tyr Leu Gly Thr Leu His Ile Ala Asn Pro Ala Gln
230                 235                 240                 245

caa gtt gat gat cca aca ctt gtt ggg cat gaa gta acc acg gga ggc   883
Gln Val Asp Asp Pro Thr Leu Val Gly His Glu Val Thr Thr Gly Gly
                250                 255                 260

ttg gct agt tcc gtg gag ccc gtc gag gac aat cct ttc aag gtg agc   931
Leu Ala Ser Ser Val Glu Pro Val Glu Asp Asn Pro Phe Lys Val Ser
            265                 270                 275
```

```
tac tgc ctg cct gga gac atc gtg tgc gat cgt tct ttt gaa cag ttc   979
Tyr Cys Leu Pro Gly Asp Ile Val Cys Asp Arg Ser Phe Glu Gln Phe
        280                 285                 290

tct gct gcg gga tcc tct ata gca gct gcg caa ttg agc acc gga aat   1027
Ser Ala Ala Gly Ser Ser Ile Ala Ala Ala Gln Leu Ser Thr Gly Asn
    295                 300                 305

atc cgt cca ggt cga gta cac gtg caa tac ttc gtt acc acc caa ccg   1075
Ile Arg Pro Gly Arg Val His Val Gln Tyr Phe Val Thr Thr Gln Pro
310                 315                 320                 325

tgg gat gag cag att ttt gac gaa gtc gca tcg tgg att gaa gct gcc   1123
Trp Asp Glu Gln Ile Phe Asp Glu Val Ala Ser Trp Ile Glu Ala Ala
                330                 335                 340

taaaaactcg cgaggacgca tgc                                       1146


<210> 1132
<211> 341
<212> PRT
<213> Corynebacterium glutamicum

<400> 1132
Met Ser Val Thr Asn Phe Arg Arg Phe Leu Ala Gly Ile Ala Val Ile
  1               5                  10                  15

Ala Ala Cys Val Ala Ala Thr Pro Thr Ala Gln Ala Gln Ser Ser Gly
            20                  25                  30

Ser Ser Gly Ser Ser Gly Ser Ser Ala Gly Ser Ser Gly Leu Trp Asp
        35                  40                  45

Leu Leu Phe Pro Glu Ser His Glu Ser Phe Ile Glu Arg Leu Leu Asp
    50                  55                  60

Pro Leu Asp Asp Ser His Ile Ser Ile His Pro Asp Leu Thr Pro Asp
65                  70                  75                  80

Leu Tyr Glu Glu Val Phe Asp Pro Pro Gln Ile Gly Glu Cys Pro Ala
                85                  90                  95

Val Val Ala Val Val Ala Arg Gly Ser Glu Gln Asn Leu Gln Ile Arg
            100                 105                 110

Pro Ala Arg Tyr Ser Glu Glu Ser Pro Trp Thr Ser Asn Gly Phe Glu
        115                 120                 125

Glu Lys Asn Phe Arg Ser Phe Phe Gly Arg Met Glu Lys His Tyr Arg
    130                 135                 140

Glu Ser Thr Gly Glu Ser Leu Met Lys Asp Val Tyr Val Met Gly Leu
145                 150                 155                 160

Asn Asn Ile Glu Tyr Pro Ala Ser Leu Pro Leu Ser Ser Glu Gly Ser
                165                 170                 175

Ser Ala Ile Glu Leu Gly Thr Ser Ile Ser Ser Gly Arg Asp Asn Val
            180                 185                 190
```

```
Ile Ser Ala Ile Asp Arg Phe Glu Ser Ala Thr Gly Cys Thr Pro Lys
        195                 200                 205

Tyr Leu Leu Ala Gly Tyr Ser Gln Gly Val Leu Ile Val Asp Gly Tyr
    210                 215                 220

Glu Glu Glu Leu Ile Ala Arg Asp Gln Tyr Leu Gly Thr Leu His Ile
225                 230                 235                 240

Ala Asn Pro Ala Gln Gln Val Asp Asp Pro Thr Leu Val Gly His Glu
                245                 250                 255

Val Thr Thr Gly Gly Leu Ala Ser Ser Val Glu Pro Val Glu Asp Asn
            260                 265                 270

Pro Phe Lys Val Ser Tyr Cys Leu Pro Gly Asp Ile Val Cys Asp Arg
        275                 280                 285

Ser Phe Glu Gln Phe Ser Ala Ala Gly Ser Ser Ile Ala Ala Ala Gln
    290                 295                 300

Leu Ser Thr Gly Asn Ile Arg Pro Gly Arg Val His Val Gln Tyr Phe
305                 310                 315                 320

Val Thr Thr Gln Pro Trp Asp Glu Gln Ile Phe Asp Glu Val Ala Ser
                325                 330                 335

Trp Ile Glu Ala Ala
            340


<210> 1133
<211> 736
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(736)
<223> RXN02383

<400> 1133
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gtaaagaaga tggcaataaa aatgtggagg agtaaaggcg atg cca gtt cgg gta   115
                                               Met Pro Val Arg Val
                                                 1               5

att gtt gat tcc tcc gca tgc ttg cca acg cat gtg gcc gag gac ctc   163
Ile Val Asp Ser Ser Ala Cys Leu Pro Thr His Val Ala Glu Asp Leu
                 10                  15                  20

gac atc acg gtg att aac ttg cac gtg atg aat aac ggt gaa gaa cgc   211
Asp Ile Thr Val Ile Asn Leu His Val Met Asn Asn Gly Glu Glu Arg
             25                  30                  35

agt aca tcc ggg ttg tcg tcg ttg gaa ctt gca gca agt tac gcc cgc   259
Ser Thr Ser Gly Leu Ser Ser Leu Glu Leu Ala Ala Ser Tyr Ala Arg
         40                  45                  50

cag ctt gaa cgc ggt ggc gat gac ggt gtg ctt gcg ctg cat att tct   307
```

```
Gln Leu Glu Arg Gly Gly Asp Asp Gly Val Leu Ala Leu His Ile Ser
     55                  60                  65

aaa gag ctc tcg tcc acg tgg tcc gca gcg gtg aca gca gcc gct gtg   355
Lys Glu Leu Ser Ser Thr Trp Ser Ala Ala Val Thr Ala Ala Ala Val
 70                  75                  80                  85

ttt gat gat gat tct gtg cgc gtg gtg gat acc agt tcg ctc ggt atg   403
Phe Asp Asp Asp Ser Val Arg Val Val Asp Thr Ser Ser Leu Gly Met
                 90                  95                 100

gct gtg ggt gct gcc gcg atg gct gct gcc cgc atg gct aaa gat ggc   451
Ala Val Gly Ala Ala Ala Met Ala Ala Ala Arg Met Ala Lys Asp Gly
            105                 110                 115

gcg tct ttg cag gaa tgc tac gac atc gcg gtg gat acc ttg aag cgt   499
Ala Ser Leu Gln Glu Cys Tyr Asp Ile Ala Val Asp Thr Leu Lys Arg
        120                 125                 130

tca gaa acc tgg atc tac ctg cac cgc att gat gaa atc tgg aag tcg   547
Ser Glu Thr Trp Ile Tyr Leu His Arg Ile Asp Glu Ile Trp Lys Ser
    135                 140                 145

gga cgg att tcc act gca acc gcc atg gtg tca acg gct ctg gca acc   595
Gly Arg Ile Ser Thr Ala Thr Ala Met Val Ser Thr Ala Leu Ala Thr
150                 155                 160                 165

cgc ccc atc atg cgt ttc aac ggt ggt cgc atg gag atc gcc gct aag   643
Arg Pro Ile Met Arg Phe Asn Gly Gly Arg Met Glu Ile Ala Ala Lys
                170                 175                 180

acc cgc acc caa tct aaa gcg ttt gcc aaa ttg gtg gaa tta gcc cag   691
Thr Arg Thr Gln Ser Lys Ala Phe Ala Lys Leu Val Glu Leu Ala Gln
            185                 190                 195

atc agg gca gat ggt gaa ccc gta ttc att gcg att ggc caa aac       736
Ile Arg Ala Asp Gly Glu Pro Val Phe Ile Ala Ile Gly Gln Asn
        200                 205                 210
```

SUBSTITUTE SHEET (RULE 26)

<210> 1134
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 1134

```
Met Pro Val Arg Val Ile Val Asp Ser Ser Ala Cys Leu Pro Thr His
  1               5                  10                  15

Val Ala Glu Asp Leu Asp Ile Thr Val Ile Asn Leu His Val Met Asn
             20                  25                  30

Asn Gly Glu Glu Arg Ser Thr Ser Gly Leu Ser Ser Leu Glu Leu Ala
         35                  40                  45

Ala Ser Tyr Ala Arg Gln Leu Glu Arg Gly Gly Asp Asp Gly Val Leu
     50                  55                  60

Ala Leu His Ile Ser Lys Glu Leu Ser Ser Thr Trp Ser Ala Ala Val
 65                  70                  75                  80
```

```
Thr Ala Ala Ala Val Phe Asp Asp Asp Ser Val Arg Val Val Asp Thr
                 85                  90                  95

Ser Ser Leu Gly Met Ala Val Gly Ala Ala Ala Met Ala Ala Ala Arg
            100                 105                 110

Met Ala Lys Asp Gly Ala Ser Leu Gln Glu Cys Tyr Asp Ile Ala Val
        115                 120                 125

Asp Thr Leu Lys Arg Ser Glu Thr Trp Ile Tyr Leu His Arg Ile Asp
    130                 135                 140

Glu Ile Trp Lys Ser Gly Arg Ile Ser Thr Ala Thr Ala Met Val Ser
145                 150                 155                 160

Thr Ala Leu Ala Thr Arg Pro Ile Met Arg Phe Asn Gly Gly Arg Met
                165                 170                 175

Glu Ile Ala Ala Lys Thr Arg Thr Gln Ser Lys Ala Phe Ala Lys Leu
            180                 185                 190

Val Glu Leu Ala Gln Ile Arg Ala Asp Gly Glu Pro Val Phe Ile Ala
        195                 200                 205

Ile Gly Gln Asn
    210


<210> 1135
<211> 703
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> FRXA02383

<400> 1135
gggcaacaat gtggaaaacg cccagtggta tcttgacggc tggaacatgg gtgttacgca 60

gtaaagaaga tggcaataaa aatgtggagg agtaaaggcg atg cca gtt cgg gta   115
                                               Met Pro Val Arg Val
                                                 1               5

att gtt gat tcc tcc gca tgc ttg cca acg cat gtg gcc gag gac ctc   163
Ile Val Asp Ser Ser Ala Cys Leu Pro Thr His Val Ala Glu Asp Leu
                10                  15                  20

gac atc acg gtg att aac ttg cac gtg atg aat aac ggt gaa gaa cgc   211
Asp Ile Thr Val Ile Asn Leu His Val Met Asn Asn Gly Glu Glu Arg
            25                  30                  35

agt aca tcc ggg ttg tcg tcg ttg gaa ctt gca gca agt tac gcc cgc   259
Ser Thr Ser Gly Leu Ser Ser Leu Glu Leu Ala Ala Ser Tyr Ala Arg
        40                  45                  50

cag ctt gaa cgc ggt ggc gat gac ggt gtg ctt gcg ctg cat att tct   307
Gln Leu Glu Arg Gly Gly Asp Asp Gly Val Leu Ala Leu His Ile Ser
    55                  60                  65
```

```
aaa gag ctc tcg tcc acg tgg tcc gca gcg gtg aca gca gcc gct gtg   355
Lys Glu Leu Ser Ser Thr Trp Ser Ala Ala Val Thr Ala Ala Ala Val
 70                  75                  80                  85

ttt gat gat gat tct gtg cgc gtg gtg gat acc agt tcg ctc ggt atg   403
Phe Asp Asp Asp Ser Val Arg Val Val Asp Thr Ser Ser Leu Gly Met
                 90                  95                 100

gct gtg ggt gct gcc gcg atg gct gct gcc cgc atg gct aaa gat ggc   451
Ala Val Gly Ala Ala Ala Met Ala Ala Ala Arg Met Ala Lys Asp Gly
            105                 110                 115

gcg tct ttg cag gaa tgc tac gac atc gcg gtg gat acc ttg aag cgt   499
Ala Ser Leu Gln Glu Cys Tyr Asp Ile Ala Val Asp Thr Leu Lys Arg
        120                 125                 130

tca gaa acc tgg atc tac ctg cac cgc att gat gaa atc tgg aag tcg   547
Ser Glu Thr Trp Ile Tyr Leu His Arg Ile Asp Glu Ile Trp Lys Ser
    135                 140                 145

gga cgg att tcc act gca acc gcc atg gtg tca acg gct ctg gca acc   595
Gly Arg Ile Ser Thr Ala Thr Ala Met Val Ser Thr Ala Leu Ala Thr
150                 155                 160                 165

cgc ccc atc atg cgt ttc aac ggt ggt cgc atg gag atc gcc gct aag   643
Arg Pro Ile Met Arg Phe Asn Gly Gly Arg Met Glu Ile Ala Ala Lys
                170                 175                 180

acc cgc acc caa tct aaa gcg ttt gcc aaa ttg gtg gaa tta gcc cag   691
Thr Arg Thr Gln Ser Lys Ala Phe Ala Lys Leu Val Glu Leu Ala Gln
            185                 190                 195

atc agg gca gat                                                  703
Ile Arg Ala Asp
        200
```

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<210> 1136
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 1136

```
Met Pro Val Arg Val Ile Val Asp Ser Ser Ala Cys Leu Pro Thr His
  1               5                  10                  15

Val Ala Glu Asp Leu Asp Ile Thr Val Ile Asn Leu His Val Met Asn
             20                  25                  30

Asn Gly Glu Glu Arg Ser Thr Ser Gly Leu Ser Ser Leu Glu Leu Ala
         35                  40                  45

Ala Ser Tyr Ala Arg Gln Leu Glu Arg Gly Gly Asp Asp Gly Val Leu
     50                  55                  60

Ala Leu His Ile Ser Lys Glu Leu Ser Ser Thr Trp Ser Ala Ala Val
 65                  70                  75                  80

Thr Ala Ala Ala Val Phe Asp Asp Asp Ser Val Arg Val Val Asp Thr
                 85                  90                  95
```

```
Ser Ser Leu Gly Met Ala Val Gly Ala Ala Ala Met Ala Ala Ala Arg
            100                 105                 110

Met Ala Lys Asp Gly Ala Ser Leu Gln Glu Cys Tyr Asp Ile Ala Val
        115                 120                 125

Asp Thr Leu Lys Arg Ser Glu Thr Trp Ile Tyr Leu His Arg Ile Asp
    130                 135                 140

Glu Ile Trp Lys Ser Gly Arg Ile Ser Thr Ala Thr Ala Met Val Ser
145                 150                 155                 160

Thr Ala Leu Ala Thr Arg Pro Ile Met Arg Phe Asn Gly Gly Arg Met
                165                 170                 175

Glu Ile Ala Ala Lys Thr Arg Thr Gln Ser Lys Ala Phe Ala Lys Leu
            180                 185                 190

Val Glu Leu Ala Gln Ile Arg Ala Asp
        195                 200
```

<210> 1137
<211> 885
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(862)
<223> RXN02387

<400> 1137

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gctagccccg attcgcttca ggtcaccacc ttgaaggcca gcgaaattac tcagggtgaa 60

ttgttggatg cgttaagccc atccttgttt gctgaagacc gtg tgg tgg tgc tta   115
                                          Val Trp Trp Cys Leu
                                            1               5

cca aca tgg atc aaa gca ggc caa gat gct gta gat cta gcc tta tcc   163
Pro Thr Trp Ile Lys Ala Gly Gln Asp Ala Val Asp Leu Ala Leu Ser
                10                  15                  20

gca gca gtt gat ccc agc cct ggt acc tac ttg atc gtc atg cac tct   211
Ala Ala Val Asp Pro Ser Pro Gly Thr Tyr Leu Ile Val Met His Ser
            25                  30                  35

ggc ggt gga cgc tct aag tcg atg gtg aag aag ctg gaa aaa gtc gcg   259
Gly Gly Gly Arg Ser Lys Ser Met Val Lys Lys Leu Glu Lys Val Ala
        40                  45                  50

gtg gtg cac gat gcc gca aag ctg aaa gac cgg gat cgt cca ggt tgg   307
Val Val His Asp Ala Ala Lys Leu Lys Asp Arg Asp Arg Pro Gly Trp
    55                  60                  65

gta aaa caa gag ttc aaa aac cac aaa gtc cag gtc acc cca gat gtc   355
Val Lys Gln Glu Phe Lys Asn His Lys Val Gln Val Thr Pro Asp Val
70                  75                  80                  85

att cat gct ctt tta gag ggc gtg ggt tca gat ctt aga gag ctg gcg   403
Ile His Ala Leu Leu Glu Gly Val Gly Ser Asp Leu Arg Glu Leu Ala
```

```
                  90                  95                 100

tcc gcc gta tcc caa ttg gtt gag gac acc caa ggc aac gtg acg gtg   451
Ser Ala Val Ser Gln Leu Val Glu Asp Thr Gln Gly Asn Val Thr Val
            105                 110                 115

gaa aaa gtc cgt gcc tat tac gtg ggt gtt gct gag gta tcg ggt ttc   499
Glu Lys Val Arg Ala Tyr Tyr Val Gly Val Ala Glu Val Ser Gly Phe
        120                 125                 130

gac atc gcc gat tct gca tgc gcc ggt caa atg tca aag gcc gtg gcc   547
Asp Ile Ala Asp Ser Ala Cys Ala Gly Gln Met Ser Lys Ala Val Ala
    135                 140                 145

agc acc aga cgt gcc ctt caa ttg ggt acc agc ccg gtt gca ttg gca   595
Ser Thr Arg Arg Ala Leu Gln Leu Gly Thr Ser Pro Val Ala Leu Ala
150                 155                 160                 165

gct gcg ttg agt atg aaa gtt ggc cag atc gcc agg ctg tat tcc acc   643
Ala Ala Leu Ser Met Lys Val Gly Gln Ile Ala Arg Leu Tyr Ser Thr
                170                 175                 180

agg gga cgc atc aac ggt ttt gag ctg gcc aaa gaa ttg ggc atg ccg   691
Arg Gly Arg Ile Asn Gly Phe Glu Leu Ala Lys Glu Leu Gly Met Pro
            185                 190                 195

ccg ttc gtg gtg gag aag act gcg aaa gtg gcc cga aac tgg tcg gga   739
Pro Phe Val Val Glu Lys Thr Ala Lys Val Ala Arg Asn Trp Ser Gly
        200                 205                 210

gat gcg gtc agc gag gcc gtg att ttg atg gcc gat ctg gat gcc gct   787
Asp Ala Val Ser Glu Ala Val Ile Leu Met Ala Asp Leu Asp Ala Ala
    215                 220                 225

gta aaa gga caa agt ggc gat cct gaa ttt gcc atc gaa tct gcc gtg   835
Val Lys Gly Gln Ser Gly Asp Pro Glu Phe Ala Ile Glu Ser Ala Val
230                 235                 240                 245

aga aga gtt gca gag ctg gcg agg cgg taacgctgaa cggcggcggg         882
Arg Arg Val Ala Glu Leu Ala Arg Arg
                250

taa                                                              885


<210> 1138
<211> 254
<212> PRT
<213> Corynebacterium glutamicum

<400> 1138
Val Trp Trp Cys Leu Pro Thr Trp Ile Lys Ala Gly Gln Asp Ala Val
  1               5                  10                  15

Asp Leu Ala Leu Ser Ala Ala Val Asp Pro Ser Pro Gly Thr Tyr Leu
             20                  25                  30

Ile Val Met His Ser Gly Gly Gly Arg Ser Lys Ser Met Val Lys Lys
         35                  40                  45

Leu Glu Lys Val Ala Val Val His Asp Ala Ala Lys Leu Lys Asp Arg
```

```
     50                  55                  60

Asp Arg Pro Gly Trp Val Lys Gln Glu Phe Lys Asn His Lys Val Gln
 65                  70                  75                  80

Val Thr Pro Asp Val Ile His Ala Leu Leu Glu Gly Val Gly Ser Asp
                 85                  90                  95

Leu Arg Glu Leu Ala Ser Ala Val Ser Gln Leu Val Glu Asp Thr Gln
            100                 105                 110

Gly Asn Val Thr Val Glu Lys Val Arg Ala Tyr Tyr Val Gly Val Ala
        115                 120                 125

Glu Val Ser Gly Phe Asp Ile Ala Asp Ser Ala Cys Ala Gly Gln Met
    130                 135                 140

Ser Lys Ala Val Ala Ser Thr Arg Arg Ala Leu Gln Leu Gly Thr Ser
145                 150                 155                 160

Pro Val Ala Leu Ala Ala Ala Leu Ser Met Lys Val Gly Gln Ile Ala
                165                 170                 175

Arg Leu Tyr Ser Thr Arg Gly Arg Ile Asn Gly Phe Glu Leu Ala Lys
            180                 185                 190

Glu Leu Gly Met Pro Pro Phe Val Val Glu Lys Thr Ala Lys Val Ala
        195                 200                 205

Arg Asn Trp Ser Gly Asp Ala Val Ser Glu Ala Val Ile Leu Met Ala
    210                 215                 220

Asp Leu Asp Ala Ala Val Lys Gly Gln Ser Gly Asp Pro Glu Phe Ala
225                 230                 235                 240

Ile Glu Ser Ala Val Arg Arg Val Ala Glu Leu Ala Arg Arg
                245                 250
```

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<210> 1139
<211> 778
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(778)
<223> FRXA02387

<400> 1139
gctagccccg attcgcttca ggtcaccacc ttgaaggcca gcgaaattac tcagggtgaa 60

ttgttggatg cgttaagccc atccttgttt gctgaagacc gtg tgg tgg tgc tta 115
                                    Val Trp Trp Cys Leu
                                      1   5

cca aca tgg atc aaa gca ggc caa gat gct gta gat cta gcc tta tcc 163
Pro Thr Trp Ile Lys Ala Gly Gln Asp Ala Val Asp Leu Ala Leu Ser
                  10   15   20

gca gca gtt gat ccc agc cct ggt acc tac ttg atc gtc atg cac tct 211

```
Ala Ala Val Asp Pro Ser Pro Gly Thr Tyr Leu Ile Val Met His Ser
            25                  30                  35

ggc ggt gga cgc tct aag tcg atg gtg aag aag ctg gaa aaa gtc gcg   259
Gly Gly Gly Arg Ser Lys Ser Met Val Lys Lys Leu Glu Lys Val Ala
         40                  45                  50

gtg gtg cac gat gcc gca aag ctg aaa gac cgg gat cgt cca ggt tgg   307
Val Val His Asp Ala Ala Lys Leu Lys Asp Arg Asp Arg Pro Gly Trp
     55                  60                  65

gta aaa caa gag ttc aaa aac cac aaa gtc cag gtc acc cca gat gtc   355
Val Lys Gln Glu Phe Lys Asn His Lys Val Gln Val Thr Pro Asp Val
 70                  75                  80                  85

att cat gct ctt tta gag ggc gtg ggt tca gat ctt aga gag ctg gcg   403
Ile His Ala Leu Leu Glu Gly Val Gly Ser Asp Leu Arg Glu Leu Ala
                90                  95                 100

tcc gcc gta tcc caa ttg gtt gag gac acc caa ggc aac gtg acg gtg   451
Ser Ala Val Ser Gln Leu Val Glu Asp Thr Gln Gly Asn Val Thr Val
            105                 110                 115

gaa aaa gtc cgt gcc tat tac gtg ggt gtt gct gag gta tcg ggt ttc   499
Glu Lys Val Arg Ala Tyr Tyr Val Gly Val Ala Glu Val Ser Gly Phe
        120                 125                 130

gac atc gcc gat tct gca tgc gcc ggt caa atg tca aag gcc gtg gcc   547
Asp Ile Ala Asp Ser Ala Cys Ala Gly Gln Met Ser Lys Ala Val Ala
    135                 140                 145

agc acc aga cgt gcc ctt caa ttg ggt acc agc ccg gtt gca ttg gca   595
Ser Thr Arg Arg Ala Leu Gln Leu Gly Thr Ser Pro Val Ala Leu Ala
150                 155                 160                 165

gct gcg ttg agt atg aaa gtt ggc cag atc gcc agg ctg tat tcc acc   643
Ala Ala Leu Ser Met Lys Val Gly Gln Ile Ala Arg Leu Tyr Ser Thr
                170                 175                 180

agg gga cgc atc aac ggt ttt gag ctg gcc aaa gaa ttg ggc atg ccg   691
Arg Gly Arg Ile Asn Gly Phe Glu Leu Ala Lys Glu Leu Gly Met Pro
            185                 190                 195

ccg ttc gtg gtg gag aag act gcg aaa gtg gcc cga aac tgg tcg gga   739
Pro Phe Val Val Glu Lys Thr Ala Lys Val Ala Arg Asn Trp Ser Gly
        200                 205                 210

gat gcg gtc agc gag gcc gtg att ttg atg gcc gat ctg               778
Asp Ala Val Ser Glu Ala Val Ile Leu Met Ala Asp Leu
    215                 220                 225
```

<210> 1140
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 1140

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Val Trp Trp Cys Leu Pro Thr Trp Ile Lys Ala Gly Gln Asp Ala Val
  1               5                  10                  15
```

```
Asp Leu Ala Leu Ser Ala Ala Val Asp Pro Ser Pro Gly Thr Tyr Leu
            20                  25                  30

Ile Val Met His Ser Gly Gly Gly Arg Ser Lys Ser Met Val Lys Lys
        35                  40                  45

Leu Glu Lys Val Ala Val Val His Asp Ala Ala Lys Leu Lys Asp Arg
    50                  55                  60

Asp Arg Pro Gly Trp Val Lys Gln Glu Phe Lys Asn His Lys Val Gln
65                  70                  75                  80

Val Thr Pro Asp Val Ile His Ala Leu Leu Glu Gly Val Gly Ser Asp
                85                  90                  95

Leu Arg Glu Leu Ala Ser Ala Val Ser Gln Leu Val Glu Asp Thr Gln
            100                 105                 110

Gly Asn Val Thr Val Glu Lys Val Arg Ala Tyr Tyr Val Gly Val Ala
        115                 120                 125

Glu Val Ser Gly Phe Asp Ile Ala Asp Ser Ala Cys Ala Gly Gln Met
    130                 135                 140

Ser Lys Ala Val Ala Ser Thr Arg Arg Ala Leu Gln Leu Gly Thr Ser
145                 150                 155                 160

Pro Val Ala Leu Ala Ala Ala Leu Ser Met Lys Val Gly Gln Ile Ala
                165                 170                 175

Arg Leu Tyr Ser Thr Arg Gly Arg Ile Asn Gly Phe Glu Leu Ala Lys
            180                 185                 190

Glu Leu Gly Met Pro Pro Phe Val Val Glu Lys Thr Ala Lys Val Ala
        195                 200                 205

Arg Asn Trp Ser Gly Asp Ala Val Ser Glu Ala Val Ile Leu Met Ala
    210                 215                 220

Asp Leu
225
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<210> 1141
<211> 1725
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1702)
<223> RXN02398

<400> 1141
gtgtccaatg aatgcgttca ataaatgccc tctttaagca tattctctga gtgcattcat 60

tacaggcgtt aattaaatgc gttcatagaa gaacttgaaa gtg gtt gaa gtg aag 115
                                            Val Val Glu Val Lys
                                              1   5

aag cgt aat ctc ctc gta gct ccc ctc act gct tcc ctg gtg ttc tgt 163

```
Lys Arg Asn Leu Leu Val Ala Pro Leu Thr Ala Ser Leu Val Phe Cys
                 10                  15                  20

aac ttg gct gtt gca gca aac gcc gtt gaa gtt gag gcc gaa tca cca   211
Asn Leu Ala Val Ala Ala Asn Ala Val Glu Val Glu Ala Glu Ser Pro
            25                  30                  35

gtt gtc atc aat gaa gtt gaa tcc aac agc gac cca gtt ggt gac tgg   259
Val Val Ile Asn Glu Val Glu Ser Asn Ser Asp Pro Val Gly Asp Trp
        40                  45                  50

gtg gag ttg gct aac acc gac aac aac aac tcc atc gac att tcc ggt   307
Val Glu Leu Ala Asn Thr Asp Asn Asn Asn Ser Ile Asp Ile Ser Gly
    55                  60                  65

tgg tcc tta gtc gat gac aag gaa gac ctg gaa aat gcc ctc gtc ctt   355
Trp Ser Leu Val Asp Asp Lys Glu Asp Leu Glu Asn Ala Leu Val Leu
70                  75                  80                  85

cct gaa ggc act gag att gag tcc ggt gga tac ttt gtt atc tac acc   403
Pro Glu Gly Thr Glu Ile Glu Ser Gly Gly Tyr Phe Val Ile Tyr Thr
                90                  95                 100

gac tct gct gat tac gtg cct acc aac aac acc ttt ggt ggc cag gaa   451
Asp Ser Ala Asp Tyr Val Pro Thr Asn Asn Thr Phe Gly Gly Gln Glu
            105                 110                 115

tac ttc ggc ctc ggc aaa gat gac act gtt act ctg cgc aac gct gaa   499
Tyr Phe Gly Leu Gly Lys Asp Asp Thr Val Thr Leu Arg Asn Ala Glu
        120                 125                 130

ggc gaa gta gtt gct acc tat tcc tgg aag gat ctg ggc gag cac gca   547
Gly Glu Val Val Ala Thr Tyr Ser Trp Lys Asp Leu Gly Glu His Ala
    135                 140                 145

gaa aac acc tat ggt cgc atc cca gat atg act ggt gat ttc gca aac   595
Glu Asn Thr Tyr Gly Arg Ile Pro Asp Met Thr Gly Asp Phe Ala Asn
150                 155                 160                 165

acc ggc gtt cca acc cca ggt gca aag aat gtt gct gct gaa ggc tcc   643
Thr Gly Val Pro Thr Pro Gly Ala Lys Asn Val Ala Ala Glu Gly Ser
                170                 175                 180

ggc gaa gaa gaa ggc gtt gtt gca aac gcc cag ctt cca ttc cac aac   691
Gly Glu Glu Glu Gly Val Val Ala Asn Ala Gln Leu Pro Phe His Asn
            185                 190                 195

gtt gaa atc acc cca att cac ctc ggt gga gat ttc acc ggt gaa gat   739
Val Glu Ile Thr Pro Ile His Leu Gly Gly Asp Phe Thr Gly Glu Asp
        200                 205                 210

atg tcc ggc gtt gat ttc gat gca aac agc acc gca tgg atc gcc aac   787
Met Ser Gly Val Asp Phe Asp Ala Asn Ser Thr Ala Trp Ile Ala Asn
    215                 220                 225

aat gac att gga aag atc tac tcc ctc gcc cac gac ata gct aac aac   835
Asn Asp Ile Gly Lys Ile Tyr Ser Leu Ala His Asp Ile Ala Asn Asn
230                 235                 240                 245

acc tac aag ctg act ggc gaa tgg gaa acc ggc tac cca gaa ggc ggc   883
Thr Tyr Lys Leu Thr Gly Glu Trp Glu Thr Gly Tyr Pro Glu Gly Gly
```

```
                    250                 255                 260

gga gag cca gac gct gaa ggc atc gtc gca gct acc aac ggt gac atc   931
Gly Glu Pro Asp Ala Glu Gly Ile Val Ala Ala Thr Asn Gly Asp Ile
            265                 270                 275

tac ctg tcc acc gag cgc aac aac gct gac aag aac gtc tct cgc cca   979
Tyr Leu Ser Thr Glu Arg Asn Asn Ala Asp Lys Asn Val Ser Arg Pro
        280                 285                 290

tcc atc ctg cgt ttt gct acc cca act ggc aag act ggc gta caa aac   1027
Ser Ile Leu Arg Phe Ala Thr Pro Thr Gly Lys Thr Gly Val Gln Asn
    295                 300                 305

gca gtt cag gaa tgg gac ctg tct gag ttc gtc ggc gac att cag ccc   1075
Ala Val Gln Glu Trp Asp Leu Ser Glu Phe Val Gly Asp Ile Gln Pro
310                 315                 320                 325

aat ggt ggt ctt gag gca atc gcg cag ctc gag gac aac atc ttc gtt   1123
Asn Gly Gly Leu Glu Ala Ile Ala Gln Leu Glu Asp Asn Ile Phe Val
                330                 335                 340

gtc ggt gtc gaa gag aca ggt gat gtc atc gtt gtt gat ctt tcc gct   1171
Val Gly Val Glu Glu Thr Gly Asp Val Ile Val Val Asp Leu Ser Ala
            345                 350                 355

gac cag cca gtt ctg gtt caa agg tac gaa tct tcc ttc gac ggt gtc   1219
Asp Gln Pro Val Leu Val Gln Arg Tyr Glu Ser Ser Phe Asp Gly Val
        360                 365                 370

atg tcg ctt gat tac aac gca gca acc aag cag ctc agc gtt gtg tgc   1267
Met Ser Leu Asp Tyr Asn Ala Ala Thr Lys Gln Leu Ser Val Val Cys
    375                 380                 385

gac gaa gca tgt gac ggc ttg tct gaa atc ctc gaa tgg gat ggc gag   1315
Asp Glu Ala Cys Asp Gly Leu Ser Glu Ile Leu Glu Trp Asp Gly Glu
390                 395                 400                 405

aag ctg tac aag tcc gac gac aag atc tac gag cgt cca gca aac ctg   1363
Lys Leu Tyr Lys Ser Asp Asp Lys Ile Tyr Glu Arg Pro Ala Asn Leu
                410                 415                 420

ggc aac tgg gct aac gaa ggc ttc ggc acc tac acc tca gag ctt aaa   1411
Gly Asn Trp Ala Asn Glu Gly Phe Gly Thr Tyr Thr Ser Glu Leu Lys
            425                 430                 435

tgc gag aac ggc aac acc gtt tct gtc acc agc tac ctc tgg gct gac   1459
Cys Glu Asn Gly Asn Thr Val Ser Val Thr Ser Tyr Leu Trp Ala Asp
        440                 445                 450

gat gca gca acc aac gaa ggc acc tcc ctc aac tcc gca cag gtc atc   1507
Asp Ala Ala Thr Asn Glu Gly Thr Ser Leu Asn Ser Ala Gln Val Ile
    455                 460                 465

aac gga gat tgc ggc gac gtc aac atc cct gga gag tcc tct tcc gac   1555
Asn Gly Asp Cys Gly Asp Val Asn Ile Pro Gly Glu Ser Ser Ser Asp
470                 475                 480                 485

aat tcc tct tct gac ttt gca acc ggc agc atc gca ggc gcc ttt gca   1603
Asn Ser Ser Ser Asp Phe Ala Thr Gly Ser Ile Ala Gly Ala Phe Ala
                490                 495                 500
```

```
acc gca gtg ctc gca gtc gta ggc att gcg ggc gca ctg ggt gga ttc   1651
Thr Ala Val Leu Ala Val Val Gly Ile Ala Gly Ala Leu Gly Gly Phe
            505                 510                 515

ttc cag cag atc ctc gca gcg ttc cca gca ttg cag cag gtc atc cgt   1699
Phe Gln Gln Ile Leu Ala Ala Phe Pro Ala Leu Gln Gln Val Ile Arg
        520                 525                 530

ttc taaacccact gcttgaaaca ctt                                     1725
Phe
```

<210> 1142
<211> 534
<212> PRT
<213> Corynebacterium glutamicum

<400> 1142

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Val Val Glu Val Lys Lys Arg Asn Leu Leu Val Ala Pro Leu Thr Ala
  1               5                  10                  15

Ser Leu Val Phe Cys Asn Leu Ala Val Ala Ala Asn Ala Val Glu Val
             20                  25                  30

Glu Ala Glu Ser Pro Val Val Ile Asn Glu Val Glu Ser Asn Ser Asp
         35                  40                  45

Pro Val Gly Asp Trp Val Glu Leu Ala Asn Thr Asp Asn Asn Asn Ser
     50                  55                  60

Ile Asp Ile Ser Gly Trp Ser Leu Val Asp Asp Lys Glu Asp Leu Glu
 65                  70                  75                  80

Asn Ala Leu Val Leu Pro Glu Gly Thr Glu Ile Glu Ser Gly Gly Tyr
                 85                  90                  95

Phe Val Ile Tyr Thr Asp Ser Ala Asp Tyr Val Pro Thr Asn Asn Thr
            100                 105                 110

Phe Gly Gly Gln Glu Tyr Phe Gly Leu Gly Lys Asp Asp Thr Val Thr
        115                 120                 125

Leu Arg Asn Ala Glu Gly Glu Val Val Ala Thr Tyr Ser Trp Lys Asp
    130                 135                 140

Leu Gly Glu His Ala Glu Asn Thr Tyr Gly Arg Ile Pro Asp Met Thr
145                 150                 155                 160

Gly Asp Phe Ala Asn Thr Gly Val Pro Thr Pro Gly Ala Lys Asn Val
                165                 170                 175

Ala Ala Glu Gly Ser Gly Glu Glu Glu Gly Val Val Ala Asn Ala Gln
            180                 185                 190

Leu Pro Phe His Asn Val Glu Ile Thr Pro Ile His Leu Gly Gly Asp
        195                 200                 205

Phe Thr Gly Glu Asp Met Ser Gly Val Asp Phe Asp Ala Asn Ser Thr
    210                 215                 220
```

```
Ala Trp Ile Ala Asn Asn Asp Ile Gly Lys Ile Tyr Ser Leu Ala His
225                 230                 235                 240

Asp Ile Ala Asn Asn Thr Tyr Lys Leu Thr Gly Glu Trp Glu Thr Gly
                245                 250                 255

Tyr Pro Glu Gly Gly Gly Glu Pro Asp Ala Glu Gly Ile Val Ala Ala
            260                 265                 270

Thr Asn Gly Asp Ile Tyr Leu Ser Thr Glu Arg Asn Asn Ala Asp Lys
        275                 280                 285

Asn Val Ser Arg Pro Ser Ile Leu Arg Phe Ala Thr Pro Thr Gly Lys
    290                 295                 300

Thr Gly Val Gln Asn Ala Val Gln Glu Trp Asp Leu Ser Glu Phe Val
305                 310                 315                 320

Gly Asp Ile Gln Pro Asn Gly Gly Leu Glu Ala Ile Ala Gln Leu Glu
                325                 330                 335

Asp Asn Ile Phe Val Val Gly Val Glu Glu Thr Gly Asp Val Ile Val
            340                 345                 350

Val Asp Leu Ser Ala Asp Gln Pro Val Leu Val Gln Arg Tyr Glu Ser
        355                 360                 365

Ser Phe Asp Gly Val Met Ser Leu Asp Tyr Asn Ala Ala Thr Lys Gln
    370                 375                 380

Leu Ser Val Val Cys Asp Glu Ala Cys Asp Gly Leu Ser Glu Ile Leu
385                 390                 395                 400

Glu Trp Asp Gly Glu Lys Leu Tyr Lys Ser Asp Asp Lys Ile Tyr Glu
                405                 410                 415

Arg Pro Ala Asn Leu Gly Asn Trp Ala Asn Glu Gly Phe Gly Thr Tyr
            420                 425                 430

Thr Ser Glu Leu Lys Cys Glu Asn Gly Asn Thr Val Ser Val Thr Ser
        435                 440                 445

Tyr Leu Trp Ala Asp Asp Ala Ala Thr Asn Glu Gly Thr Ser Leu Asn
    450                 455                 460

Ser Ala Gln Val Ile Asn Gly Asp Cys Gly Asp Val Asn Ile Pro Gly
465                 470                 475                 480

Glu Ser Ser Ser Asp Asn Ser Ser Ser Asp Phe Ala Thr Gly Ser Ile
                485                 490                 495

Ala Gly Ala Phe Ala Thr Ala Val Leu Ala Val Val Gly Ile Ala Gly
            500                 505                 510

Ala Leu Gly Gly Phe Phe Gln Gln Ile Leu Ala Ala Phe Pro Ala Leu
        515                 520                 525

Gln Gln Val Ile Arg Phe
    530
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<210> 1143
<211> 1630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1630)
<223> FRXA02398

<400> 1143
gtgtccaatg aatgcgttca ataaatgccc tctttaagca tattctctga gtgcattcat 60

tacaggcgtt aattaaatgc gttcatagaa gaacttgaaa gtg gtt gaa gtg aag 115
Val Val Glu Val Lys
1 5

aag cgt aat ctc ctc gta gct ccc ctc act gct tcc ctg gtg ttc tgt 163
Lys Arg Asn Leu Leu Val Ala Pro Leu Thr Ala Ser Leu Val Phe Cys
10 15 20

aac ttg gct gtt gca gca aac gcc gtt gaa gtt gag gcc gaa tca cca 211
Asn Leu Ala Val Ala Ala Asn Ala Val Glu Val Glu Ala Glu Ser Pro
25 30 35

gtt gtc atc aat gaa gtt gaa tcc aac agc gac cca gtt ggt gac tgg 259
Val Val Ile Asn Glu Val Glu Ser Asn Ser Asp Pro Val Gly Asp Trp
40 45 50

gtg gag ttg gct aac acc gac aac aac aac tcc atc gac att tcc ggt 307
Val Glu Leu Ala Asn Thr Asp Asn Asn Asn Ser Ile Asp Ile Ser Gly
55 60 65

tgg tcc tta gtc gat gac aag gaa gac ctg gaa aat gcc ctc gtc ctt 355
Trp Ser Leu Val Asp Asp Lys Glu Asp Leu Glu Asn Ala Leu Val Leu
70 75 80 85

cct gaa ggc act gag att gag tcc ggt gga tac ttt gtt atc tac acc 403
Pro Glu Gly Thr Glu Ile Glu Ser Gly Gly Tyr Phe Val Ile Tyr Thr
90 95 100

gac tct gct gat tac gtg cct acc aac aac acc ttt ggt ggc cag gaa 451
Asp Ser Ala Asp Tyr Val Pro Thr Asn Asn Thr Phe Gly Gly Gln Glu
105 110 115

tac ttc ggc ctc ggc aaa gat gac act gtt act ctg cgc aac gct gaa 499
Tyr Phe Gly Leu Gly Lys Asp Asp Thr Val Thr Leu Arg Asn Ala Glu
120 125 130

ggc gaa gta gtt gct acc tat tcc tgg aag gat ctg ggc gag cac gca 547
Gly Glu Val Val Ala Thr Tyr Ser Trp Lys Asp Leu Gly Glu His Ala
135 140 145

gaa aac acc tat ggt cgc atc cca gat atg act ggt gat ttc gca aac 595
Glu Asn Thr Tyr Gly Arg Ile Pro Asp Met Thr Gly Asp Phe Ala Asn
150 155 160 165

acc ggc gtt cca acc cca ggt gca aag aat gtt gct gct gaa ggc tcc 643
Thr Gly Val Pro Thr Pro Gly Ala Lys Asn Val Ala Ala Glu Gly Ser
170 175 180

```
ggc gaa gaa gaa ggc gtt gtt gca aac gcc cag ctt cca ttc cac aac   691
Gly Glu Glu Glu Gly Val Val Ala Asn Ala Gln Leu Pro Phe His Asn
            185                 190                 195

gtt gaa atc acc cca att cac ctc ggt gga gat ttc acc ggt gaa gat   739
Val Glu Ile Thr Pro Ile His Leu Gly Gly Asp Phe Thr Gly Glu Asp
        200                 205                 210

atg tcc ggc gtt gat ttc gat gca aac agc acc gca tgg atc gcc aac   787
Met Ser Gly Val Asp Phe Asp Ala Asn Ser Thr Ala Trp Ile Ala Asn
    215                 220                 225

aat gac att gga aag atc tac tcc ctc gcc cac gac ata gct aac aac   835
Asn Asp Ile Gly Lys Ile Tyr Ser Leu Ala His Asp Ile Ala Asn Asn
230                 235                 240                 245

acc tac aag ctg act ggc gaa tgg gaa acc ggc tac cca gaa ggc ggc   883
Thr Tyr Lys Leu Thr Gly Glu Trp Glu Thr Gly Tyr Pro Glu Gly Gly
                250                 255                 260

gga gag cca gac gct gaa ggc atc gtc gca gct acc aac ggt gac atc   931
Gly Glu Pro Asp Ala Glu Gly Ile Val Ala Ala Thr Asn Gly Asp Ile
            265                 270                 275

tac ctg tcc acc gag cgc aac aac gct gac aag aac gtc tct cgc cca   979
Tyr Leu Ser Thr Glu Arg Asn Asn Ala Asp Lys Asn Val Ser Arg Pro
        280                 285                 290

tcc atc ctg cgt ttt gct acc cca act ggc aag act ggc gta caa aac   1027
Ser Ile Leu Arg Phe Ala Thr Pro Thr Gly Lys Thr Gly Val Gln Asn
    295                 300                 305

gca gtt cag gaa tgg gac ctg tct gag ttc gtc ggc gac att cag ccc   1075
Ala Val Gln Glu Trp Asp Leu Ser Glu Phe Val Gly Asp Ile Gln Pro
310                 315                 320                 325

aat ggt ggt ctt gag gca atc gcg cag ctc gag gac aac atc ttc gtt   1123
Asn Gly Gly Leu Glu Ala Ile Ala Gln Leu Glu Asp Asn Ile Phe Val
                330                 335                 340

gtc ggt gtc gaa gag aca ggt gat gtc atc gtt gtt gat ctt tcc gct   1171
Val Gly Val Glu Glu Thr Gly Asp Val Ile Val Val Asp Leu Ser Ala
            345                 350                 355

gac cag cca gtt ctg gtt caa agg tac gaa tct tcc ttc gac ggt gtc   1219
Asp Gln Pro Val Leu Val Gln Arg Tyr Glu Ser Ser Phe Asp Gly Val
        360                 365                 370

atg tcg ctt gat tac aac gca gca acc aag cag ctc agc gtt gtg tgc   1267
Met Ser Leu Asp Tyr Asn Ala Ala Thr Lys Gln Leu Ser Val Val Cys
    375                 380                 385

gac gaa gca tgt gac ggc ttg tct gaa atc ctc gaa tgg gat ggc gag   1315
Asp Glu Ala Cys Asp Gly Leu Ser Glu Ile Leu Glu Trp Asp Gly Glu
390                 395                 400                 405

aag ctg tac aag tcc gac gac aag atc tac gag cgt cca gca aac ctg   1363
Lys Leu Tyr Lys Ser Asp Asp Lys Ile Tyr Glu Arg Pro Ala Asn Leu
                410                 415                 420
```

```
ggc aac tgg gct aac gaa ggc ttc ggc acc tac acc tca gag ctt aaa   1411
Gly Asn Trp Ala Asn Glu Gly Phe Gly Thr Tyr Thr Ser Glu Leu Lys
            425                 430                 435

tgc gag aac ggc aac acc gtt tct gtc acc agc tac ctc tgg gct gac   1459
Cys Glu Asn Gly Asn Thr Val Ser Val Thr Ser Tyr Leu Trp Ala Asp
        440                 445                 450

gat gca gca acc aac gaa ggc acc tcc ctc aac tcc gca cag gtc atc   1507
Asp Ala Ala Thr Asn Glu Gly Thr Ser Leu Asn Ser Ala Gln Val Ile
    455                 460                 465

aac gga gat tgc ggc gac gtc aac atc cct gga gag tcc tct tcc gac   1555
Asn Gly Asp Cys Gly Asp Val Asn Ile Pro Gly Glu Ser Ser Ser Asp
470                 475                 480                 485

aat tcc tct tct gac ttt gca acc ggc agc atc gca ggc gcc ttt gca   1603
Asn Ser Ser Ser Asp Phe Ala Thr Gly Ser Ile Ala Gly Ala Phe Ala
                490                 495                 500

acc gca gtg ctc gca gtc gta ggc att                              1630
Thr Ala Val Leu Ala Val Val Gly Ile
            505                 510
```

<210> 1144
<211> 510
<212> PRT
<213> Corynebacterium glutamicum

<400> 1144

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Val Val Glu Val Lys Lys Arg Asn Leu Leu Val Ala Pro Leu Thr Ala
  1               5                  10                  15

Ser Leu Val Phe Cys Asn Leu Ala Val Ala Ala Asn Ala Val Glu Val
             20                  25                  30

Glu Ala Glu Ser Pro Val Val Ile Asn Glu Val Glu Ser Asn Ser Asp
         35                  40                  45

Pro Val Gly Asp Trp Val Glu Leu Ala Asn Thr Asp Asn Asn Asn Ser
     50                  55                  60

Ile Asp Ile Ser Gly Trp Ser Leu Val Asp Asp Lys Glu Asp Leu Glu
 65                  70                  75                  80

Asn Ala Leu Val Leu Pro Glu Gly Thr Glu Ile Glu Ser Gly Gly Tyr
                 85                  90                  95

Phe Val Ile Tyr Thr Asp Ser Ala Asp Tyr Val Pro Thr Asn Asn Thr
            100                 105                 110

Phe Gly Gly Gln Glu Tyr Phe Gly Leu Gly Lys Asp Asp Thr Val Thr
        115                 120                 125

Leu Arg Asn Ala Glu Gly Glu Val Val Ala Thr Tyr Ser Trp Lys Asp
    130                 135                 140

Leu Gly Glu His Ala Glu Asn Thr Tyr Gly Arg Ile Pro Asp Met Thr
145                 150                 155                 160
```

```
Gly Asp Phe Ala Asn Thr Gly Val Pro Thr Pro Gly Ala Lys Asn Val
                165                 170                 175

Ala Ala Glu Gly Ser Gly Glu Glu Glu Gly Val Val Ala Asn Ala Gln
            180                 185                 190

Leu Pro Phe His Asn Val Glu Ile Thr Pro Ile His Leu Gly Gly Asp
        195                 200                 205

Phe Thr Gly Glu Asp Met Ser Gly Val Asp Phe Asp Ala Asn Ser Thr
    210                 215                 220

Ala Trp Ile Ala Asn Asn Asp Ile Gly Lys Ile Tyr Ser Leu Ala His
225                 230                 235                 240

Asp Ile Ala Asn Asn Thr Tyr Lys Leu Thr Gly Glu Trp Glu Thr Gly
                245                 250                 255

Tyr Pro Glu Gly Gly Gly Glu Pro Asp Ala Glu Gly Ile Val Ala Ala
            260                 265                 270

Thr Asn Gly Asp Ile Tyr Leu Ser Thr Glu Arg Asn Asn Ala Asp Lys
        275                 280                 285

Asn Val Ser Arg Pro Ser Ile Leu Arg Phe Ala Thr Pro Thr Gly Lys
    290                 295                 300

Thr Gly Val Gln Asn Ala Val Gln Glu Trp Asp Leu Ser Glu Phe Val
305                 310                 315                 320

Gly Asp Ile Gln Pro Asn Gly Gly Leu Glu Ala Ile Ala Gln Leu Glu
                325                 330                 335

Asp Asn Ile Phe Val Val Gly Val Glu Glu Thr Gly Asp Val Ile Val
            340                 345                 350

Val Asp Leu Ser Ala Asp Gln Pro Val Leu Val Gln Arg Tyr Glu Ser
        355                 360                 365

Ser Phe Asp Gly Val Met Ser Leu Asp Tyr Asn Ala Ala Thr Lys Gln
    370                 375                 380

Leu Ser Val Val Cys Asp Glu Ala Cys Asp Gly Leu Ser Glu Ile Leu
385                 390                 395                 400

Glu Trp Asp Gly Glu Lys Leu Tyr Lys Ser Asp Asp Lys Ile Tyr Glu
                405                 410                 415

Arg Pro Ala Asn Leu Gly Asn Trp Ala Asn Glu Gly Phe Gly Thr Tyr
            420                 425                 430

Thr Ser Glu Leu Lys Cys Glu Asn Gly Asn Thr Val Ser Val Thr Ser
        435                 440                 445

Tyr Leu Trp Ala Asp Asp Ala Ala Thr Asn Glu Gly Thr Ser Leu Asn
    450                 455                 460

Ser Ala Gln Val Ile Asn Gly Asp Cys Gly Asp Val Asn Ile Pro Gly
465                 470                 475                 480

Glu Ser Ser Ser Asp Asn Ser Ser Ser Asp Phe Ala Thr Gly Ser Ile
```

```
                485                 490                 495

Ala Gly Ala Phe Ala Thr Ala Val Leu Ala Val Val Gly Ile
            500                 505                 510


<210> 1145
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
<223> RXN02406

<400> 1145
cactctgata gccttttctc tgaaattgta ccgagcattt gattttgttc ccctatcaat 60

gctggttttg gtgacaaaaa ctcggcggaa ggaccaccga atg gaa acc ctt gca   115
                                              Met Glu Thr Leu Ala
                                                1               5

gca caa gcg cgc acc ctg cta gaa aaa tgg ggc gtc gcg ccg acg cac   163
Ala Gln Ala Arg Thr Leu Leu Glu Lys Trp Gly Val Ala Pro Thr His
                  10                  15                  20

gca tct ttc gtc gaa tcc att gca aag gcc atc ccg att ctg tcg atc   211
Ala Ser Phe Val Glu Ser Ile Ala Lys Ala Ile Pro Ile Leu Ser Ile
              25                  30                  35

ctg ctg acg ctg att gtc acc gtg aat gga att tca agc gga aat ccg   259
Leu Leu Thr Leu Ile Val Thr Val Asn Gly Ile Ser Ser Gly Asn Pro
          40                  45                  50

gtc cag cca cca gca ctg gaa cag gta cgg acc gat gta gtg aac aag   307
Val Gln Pro Pro Ala Leu Glu Gln Val Arg Thr Asp Val Val Asn Lys
      55                  60                  65

atc aac tac gaa cgc aac cta aag ggc ctc gtc tcg atc agc ccg gag   355
Ile Asn Tyr Glu Arg Asn Leu Lys Gly Leu Val Ser Ile Ser Pro Glu
  70                  75                  80                  85

ctt gaa tta cac acg gca gcc caa aca att gcg cag cga aat gca gac   403
Leu Glu Leu His Thr Ala Ala Gln Thr Ile Ala Gln Arg Asn Ala Asp
                  90                  95                 100

tca gat tcc gaa gaa aaa gta ccg gat cca gag ggc aac ctg gtg gtt   451
Ser Asp Ser Glu Glu Lys Val Pro Asp Pro Glu Gly Asn Leu Val Val
             105                 110                 115

ctg caa cag aat ctg ccc tat gca aat gcc aac gcc gat acc atc gtt   499
Leu Gln Gln Asn Leu Pro Tyr Ala Asn Ala Asn Ala Asp Thr Ile Val
         120                 125                 130

gat cgg ttc tta aac tct cct gat cat gtc aaa cta ctg ctt gca aac   547
Asp Arg Phe Leu Asn Ser Pro Asp His Val Lys Leu Leu Leu Ala Asn
     135                 140                 145

gat tat gaa gcc atc gga gtt ggt gtg gcc tac aag ggt gat cat gcg   595
Asp Tyr Glu Ala Ile Gly Val Gly Val Ala Tyr Lys Gly Asp His Ala
```

```
150                 155                 160                 165

tgg ata gtg gtg gag ttc act gta gct ccc gct gat tcc gta gaa tca   643
Trp Ile Val Val Glu Phe Thr Val Ala Pro Ala Asp Ser Val Glu Ser
                170                 175                 180

aca gag tgaataccaa tccgtctgaa ttc                                 672
Thr Glu
```

<210> 1146
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 1146

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Met Glu Thr Leu Ala Ala Gln Ala Arg Thr Leu Leu Glu Lys Trp Gly
  1               5                  10                  15

Val Ala Pro Thr His Ala Ser Phe Val Glu Ser Ile Ala Lys Ala Ile
             20                  25                  30

Pro Ile Leu Ser Ile Leu Leu Thr Leu Ile Val Thr Val Asn Gly Ile
         35                  40                  45

Ser Ser Gly Asn Pro Val Gln Pro Pro Ala Leu Glu Gln Val Arg Thr
     50                  55                  60

Asp Val Val Asn Lys Ile Asn Tyr Glu Arg Asn Leu Lys Gly Leu Val
 65                  70                  75                  80

Ser Ile Ser Pro Glu Leu Glu Leu His Thr Ala Ala Gln Thr Ile Ala
                 85                  90                  95

Gln Arg Asn Ala Asp Ser Asp Ser Glu Glu Lys Val Pro Asp Pro Glu
            100                 105                 110

Gly Asn Leu Val Val Leu Gln Gln Asn Leu Pro Tyr Ala Asn Ala Asn
        115                 120                 125

Ala Asp Thr Ile Val Asp Arg Phe Leu Asn Ser Pro Asp His Val Lys
    130                 135                 140

Leu Leu Leu Ala Asn Asp Tyr Glu Ala Ile Gly Val Gly Val Ala Tyr
145                 150                 155                 160

Lys Gly Asp His Ala Trp Ile Val Val Glu Phe Thr Val Ala Pro Ala
                165                 170                 175

Asp Ser Val Glu Ser Thr Glu
            180
```

<210> 1147
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(649)
<223> FRXA02406

<400> 1147
cactctgata gccttttctc tgaaattgta ccgagcattt gattttgttc ccctatcaat 60

gctggttttg gtgacaaaaa ctcggcggaa ggaccaccga atg gaa acc ctt gca 115
Met Glu Thr Leu Ala
1 5

gca caa gcg cgc acc ctg cta gaa aaa tgg ggc gtc gcg ccg acg cac 163
Ala Gln Ala Arg Thr Leu Leu Glu Lys Trp Gly Val Ala Pro Thr His
10 15 20

gca tct ttc gtc gaa tcc att gca aag gcc atc ccg att ctg tcg atc 211
Ala Ser Phe Val Glu Ser Ile Ala Lys Ala Ile Pro Ile Leu Ser Ile
25 30 35

ctg ctg acg ctg att gtc acc gtg aat gga att tca agc gga aat ccg 259
Leu Leu Thr Leu Ile Val Thr Val Asn Gly Ile Ser Ser Gly Asn Pro
40 45 50

gtc cag cca cca gca ctg gaa cag gta cgg acc gat gta gtg aac aag 307
Val Gln Pro Pro Ala Leu Glu Gln Val Arg Thr Asp Val Val Asn Lys
55 60 65

atc aac tac gaa cgc aac cta aag ggc ctc gtc tcg atc agc ccg gag 355
Ile Asn Tyr Glu Arg Asn Leu Lys Gly Leu Val Ser Ile Ser Pro Glu
70 75 80 85

ctt gaa tta cac acg gca gcc caa aca att gcg cag cga aat gca gac 403
Leu Glu Leu His Thr Ala Ala Gln Thr Ile Ala Gln Arg Asn Ala Asp
90 95 100

tca gat tcc gaa gaa aaa gta ccg gat cca gag gga acc ttg gtg gtt 451
Ser Asp Ser Glu Glu Lys Val Pro Asp Pro Glu Gly Thr Leu Val Val
105 110 115

ctg caa cag aat ctg ccc tat gca aat gcc aac gcc gat acc atc gtt 499
Leu Gln Gln Asn Leu Pro Tyr Ala Asn Ala Asn Ala Asp Thr Ile Val
120 125 130

gat cgg ttc tta aac tct cct gat cat gtc aaa cta ctg ctt gca aac 547
Asp Arg Phe Leu Asn Ser Pro Asp His Val Lys Leu Leu Leu Ala Asn
135 140 145

gat tat gaa gcc atc gga gtt ggt gtg gcc tac aag ggt gat cat gcg 595
Asp Tyr Glu Ala Ile Gly Val Gly Val Ala Tyr Lys Gly Asp His Ala
150 155 160 165

tgg ata gtg gtg gag ttc act gta gct ccc gct gat tcc gta gaa tca 643
Trp Ile Val Val Glu Phe Thr Val Ala Pro Ala Asp Ser Val Glu Ser
170 175 180

aca gag tgaataccaa tccgtctgaa ttc 672
Thr Glu

<210> 1148
<211> 183

<212> PRT
<213> Corynebacterium glutamicum

<400> 1148

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Met Glu Thr Leu Ala Ala Gln Ala Arg Thr Leu Leu Glu Lys Trp Gly
  1               5                  10                  15

Val Ala Pro Thr His Ala Ser Phe Val Glu Ser Ile Ala Lys Ala Ile
             20                  25                  30

Pro Ile Leu Ser Ile Leu Leu Thr Leu Ile Val Thr Val Asn Gly Ile
         35                  40                  45

Ser Ser Gly Asn Pro Val Gln Pro Pro Ala Leu Glu Gln Val Arg Thr
     50                  55                  60

Asp Val Val Asn Lys Ile Asn Tyr Glu Arg Asn Leu Lys Gly Leu Val
 65                  70                  75                  80

Ser Ile Ser Pro Glu Leu Glu Leu His Thr Ala Ala Gln Thr Ile Ala
                 85                  90                  95

Gln Arg Asn Ala Asp Ser Asp Ser Glu Glu Lys Val Pro Asp Pro Glu
            100                 105                 110

Gly Thr Leu Val Val Leu Gln Gln Asn Leu Pro Tyr Ala Asn Ala Asn
        115                 120                 125

Ala Asp Thr Ile Val Asp Arg Phe Leu Asn Ser Pro Asp His Val Lys
    130                 135                 140

Leu Leu Leu Ala Asn Asp Tyr Glu Ala Ile Gly Val Gly Val Ala Tyr
145                 150                 155                 160

Lys Gly Asp His Ala Trp Ile Val Val Glu Phe Thr Val Ala Pro Ala
                165                 170                 175

Asp Ser Val Glu Ser Thr Glu
            180
```

<210> 1149
<211> 495
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(472)
<223> RXN02407

<400> 1149

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ggataaaaat ttggatgaca tatcacctaa gcttgcaatt tctactggaa tagcgcgact 60

actctgcacc aacgcatagt tgttgactag gctatttgtc atg aat agg caa aac   115
                                               Met Asn Arg Gln Asn
                                                 1               5

caa ctt cac tac ccg cag gaa gtg aag gca gtg gaa agt gtg gaa tca   163
Gln Leu His Tyr Pro Gln Glu Val Lys Ala Val Glu Ser Val Glu Ser
                10                  15                  20
```

```
agc ttg aac atg tcg tca cct tct gca ccg ctt gcc acg cca gat gtt   211
Ser Leu Asn Met Ser Ser Pro Ser Ala Pro Leu Ala Thr Pro Asp Val
            25                  30                  35

gag ctt gat gtg cac acg ttg tcg agc gaa aac ctg cct tgg ttg tgc   259
Glu Leu Asp Val His Thr Leu Ser Ser Glu Asn Leu Pro Trp Leu Cys
        40                  45                  50

atc gtg tgg gat gat ccg gtc aat ttg atg agc tat gtc acc tac gtt   307
Ile Val Trp Asp Asp Pro Val Asn Leu Met Ser Tyr Val Thr Tyr Val
    55                  60                  65

ttt cag act gtg ttg ggc ttc agt aag aag agg gcc act gag ctg atg   355
Phe Gln Thr Val Leu Gly Phe Ser Lys Lys Arg Ala Thr Glu Leu Met
70                  75                  80                  85

atg cag gtg cac acc gaa ggt aaa gcc gtg gtg agt tct ggc gag aag   403
Met Gln Val His Thr Glu Gly Lys Ala Val Val Ser Ser Gly Glu Lys
                90                  95                  100

gac aaa gtg gag ggt gat gtg aag aaa ctc cac acc gca ggg ctg tgg   451
Asp Lys Val Glu Gly Asp Val Lys Lys Leu His Thr Ala Gly Leu Trp
            105                 110                 115

gcg aca atg cag cag gca ggg taggggagaa ttttcatgca gca            495
Ala Thr Met Gln Gln Ala Gly
        120
```

09503703.090703

<210> 1150
<211> 124
<212> PRT
<213> Corynebacterium glutamicum

<400> 1150

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Met Asn Arg Gln Asn Gln Leu His Tyr Pro Gln Glu Val Lys Ala Val
  1               5                  10                  15

Glu Ser Val Glu Ser Ser Leu Asn Met Ser Ser Pro Ser Ala Pro Leu
            20                  25                  30

Ala Thr Pro Asp Val Glu Leu Asp Val His Thr Leu Ser Ser Glu Asn
        35                  40                  45

Leu Pro Trp Leu Cys Ile Val Trp Asp Asp Pro Val Asn Leu Met Ser
    50                  55                  60

Tyr Val Thr Tyr Val Phe Gln Thr Val Leu Gly Phe Ser Lys Lys Arg
65                  70                  75                  80

Ala Thr Glu Leu Met Met Gln Val His Thr Glu Gly Lys Ala Val Val
                85                  90                  95

Ser Ser Gly Glu Lys Asp Lys Val Glu Gly Asp Val Lys Lys Leu His
            100                 105                 110

Thr Ala Gly Leu Trp Ala Thr Met Gln Gln Ala Gly
        115                 120
```

<210> 1151
<211> 406
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(406)
<223> FRXA02407

<400> 1151
ggataaaaat ttggatgaca tatcacctaa gcttgcaatt tctactggaa tagcgcgact 60

actctgcacc aacgcatagt tgttgactag gctatttgtc atg aat agg caa aac 115
Met Asn Arg Gln Asn
1 5

caa ctt cac tac ccg cag gaa gtg aag gca gtg gaa agt gtg gaa tca 163
Gln Leu His Tyr Pro Gln Glu Val Lys Ala Val Glu Ser Val Glu Ser
10 15 20

agc ttg aac atg tcg tca cct tct gca ccg ctt gcc acg cca gat gtt 211
Ser Leu Asn Met Ser Ser Pro Ser Ala Pro Leu Ala Thr Pro Asp Val
25 30 35

gag ctt gat gtg cac acg ttg tcg agc gaa aac ctg cct tgg ttg tgc 259
Glu Leu Asp Val His Thr Leu Ser Ser Glu Asn Leu Pro Trp Leu Cys
40 45 50

atc gtg tgg gat gat ccg gtc aat ttg atg agc tat gtc acc tac gtt 307
Ile Val Trp Asp Asp Pro Val Asn Leu Met Ser Tyr Val Thr Tyr Val
55 60 65

ttt cag act gtg ttg ggc ttc agt aag aag agg gcc act gag ctg atg 355
Phe Gln Thr Val Leu Gly Phe Ser Lys Lys Arg Ala Thr Glu Leu Met
70 75 80 85

atg cag gtg cac acc gaa ggt aaa gcc gtg gtg agt tct ggc gag aag 403
Met Gln Val His Thr Glu Gly Lys Ala Val Val Ser Ser Gly Glu Lys
90 95 100

gac 406
Asp

<210> 1152
<211> 102
<212> PRT
<213> Corynebacterium glutamicum

<400> 1152
Met Asn Arg Gln Asn Gln Leu His Tyr Pro Gln Glu Val Lys Ala Val
1 5 10 15

Glu Ser Val Glu Ser Ser Leu Asn Met Ser Ser Pro Ser Ala Pro Leu
20 25 30

Ala Thr Pro Asp Val Glu Leu Asp Val His Thr Leu Ser Ser Glu Asn
35 40 45

```
Leu Pro Trp Leu Cys Ile Val Trp Asp Asp Pro Val Asn Leu Met Ser
     50                  55                  60

Tyr Val Thr Tyr Val Phe Gln Thr Val Leu Gly Phe Ser Lys Lys Arg
 65                  70                  75                  80

Ala Thr Glu Leu Met Met Gln Val His Thr Glu Gly Lys Ala Val Val
                 85                  90                  95

Ser Ser Gly Glu Lys Asp
            100


<210> 1153
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> RXN02408

<400> 1153
gtgatgtacg cggcggggaa gccgccgagg aagaccgcga aaacctcgtg cagtggcttg 60

cctacaatca agagtccttg ctggaagcga tgatgaatta atg ctt atc gac gtc   115
                                        Met Leu Ile Asp Val
                                          1               5

gcg ggc ttc ctt tta ggc cac gtc acg aag ggg gat acg ggt tgc tca   163
Ala Gly Phe Leu Leu Gly His Val Thr Lys Gly Asp Thr Gly Cys Ser
                10                  15                  20

gtg gtc att gca cct aac ggt gca ttt gcg ggc gtc gat gtc cgt ggg   211
Val Val Ile Ala Pro Asn Gly Ala Phe Ala Gly Val Asp Val Arg Gly
            25                  30                  35

gga ggc cca ggc acc agg gaa acc gac ctt cta gaa cca cac aat tct   259
Gly Gly Pro Gly Thr Arg Glu Thr Asp Leu Leu Glu Pro His Asn Ser
        40                  45                  50

gtg cag caa gca cat gcc gtg gtg ttg tgt ggc ggt tcg gcg ttc ggg   307
Val Gln Gln Ala His Ala Val Val Leu Cys Gly Gly Ser Ala Phe Gly
    55                  60                  65

ttg gct gct gcc gat gga gtg atg aca gcc cta gaa aac cgc ggt att   355
Leu Ala Ala Ala Asp Gly Val Met Thr Ala Leu Glu Asn Arg Gly Ile
70                  75                  80                  85

ggt ttc cct gtc cgt ccc gaa ggg cct atc gtg cca atc gtt cca ggc   403
Gly Phe Pro Val Arg Pro Glu Gly Pro Ile Val Pro Ile Val Pro Gly
                90                  95                 100

gct gtg att ttt gat ttg ttg gtg ggc gat ccc aaa aac agg ccc acg   451
Ala Val Ile Phe Asp Leu Leu Val Gly Asp Pro Lys Asn Arg Pro Thr
            105                 110                 115

gca gct gat ggg gaa caa gca gtt gaa aac gct ttc gct ggt aca cac   499
Ala Ala Asp Gly Glu Gln Ala Val Glu Asn Ala Phe Ala Gly Thr His
        120                 125                 130
```

```
aac ggt tcg ggc agc gtc ggt gca gga acg ggt gct aca gca ggt cgg   547
Asn Gly Ser Gly Ser Val Gly Ala Gly Thr Gly Ala Thr Ala Gly Arg
    135                 140                 145

ctg cgt ggc ggt ttt ggc caa agc tcg cgc cgg gtc gga aag tac acc   595
Leu Arg Gly Gly Phe Gly Gln Ser Ser Arg Arg Val Gly Lys Tyr Thr
150                 155                 160                 165

atc gcg gca ggg gtc gtg gcg aat cct gtt ggg gaa gtc gtg gac cta   643
Ile Ala Ala Gly Val Val Ala Asn Pro Val Gly Glu Val Val Asp Leu
                170                 175                 180

aca act gga gct ttg ttt ggt agg ccc gaa gtg atg ggg gtg ggc gtc   691
Thr Thr Gly Ala Leu Phe Gly Arg Pro Glu Val Met Gly Val Gly Val
            185                 190                 195

gat aag cta aaa agc gcg gca gag acg ctg aac acg acc atc ggc gtc   739
Asp Lys Leu Lys Ser Ala Ala Glu Thr Leu Asn Thr Thr Ile Gly Val
        200                 205                 210

gtg gca act gac gcg ccg gtg aca aaa gcc caa gcg aag cgc ttg gcg   787
Val Ala Thr Asp Ala Pro Val Thr Lys Ala Gln Ala Lys Arg Leu Ala
    215                 220                 225

ctg gtg gcc cat gat ggt ttg gcg agg gca gtg cgg ccg tcg cat tca   835
Leu Val Ala His Asp Gly Leu Ala Arg Ala Val Arg Pro Ser His Ser
230                 235                 240                 245

ccg atg gac ggt gac aca ttt ttc gcc atg tca tcg ggt gat ggt agt   883
Pro Met Asp Gly Asp Thr Phe Phe Ala Met Ser Ser Gly Asp Gly Ser
                250                 255                 260

ggc gtt acc ccg gtt gag ctg gcg gaa ttg tcg gct cat gct gca gat   931
Gly Val Thr Pro Val Glu Leu Ala Glu Leu Ser Ala His Ala Ala Asp
            265                 270                 275

tgc gta cag gac gct atc atc gac gcc ata ctt acc gcg agt ccg gga   979
Cys Val Gln Asp Ala Ile Ile Asp Ala Ile Leu Thr Ala Ser Pro Gly
        280                 285                 290

ctc ggg ctc aaa agc ttc agg gaa ctt tta cca tgagttacaa cagcccgtat 1032
Leu Gly Leu Lys Ser Phe Arg Glu Leu Leu Pro
    295                 300

aac                                                               1035
```

09620350.0

<210> 1154
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 1154

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Met Leu Ile Asp Val Ala Gly Phe Leu Leu Gly His Val Thr Lys Gly
  1               5                  10                  15

Asp Thr Gly Cys Ser Val Val Ile Ala Pro Asn Gly Ala Phe Ala Gly
             20                  25                  30

Val Asp Val Arg Gly Gly Gly Pro Gly Thr Arg Glu Thr Asp Leu Leu
```

```
          35                  40                  45

Glu Pro His Asn Ser Val Gln Gln Ala His Ala Val Val Leu Cys Gly
      50                  55                  60

Gly Ser Ala Phe Gly Leu Ala Ala Ala Asp Gly Val Met Thr Ala Leu
 65                  70                  75                  80

Glu Asn Arg Gly Ile Gly Phe Pro Val Arg Pro Glu Gly Pro Ile Val
                 85                  90                  95

Pro Ile Val Pro Gly Ala Val Ile Phe Asp Leu Leu Val Gly Asp Pro
            100                 105                 110

Lys Asn Arg Pro Thr Ala Ala Asp Gly Glu Gln Ala Val Glu Asn Ala
        115                 120                 125

Phe Ala Gly Thr His Asn Gly Ser Gly Ser Val Gly Ala Gly Thr Gly
    130                 135                 140

Ala Thr Ala Gly Arg Leu Arg Gly Gly Phe Gly Gln Ser Ser Arg Arg
145                 150                 155                 160

Val Gly Lys Tyr Thr Ile Ala Ala Gly Val Val Ala Asn Pro Val Gly
                165                 170                 175

Glu Val Val Asp Leu Thr Thr Gly Ala Leu Phe Gly Arg Pro Glu Val
            180                 185                 190

Met Gly Val Gly Val Asp Lys Leu Lys Ser Ala Ala Glu Thr Leu Asn
        195                 200                 205

Thr Thr Ile Gly Val Val Ala Thr Asp Ala Pro Val Thr Lys Ala Gln
    210                 215                 220

Ala Lys Arg Leu Ala Leu Val Ala His Asp Gly Leu Ala Arg Ala Val
225                 230                 235                 240

Arg Pro Ser His Ser Pro Met Asp Gly Asp Thr Phe Phe Ala Met Ser
                245                 250                 255

Ser Gly Asp Gly Ser Gly Val Thr Pro Val Glu Leu Ala Glu Leu Ser
            260                 265                 270

Ala His Ala Ala Asp Cys Val Gln Asp Ala Ile Ile Asp Ala Ile Leu
        275                 280                 285

Thr Ala Ser Pro Gly Leu Gly Leu Lys Ser Phe Arg Glu Leu Leu Pro
    290                 295                 300
```

<210> 1155
<211> 928
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(928)
<223> FRXA02408

<400> 1155
gtgatgtacg cggcggggaa gccgccgagg aagaccgcga aaacctcgtg cagtggcttg 60

cctacaatca agagtccttg ctggaagcga tgatgaatta atg ctt atc gac gtc 115
Met Leu Ile Asp Val
1 5

gcg ggc ttc ctt tta ggc cac gtc acg aag ggg gat acg ggt tgc tca 163
Ala Gly Phe Leu Leu Gly His Val Thr Lys Gly Asp Thr Gly Cys Ser
10 15 20

gtg gtc att gca cct aac ggt gca ttt gcg ggc gtc gat gtc cgt ggg 211
Val Val Ile Ala Pro Asn Gly Ala Phe Ala Gly Val Asp Val Arg Gly
25 30 35

gga ggc cca ggc acc agg gaa acc gac ctt cta gaa cca cac aat tct 259
Gly Gly Pro Gly Thr Arg Glu Thr Asp Leu Leu Glu Pro His Asn Ser
40 45 50

gtg cag caa gca cat gcc gtg gtg ttg tgt ggc ggt tcg gcg ttc ggg 307
Val Gln Gln Ala His Ala Val Val Leu Cys Gly Gly Ser Ala Phe Gly
55 60 65

ttg gct gct gcc gat gga gtg atg aca gcc cta gaa aac cgc ggt att 355
Leu Ala Ala Ala Asp Gly Val Met Thr Ala Leu Glu Asn Arg Gly Ile
70 75 80 85

ggt ttc cct gtc cgt ccc gaa ggg cct atc gtg cca atc gtt cca ggc 403
Gly Phe Pro Val Arg Pro Glu Gly Pro Ile Val Pro Ile Val Pro Gly
90 95 100

gct gtg att ttt gat ttg ttg gtg ggc gat ccc aaa aac agg ccc acg 451
Ala Val Ile Phe Asp Leu Leu Val Gly Asp Pro Lys Asn Arg Pro Thr
105 110 115

gca gct gat ggg gaa caa gca gtt gaa aac gct ttc gct ggt aca cac 499
Ala Ala Asp Gly Glu Gln Ala Val Glu Asn Ala Phe Ala Gly Thr His
120 125 130

aac ggt tcg ggc agc gtc ggt gca gga acg ggt gct aca gca ggt cgg 547
Asn Gly Ser Gly Ser Val Gly Ala Gly Thr Gly Ala Thr Ala Gly Arg
135 140 145

ctg cgt ggc ggt ttt ggc caa agc tcg cgc cgg gtc gga aag tac acc 595
Leu Arg Gly Gly Phe Gly Gln Ser Ser Arg Arg Val Gly Lys Tyr Thr
150 155 160 165

atc gcg gca ggg gtc gtg gcg aat cct gtt ggg gaa gtc gtg gac cta 643
Ile Ala Ala Gly Val Val Ala Asn Pro Val Gly Glu Val Val Asp Leu
170 175 180

aca act gga gct ttg ttt ggt agg ccc gaa gtg atg ggg gtg ggc gtc 691
Thr Thr Gly Ala Leu Phe Gly Arg Pro Glu Val Met Gly Val Gly Val
185 190 195

gat aag cta aaa agc gcg gca gag acg ctg aac acg acc atc ggc gtc 739
Asp Lys Leu Lys Ser Ala Ala Glu Thr Leu Asn Thr Thr Ile Gly Val
200 205 210

```
gtg gca act gac gcg ccg gtg aca aaa gcc caa gcg aag cgc ttg gcg   787
Val Ala Thr Asp Ala Pro Val Thr Lys Ala Gln Ala Lys Arg Leu Ala
    215                 220                 225

ctg gtg gcc cat gat ggt ttg gcg agg gca gtg cgg ccg tcg cat tca   835
Leu Val Ala His Asp Gly Leu Ala Arg Ala Val Arg Pro Ser His Ser
230                 235                 240                 245

ccg atg gac ggt gac aca ttt ttc gcc atg tca tcg ggt gat ggt agt   883
Pro Met Asp Gly Asp Thr Phe Phe Ala Met Ser Ser Gly Asp Gly Ser
                250                 255                 260

ggc gtt acc ccg gtt gag ctg ggg gaa ttg tcg gct cat gct gca       928
Gly Val Thr Pro Val Glu Leu Gly Glu Leu Ser Ala His Ala Ala
            265                 270                 275
```

<210> 1156
<211> 276
<212> PRT
<213> Corynebacterium glutamicum

<400> 1156

```
Met Leu Ile Asp Val Ala Gly Phe Leu Leu Gly His Val Thr Lys Gly
  1               5                  10                  15

Asp Thr Gly Cys Ser Val Val Ile Ala Pro Asn Gly Ala Phe Ala Gly
             20                  25                  30

Val Asp Val Arg Gly Gly Gly Pro Gly Thr Arg Glu Thr Asp Leu Leu
         35                  40                  45

Glu Pro His Asn Ser Val Gln Gln Ala His Ala Val Val Leu Cys Gly
     50                  55                  60

Gly Ser Ala Phe Gly Leu Ala Ala Ala Asp Gly Val Met Thr Ala Leu
 65                  70                  75                  80

Glu Asn Arg Gly Ile Gly Phe Pro Val Arg Pro Glu Gly Pro Ile Val
                 85                  90                  95

Pro Ile Val Pro Gly Ala Val Ile Phe Asp Leu Leu Val Gly Asp Pro
            100                 105                 110

Lys Asn Arg Pro Thr Ala Ala Asp Gly Glu Gln Ala Val Glu Asn Ala
        115                 120                 125

Phe Ala Gly Thr His Asn Gly Ser Gly Ser Val Gly Ala Gly Thr Gly
    130                 135                 140

Ala Thr Ala Gly Arg Leu Arg Gly Gly Phe Gly Gln Ser Ser Arg Arg
145                 150                 155                 160

Val Gly Lys Tyr Thr Ile Ala Ala Gly Val Val Ala Asn Pro Val Gly
                165                 170                 175

Glu Val Val Asp Leu Thr Thr Gly Ala Leu Phe Gly Arg Pro Glu Val
            180                 185                 190

Met Gly Val Gly Val Asp Lys Leu Lys Ser Ala Ala Glu Thr Leu Asn
```

```
        195                 200                 205

Thr Thr Ile Gly Val Val Ala Thr Asp Ala Pro Val Thr Lys Ala Gln
    210                 215                 220

Ala Lys Arg Leu Ala Leu Val Ala His Asp Gly Leu Ala Arg Ala Val
225                 230                 235                 240

Arg Pro Ser His Ser Pro Met Asp Gly Asp Thr Phe Phe Ala Met Ser
                245                 250                 255

Ser Gly Asp Gly Ser Gly Val Thr Pro Val Glu Leu Gly Glu Leu Ser
            260                 265                 270

Ala His Ala Ala
        275


<210> 1157
<211> 660
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(637)
<223> RXN02409

<400> 1157
gagttctggc gagaaggaca aagtggaggg tgatgtgaag aaactccaca ccgcagggct 60

gtgggcgaca atgcagcagg cagggtaggg gagaattttc atg cag cag tgg aag   115
                                            Met Gln Gln Trp Lys
                                              1               5

aag aaa aaa ggg ctg atg cgc cag gct cgt tac gcg gtg gtt ttt gag   163
Lys Lys Lys Gly Leu Met Arg Gln Ala Arg Tyr Ala Val Val Phe Glu
                 10                  15                  20

ccg atg gag cgg gaa gtg ttg ggt gat ttg tca gct gcg gtc agt gag   211
Pro Met Glu Arg Glu Val Leu Gly Asp Leu Ser Ala Ala Val Ser Glu
             25                  30                  35

gcg ttg att cag cgt gca cag tct gtg ccg aag gat cct ctg gca gag   259
Ala Leu Ile Gln Arg Ala Gln Ser Val Pro Lys Asp Pro Leu Ala Glu
         40                  45                  50

atg acc ggc atg aca agt gga cac aaa gaa gca cca acc gat ccg gcg   307
Met Thr Gly Met Thr Ser Gly His Lys Glu Ala Pro Thr Asp Pro Ala
     55                  60                  65

ctt gcg cgt ttg ctc cct gat ttt cag cac gag ggc gat gag gaa tac   355
Leu Ala Arg Leu Leu Pro Asp Phe Gln His Glu Gly Asp Glu Glu Tyr
 70                  75                  80                  85

gac ggc gat aat tct ttc ctc cgt tca ctc cat gaa ggc gac atc acc   403
Asp Gly Asp Asn Ser Phe Leu Arg Ser Leu His Glu Gly Asp Ile Thr
                 90                  95                 100

cga gca aaa ctg gaa aat ctg cgc gtg att aac gat gcg ctg gga ccc   451
Arg Ala Lys Leu Glu Asn Leu Arg Val Ile Asn Asp Ala Leu Gly Pro
```

```
            105                 110                 115

gac gga aat gtt gcg gtc acc gcc tct gag gag gaa gcg cac gct tgg   499
Asp Gly Asn Val Ala Val Thr Ala Ser Glu Glu Glu Ala His Ala Trp
        120                 125                 130

ttg gct gcg ctc aat gac atc cgc ctg tac gtt gcc tcc ggt gat gta   547
Leu Ala Ala Leu Asn Asp Ile Arg Leu Tyr Val Ala Ser Gly Asp Val
    135                 140                 145

cgc ggc ggg gaa gcc gcc gag gaa gac cgc gaa aac ctc gtg cag tgg   595
Arg Gly Gly Glu Ala Ala Glu Glu Asp Arg Glu Asn Leu Val Gln Trp
150                 155                 160                 165

ctt gcc tac aat caa gag tcc ttg ctg gaa gcg atg atg aat           637
Leu Ala Tyr Asn Gln Glu Ser Leu Leu Glu Ala Met Met Asn
                170                 175

taatgcttat cgacgtcgcg ggc                                        660


<210> 1158
<211> 179
<212> PRT
<213> Corynebacterium glutamicum

<400> 1158
Met Gln Gln Trp Lys Lys Lys Lys Gly Leu Met Arg Gln Ala Arg Tyr
  1               5                  10                  15

Ala Val Val Phe Glu Pro Met Glu Arg Glu Val Leu Gly Asp Leu Ser
             20                  25                  30

Ala Ala Val Ser Glu Ala Leu Ile Gln Arg Ala Gln Ser Val Pro Lys
         35                  40                  45

Asp Pro Leu Ala Glu Met Thr Gly Met Thr Ser Gly His Lys Glu Ala
     50                  55                  60

Pro Thr Asp Pro Ala Leu Ala Arg Leu Leu Pro Asp Phe Gln His Glu
 65                  70                  75                  80

Gly Asp Glu Glu Tyr Asp Gly Asp Asn Ser Phe Leu Arg Ser Leu His
                 85                  90                  95

Glu Gly Asp Ile Thr Arg Ala Lys Leu Glu Asn Leu Arg Val Ile Asn
            100                 105                 110

Asp Ala Leu Gly Pro Asp Gly Asn Val Ala Val Thr Ala Ser Glu Glu
        115                 120                 125

Glu Ala His Ala Trp Leu Ala Ala Leu Asn Asp Ile Arg Leu Tyr Val
    130                 135                 140

Ala Ser Gly Asp Val Arg Gly Gly Glu Ala Ala Glu Glu Asp Arg Glu
145                 150                 155                 160

Asn Leu Val Gln Trp Leu Ala Tyr Asn Gln Glu Ser Leu Leu Glu Ala
                165                 170                 175

Met Met Asn
```

<210> 1159
<211> 437
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(414)
<223> FRXA02409

<400> 1159
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cgt gca cag tct gtg ccg aag gat cct ctg gca gag atg acc ggc atg   48
Arg Ala Gln Ser Val Pro Lys Asp Pro Leu Ala Glu Met Thr Gly Met
  1               5                  10                  15

aca agt gga cac aaa gaa gca cca acc gat ccg gcg ctt gcg cgt ttg   96
Thr Ser Gly His Lys Glu Ala Pro Thr Asp Pro Ala Leu Ala Arg Leu
             20                  25                  30

ctc cct gat ttt cag cac gag ggc gat gag gaa tac gac ggc gat aat  144
Leu Pro Asp Phe Gln His Glu Gly Asp Glu Glu Tyr Asp Gly Asp Asn
         35                  40                  45

tct ttc ctc cgt tca ctc cat gaa ggc gac atc acc cga gca aaa ctg  192
Ser Phe Leu Arg Ser Leu His Glu Gly Asp Ile Thr Arg Ala Lys Leu
     50                  55                  60

gaa aat ctg cgc gtg att aac gat gcg ctg gga ccc gac gga aat gtt  240
Glu Asn Leu Arg Val Ile Asn Asp Ala Leu Gly Pro Asp Gly Asn Val
 65                  70                  75                  80

gcg gtc acc gcc tct gag gag gaa gcg cac gct tgg ttg gct gcg ctc  288
Ala Val Thr Ala Ser Glu Glu Glu Ala His Ala Trp Leu Ala Ala Leu
                 85                  90                  95

aat gac atc cgc ctg tac gtt gcc tcc ggt gat gta cgc ggc ggg gaa  336
Asn Asp Ile Arg Leu Tyr Val Ala Ser Gly Asp Val Arg Gly Gly Glu
            100                 105                 110

gcc gcc gag gaa gac cgc gaa aac ctc gtg cag tgg ctt gcc tac aat  384
Ala Ala Glu Glu Asp Arg Glu Asn Leu Val Gln Trp Leu Ala Tyr Asn
        115                 120                 125

caa gag tcc ttg ctg gaa gcg atg atg aat taatgcttat cgacgtcgcg    434
Gln Glu Ser Leu Leu Glu Ala Met Met Asn
    130                 135

ggc                                                             437
```

<210> 1160
<211> 138
<212> PRT
<213> Corynebacterium glutamicum

<400> 1160
```
Arg Ala Gln Ser Val Pro Lys Asp Pro Leu Ala Glu Met Thr Gly Met
  1               5                  10                  15
```

```
Thr Ser Gly His Lys Glu Ala Pro Thr Asp Pro Ala Leu Ala Arg Leu
            20                  25                  30

Leu Pro Asp Phe Gln His Glu Gly Asp Glu Glu Tyr Asp Gly Asp Asn
        35                  40                  45

Ser Phe Leu Arg Ser Leu His Glu Gly Asp Ile Thr Arg Ala Lys Leu
    50                  55                  60

Glu Asn Leu Arg Val Ile Asn Asp Ala Leu Gly Pro Asp Gly Asn Val
65                  70                  75                  80

Ala Val Thr Ala Ser Glu Glu Glu Ala His Ala Trp Leu Ala Ala Leu
                85                  90                  95

Asn Asp Ile Arg Leu Tyr Val Ala Ser Gly Asp Val Arg Gly Gly Glu
            100                 105                 110

Ala Ala Glu Glu Asp Arg Glu Asn Leu Val Gln Trp Leu Ala Tyr Asn
        115                 120                 125

Gln Glu Ser Leu Leu Glu Ala Met Met Asn
    130                 135
```

<210> 1161
<211> 1257
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1234)
<223> RXN02428

<400> 1161

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cgaaagatat gcataaagtg atgatgaaat agctttgtcg aaaggtttgc tcccggtgca 60

ttcagttagc gtgaaggtgc catcatcaca agggttgatg atg gcc gcg acg tta   115
                                              Met Ala Ala Thr Leu
                                                1               5

gat ctt cca gat aca gat ccc att gcc tat gca atg ttt gcc cac tgt   163
Asp Leu Pro Asp Thr Asp Pro Ile Ala Tyr Ala Met Phe Ala His Cys
            10                  15                  20

ttc acc ggc tca cgg ttc acg cca gcc gcc gcg cga gtc agt aaa aca   211
Phe Thr Gly Ser Arg Phe Thr Pro Ala Ala Ala Arg Val Ser Lys Thr
        25                  30                  35

ctc gca gaa tcc ggc gtc gcc tgc ctg cgt ttc gat ttc cca gga ctg   259
Leu Ala Glu Ser Gly Val Ala Cys Leu Arg Phe Asp Phe Pro Gly Leu
    40                  45                  50

agc caa tca gaa ggt gac ttc tcc aaa acc acc ttc aac tcc aat gtg   307
Ser Gln Ser Glu Gly Asp Phe Ser Lys Thr Thr Phe Asn Ser Asn Val
55                  60                  65

gac gat atc gtg gcg gcc tcg cag tgg ttg acg gaa cac tac tcc gct   355
Asp Asp Ile Val Ala Ala Ser Gln Trp Leu Thr Glu His Tyr Ser Ala
```

```
 70                  75                  80                  85

cca cag ttg ctc att gga cac tcc ttg ggt ggt gca gca tca ctg aaa   403
Pro Gln Leu Leu Ile Gly His Ser Leu Gly Gly Ala Ala Ser Leu Lys
                 90                  95                 100

gct gcc acc aaa atc tcc tgc ctc aaa gca gta gca acg ata ggt gca   451
Ala Ala Thr Lys Ile Ser Cys Leu Lys Ala Val Ala Thr Ile Gly Ala
             105                 110                 115

cct ttt gat cct gcg cac gca gtc ctg cac ttt gct gat cgc ata tgt   499
Pro Phe Asp Pro Ala His Ala Val Leu His Phe Ala Asp Arg Ile Cys
         120                 125                 130

gat gta gat gat caa ggt gct gtc act ctg cag ctc gga ggc cgg gat   547
Asp Val Asp Asp Gln Gly Ala Val Thr Leu Gln Leu Gly Gly Arg Asp
     135                 140                 145

gtc acc att tcc cgc gaa ttc ctc gaa gac ctt gca gag gtc aac ccc   595
Val Thr Ile Ser Arg Glu Phe Leu Glu Asp Leu Ala Glu Val Asn Pro
150                 155                 160                 165

gaa gat cac ctc cgc agg ctc cgc aaa cca ctg ctt tta ctg cat tcc   643
Glu Asp His Leu Arg Arg Leu Arg Lys Pro Leu Leu Leu Leu His Ser
                 170                 175                 180

ccc acc gac caa acc gtc ggc gtg gac aac gcg cag ctc atc ttc aga   691
Pro Thr Asp Gln Thr Val Gly Val Asp Asn Ala Gln Leu Ile Phe Arg
             185                 190                 195

gtc act cgc tac cct aaa tcc ttg atg act ttg gac aag gca gat cac   739
Val Thr Arg Tyr Pro Lys Ser Leu Met Thr Leu Asp Lys Ala Asp His
         200                 205                 210

ctg ctc acc aaa gat ggc acc gca cag cgt gca gcc cgg atc atc gcg   787
Leu Leu Thr Lys Asp Gly Thr Ala Gln Arg Ala Ala Arg Ile Ile Ala
     215                 220                 225

aac tgg gtc gag ccc tac ctg gtt cca gaa aac gtc tgt gag gat ctt   835
Asn Trp Val Glu Pro Tyr Leu Val Pro Glu Asn Val Cys Glu Asp Leu
230                 235                 240                 245

ccg gag ttt gtc gcc gaa gcc tca acc atc aaa gcc agc aaa tac ggc   883
Pro Glu Phe Val Ala Glu Ala Ser Thr Ile Lys Ala Ser Lys Tyr Gly
                 250                 255                 260

gca gcc atc cgc acc ggt ggt cac aat ttc atc acc gac cgc gac aaa   931
Ala Ala Ile Arg Thr Gly Gly His Asn Phe Ile Thr Asp Arg Asp Lys
             265                 270                 275

tcc cag ggt ggc aaa aac ctc ggc ttc acc cct act tcc ctg ctg gtt   979
Ser Gln Gly Gly Lys Asn Leu Gly Phe Thr Pro Thr Ser Leu Leu Val
         280                 285                 290

tcc gcg ctt gct gct gca aac tct caa acg atc aaa caa gca gcc atc   1027
Ser Ala Leu Ala Ala Ala Asn Ser Gln Thr Ile Lys Gln Ala Ala Ile
     295                 300                 305

gac aac cgc atc aaa ggc ctt gac gat gtc aaa gtg acg atc tcc cag   1075
Asp Asn Arg Ile Lys Gly Leu Asp Asp Val Lys Val Thr Ile Ser Gln
310                 315                 320                 325
```

```
gaa caa tca gcc gac cac ggc cag atc aaa ctc cgc cga aag atc tct   1123
Glu Gln Ser Ala Asp His Gly Gln Ile Lys Leu Arg Arg Lys Ile Ser
                330                 335                 340

ttg atc ggc aac ctc agc gat gct gac agt gct tca ctt cgg gcc gca   1171
Leu Ile Gly Asn Leu Ser Asp Ala Asp Ser Ala Ser Leu Arg Ala Ala
            345                 350                 355

tct aat tcc tgc tcg att acc caa ctg ctc gcg cag gga atc gtc atc   1219
Ser Asn Ser Cys Ser Ile Thr Gln Leu Leu Ala Gln Gly Ile Val Ile
        360                 365                 370

gac gac gag gtg aac tagcgtggat tttgagttgg gta                    1257
Asp Asp Glu Val Asn
    375
```

<210> 1162
<211> 378
<212> PRT
<213> Corynebacterium glutamicum

<400> 1162

```
Met Ala Ala Thr Leu Asp Leu Pro Asp Thr Asp Pro Ile Ala Tyr Ala
  1               5                  10                  15

Met Phe Ala His Cys Phe Thr Gly Ser Arg Phe Thr Pro Ala Ala Ala
             20                  25                  30

Arg Val Ser Lys Thr Leu Ala Glu Ser Gly Val Ala Cys Leu Arg Phe
         35                  40                  45

Asp Phe Pro Gly Leu Ser Gln Ser Glu Gly Asp Phe Ser Lys Thr Thr
     50                  55                  60

Phe Asn Ser Asn Val Asp Asp Ile Val Ala Ala Ser Gln Trp Leu Thr
 65                  70                  75                  80

Glu His Tyr Ser Ala Pro Gln Leu Leu Ile Gly His Ser Leu Gly Gly
                 85                  90                  95

Ala Ala Ser Leu Lys Ala Ala Thr Lys Ile Ser Cys Leu Lys Ala Val
            100                 105                 110

Ala Thr Ile Gly Ala Pro Phe Asp Pro Ala His Ala Val Leu His Phe
        115                 120                 125

Ala Asp Arg Ile Cys Asp Val Asp Asp Gln Gly Ala Val Thr Leu Gln
    130                 135                 140

Leu Gly Gly Arg Asp Val Thr Ile Ser Arg Glu Phe Leu Glu Asp Leu
145                 150                 155                 160

Ala Glu Val Asn Pro Glu Asp His Leu Arg Arg Leu Arg Lys Pro Leu
                165                 170                 175

Leu Leu Leu His Ser Pro Thr Asp Gln Thr Val Gly Val Asp Asn Ala
            180                 185                 190

Gln Leu Ile Phe Arg Val Thr Arg Tyr Pro Lys Ser Leu Met Thr Leu
```

```
        195                 200                 205

Asp Lys Ala Asp His Leu Leu Thr Lys Asp Gly Thr Ala Gln Arg Ala
    210                 215                 220

Ala Arg Ile Ile Ala Asn Trp Val Glu Pro Tyr Leu Val Pro Glu Asn
225                 230                 235                 240

Val Cys Glu Asp Leu Pro Glu Phe Val Ala Glu Ala Ser Thr Ile Lys
                245                 250                 255

Ala Ser Lys Tyr Gly Ala Ala Ile Arg Thr Gly Gly His Asn Phe Ile
            260                 265                 270

Thr Asp Arg Asp Lys Ser Gln Gly Gly Lys Asn Leu Gly Phe Thr Pro
        275                 280                 285

Thr Ser Leu Leu Val Ser Ala Leu Ala Ala Ala Asn Ser Gln Thr Ile
    290                 295                 300

Lys Gln Ala Ala Ile Asp Asn Arg Ile Lys Gly Leu Asp Asp Val Lys
305                 310                 315                 320

Val Thr Ile Ser Gln Glu Gln Ser Ala Asp His Gly Gln Ile Lys Leu
                325                 330                 335

Arg Arg Lys Ile Ser Leu Ile Gly Asn Leu Ser Asp Ala Asp Ser Ala
            340                 345                 350

Ser Leu Arg Ala Ala Ser Asn Ser Cys Ser Ile Thr Gln Leu Leu Ala
        355                 360                 365

Gln Gly Ile Val Ile Asp Asp Glu Val Asn
    370                 375


<210> 1163
<211> 1257
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1234)
<223> FRXA02428

<400> 1163
cgaaagatat gcataaagtg atgatgaaat agctttgtcg aaaggtttgc tcccggtgca 60

ttcagttagc gtgaaggtgc catcatcaca agggttgatg atg gcc gcg acg tta   115
                                              Met Ala Ala Thr Leu
                                                1               5

gat ctt cca gat aca gat ccc att gcc tat gca atg ttt gcc cac tgt   163
Asp Leu Pro Asp Thr Asp Pro Ile Ala Tyr Ala Met Phe Ala His Cys
                10                  15                  20

ttc acc ggc tca cgg ttc acg cca gcc gcc gcg cga gtc agt aaa aca   211
Phe Thr Gly Ser Arg Phe Thr Pro Ala Ala Ala Arg Val Ser Lys Thr
            25                  30                  35
```

```
ctc gca gaa tcc ggc gtc gcc tgc ctg cgt ttc gat ttc cca gga ctg   259
Leu Ala Glu Ser Gly Val Ala Cys Leu Arg Phe Asp Phe Pro Gly Leu
         40                  45                  50

agc caa tca gaa ggt gac ttc tcc aaa acc acc ttc aac tcc aat gtg   307
Ser Gln Ser Glu Gly Asp Phe Ser Lys Thr Thr Phe Asn Ser Asn Val
     55                  60                  65

gac gat atc gtg gcg gcc tcg cag tgg ttg acg gaa cac tac tcc gct   355
Asp Asp Ile Val Ala Ala Ser Gln Trp Leu Thr Glu His Tyr Ser Ala
 70                  75                  80                  85

cca cag ttg ctc att gga cac tcc ttg ggt ggt gca gca tca ctg aaa   403
Pro Gln Leu Leu Ile Gly His Ser Leu Gly Gly Ala Ala Ser Leu Lys
                 90                  95                 100

gct gcc acc aaa atc tcc tgc ctc aaa gca gta gca acg ata ggt gca   451
Ala Ala Thr Lys Ile Ser Cys Leu Lys Ala Val Ala Thr Ile Gly Ala
            105                 110                 115

cct ttt gat cct gcg cac gca gtc ctg cac ttt gct gat cgc ata tgt   499
Pro Phe Asp Pro Ala His Ala Val Leu His Phe Ala Asp Arg Ile Cys
        120                 125                 130

gat gta gat gat caa ggt gct gtc act ctg cag ctc gga ggc cgg gat   547
Asp Val Asp Asp Gln Gly Ala Val Thr Leu Gln Leu Gly Gly Arg Asp
    135                 140                 145

gtc acc att tcc cgc gaa ttc ctc gaa gac ctt gca gag gtc aac ccc   595
Val Thr Ile Ser Arg Glu Phe Leu Glu Asp Leu Ala Glu Val Asn Pro
150                 155                 160                 165

gaa gat cac ctc cgc agg ctc cgc aaa cca ctg ctt tta ctg cat tcc   643
Glu Asp His Leu Arg Arg Leu Arg Lys Pro Leu Leu Leu Leu His Ser
                170                 175                 180

ccc acc gac caa acc gtc ggc gtg gac aac gcg cag ctc atc ttc aga   691
Pro Thr Asp Gln Thr Val Gly Val Asp Asn Ala Gln Leu Ile Phe Arg
            185                 190                 195

gtc act cgc tac cct aaa tcc ttg atg act ttg gac aag gca gat cac   739
Val Thr Arg Tyr Pro Lys Ser Leu Met Thr Leu Asp Lys Ala Asp His
        200                 205                 210

ctg ctc acc aaa gat ggc acc gca cag cgt gca gcc cgg atc atc gcg   787
Leu Leu Thr Lys Asp Gly Thr Ala Gln Arg Ala Ala Arg Ile Ile Ala
    215                 220                 225

aac tgg gtc gag ccc tac ctg gtt cca gaa aac gtc tgt gag gat ctt   835
Asn Trp Val Glu Pro Tyr Leu Val Pro Glu Asn Val Cys Glu Asp Leu
230                 235                 240                 245

ccg gag ttt gtc gcc gaa gcc tca acc atc aaa gcc agc aaa tac ggc   883
Pro Glu Phe Val Ala Glu Ala Ser Thr Ile Lys Ala Ser Lys Tyr Gly
                250                 255                 260

gca gcc atc cgc acc ggt ggt cac aat ttc atc acc gac cgc gac aaa   931
Ala Ala Ile Arg Thr Gly Gly His Asn Phe Ile Thr Asp Arg Asp Lys
            265                 270                 275

tcc cag ggt ggc aaa aac ctc ggc ttc acc cct act tcc ctg ctg gtt   979
```

```
Ser Gln Gly Gly Lys Asn Leu Gly Phe Thr Pro Thr Ser Leu Leu Val
        280                 285                 290

tcc gcg ctt gct gct gca aac tct caa acg atc aaa caa gca gcc atc   1027
Ser Ala Leu Ala Ala Ala Asn Ser Gln Thr Ile Lys Gln Ala Ala Ile
    295                 300                 305

gac aac cgc atc aaa ggc ctt gac gat gtc aaa gtg acg atc tcc cag   1075
Asp Asn Arg Ile Lys Gly Leu Asp Asp Val Lys Val Thr Ile Ser Gln
310                 315                 320                 325

gaa caa tca gcc gac cac ggc cag atc aaa ctc cgc cga aag atc tct   1123
Glu Gln Ser Ala Asp His Gly Gln Ile Lys Leu Arg Arg Lys Ile Ser
                330                 335                 340

ttg atc ggc aac ctc agc gat gct gac agt gct tca ctt cgg gcc gca   1171
Leu Ile Gly Asn Leu Ser Asp Ala Asp Ser Ala Ser Leu Arg Ala Ala
            345                 350                 355

tct aat tcc tgc tcg att acc caa ctg ctc gcg cag gga atc gtc atc   1219
Ser Asn Ser Cys Ser Ile Thr Gln Leu Leu Ala Gln Gly Ile Val Ile
        360                 365                 370

gac gac gag gtg aac tagcgtggat tttgagttgg gta                    1257
Asp Asp Glu Val Asn
    375


<210> 1164
<211> 378
<212> PRT
<213> Corynebacterium glutamicum

<400> 1164
Met Ala Ala Thr Leu Asp Leu Pro Asp Thr Asp Pro Ile Ala Tyr Ala
  1               5                  10                  15

Met Phe Ala His Cys Phe Thr Gly Ser Arg Phe Thr Pro Ala Ala Ala
             20                  25                  30

Arg Val Ser Lys Thr Leu Ala Glu Ser Gly Val Ala Cys Leu Arg Phe
         35                  40                  45

Asp Phe Pro Gly Leu Ser Gln Ser Glu Gly Asp Phe Ser Lys Thr Thr
     50                  55                  60

Phe Asn Ser Asn Val Asp Asp Ile Val Ala Ala Ser Gln Trp Leu Thr
 65                  70                  75                  80

Glu His Tyr Ser Ala Pro Gln Leu Leu Ile Gly His Ser Leu Gly Gly
                 85                  90                  95

Ala Ala Ser Leu Lys Ala Ala Thr Lys Ile Ser Cys Leu Lys Ala Val
            100                 105                 110

Ala Thr Ile Gly Ala Pro Phe Asp Pro Ala His Ala Val Leu His Phe
        115                 120                 125

Ala Asp Arg Ile Cys Asp Val Asp Asp Gln Gly Ala Val Thr Leu Gln
    130                 135                 140
```

```
Leu Gly Gly Arg Asp Val Thr Ile Ser Arg Glu Phe Leu Glu Asp Leu
145                 150                 155                 160

Ala Glu Val Asn Pro Glu Asp His Leu Arg Arg Leu Arg Lys Pro Leu
                165                 170                 175

Leu Leu Leu His Ser Pro Thr Asp Gln Thr Val Gly Val Asp Asn Ala
            180                 185                 190

Gln Leu Ile Phe Arg Val Thr Arg Tyr Pro Lys Ser Leu Met Thr Leu
        195                 200                 205

Asp Lys Ala Asp His Leu Leu Thr Lys Asp Gly Thr Ala Gln Arg Ala
    210                 215                 220

Ala Arg Ile Ile Ala Asn Trp Val Glu Pro Tyr Leu Val Pro Glu Asn
225                 230                 235                 240

Val Cys Glu Asp Leu Pro Glu Phe Val Ala Glu Ala Ser Thr Ile Lys
                245                 250                 255

Ala Ser Lys Tyr Gly Ala Ala Ile Arg Thr Gly Gly His Asn Phe Ile
            260                 265                 270

Thr Asp Arg Asp Lys Ser Gln Gly Gly Lys Asn Leu Gly Phe Thr Pro
        275                 280                 285

Thr Ser Leu Leu Val Ser Ala Leu Ala Ala Ala Asn Ser Gln Thr Ile
    290                 295                 300

Lys Gln Ala Ala Ile Asp Asn Arg Ile Lys Gly Leu Asp Asp Val Lys
305                 310                 315                 320

Val Thr Ile Ser Gln Glu Gln Ser Ala Asp His Gly Gln Ile Lys Leu
                325                 330                 335

Arg Arg Lys Ile Ser Leu Ile Gly Asn Leu Ser Asp Ala Asp Ser Ala
            340                 345                 350

Ser Leu Arg Ala Ala Ser Asn Ser Cys Ser Ile Thr Gln Leu Leu Ala
        355                 360                 365

Gln Gly Ile Val Ile Asp Asp Glu Val Asn
    370                 375


<210> 1165
<211> 1365
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1342)
<223> RXN02454

<400> 1165
ggcaagcgcc tcccttaagc ccgcgtaccg gctaccccga ggcacgtaat gagtagggca 60

gttctagcca taatcagcag aaaaggtgga gtgattcgcc atg aaa gag tcc atg   115
                                               Met Lys Glu Ser Met
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                                                        1               5

agc atc acc tcg tcg acg tac gcg tcg gca ctg ctg aca ctg ccc tgg   163
Ser Ile Thr Ser Ser Thr Tyr Ala Ser Ala Leu Leu Thr Leu Pro Trp
                  10                  15                  20

ggt aca ccc ctg gaa cag tgg ccc gat aat ctc atc gcc gcg ctg ccc   211
Gly Thr Pro Leu Glu Gln Trp Pro Asp Asn Leu Ile Ala Ala Leu Pro
             25                  30                  35

agg ggt att tcc cgg cac atc gtg cgt ttc gtg ggg atc aac cgt ggc   259
Arg Gly Ile Ser Arg His Ile Val Arg Phe Val Gly Ile Asn Arg Gly
         40                  45                  50

atc gtc gcg gtc aaa gaa att ggt gcg cgt acc gcc cac cac gag tac   307
Ile Val Ala Val Lys Glu Ile Gly Ala Arg Thr Ala His His Glu Tyr
     55                  60                  65

aag atg ctg cgt gaa ctg cag cgc ctt ggt gcc ccc agt gtg cgc ccc   355
Lys Met Leu Arg Glu Leu Gln Arg Leu Gly Ala Pro Ser Val Arg Pro
 70                  75                  80                  85

gta gcc gtg atc acc gga cgc cat ccg gca gag gaa gac tac ggg gag   403
Val Ala Val Ile Thr Gly Arg His Pro Ala Glu Glu Asp Tyr Gly Glu
                 90                  95                 100

ctc acc gca gct ttg gtg acc gag cac ttg gag ttt tcc ctg ccc tat   451
Leu Thr Ala Ala Leu Val Thr Glu His Leu Glu Phe Ser Leu Pro Tyr
            105                 110                 115

cgc gag atc ttt tct cgg cac ctc acg gtc gtg gaa tcg gag aag ctc   499
Arg Glu Ile Phe Ser Arg His Leu Thr Val Val Glu Ser Glu Lys Leu
        120                 125                 130

atc cgc gcc ctg tcc gtg ctg ttg gtg cgg atg cat ctg ctc aac ttc   547
Ile Arg Ala Leu Ser Val Leu Leu Val Arg Met His Leu Leu Asn Phe
    135                 140                 145

tac tgg gga gat gtg tca ctg tct aat act ctc ttt cgt cgc gat gct   595
Tyr Trp Gly Asp Val Ser Leu Ser Asn Thr Leu Phe Arg Arg Asp Ala
150                 155                 160                 165

gaa acc tat tcc gcc tat ctc gtc gat gcc gaa acc ggg gag ttc cag   643
Glu Thr Tyr Ser Ala Tyr Leu Val Asp Ala Glu Thr Gly Glu Phe Gln
                170                 175                 180

ccc aac ctc tct gaa tca cgc agg ctt tac gac gtc gac atc gcc cgc   691
Pro Asn Leu Ser Glu Ser Arg Arg Leu Tyr Asp Val Asp Ile Ala Arg
            185                 190                 195

gtc aac atc att ggc gaa ctc atg gac cta cag gcg ggt gaa tgc cta   739
Val Asn Ile Ile Gly Glu Leu Met Asp Leu Gln Ala Gly Glu Cys Leu
        200                 205                 210

gat aag tcc atc gat gtc atc gcc cta gga ggc ctt gtc gaa agc tct   787
Asp Lys Ser Ile Asp Val Ile Ala Leu Gly Gly Leu Val Glu Ser Ser
    215                 220                 225

tat ctt gaa ttg tgg acg gag ctc acc gcg gag gaa tcc gtc gat gcc   835
Tyr Leu Glu Leu Trp Thr Glu Leu Thr Ala Glu Glu Ser Val Asp Ala
230                 235                 240                 245
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```
agt gaa tat tgg cgc ctc tct gag aga att gac cgg ctc aat caa ctg   883
Ser Glu Tyr Trp Arg Leu Ser Glu Arg Ile Asp Arg Leu Asn Gln Leu
                250                 255                 260

ggc ttt gac gta ggg gag ctc aag gtc acg aag gac gat tcg cgg cag   931
Gly Phe Asp Val Gly Glu Leu Lys Val Thr Lys Asp Asp Ser Arg Gln
            265                 270                 275

gtt gtg cgc att cgc cct gta gtg gtg gat ccg ggc cac tat cgt gca   979
Val Val Arg Ile Arg Pro Val Val Val Asp Pro Gly His Tyr Arg Ala
        280                 285                 290

gag cta ttg agc tta acc ggg ctg agc gtc gag gaa cac cag gcc caa   1027
Glu Leu Leu Ser Leu Thr Gly Leu Ser Val Glu Glu His Gln Ala Gln
    295                 300                 305

cgc cta ttg ggc tcg atc cag gcc tat cag gcc gtc gaa tgc gga ccg   1075
Arg Leu Leu Gly Ser Ile Gln Ala Tyr Gln Ala Val Glu Cys Gly Pro
310                 315                 320                 325

cat gta ggt ctt acc caa gcc gcg cat ctc tgg atg acg aat gaa tac   1123
His Val Gly Leu Thr Gln Ala Ala His Leu Trp Met Thr Asn Glu Tyr
                330                 335                 340

gaa ccg act atc gcc gcc gtc ccc gtg gag atg tta gac aag ctg gag   1171
Glu Pro Thr Ile Ala Ala Val Pro Val Glu Met Leu Asp Lys Leu Glu
            345                 350                 355

cca gca caa atc ttc cac gaa atc gtc gac cac cgc tgg ttc ctc gcc   1219
Pro Ala Gln Ile Phe His Glu Ile Val Asp His Arg Trp Phe Leu Ala
        360                 365                 370

caa gaa agg gga ggg gct gtc acc ctc cca gag gcc acg gca tcc tat   1267
Gln Glu Arg Gly Gly Ala Val Thr Leu Pro Glu Ala Thr Ala Ser Tyr
    375                 380                 385

ctt gaa tcc gtg ctt ccg gcc cgc cgc gac gag gct cgc ctc ctc agc   1315
Leu Glu Ser Val Leu Pro Ala Arg Arg Asp Glu Ala Arg Leu Leu Ser
390                 395                 400                 405

aca aac cct tca gac gaa gac ttg tca taacctctcg cgtgccccaa         1362
Thr Asn Pro Ser Asp Glu Asp Leu Ser
                410

cgg                                                              1365
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<210> 1166
<211> 414
<212> PRT
<213> Corynebacterium glutamicum

<400> 1166

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Met Lys Glu Ser Met Ser Ile Thr Ser Ser Thr Tyr Ala Ser Ala Leu
  1               5                  10                  15

Leu Thr Leu Pro Trp Gly Thr Pro Leu Glu Gln Trp Pro Asp Asn Leu
             20                  25                  30

Ile Ala Ala Leu Pro Arg Gly Ile Ser Arg His Ile Val Arg Phe Val
```

```
         35                  40                  45

Gly Ile Asn Arg Gly Ile Val Ala Val Lys Glu Ile Gly Ala Arg Thr
     50                  55                  60

Ala His His Glu Tyr Lys Met Leu Arg Glu Leu Gln Arg Leu Gly Ala
 65                  70                  75                  80

Pro Ser Val Arg Pro Val Ala Val Ile Thr Gly Arg His Pro Ala Glu
                 85                  90                  95

Glu Asp Tyr Gly Glu Leu Thr Ala Ala Leu Val Thr Glu His Leu Glu
            100                 105                 110

Phe Ser Leu Pro Tyr Arg Glu Ile Phe Ser Arg His Leu Thr Val Val
        115                 120                 125

Glu Ser Glu Lys Leu Ile Arg Ala Leu Ser Val Leu Leu Val Arg Met
    130                 135                 140

His Leu Leu Asn Phe Tyr Trp Gly Asp Val Ser Leu Ser Asn Thr Leu
145                 150                 155                 160

Phe Arg Arg Asp Ala Glu Thr Tyr Ser Ala Tyr Leu Val Asp Ala Glu
                165                 170                 175

Thr Gly Glu Phe Gln Pro Asn Leu Ser Glu Ser Arg Arg Leu Tyr Asp
            180                 185                 190

Val Asp Ile Ala Arg Val Asn Ile Ile Gly Glu Leu Met Asp Leu Gln
        195                 200                 205

Ala Gly Glu Cys Leu Asp Lys Ser Ile Asp Val Ile Ala Leu Gly Gly
    210                 215                 220

Leu Val Glu Ser Ser Tyr Leu Glu Leu Trp Thr Glu Leu Thr Ala Glu
225                 230                 235                 240

Glu Ser Val Asp Ala Ser Glu Tyr Trp Arg Leu Ser Glu Arg Ile Asp
                245                 250                 255

Arg Leu Asn Gln Leu Gly Phe Asp Val Gly Glu Leu Lys Val Thr Lys
            260                 265                 270

Asp Asp Ser Arg Gln Val Val Arg Ile Arg Pro Val Val Val Asp Pro
        275                 280                 285

Gly His Tyr Arg Ala Glu Leu Leu Ser Leu Thr Gly Leu Ser Val Glu
    290                 295                 300

Glu His Gln Ala Gln Arg Leu Leu Gly Ser Ile Gln Ala Tyr Gln Ala
305                 310                 315                 320

Val Glu Cys Gly Pro His Val Gly Leu Thr Gln Ala Ala His Leu Trp
                325                 330                 335

Met Thr Asn Glu Tyr Glu Pro Thr Ile Ala Ala Val Pro Val Glu Met
            340                 345                 350

Leu Asp Lys Leu Glu Pro Ala Gln Ile Phe His Glu Ile Val Asp His
        355                 360                 365
```

```
Arg Trp Phe Leu Ala Gln Glu Arg Gly Gly Ala Val Thr Leu Pro Glu
    370                 375                 380

Ala Thr Ala Ser Tyr Leu Glu Ser Val Leu Pro Ala Arg Arg Asp Glu
385                 390                 395                 400

Ala Arg Leu Leu Ser Thr Asn Pro Ser Asp Glu Asp Leu Ser
                405                 410


<210> 1167
<211> 836
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(813)
<223> FRXA02454

<400> 1167
atg cat ctg ctc aac ttc tac tgg gga gat gtg tca ctg tct aat act   48
Met His Leu Leu Asn Phe Tyr Trp Gly Asp Val Ser Leu Ser Asn Thr
  1               5                  10                  15

ctc ttt cgt cgc gat gct gaa acc tat tcc gcc tat ctc gtc gat gcc   96
Leu Phe Arg Arg Asp Ala Glu Thr Tyr Ser Ala Tyr Leu Val Asp Ala
             20                  25                  30

gaa acc ggg gag ttc cag ccc aac ctc tct gaa tca cgc agg ctt tac   144
Glu Thr Gly Glu Phe Gln Pro Asn Leu Ser Glu Ser Arg Arg Leu Tyr
         35                  40                  45

gac gtc gac atc gcc cgc gtc aac atc att ggc gaa ctc atg gac cta   192
Asp Val Asp Ile Ala Arg Val Asn Ile Ile Gly Glu Leu Met Asp Leu
     50                  55                  60

cag gcg ggt gaa tgc cta gat aag tcc atc gat gtc atc gcc cta gga   240
Gln Ala Gly Glu Cys Leu Asp Lys Ser Ile Asp Val Ile Ala Leu Gly
 65                  70                  75                  80

ggc ctt gtc gaa agc tct tat ctt gaa ttg tgg acg gag ctc acc gcg   288
Gly Leu Val Glu Ser Ser Tyr Leu Glu Leu Trp Thr Glu Leu Thr Ala
                 85                  90                  95

gag gaa tcc gtc gat gcc agt gaa tat tgg cgc ctc tct gag aga att   336
Glu Glu Ser Val Asp Ala Ser Glu Tyr Trp Arg Leu Ser Glu Arg Ile
            100                 105                 110

gac cgg ctc aat caa ctg ggc ttt gac gta ggg gag ctc aag gtc acg   384
Asp Arg Leu Asn Gln Leu Gly Phe Asp Val Gly Glu Leu Lys Val Thr
        115                 120                 125

aag gac gat tcg cgg cag gtt gtg cgc att cgc cct gta gtg gtg gat   432
Lys Asp Asp Ser Arg Gln Val Val Arg Ile Arg Pro Val Val Val Asp
    130                 135                 140

ccg ggc cac tat cgt gca gag cta ttg agc tta acc ggg ctg agc gtc   480
Pro Gly His Tyr Arg Ala Glu Leu Leu Ser Leu Thr Gly Leu Ser Val
145                 150                 155                 160
```

```
gag gaa cac cag gcc caa cgc cta ttg ggc tcg atc cag gcc tat cag   528
Glu Glu His Gln Ala Gln Arg Leu Leu Gly Ser Ile Gln Ala Tyr Gln
                165                 170                 175

gcc gtc gaa tgc gga ccg cat gta ggt ctt acc caa gcc gcg cat ctc   576
Ala Val Glu Cys Gly Pro His Val Gly Leu Thr Gln Ala Ala His Leu
            180                 185                 190

tgg atg acg aat gaa tac gaa ccg act atc gcc gcc gtc ccc gtg gag   624
Trp Met Thr Asn Glu Tyr Glu Pro Thr Ile Ala Ala Val Pro Val Glu
        195                 200                 205

atg tta gac aag ctg gag cca gca caa atc ttc cac gaa atc gtc gac   672
Met Leu Asp Lys Leu Glu Pro Ala Gln Ile Phe His Glu Ile Val Asp
    210                 215                 220

cac cgc tgg ttc ctc gcc caa gaa agg gga ggg gct gtc acc ctc cca   720
His Arg Trp Phe Leu Ala Gln Glu Arg Gly Gly Ala Val Thr Leu Pro
225                 230                 235                 240

gag gcc acg gca tcc tat ctt gaa tcc gtg ctt ccg gcc cgc cgc gac   768
Glu Ala Thr Ala Ser Tyr Leu Glu Ser Val Leu Pro Ala Arg Arg Asp
                245                 250                 255

gag gct cgc ctc ctc agc aca aac cct tca gac gaa gac ttg tca       813
Glu Ala Arg Leu Leu Ser Thr Asn Pro Ser Asp Glu Asp Leu Ser
            260                 265                 270

taacctctcg cgtgccccaa cgg                                        836


<210> 1168
<211> 271
<212> PRT
<213> Corynebacterium glutamicum

<400> 1168
Met His Leu Leu Asn Phe Tyr Trp Gly Asp Val Ser Leu Ser Asn Thr
  1               5                  10                  15

Leu Phe Arg Arg Asp Ala Glu Thr Tyr Ser Ala Tyr Leu Val Asp Ala
             20                  25                  30

Glu Thr Gly Glu Phe Gln Pro Asn Leu Ser Glu Ser Arg Arg Leu Tyr
         35                  40                  45

Asp Val Asp Ile Ala Arg Val Asn Ile Ile Gly Glu Leu Met Asp Leu
     50                  55                  60

Gln Ala Gly Glu Cys Leu Asp Lys Ser Ile Asp Val Ile Ala Leu Gly
 65                  70                  75                  80

Gly Leu Val Glu Ser Ser Tyr Leu Glu Leu Trp Thr Glu Leu Thr Ala
                 85                  90                  95

Glu Glu Ser Val Asp Ala Ser Glu Tyr Trp Arg Leu Ser Glu Arg Ile
            100                 105                 110

Asp Arg Leu Asn Gln Leu Gly Phe Asp Val Gly Glu Leu Lys Val Thr
        115                 120                 125
```

```
Lys Asp Asp Ser Arg Gln Val Val Arg Ile Arg Pro Val Val Val Asp
    130                 135                 140

Pro Gly His Tyr Arg Ala Glu Leu Leu Ser Leu Thr Gly Leu Ser Val
145                 150                 155                 160

Glu Glu His Gln Ala Gln Arg Leu Leu Gly Ser Ile Gln Ala Tyr Gln
                165                 170                 175

Ala Val Glu Cys Gly Pro His Val Gly Leu Thr Gln Ala Ala His Leu
            180                 185                 190

Trp Met Thr Asn Glu Tyr Glu Pro Thr Ile Ala Ala Val Pro Val Glu
        195                 200                 205

Met Leu Asp Lys Leu Glu Pro Ala Gln Ile Phe His Glu Ile Val Asp
    210                 215                 220

His Arg Trp Phe Leu Ala Gln Glu Arg Gly Gly Ala Val Thr Leu Pro
225                 230                 235                 240

Glu Ala Thr Ala Ser Tyr Leu Glu Ser Val Leu Pro Ala Arg Arg Asp
                245                 250                 255

Glu Ala Arg Leu Leu Ser Thr Asn Pro Ser Asp Glu Asp Leu Ser
            260                 265                 270


<210> 1169
<211> 1233
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1210)
<223> RXN02457

<400> 1169
ctgtaaagcc acgtgagctg ttgcttagac tttactctac ccccgcgtgt ccaccacatc 60

agttagaaca tatgtaccac ttcaaatcta gggggaaaca atg ttc tac ttc acc   115
                                                Met Phe Tyr Phe Thr
                                                  1               5

gtc aat aat ccg cag gat cct tta agc acc gaa att gtt gag act aat   163
Val Asn Asn Pro Gln Asp Pro Leu Ser Thr Glu Ile Val Glu Thr Asn
                 10                  15                  20

cgc cgt gac ctc gca ttt tgg cat cga tta cgc ccc aaa gat gac gat   211
Arg Arg Asp Leu Ala Phe Trp His Arg Leu Arg Pro Lys Asp Asp Asp
             25                  30                  35

gat tta gcc aca gcc atc aac aaa ata tgc gtg cgc aca ggc tta tcc   259
Asp Leu Ala Thr Ala Ile Asn Lys Ile Cys Val Arg Thr Gly Leu Ser
         40                  45                  50

cgc aaa ctg atc gcc gct tgt tta ttt agc atc tgc ttc ctg ccg tac   307
Arg Lys Leu Ile Ala Ala Cys Leu Phe Ser Ile Cys Phe Leu Pro Tyr
     55                  60                  65
```

```
tta ccc aac ttc cac aaa ctc gtc gaa aag ctt ggt cat ctc gac atg   355
Leu Pro Asn Phe His Lys Leu Val Glu Lys Leu Gly His Leu Asp Met
 70                  75                  80                  85

gcg cgc atc aac gcg atc act aaa gct ggc gaa aaa gtg cca agc gag   403
Ala Arg Ile Asn Ala Ile Thr Lys Ala Gly Glu Lys Val Pro Ser Glu
                90                  95                 100

aag aga gag ctt ttc gac gcc tac ctc gtc gat tac ctg acg cct cga   451
Lys Arg Glu Leu Phe Asp Ala Tyr Leu Val Asp Tyr Leu Thr Pro Arg
            105                 110                 115

gcg gag gct cag tgc ttg ccc cag gca agc tca att tcc gca atg atg   499
Ala Glu Ala Gln Cys Leu Pro Gln Ala Ser Ser Ile Ser Ala Met Met
        120                 125                 130

cgg aaa ttt atc gca caa cac tgc ccc gac gac aag gcc tcc tca gcc   547
Arg Lys Phe Ile Ala Gln His Cys Pro Asp Asp Lys Ala Ser Ser Ala
    135                 140                 145

acc aat gat ggc tcc atc cgc tac cgc aga aac aac aaa ggc ggg atc   595
Thr Asn Asp Gly Ser Ile Arg Tyr Arg Arg Asn Asn Lys Gly Gly Ile
150                 155                 160                 165

agt atc acc gtc gat gcc acc gcc agc gaa gta aca gaa atc aaa gct   643
Ser Ile Thr Val Asp Ala Thr Ala Ser Glu Val Thr Glu Ile Lys Ala
                170                 175                 180

gcc ctg gaa caa atg tcc aaa gat aag gac tgc aca cca ggc act tcc   691
Ala Leu Glu Gln Met Ser Lys Asp Lys Asp Cys Thr Pro Gly Thr Ser
            185                 190                 195

cta ctc cac atc att cgt ggc ctg ccg aca aaa gtc gta ctc aac acc   739
Leu Leu His Ile Ile Arg Gly Leu Pro Thr Lys Val Val Leu Asn Thr
        200                 205                 210

tac ggc acc aaa gac agc cct gaa tac tta gaa gga gga acc tgg ctg   787
Tyr Gly Thr Lys Asp Ser Pro Glu Tyr Leu Glu Gly Gly Thr Trp Leu
    215                 220                 225

tca aag gaa cag tct gag ttc tgg aaa acc cga acc acg tcc agt cgg   835
Ser Lys Glu Gln Ser Glu Phe Trp Lys Thr Arg Thr Thr Ser Ser Arg
230                 235                 240                 245

gat atg gac gcc gcc cac ttc tct tac acc acc gcc tac gct cca acc   883
Asp Met Asp Ala Ala His Phe Ser Tyr Thr Thr Ala Tyr Ala Pro Thr
                250                 255                 260

cga gaa atg cgc gtc tac atc aaa ggt cta cgc acc acc tgt agc gtc   931
Arg Glu Met Arg Val Tyr Ile Lys Gly Leu Arg Thr Thr Cys Ser Val
            265                 270                 275

cct ggc tgc agt gta gcg gtc gaa aac tgc caa ctg gac cac atc atc   979
Pro Gly Cys Ser Val Ala Val Glu Asn Cys Gln Leu Asp His Ile Ile
        280                 285                 290

ccc tgg ggt gaa gga ggg ccg aca aca ccg tgg aat att cat ccc ctg   1027
Pro Trp Gly Glu Gly Gly Pro Thr Thr Pro Trp Asn Ile His Pro Leu
    295                 300                 305
```

```
tgt gtc ttc cac cac atc cag aag act gaa ggg agg ctc cag tgc tat   1075
Cys Val Phe His His Ile Gln Lys Thr Glu Gly Arg Leu Gln Cys Tyr
310                 315                 320                 325

cca cta ccg gac ggc acc gtc cta ttc cta gtg gat gga ata ccg gtg   1123
Pro Leu Pro Asp Gly Thr Val Leu Phe Leu Val Asp Gly Ile Pro Val
                330                 335                 340

ttc tcc atc ccc gac ggg cct tta tct aaa tcg aat aaa acc tgg ggg   1171
Phe Ser Ile Pro Asp Gly Pro Leu Ser Lys Ser Asn Lys Thr Trp Gly
            345                 350                 355

aca aag ttc ggc aaa tac atg gag cgt cga atc gcc gcc taatccagca   1220
Thr Lys Phe Gly Lys Tyr Met Glu Arg Arg Ile Ala Ala
        360                 365                 370

agccagcgtg atc                                                  1233


<210> 1170
<211> 370
<212> PRT
<213> Corynebacterium glutamicum

<400> 1170
Met Phe Tyr Phe Thr Val Asn Asn Pro Gln Asp Pro Leu Ser Thr Glu
  1               5                  10                  15

Ile Val Glu Thr Asn Arg Arg Asp Leu Ala Phe Trp His Arg Leu Arg
             20                  25                  30

Pro Lys Asp Asp Asp Asp Leu Ala Thr Ala Ile Asn Lys Ile Cys Val
         35                  40                  45

Arg Thr Gly Leu Ser Arg Lys Leu Ile Ala Ala Cys Leu Phe Ser Ile
     50                  55                  60

Cys Phe Leu Pro Tyr Leu Pro Asn Phe His Lys Leu Val Glu Lys Leu
 65                  70                  75                  80

Gly His Leu Asp Met Ala Arg Ile Asn Ala Ile Thr Lys Ala Gly Glu
                 85                  90                  95

Lys Val Pro Ser Glu Lys Arg Glu Leu Phe Asp Ala Tyr Leu Val Asp
            100                 105                 110

Tyr Leu Thr Pro Arg Ala Glu Ala Gln Cys Leu Pro Gln Ala Ser Ser
        115                 120                 125

Ile Ser Ala Met Met Arg Lys Phe Ile Ala Gln His Cys Pro Asp Asp
    130                 135                 140

Lys Ala Ser Ser Ala Thr Asn Asp Gly Ser Ile Arg Tyr Arg Arg Asn
145                 150                 155                 160

Asn Lys Gly Gly Ile Ser Ile Thr Val Asp Ala Thr Ala Ser Glu Val
                165                 170                 175

Thr Glu Ile Lys Ala Ala Leu Glu Gln Met Ser Lys Asp Lys Asp Cys
            180                 185                 190
```

```
Thr Pro Gly Thr Ser Leu Leu His Ile Ile Arg Gly Leu Pro Thr Lys
        195                 200                 205

Val Val Leu Asn Thr Tyr Gly Thr Lys Asp Ser Pro Glu Tyr Leu Glu
    210                 215                 220

Gly Gly Thr Trp Leu Ser Lys Glu Gln Ser Glu Phe Trp Lys Thr Arg
225                 230                 235                 240

Thr Thr Ser Ser Arg Asp Met Asp Ala Ala His Phe Ser Tyr Thr Thr
                245                 250                 255

Ala Tyr Ala Pro Thr Arg Glu Met Arg Val Tyr Ile Lys Gly Leu Arg
            260                 265                 270

Thr Thr Cys Ser Val Pro Gly Cys Ser Val Ala Val Glu Asn Cys Gln
        275                 280                 285

Leu Asp His Ile Ile Pro Trp Gly Glu Gly Gly Pro Thr Thr Pro Trp
    290                 295                 300

Asn Ile His Pro Leu Cys Val Phe His His Ile Gln Lys Thr Glu Gly
305                 310                 315                 320

Arg Leu Gln Cys Tyr Pro Leu Pro Asp Gly Thr Val Leu Phe Leu Val
                325                 330                 335

Asp Gly Ile Pro Val Phe Ser Ile Pro Asp Gly Pro Leu Ser Lys Ser
            340                 345                 350

Asn Lys Thr Trp Gly Thr Lys Phe Gly Lys Tyr Met Glu Arg Arg Ile
        355                 360                 365

Ala Ala
    370
```

US20050009150A1

<210> 1171
<211> 1233
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1210)
<223> FRXA02457

<400> 1171
ctgtaaagcc acgtgagctg ttgcttagac tttactctac ccccgcgtgt ccaccacatc 60

agttagaaca tatgtaccac ttcaaatcta gggggaaaca atg ttc tac ttc acc 115
                                                Met Phe Tyr Phe Thr
                                                  1   5

gtc aat aat ccg cag gat cct tta agc acc gaa att gtt gag act aat 163
Val Asn Asn Pro Gln Asp Pro Leu Ser Thr Glu Ile Val Glu Thr Asn
                  10   15   20

cgc cgt gac ctc gca ttt tgg cat cga tta cgc ccc aaa gat gac gat 211
Arg Arg Asp Leu Ala Phe Trp His Arg Leu Arg Pro Lys Asp Asp Asp
              25   30   35

```
gat tta gcc aca gcc atc aac aaa ata tgc gtg cgc aca ggc tta tcc   259
Asp Leu Ala Thr Ala Ile Asn Lys Ile Cys Val Arg Thr Gly Leu Ser
         40                  45                  50

cgc aaa ctg atc gcc gct tgt tta ttt agc atc tgc ttc ctg ccg tac   307
Arg Lys Leu Ile Ala Ala Cys Leu Phe Ser Ile Cys Phe Leu Pro Tyr
     55                  60                  65

tta ccc aac ttc cac aaa ctc gtc gaa aag ctt ggt cat ctc gac atg   355
Leu Pro Asn Phe His Lys Leu Val Glu Lys Leu Gly His Leu Asp Met
 70                  75                  80                  85

gcg cgc atc aac gcg atc act aaa gct ggc gaa aaa gtg cca agc gag   403
Ala Arg Ile Asn Ala Ile Thr Lys Ala Gly Glu Lys Val Pro Ser Glu
                 90                  95                 100

aag aga gag ctt ttc gac gcc tac ctc gtc gat tac ctg acg cct cga   451
Lys Arg Glu Leu Phe Asp Ala Tyr Leu Val Asp Tyr Leu Thr Pro Arg
            105                 110                 115

gcg gag gct cag tgc ttg ccc cag gca agc tca att tcc gca atg atg   499
Ala Glu Ala Gln Cys Leu Pro Gln Ala Ser Ser Ile Ser Ala Met Met
        120                 125                 130

cgg aaa ttt atc gca caa cac tgc ccc gac gac aag gcc tcc tca gcc   547
Arg Lys Phe Ile Ala Gln His Cys Pro Asp Asp Lys Ala Ser Ser Ala
    135                 140                 145

acc aat gat ggc tcc atc cgc tac cgc aga aac aac aaa ggc ggg atc   595
Thr Asn Asp Gly Ser Ile Arg Tyr Arg Arg Asn Asn Lys Gly Gly Ile
150                 155                 160                 165

agt atc acc gtc gat gcc acc gcc agc gaa gta aca gaa atc aaa gct   643
Ser Ile Thr Val Asp Ala Thr Ala Ser Glu Val Thr Glu Ile Lys Ala
                170                 175                 180

gcc ctg gaa caa atg tcc aaa gat aag gac tgc aca cca ggc act tcc   691
Ala Leu Glu Gln Met Ser Lys Asp Lys Asp Cys Thr Pro Gly Thr Ser
            185                 190                 195

cta ctc cac atc att cgt ggc ctg ccg aca aaa gtc gta ctc aac acc   739
Leu Leu His Ile Ile Arg Gly Leu Pro Thr Lys Val Val Leu Asn Thr
        200                 205                 210

tac ggc acc aaa gac agc cct gaa tac tta gaa gga gga acc tgg ctg   787
Tyr Gly Thr Lys Asp Ser Pro Glu Tyr Leu Glu Gly Gly Thr Trp Leu
    215                 220                 225

tca aag gaa cag tct gag ttc tgg aaa acc cga acc acg tcc agt cgg   835
Ser Lys Glu Gln Ser Glu Phe Trp Lys Thr Arg Thr Thr Ser Ser Arg
230                 235                 240                 245

gat atg gac gcc gcc cac ttc tct tac acc acc gcc tac gct cca acc   883
Asp Met Asp Ala Ala His Phe Ser Tyr Thr Thr Ala Tyr Ala Pro Thr
                250                 255                 260

cga gaa atg cgc gtc tac atc aaa ggt cta cgc acc acc tgt agc gtc   931
Arg Glu Met Arg Val Tyr Ile Lys Gly Leu Arg Thr Thr Cys Ser Val
            265                 270                 275
```

```
cct ggc tgc agt gta gcg gtc gaa aac tgc caa ctg gac cac atc atc   979
Pro Gly Cys Ser Val Ala Val Glu Asn Cys Gln Leu Asp His Ile Ile
        280                 285                 290

ccc tgg ggt gaa gga ggg ccg aca aca ccg tgg aat att cat ccc ctg   1027
Pro Trp Gly Glu Gly Gly Pro Thr Thr Pro Trp Asn Ile His Pro Leu
    295                 300                 305

tgt gtc ttc cac cac atc cag aag act gaa ggg agg ctc cag tgc tat   1075
Cys Val Phe His His Ile Gln Lys Thr Glu Gly Arg Leu Gln Cys Tyr
310                 315                 320                 325

cca cta ccg gac ggc acc gtc cta ttc cta gtg gat gga ata ccg gtg   1123
Pro Leu Pro Asp Gly Thr Val Leu Phe Leu Val Asp Gly Ile Pro Val
                330                 335                 340

ttc tcc atc ccc gac ggg cct tta tct aaa tcg aat aaa acc tgg ggg   1171
Phe Ser Ile Pro Asp Gly Pro Leu Ser Lys Ser Asn Lys Thr Trp Gly
            345                 350                 355

aca aag ttc ggc aaa tac atg gag cgt cga atc gcc gcc taatccagca   1220
Thr Lys Phe Gly Lys Tyr Met Glu Arg Arg Ile Ala Ala
        360                 365                 370

agccagcgtg atc                                                  1233
```

<210> 1172
<211> 370
<212> PRT
<213> Corynebacterium glutamicum

<400> 1172

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Met Phe Tyr Phe Thr Val Asn Asn Pro Gln Asp Pro Leu Ser Thr Glu
  1               5                  10                  15

Ile Val Glu Thr Asn Arg Arg Asp Leu Ala Phe Trp His Arg Leu Arg
             20                  25                  30

Pro Lys Asp Asp Asp Asp Leu Ala Thr Ala Ile Asn Lys Ile Cys Val
         35                  40                  45

Arg Thr Gly Leu Ser Arg Lys Leu Ile Ala Ala Cys Leu Phe Ser Ile
     50                  55                  60

Cys Phe Leu Pro Tyr Leu Pro Asn Phe His Lys Leu Val Glu Lys Leu
 65                  70                  75                  80

Gly His Leu Asp Met Ala Arg Ile Asn Ala Ile Thr Lys Ala Gly Glu
                 85                  90                  95

Lys Val Pro Ser Glu Lys Arg Glu Leu Phe Asp Ala Tyr Leu Val Asp
            100                 105                 110

Tyr Leu Thr Pro Arg Ala Glu Ala Gln Cys Leu Pro Gln Ala Ser Ser
        115                 120                 125

Ile Ser Ala Met Met Arg Lys Phe Ile Ala Gln His Cys Pro Asp Asp
    130                 135                 140

Lys Ala Ser Ser Ala Thr Asn Asp Gly Ser Ile Arg Tyr Arg Arg Asn
```

```
145                 150                 155                 160

Asn Lys Gly Gly Ile Ser Ile Thr Val Asp Ala Thr Ala Ser Glu Val
                165                 170                 175

Thr Glu Ile Lys Ala Ala Leu Glu Gln Met Ser Lys Asp Lys Asp Cys
            180                 185                 190

Thr Pro Gly Thr Ser Leu Leu His Ile Ile Arg Gly Leu Pro Thr Lys
        195                 200                 205

Val Val Leu Asn Thr Tyr Gly Thr Lys Asp Ser Pro Glu Tyr Leu Glu
    210                 215                 220

Gly Gly Thr Trp Leu Ser Lys Glu Gln Ser Glu Phe Trp Lys Thr Arg
225                 230                 235                 240

Thr Thr Ser Ser Arg Asp Met Asp Ala Ala His Phe Ser Tyr Thr Thr
                245                 250                 255

Ala Tyr Ala Pro Thr Arg Glu Met Arg Val Tyr Ile Lys Gly Leu Arg
            260                 265                 270

Thr Thr Cys Ser Val Pro Gly Cys Ser Val Ala Val Glu Asn Cys Gln
        275                 280                 285

Leu Asp His Ile Ile Pro Trp Gly Glu Gly Gly Pro Thr Thr Pro Trp
    290                 295                 300

Asn Ile His Pro Leu Cys Val Phe His His Ile Gln Lys Thr Glu Gly
305                 310                 315                 320

Arg Leu Gln Cys Tyr Pro Leu Pro Asp Gly Thr Val Leu Phe Leu Val
                325                 330                 335

Asp Gly Ile Pro Val Phe Ser Ile Pro Asp Gly Pro Leu Ser Lys Ser
            340                 345                 350

Asn Lys Thr Trp Gly Thr Lys Phe Gly Lys Tyr Met Glu Arg Arg Ile
        355                 360                 365

Ala Ala
    370
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20050208

<210> 1173
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> RXN02460

<400> 1173
gcgccgtcga agccggactc gtaggcgtct actaccagca atttgaccgt gcagtcgtcg 60

aaatcgtcgg actgttcggg ctagaaggag aattctaatc ttg cgc gtc tac atc 115
                                                Leu Arg Val Tyr Ile
                                                  1   5

```
cca gca acg ttt tcc aca ctc cgc gga ctc aat gaa tcc cgc gtc atc   163
Pro Ala Thr Phe Ser Thr Leu Arg Gly Leu Asn Glu Ser Arg Val Ile
                 10                  15                  20

aca gca cgc tcc gga tac ggt ttc gca gtc acc cca gca ctc ctt gac   211
Thr Ala Arg Ser Gly Tyr Gly Phe Ala Val Thr Pro Ala Leu Leu Asp
             25                  30                  35

ttc tac acc gac ggt gac gaa gaa gaa atc gca cat gca gcc ttc caa   259
Phe Tyr Thr Asp Gly Asp Glu Glu Glu Ile Ala His Ala Ala Phe Gln
         40                  45                  50

gac gcc gca gaa gcc tcc atc cga ctc ctc gca atc ggc gac gaa gaa   307
Asp Ala Ala Glu Ala Ser Ile Arg Leu Leu Ala Ile Gly Asp Glu Glu
     55                  60                  65

aca ttt ccc tac cgc aga gtc gtc gtc tca gta gat gtt gac gac tcc   355
Thr Phe Pro Tyr Arg Arg Val Val Val Ser Val Asp Val Asp Asp Ser
 70                  75                  80                  85

gtg gtg acc tac cag cct gaa aac ggc gaa tcc gta gtc aaa ctc agc   403
Val Val Thr Tyr Gln Pro Glu Asn Gly Glu Ser Val Val Lys Leu Ser
                 90                  95                 100

cca gcg cac atc aac ctc gac gac gtg gca gca atc cac atc gac gtt   451
Pro Ala His Ile Asn Leu Asp Asp Val Ala Ala Ile His Ile Asp Val
             105                 110                 115

gaa gcc tcc gaa gca gac acc aaa aaa gct atc gaa gtc atc gac gaa   499
Glu Ala Ser Glu Ala Asp Thr Lys Lys Ala Ile Glu Val Ile Asp Glu
         120                 125                 130

tcc gac ctc ggc gaa gaa gac gcc gaa ctc acc gtc gga gac gcc caa   547
Ser Asp Leu Gly Glu Glu Asp Ala Glu Leu Thr Val Gly Asp Ala Gln
     135                 140                 145

gac aac ttc atg gcc tgg tac gac cca gaa gag ctc ccc ttc cta gtc   595
Asp Asn Phe Met Ala Trp Tyr Asp Pro Glu Glu Leu Pro Phe Leu Val
150                 155                 160                 165

gag ctc ctc tagatcacat atcccacgcg tcg                            627
Glu Leu Leu
```

<210> 1174
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 1174

```
Leu Arg Val Tyr Ile Pro Ala Thr Phe Ser Thr Leu Arg Gly Leu Asn
  1               5                  10                  15

Glu Ser Arg Val Ile Thr Ala Arg Ser Gly Tyr Gly Phe Ala Val Thr
             20                  25                  30

Pro Ala Leu Leu Asp Phe Tyr Thr Asp Gly Asp Glu Glu Glu Ile Ala
         35                  40                  45
```

```
His Ala Ala Phe Gln Asp Ala Ala Glu Ala Ser Ile Arg Leu Leu Ala
     50                  55                  60

Ile Gly Asp Glu Glu Thr Phe Pro Tyr Arg Arg Val Val Val Ser Val
 65                  70                  75                  80

Asp Val Asp Asp Ser Val Val Thr Tyr Gln Pro Glu Asn Gly Glu Ser
                 85                  90                  95

Val Val Lys Leu Ser Pro Ala His Ile Asn Leu Asp Asp Val Ala Ala
            100                 105                 110

Ile His Ile Asp Val Glu Ala Ser Glu Ala Asp Thr Lys Lys Ala Ile
        115                 120                 125

Glu Val Ile Asp Glu Ser Asp Leu Gly Glu Glu Asp Ala Glu Leu Thr
    130                 135                 140

Val Gly Asp Ala Gln Asp Asn Phe Met Ala Trp Tyr Asp Pro Glu Glu
145                 150                 155                 160

Leu Pro Phe Leu Val Glu Leu Leu
                165
```

US20030148461A1

<210> 1175
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> FRXA02460

<400> 1175

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gcgccgtcga agccggactc gtaggcgtct actaccagca atttgaccgt gcagtcgtcg 60

aaatcgtcgg actgttcggg ctagaaggag aattctaatc ttg cgc gtc tac atc   115
                                               Leu Arg Val Tyr Ile
                                                 1               5

cca gca acg ttt tcc aca ctc cgc gga ctc aat gaa tcc cgc gtc atc   163
Pro Ala Thr Phe Ser Thr Leu Arg Gly Leu Asn Glu Ser Arg Val Ile
                 10                  15                  20

aca gca cgc tcc gga tac ggt ttc gca gtc acc cca gca ctc ctt gac   211
Thr Ala Arg Ser Gly Tyr Gly Phe Ala Val Thr Pro Ala Leu Leu Asp
             25                  30                  35

ttc tac acc gac ggt gac gaa gaa gaa atc gca cat gca gcc ttc caa   259
Phe Tyr Thr Asp Gly Asp Glu Glu Glu Ile Ala His Ala Ala Phe Gln
         40                  45                  50

gac gcc gca gaa gcc tcc atc cga ctc ctc gca atc ggc gac gaa gaa   307
Asp Ala Ala Glu Ala Ser Ile Arg Leu Leu Ala Ile Gly Asp Glu Glu
     55                  60                  65

aca ttt ccc tac cgc aga gtc gtc gtc tca gta gat gtt gac gac tcc   355
Thr Phe Pro Tyr Arg Arg Val Val Val Ser Val Asp Val Asp Asp Ser
 70                  75                  80                  85
```

```
gtg gtg acc tac cag cct gaa aac ggc gaa tcc gta gtc aaa ctc agc   403
Val Val Thr Tyr Gln Pro Glu Asn Gly Glu Ser Val Val Lys Leu Ser
                 90                  95                 100

cca gcg cac atc aac ctc gac gac gtg gca gca atc cac atc gac gtt   451
Pro Ala His Ile Asn Leu Asp Asp Val Ala Ala Ile His Ile Asp Val
            105                 110                 115

gaa gcc tcc gaa gca gac acc aaa aaa gct atc gaa gtc atc gac gaa   499
Glu Ala Ser Glu Ala Asp Thr Lys Lys Ala Ile Glu Val Ile Asp Glu
        120                 125                 130

tcc gac ctc ggc gaa gaa gac gcc gaa ctc acc gtc gga gac gcc caa   547
Ser Asp Leu Gly Glu Glu Asp Ala Glu Leu Thr Val Gly Asp Ala Gln
    135                 140                 145

gac aac ttc atg gcc tgg tac gac cca gaa gag ctc ccc ttc cta gtc   595
Asp Asn Phe Met Ala Trp Tyr Asp Pro Glu Glu Leu Pro Phe Leu Val
150                 155                 160                 165

gag ctc ctc tagatcacat atcccacgcg tcg                            627
Glu Leu Leu
```

09350705.0

<210> 1176
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 1176

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Leu Arg Val Tyr Ile Pro Ala Thr Phe Ser Thr Leu Arg Gly Leu Asn
  1               5                  10                  15

Glu Ser Arg Val Ile Thr Ala Arg Ser Gly Tyr Gly Phe Ala Val Thr
             20                  25                  30

Pro Ala Leu Leu Asp Phe Tyr Thr Asp Gly Asp Glu Glu Glu Ile Ala
         35                  40                  45

His Ala Ala Phe Gln Asp Ala Ala Glu Ala Ser Ile Arg Leu Leu Ala
     50                  55                  60

Ile Gly Asp Glu Glu Thr Phe Pro Tyr Arg Arg Val Val Val Ser Val
 65                  70                  75                  80

Asp Val Asp Asp Ser Val Val Thr Tyr Gln Pro Glu Asn Gly Glu Ser
                 85                  90                  95

Val Val Lys Leu Ser Pro Ala His Ile Asn Leu Asp Asp Val Ala Ala
            100                 105                 110

Ile His Ile Asp Val Glu Ala Ser Glu Ala Asp Thr Lys Lys Ala Ile
        115                 120                 125

Glu Val Ile Asp Glu Ser Asp Leu Gly Glu Glu Asp Ala Glu Leu Thr
    130                 135                 140

Val Gly Asp Ala Gln Asp Asn Phe Met Ala Trp Tyr Asp Pro Glu Glu
145                 150                 155                 160
```

```
Leu Pro Phe Leu Val Glu Leu Leu
                165


<210> 1177
<211> 1323
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1300)
<223> RXN02464

<400> 1177
actcgacatc ccagaaggtg tcaccgaacg agtcggacca ccaaccaaag ttctaggcgg 60

aacagcccca cgaccaccac gccgcacccg gaaataactt atg gca gca aag ctt   115
                                          Met Ala Ala Lys Leu
                                            1               5

caa cca ctc aaa cgc acc aaa aaa gac ctc atc gca acc ggt gtc atc   163
Gln Pro Leu Lys Arg Thr Lys Lys Asp Leu Ile Ala Thr Gly Val Ile
                10                  15                  20

aca gca cta gca gtc att ggc gtc ggc acg gtc tgg gca acc gca cca   211
Thr Ala Leu Ala Val Ile Gly Val Gly Thr Val Trp Ala Thr Ala Pro
            25                  30                  35

ata cga gga tct gaa ctc acc ccc gcc gac gaa cca ttc att ggc tca   259
Ile Arg Gly Ser Glu Leu Thr Pro Ala Asp Glu Pro Phe Ile Gly Ser
        40                  45                  50

acc aca ctg gac gcc atc ccc gaa aca ctc agc gaa cat tgg cga gcc   307
Thr Thr Leu Asp Ala Ile Pro Glu Thr Leu Ser Glu His Trp Arg Ala
    55                  60                  65

acc gac acc tta aca aac cac aaa ccc ctc atc acc ggc gga gtc atc   355
Thr Asp Thr Leu Thr Asn His Lys Pro Leu Ile Thr Gly Gly Val Ile
70                  75                  80                  85

ttc acc gcc gac ggc aac acc att aag acc tac acc ccc gac ggc gcc   403
Phe Thr Ala Asp Gly Asn Thr Ile Lys Thr Tyr Thr Pro Asp Gly Ala
                90                  95                  100

ctc ctg tgg agc tac gaa cgc gac aaa gaa ctc tgc agc ctc tcc gta   451
Leu Leu Trp Ser Tyr Glu Arg Asp Lys Glu Leu Cys Ser Leu Ser Val
            105                 110                 115

gga ttc gac gcc gcc gtc gcc acc tac aaa acc gga atc gga tgt ggc   499
Gly Phe Asp Ala Ala Val Ala Thr Tyr Lys Thr Gly Ile Gly Cys Gly
        120                 125                 130

gac gtc acc gcc atc aac gcc aac gac ggc caa tac caa gca aca cgc   547
Asp Val Thr Ala Ile Asn Ala Asn Asp Gly Gln Tyr Gln Ala Thr Arg
    135                 140                 145

agc gca atc tcc agc gac cac gta gca ccg atc tcc tcg aac gat cgg   595
Ser Ala Ile Ser Ser Asp His Val Ala Pro Ile Ser Ser Asn Asp Arg
150                 155                 160                 165
```

```
atc ggt gtt ctc ggg aca gaa cgc ttg gag ctt tgg cga tcc gat ctg   643
Ile Gly Val Leu Gly Thr Glu Arg Leu Glu Leu Trp Arg Ser Asp Leu
                170                 175                 180

gtg cga acc atc gaa tac ggc gat gtg gaa gct cct caa gaa tct ggg   691
Val Arg Thr Ile Glu Tyr Gly Asp Val Glu Ala Pro Gln Glu Ser Gly
            185                 190                 195

caa caa cca cat ccg gaa tgc tcg att acg tcc gcc atg aca cgc aaa   739
Gln Gln Pro His Pro Glu Cys Ser Ile Thr Ser Ala Met Thr Arg Lys
        200                 205                 210

gat cta ttg gct atc acc gag gat tgc cct gac gga tct tct tac ttg   787
Asp Leu Leu Ala Ile Thr Glu Asp Cys Pro Asp Gly Ser Ser Tyr Leu
    215                 220                 225

agg ttc atg ggc aca aca cca gac gat tcc cga act cct gaa atc acc   835
Arg Phe Met Gly Thr Thr Pro Asp Asp Ser Arg Thr Pro Glu Ile Thr
230                 235                 240                 245

caa gac ata gaa ata acc gat ggc agg atc gtt gcc atc ggt caa tca   883
Gln Asp Ile Glu Ile Thr Asp Gly Arg Ile Val Ala Ile Gly Gln Ser
                250                 255                 260

gtg gct gcg gtg tat aca aac gat cct tcg cct cga atc gtc tcc tac   931
Val Ala Ala Val Tyr Thr Asn Asp Pro Ser Pro Arg Ile Val Ser Tyr
            265                 270                 275

aac gat gat ggt gaa cta gtt gga gaa caa gca gtc gat gag gtt gag   979
Asn Asp Asp Gly Glu Leu Val Gly Glu Gln Ala Val Asp Glu Val Glu
        280                 285                 290

ttc ccg gat ccg ccg ttt caa agc gcg acc gct gat ctt cca cac cat   1027
Phe Pro Asp Pro Pro Phe Gln Ser Ala Thr Ala Asp Leu Pro His His
    295                 300                 305

atg agt tgg ttc aac gga gac agc ctc gta ctg ttc tct ccc act cag   1075
Met Ser Trp Phe Asn Gly Asp Ser Leu Val Leu Phe Ser Pro Thr Gln
310                 315                 320                 325

ctc aat gta cga caa agc ttc aat gat gct tta gga acc ggc att gcg   1123
Leu Asn Val Arg Gln Ser Phe Asn Asp Ala Leu Gly Thr Gly Ile Ala
                330                 335                 340

ttg aac gga agt ctc ctc tac ccc acc gct gag ggc atc acg gta gct   1171
Leu Asn Gly Ser Leu Leu Tyr Pro Thr Ala Glu Gly Ile Thr Val Ala
            345                 350                 355

aat tgg gac acc gga gag gtg cag cgc acc att ccg gtg gac cgt gcg   1219
Asn Trp Asp Thr Gly Glu Val Gln Arg Thr Ile Pro Val Asp Arg Ala
        360                 365                 370

ggc tac gac ggt gaa gtt gcg ctc ggc gtt gta ggg cag gtg atc gtc   1267
Gly Tyr Asp Gly Glu Val Ala Leu Gly Val Val Gly Gln Val Ile Val
    375                 380                 385

gaa aag cgt ggc tct gag atc gtt gct cta ggc tagatctcgt tgttagccca 1320
Glu Lys Arg Gly Ser Glu Ile Val Ala Leu Gly
390                 395                 400
```

aag 1323

<210> 1178
<211> 400
<212> PRT
<213> Corynebacterium glutamicum

<400> 1178

```
Met Ala Ala Lys Leu Gln Pro Leu Lys Arg Thr Lys Lys Asp Leu Ile
  1               5                  10                  15

Ala Thr Gly Val Ile Thr Ala Leu Ala Val Ile Gly Val Gly Thr Val
             20                  25                  30

Trp Ala Thr Ala Pro Ile Arg Gly Ser Glu Leu Thr Pro Ala Asp Glu
         35                  40                  45

Pro Phe Ile Gly Ser Thr Thr Leu Asp Ala Ile Pro Glu Thr Leu Ser
     50                  55                  60

Glu His Trp Arg Ala Thr Asp Thr Leu Thr Asn His Lys Pro Leu Ile
 65                  70                  75                  80

Thr Gly Gly Val Ile Phe Thr Ala Asp Gly Asn Thr Ile Lys Thr Tyr
                 85                  90                  95

Thr Pro Asp Gly Ala Leu Leu Trp Ser Tyr Glu Arg Asp Lys Glu Leu
            100                 105                 110

Cys Ser Leu Ser Val Gly Phe Asp Ala Ala Val Ala Thr Tyr Lys Thr
        115                 120                 125

Gly Ile Gly Cys Gly Asp Val Thr Ala Ile Asn Ala Asn Asp Gly Gln
    130                 135                 140

Tyr Gln Ala Thr Arg Ser Ala Ile Ser Ser Asp His Val Ala Pro Ile
145                 150                 155                 160

Ser Ser Asn Asp Arg Ile Gly Val Leu Gly Thr Glu Arg Leu Glu Leu
                165                 170                 175

Trp Arg Ser Asp Leu Val Arg Thr Ile Glu Tyr Gly Asp Val Glu Ala
            180                 185                 190

Pro Gln Glu Ser Gly Gln Gln Pro His Pro Glu Cys Ser Ile Thr Ser
        195                 200                 205

Ala Met Thr Arg Lys Asp Leu Leu Ala Ile Thr Glu Asp Cys Pro Asp
    210                 215                 220

Gly Ser Ser Tyr Leu Arg Phe Met Gly Thr Thr Pro Asp Asp Ser Arg
225                 230                 235                 240

Thr Pro Glu Ile Thr Gln Asp Ile Glu Ile Thr Asp Gly Arg Ile Val
                245                 250                 255

Ala Ile Gly Gln Ser Val Ala Ala Val Tyr Thr Asn Asp Pro Ser Pro
            260                 265                 270

Arg Ile Val Ser Tyr Asn Asp Asp Gly Glu Leu Val Gly Glu Gln Ala
```

```
        275                 280                 285

Val Asp Glu Val Glu Phe Pro Asp Pro Pro Phe Gln Ser Ala Thr Ala
    290                 295                 300

Asp Leu Pro His His Met Ser Trp Phe Asn Gly Asp Ser Leu Val Leu
305                 310                 315                 320

Phe Ser Pro Thr Gln Leu Asn Val Arg Gln Ser Phe Asn Asp Ala Leu
                325                 330                 335

Gly Thr Gly Ile Ala Leu Asn Gly Ser Leu Leu Tyr Pro Thr Ala Glu
            340                 345                 350

Gly Ile Thr Val Ala Asn Trp Asp Thr Gly Glu Val Gln Arg Thr Ile
        355                 360                 365

Pro Val Asp Arg Ala Gly Tyr Asp Gly Glu Val Ala Leu Gly Val Val
    370                 375                 380

Gly Gln Val Ile Val Glu Lys Arg Gly Ser Glu Ile Val Ala Leu Gly
385                 390                 395                 400
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EP 2 036 983 A2

<210> 1179
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(607)
<223> FRXA02464

<400> 1179

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acaaccacat ccggaatgct cgattacgtc cgccatgaca cgcaaagatc tattggctat 60

caccgaggat tgccctgacg gatcttctta cttgaggttc atg ggc aca aca cca   115
                                            Met Gly Thr Thr Pro
                                              1               5

gac gat tcc cga act cct gaa atc acc caa gac ata gaa ata acc gat   163
Asp Asp Ser Arg Thr Pro Glu Ile Thr Gln Asp Ile Glu Ile Thr Asp
                 10                  15                  20

ggc agg atc gtt gcc atc ggt caa tca gtg gct gcg gtg tat aca aac   211
Gly Arg Ile Val Ala Ile Gly Gln Ser Val Ala Ala Val Tyr Thr Asn
             25                  30                  35

gat cct tcg cct cga atc gtc tcc tac aac gat gat ggt gaa cta gtt   259
Asp Pro Ser Pro Arg Ile Val Ser Tyr Asn Asp Asp Gly Glu Leu Val
         40                  45                  50

gga gaa caa gca gtc gat gag gtt gag ttc ccg gat ccg ccg ttt caa   307
Gly Glu Gln Ala Val Asp Glu Val Glu Phe Pro Asp Pro Pro Phe Gln
     55                  60                  65

agc gcg acc gct gat ctt cca cac cat atg agt tgg ttc aac gga gac   355
```

```
Ser Ala Thr Ala Asp Leu Pro His His Met Ser Trp Phe Asn Gly Asp
 70                  75                  80                  85

agc ctc gta ctg ttc tct ccc act cag ctc aat gta cga caa agc ttc   403
Ser Leu Val Leu Phe Ser Pro Thr Gln Leu Asn Val Arg Gln Ser Phe
                 90                  95                 100

aat gat gct tta gga acc ggc att gcg ttg aac gga agt ctc ctc tac   451
Asn Asp Ala Leu Gly Thr Gly Ile Ala Leu Asn Gly Ser Leu Leu Tyr
            105                 110                 115

ccc acc gct gag ggc atc acg gta gct aat tgg gac acc gga gag gtg   499
Pro Thr Ala Glu Gly Ile Thr Val Ala Asn Trp Asp Thr Gly Glu Val
        120                 125                 130

cag cgc acc att ccg gtg gac cgt gcg ggc tac gac ggt gaa gtt gcg   547
Gln Arg Thr Ile Pro Val Asp Arg Ala Gly Tyr Asp Gly Glu Val Ala
    135                 140                 145

ctc ggc gtt gta ggg cag gtg atc gtc gaa aag cgt ggc tct gag atc   595
Leu Gly Val Val Gly Gln Val Ile Val Glu Lys Arg Gly Ser Glu Ile
150                 155                 160                 165

gtt gct cta ggc tagatctcgt tgttagccca aag                        630
Val Ala Leu Gly
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5,668,168 5,705,483 5,770,435 5,830,716

<210> 1180
<211> 169
<212> PRT
<213> Corynebacterium glutamicum

<400> 1180

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Met Gly Thr Thr Pro Asp Asp Ser Arg Thr Pro Glu Ile Thr Gln Asp
  1               5                  10                  15

Ile Glu Ile Thr Asp Gly Arg Ile Val Ala Ile Gly Gln Ser Val Ala
             20                  25                  30

Ala Val Tyr Thr Asn Asp Pro Ser Pro Arg Ile Val Ser Tyr Asn Asp
         35                  40                  45

Asp Gly Glu Leu Val Gly Glu Gln Ala Val Asp Glu Val Glu Phe Pro
     50                  55                  60

Asp Pro Pro Phe Gln Ser Ala Thr Ala Asp Leu Pro His His Met Ser
 65                  70                  75                  80

Trp Phe Asn Gly Asp Ser Leu Val Leu Phe Ser Pro Thr Gln Leu Asn
                 85                  90                  95

Val Arg Gln Ser Phe Asn Asp Ala Leu Gly Thr Gly Ile Ala Leu Asn
            100                 105                 110

Gly Ser Leu Leu Tyr Pro Thr Ala Glu Gly Ile Thr Val Ala Asn Trp
        115                 120                 125

Asp Thr Gly Glu Val Gln Arg Thr Ile Pro Val Asp Arg Ala Gly Tyr
    130                 135                 140
```

```
Asp Gly Glu Val Ala Leu Gly Val Val Gly Gln Val Ile Val Glu Lys
145                 150                 155                 160

Arg Gly Ser Glu Ile Val Ala Leu Gly
                165
```

<210> 1181
<211> 522
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(499)
<223> RXN02465

<400> 1181

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ctggtgcaat ataaaagtta accaaccagt catccaatat gtcgcctaag tagtcttccc 60

aaagttaaca gctagaatca tggccgtgac ttctccgaac atg cct gca tca att   115
                                            Met Pro Ala Ser Ile
                                              1               5

cgc tgg ggc ggc atc gtc gcc ctc att caa tcc acc atc gga ttc ggt   163
Arg Trp Gly Gly Ile Val Ala Leu Ile Gln Ser Thr Ile Gly Phe Gly
                 10                  15                  20

tac gcc ttt ttc ctt att tac agg gaa gct acg ggc gag acg gat cca   211
Tyr Ala Phe Phe Leu Ile Tyr Arg Glu Ala Thr Gly Glu Thr Asp Pro
             25                  30                  35

agc atc gtc tac gaa acc gat aac gcc aac acg tgg gtt ggc tac ggt   259
Ser Ile Val Tyr Glu Thr Asp Asn Ala Asn Thr Trp Val Gly Tyr Gly
         40                  45                  50

acc gct gca ttc ttc atc att gtg ttc gga acg gtt gtt gca ggc gca   307
Thr Ala Ala Phe Phe Ile Ile Val Phe Gly Thr Val Val Ala Gly Ala
     55                  60                  65

atc aac atg atg aag ggg cat cgc tgg gga cgc gga gct gtc gtc atg   355
Ile Asn Met Met Lys Gly His Arg Trp Gly Arg Gly Ala Val Val Met
 70                  75                  80                  85

ctg aat att att ttg ttg ccg gct gcg tat tac atg ttt atc gaa ggc   403
Leu Asn Ile Ile Leu Leu Pro Ala Ala Tyr Tyr Met Phe Ile Glu Gly
                 90                  95                 100

cga ttc tcc tgg gcg atc gtc aca gga atc tca gct ctc ttc gtt ttg   451
Arg Phe Ser Trp Ala Ile Val Thr Gly Ile Ser Ala Leu Phe Val Leu
            105                 110                 115

ggc gca ctg ttt aat aag cgc gcc gtc ctt tgg gct aac aac gag atc   499
Gly Ala Leu Phe Asn Lys Arg Ala Val Leu Trp Ala Asn Asn Glu Ile
        120                 125                 130

tagcctagag caacgatctc aga                                       522
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<210> 1182
<211> 133

<212> PRT
<213> Corynebacterium glutamicum

<400> 1182
Met Pro Ala Ser Ile Arg Trp Gly Gly Ile Val Ala Leu Ile Gln Ser
1 5 10 15

Thr Ile Gly Phe Gly Tyr Ala Phe Phe Leu Ile Tyr Arg Glu Ala Thr
20 25 30

Gly Glu Thr Asp Pro Ser Ile Val Tyr Glu Thr Asp Asn Ala Asn Thr
35 40 45

Trp Val Gly Tyr Gly Thr Ala Ala Phe Phe Ile Ile Val Phe Gly Thr
50 55 60

Val Val Ala Gly Ala Ile Asn Met Met Lys Gly His Arg Trp Gly Arg
65 70 75 80

Gly Ala Val Val Met Leu Asn Ile Ile Leu Leu Pro Ala Ala Tyr Tyr
85 90 95

Met Phe Ile Glu Gly Arg Phe Ser Trp Ala Ile Val Thr Gly Ile Ser
100 105 110

Ala Leu Phe Val Leu Gly Ala Leu Phe Asn Lys Arg Ala Val Leu Trp
115 120 125

Ala Asn Asn Glu Ile
130

<210> 1183
<211> 522
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(499)
<223> FRXA02465

<400> 1183
ctggtgcaat ataaaagtta accaaccagt catccaatat gtcgcctaag tagtcttccc 60

aaagttaaca gctagaatca tggccgtgac ttctccgaac atg cct gca tca att 115
Met Pro Ala Ser Ile
1 5

cgc tgg ggc ggc atc gtc gcc ctc att caa tcc acc atc gga ttc ggt 163
Arg Trp Gly Gly Ile Val Ala Leu Ile Gln Ser Thr Ile Gly Phe Gly
10 15 20

tac gcc ttt ttc ctt att tac agg gaa gct acg ggc gag acg gat cca 211
Tyr Ala Phe Phe Leu Ile Tyr Arg Glu Ala Thr Gly Glu Thr Asp Pro
25 30 35

agc atc gtc tac gaa acc gat aac gcc aac acg tgg gtt ggc tac ggt 259
Ser Ile Val Tyr Glu Thr Asp Asn Ala Asn Thr Trp Val Gly Tyr Gly
40 45 50

```
acc gct gca ttc ttc atc att gtg ttc gga acg gtt gtt gca ggc gca   307
Thr Ala Ala Phe Phe Ile Ile Val Phe Gly Thr Val Val Ala Gly Ala
     55                  60                  65

atc aac atg atg aag ggg cat cgc tgg gga cgc gga gct gtc gtc atg   355
Ile Asn Met Met Lys Gly His Arg Trp Gly Arg Gly Ala Val Val Met
 70                  75                  80                  85

ctg aat att att ttg ttg ccg gct gcg tat tac atg ttt atc gaa ggc   403
Leu Asn Ile Ile Leu Leu Pro Ala Ala Tyr Tyr Met Phe Ile Glu Gly
                 90                  95                 100

cga ttc tcc tgg gcg atc gtc aca gga atc tca gct ctc ttc gtt ttg   451
Arg Phe Ser Trp Ala Ile Val Thr Gly Ile Ser Ala Leu Phe Val Leu
            105                 110                 115

ggc gca ctg ttt aat aag cgc gcc gtc ctt tgg gct aac aac gag atc   499
Gly Ala Leu Phe Asn Lys Arg Ala Val Leu Trp Ala Asn Asn Glu Ile
        120                 125                 130

tagcctagag caacgatctc aga                                       522
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<210> 1184
<211> 133
<212> PRT
<213> Corynebacterium glutamicum

<400> 1184

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Met Pro Ala Ser Ile Arg Trp Gly Gly Ile Val Ala Leu Ile Gln Ser
  1               5                  10                  15

Thr Ile Gly Phe Gly Tyr Ala Phe Phe Leu Ile Tyr Arg Glu Ala Thr
             20                  25                  30

Gly Glu Thr Asp Pro Ser Ile Val Tyr Glu Thr Asp Asn Ala Asn Thr
         35                  40                  45

Trp Val Gly Tyr Gly Thr Ala Ala Phe Phe Ile Ile Val Phe Gly Thr
     50                  55                  60

Val Val Ala Gly Ala Ile Asn Met Met Lys Gly His Arg Trp Gly Arg
 65                  70                  75                  80

Gly Ala Val Val Met Leu Asn Ile Ile Leu Leu Pro Ala Ala Tyr Tyr
                 85                  90                  95

Met Phe Ile Glu Gly Arg Phe Ser Trp Ala Ile Val Thr Gly Ile Ser
            100                 105                 110

Ala Leu Phe Val Leu Gly Ala Leu Phe Asn Lys Arg Ala Val Leu Trp
        115                 120                 125

Ala Asn Asn Glu Ile
    130
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<210> 1185
<211> 187
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(187)
<223> RXN02466

<400> 1185
cgaaccgcaa agcgttccgc tgacggaact gccgcctggc ggcagctaca ccgaaaccgg 60

tgctggcact ttccgccagg tcggcgctgc tcttcctcgc gtg ggc gag ggg cag 115
Val Gly Glu Gly Gln
1 5

gaa caa act ttt acg tac gtc att gag att gag gat ggc gtc aac acg 163
Glu Gln Thr Phe Thr Tyr Val Ile Glu Ile Glu Asp Gly Val Asn Thr
10 15 20

gcc gct tat ggt ggc gac gat gcg 187
Ala Ala Tyr Gly Gly Asp Asp Ala
25

<210> 1186
<211> 29
<212> PRT
<213> Corynebacterium glutamicum

<400> 1186
Val Gly Glu Gly Gln Glu Gln Thr Phe Thr Tyr Val Ile Glu Ile Glu
1 5 10 15

Asp Gly Val Asn Thr Ala Ala Tyr Gly Gly Asp Asp Ala
20 25

<210> 1187
<211> 187
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(187)
<223> FRXA02466

<400> 1187
cgaaccgcaa agcgttccgc tgacggaact gccgcctggc ggcagctaca ccgaaaccgg 60

tgctggcact ttccgccagg tcggcgctgc tcttcctcgc gtg ggc gag ggg cag 115
Val Gly Glu Gly Gln
1 5

gaa caa act ttt acg tac gtc att gag att gag gat ggc gtc aac acg 163
Glu Gln Thr Phe Thr Tyr Val Ile Glu Ile Glu Asp Gly Val Asn Thr
10 15 20

gcc gct tat ggt ggc gac gat gcg 187
Ala Ala Tyr Gly Gly Asp Asp Ala
25

<210> 1188
<211> 29
<212> PRT
<213> Corynebacterium glutamicum

<400> 1188
Val Gly Glu Gly Gln Glu Gln Thr Phe Thr Tyr Val Ile Glu Ile Glu
1 5 10 15

Asp Gly Val Asn Thr Ala Ala Tyr Gly Gly Asp Asp Ala
20 25

<210> 1189
<211> 294
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(271)
<223> RXN02505

<400> 1189
tcggaaagca atccggaaca ttcaggttgt agacaatgtc atcagttcag ttgaccgtcc 60

cattaagcgc actggtcgtt tgcgtattcc gggggtcttt gtg gct ggc act cat 115
Val Ala Gly Thr His
1 5

gcg tat gtc aat gaa act ctt tcg gaa aat gag ttc agc atg tgc cga 163
Ala Tyr Val Asn Glu Thr Leu Ser Glu Asn Glu Phe Ser Met Cys Arg
10 15 20

aag aat gaa cct ggt ttg gtc att gag ctg gag aac atc agc atc gat 211
Lys Asn Glu Pro Gly Leu Val Ile Glu Leu Glu Asn Ile Ser Ile Asp
25 30 35

cgc att gtc att tcc aca cca gat gcc cac cgc tat gcg gat gag ctc 259
Arg Ile Val Ile Ser Thr Pro Asp Ala His Arg Tyr Ala Asp Glu Leu
40 45 50

atg gcg gct gtt tagaactcag tttccgtcaa taa 294
Met Ala Ala Val
55

<210> 1190
<211> 57
<212> PRT
<213> Corynebacterium glutamicum

<400> 1190
Val Ala Gly Thr His Ala Tyr Val Asn Glu Thr Leu Ser Glu Asn Glu
1 5 10 15

Phe Ser Met Cys Arg Lys Asn Glu Pro Gly Leu Val Ile Glu Leu Glu
20 25 30

Asn Ile Ser Ile Asp Arg Ile Val Ile Ser Thr Pro Asp Ala His Arg
35 40 45

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Tyr Ala Asp Glu Leu Met Ala Ala Val
     50                  55


<210> 1191
<211> 294
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(271)
<223> FRXA02505

<400> 1191
tcggaaagca atccggaaca ttcaggttgt agacaatgtc atcagttcag ttgaccgtcc 60

cattaagcgc actggtcgtt tgcgtattcc gggggtcttt gtg gct ggc act cat   115
                                              Val Ala Gly Thr His
                                                1               5

gcg tat gtc aat gaa act ctt tcg gaa aat gag ttc agc atg tgc cga   163
Ala Tyr Val Asn Glu Thr Leu Ser Glu Asn Glu Phe Ser Met Cys Arg
                10                  15                  20

aag aat gaa cct ggt ttg gtc att gag ctg gag aac atc agc atc gat   211
Lys Asn Glu Pro Gly Leu Val Ile Glu Leu Glu Asn Ile Ser Ile Asp
            25                  30                  35

cgc att gtc att tcc aca cca gat gcc cac cgc tat gcg gat gag ctc   259
Arg Ile Val Ile Ser Thr Pro Asp Ala His Arg Tyr Ala Asp Glu Leu
        40                  45                  50

atg gcg gct gtt tagaactcag tttccgtcaa taa                        294
Met Ala Ala Val
     55


<210> 1192
<211> 57
<212> PRT
<213> Corynebacterium glutamicum

<400> 1192
Val Ala Gly Thr His Ala Tyr Val Asn Glu Thr Leu Ser Glu Asn Glu
  1               5                  10                  15

Phe Ser Met Cys Arg Lys Asn Glu Pro Gly Leu Val Ile Glu Leu Glu
            20                  25                  30

Asn Ile Ser Ile Asp Arg Ile Val Ile Ser Thr Pro Asp Ala His Arg
        35                  40                  45

Tyr Ala Asp Glu Leu Met Ala Ala Val
     50                  55


<210> 1193
<211> 759
<212> DNA
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<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(736)
<223> RXN02510

<400> 1193
cccgtcgatg aggcaatcgc tgtgatttct tcctggattg gtgaccgcat caatgatcag 60

ccgagcgagg actccattgc agctcgcagg tagccctgag atg gac tca tct gac 115
Met Asp Ser Ser Asp
1 5

agc cac gtt ggt cag gat gta tat gtt gat caa ggt cta ggg gag ccc 163
Ser His Val Gly Gln Asp Val Tyr Val Asp Gln Gly Leu Gly Glu Pro
10 15 20

gac aga ctg gaa cgt ctg tgg gcg ccc tac cgg atg agc tac atc aac 211
Asp Arg Leu Glu Arg Leu Trp Ala Pro Tyr Arg Met Ser Tyr Ile Asn
25 30 35

act cga tct ggc ggt aag caa tca act acc gcc aag cgg gac ccc ttc 259
Thr Arg Ser Gly Gly Lys Gln Ser Thr Thr Ala Lys Arg Asp Pro Phe
40 45 50

att gag gtt ccc aaa atg agt gat gag gac ggc ctg atc gtt gcg cgg 307
Ile Glu Val Pro Lys Met Ser Asp Glu Asp Gly Leu Ile Val Ala Arg
55 60 65

ggt gag ctg gtg tat tgc gta ctc aac ttg tat ccc tac aac gct gga 355
Gly Glu Leu Val Tyr Cys Val Leu Asn Leu Tyr Pro Tyr Asn Ala Gly
70 75 80 85

cac atg atg gtg atc cca ttc cgt aag gaa aag aat cta gag gat ttg 403
His Met Met Val Ile Pro Phe Arg Lys Glu Lys Asn Leu Glu Asp Leu
90 95 100

agc ttg gca gaa tct gcg gag ttg atg ctc ttt acc caa acg gcc atc 451
Ser Leu Ala Glu Ser Ala Glu Leu Met Leu Phe Thr Gln Thr Ala Ile
105 110 115

aag gcg ctg aag cag gtg tca aac cct gat gct gtc aat gtt ggt tta 499
Lys Ala Leu Lys Gln Val Ser Asn Pro Asp Ala Val Asn Val Gly Leu
120 125 130

aac ctt ggc aaa gca tcg ggt ggc tca gtg gga gat cac ctt cat gtc 547
Asn Leu Gly Lys Ala Ser Gly Gly Ser Val Gly Asp His Leu His Val
135 140 145

cat gtg gtg cct agg tgg tcg ggt gat gct aat ttc atg act gtg att 595
His Val Val Pro Arg Trp Ser Gly Asp Ala Asn Phe Met Thr Val Ile
150 155 160 165

gac ggt gtc aaa gtg cta ccg cag acc ctg cgt caa acc agg gcc atg 643
Asp Gly Val Lys Val Leu Pro Gln Thr Leu Arg Gln Thr Arg Ala Met
170 175 180

ctt gcg caa gca tgg ggc acc att gat ggg gca cca ggc act gtc gac 691
Leu Ala Gln Ala Trp Gly Thr Ile Asp Gly Ala Pro Gly Thr Val Asp
185 190 195

```
cca acg ctg act tca gcg atc cgt acc gca gca ccg aag gag cac       736
Pro Thr Leu Thr Ser Ala Ile Arg Thr Ala Ala Pro Lys Glu His
        200                 205                 210

tgatgctggg acttcatgga cgt                                         759


<210> 1194
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 1194
Met Asp Ser Ser Asp Ser His Val Gly Gln Asp Val Tyr Val Asp Gln
  1               5                  10                  15

Gly Leu Gly Glu Pro Asp Arg Leu Glu Arg Leu Trp Ala Pro Tyr Arg
             20                  25                  30

Met Ser Tyr Ile Asn Thr Arg Ser Gly Gly Lys Gln Ser Thr Thr Ala
         35                  40                  45

Lys Arg Asp Pro Phe Ile Glu Val Pro Lys Met Ser Asp Glu Asp Gly
     50                  55                  60

Leu Ile Val Ala Arg Gly Glu Leu Val Tyr Cys Val Leu Asn Leu Tyr
 65                  70                  75                  80

Pro Tyr Asn Ala Gly His Met Met Val Ile Pro Phe Arg Lys Glu Lys
                 85                  90                  95

Asn Leu Glu Asp Leu Ser Leu Ala Glu Ser Ala Glu Leu Met Leu Phe
            100                 105                 110

Thr Gln Thr Ala Ile Lys Ala Leu Lys Gln Val Ser Asn Pro Asp Ala
        115                 120                 125

Val Asn Val Gly Leu Asn Leu Gly Lys Ala Ser Gly Gly Ser Val Gly
    130                 135                 140

Asp His Leu His Val His Val Val Pro Arg Trp Ser Gly Asp Ala Asn
145                 150                 155                 160

Phe Met Thr Val Ile Asp Gly Val Lys Val Leu Pro Gln Thr Leu Arg
                165                 170                 175

Gln Thr Arg Ala Met Leu Ala Gln Ala Trp Gly Thr Ile Asp Gly Ala
            180                 185                 190

Pro Gly Thr Val Asp Pro Thr Leu Thr Ser Ala Ile Arg Thr Ala Ala
        195                 200                 205

Pro Lys Glu His
    210


<210> 1195
<211> 759
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(736)
<223> FRXA02510

<400> 1195
cccgtcgatg aggcaatcgc tgtgatttct tcctggattg gtgaccgcat caatgatcag 60

ccgagcgagg actccattgc agctcgcagg tagccctgag atg gac tca tct gac 115
Met Asp Ser Ser Asp
1 5

agc cac gtt ggt cag gat gta tat gtt gat caa ggt cta ggg gag ccc 163
Ser His Val Gly Gln Asp Val Tyr Val Asp Gln Gly Leu Gly Glu Pro
10 15 20

gac aga ctg gaa cgt ctg tgg gcg ccc tac cgg atg agc tac atc aac 211
Asp Arg Leu Glu Arg Leu Trp Ala Pro Tyr Arg Met Ser Tyr Ile Asn
25 30 35

act cga tct ggc ggt aag caa tca act acc gcc aag cgg gac ccc ttc 259
Thr Arg Ser Gly Gly Lys Gln Ser Thr Thr Ala Lys Arg Asp Pro Phe
40 45 50

att gag gtt ccc aaa atg agt gat gag gac ggc ctg atc gtt gcg cgg 307
Ile Glu Val Pro Lys Met Ser Asp Glu Asp Gly Leu Ile Val Ala Arg
55 60 65

ggt gag ctg gtg tat tgc gta ctc aac ttg tat ccc tac aac gct gga 355
Gly Glu Leu Val Tyr Cys Val Leu Asn Leu Tyr Pro Tyr Asn Ala Gly
70 75 80 85

cac atg atg gtg atc cca ttc cgt aag gaa aag aat cta gag gat ttg 403
His Met Met Val Ile Pro Phe Arg Lys Glu Lys Asn Leu Glu Asp Leu
90 95 100

agc ttg gca gaa tct gcg gag ttg atg ctc ttt acc caa acg gcc atc 451
Ser Leu Ala Glu Ser Ala Glu Leu Met Leu Phe Thr Gln Thr Ala Ile
105 110 115

aag gcg ctg aag cag gtg tca aac cct gat gct gtc aat gtt ggt tta 499
Lys Ala Leu Lys Gln Val Ser Asn Pro Asp Ala Val Asn Val Gly Leu
120 125 130

aac ctt ggc aaa gca tcg ggt ggc tca gtg gga gat cac ctt cat gtc 547
Asn Leu Gly Lys Ala Ser Gly Gly Ser Val Gly Asp His Leu His Val
135 140 145

cat gtg gtg cct agg tgg tcg ggt gat gct aat ttc atg act gtg att 595
His Val Val Pro Arg Trp Ser Gly Asp Ala Asn Phe Met Thr Val Ile
150 155 160 165

gac ggt gtc aaa gtg cta ccg cag acc ctg cgt caa acc agg gcc atg 643
Asp Gly Val Lys Val Leu Pro Gln Thr Leu Arg Gln Thr Arg Ala Met
170 175 180

ctt gcg caa gca tgg ggc acc att gat ggg gca cca ggc act gtc gac 691
Leu Ala Gln Ala Trp Gly Thr Ile Asp Gly Ala Pro Gly Thr Val Asp
185 190 195

```
cca acg ctg act tca gcg atc cgt acc gca gca ccg aag gag cac       736
Pro Thr Leu Thr Ser Ala Ile Arg Thr Ala Ala Pro Lys Glu His
        200                 205                 210

tgatgctggg acttcatgga cgt                                         759
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<210> 1196
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 1196

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Met Asp Ser Ser Asp Ser His Val Gly Gln Asp Val Tyr Val Asp Gln
  1               5                  10                  15

Gly Leu Gly Glu Pro Asp Arg Leu Glu Arg Leu Trp Ala Pro Tyr Arg
             20                  25                  30

Met Ser Tyr Ile Asn Thr Arg Ser Gly Gly Lys Gln Ser Thr Thr Ala
         35                  40                  45

Lys Arg Asp Pro Phe Ile Glu Val Pro Lys Met Ser Asp Glu Asp Gly
     50                  55                  60

Leu Ile Val Ala Arg Gly Glu Leu Val Tyr Cys Val Leu Asn Leu Tyr
 65                  70                  75                  80

Pro Tyr Asn Ala Gly His Met Met Val Ile Pro Phe Arg Lys Glu Lys
                 85                  90                  95

Asn Leu Glu Asp Leu Ser Leu Ala Glu Ser Ala Glu Leu Met Leu Phe
            100                 105                 110

Thr Gln Thr Ala Ile Lys Ala Leu Lys Gln Val Ser Asn Pro Asp Ala
        115                 120                 125

Val Asn Val Gly Leu Asn Leu Gly Lys Ala Ser Gly Gly Ser Val Gly
    130                 135                 140

Asp His Leu His Val His Val Val Pro Arg Trp Ser Gly Asp Ala Asn
145                 150                 155                 160

Phe Met Thr Val Ile Asp Gly Val Lys Val Leu Pro Gln Thr Leu Arg
                165                 170                 175

Gln Thr Arg Ala Met Leu Ala Gln Ala Trp Gly Thr Ile Asp Gly Ala
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Pro Gly Thr Val Asp Pro Thr Leu Thr Ser Ala Ile Arg Thr Ala Ala
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<223> RXN02519

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gcgcatcggc accgctggtt ccagatcagc gaccctccac gtg gaa gac gag cag 115
Val Glu Asp Glu Gln
1 5

agc cct tta ggg gca acg ctt ttc gac gtc gcg acc ggc gcg agc tcc 163
Ser Pro Leu Gly Ala Thr Leu Phe Asp Val Ala Thr Gly Ala Ser Ser
10 15 20

atc aac gac cgc gat acc gac gcc tca ggg ctt gag cct gaa aag att 211
Ile Asn Asp Arg Asp Thr Asp Ala Ser Gly Leu Glu Pro Glu Lys Ile
25 30 35

cgc cga ttt gca tgg ctg cgc ctg atc ggc acc atg ggt gcg tta atg 259
Arg Arg Phe Ala Trp Leu Arg Leu Ile Gly Thr Met Gly Ala Leu Met
40 45 50

atc gcg ttt ggt gcg ctg ggc gcg ggt gca ctt ccg gtg gtg aat aat 307
Ile Ala Phe Gly Ala Leu Gly Ala Gly Ala Leu Pro Val Val Asn Asn
55 60 65

ccg tat gtg gat ttc cct ggc gga aac ttc atg agc cga atg ctg cag 355
Pro Tyr Val Asp Phe Pro Gly Gly Asn Phe Met Ser Arg Met Leu Gln
70 75 80 85

acc tct tcc atg atc gtg ctc atc ggc gtg gga ttt ttg gtg ctg gcg 403
Thr Ser Ser Met Ile Val Leu Ile Gly Val Gly Phe Leu Val Leu Ala
90 95 100

tgg gtg tta atg gca ccg ctg gtg ggt att cct ttt aaa cgc agc gga 451
Trp Val Leu Met Ala Pro Leu Val Gly Ile Pro Phe Lys Arg Ser Gly
105 110 115

aac aga aca gcc agc gtg agt ttg tcc atg ctg cgc cgc aca ttt ggc 499
Asn Arg Thr Ala Ser Val Ser Leu Ser Met Leu Arg Arg Thr Phe Gly
120 125 130

gcc tgg gta gcg ccc atc atg ctc acc gcc cca ctg ttt act caa gac 547
Ala Trp Val Ala Pro Ile Met Leu Thr Ala Pro Leu Phe Thr Gln Asp
135 140 145

att tat tct tat ctg gca caa ggc tct gtg acc gcg cag gga atg gat 595
Ile Tyr Ser Tyr Leu Ala Gln Gly Ser Val Thr Ala Gln Gly Met Asp
150 155 160 165

gcc tac gcc ggt gga ccg ctt gaa cta ttg ggg ccc gat aat cat ctg 643
Ala Tyr Ala Gly Gly Pro Leu Glu Leu Leu Gly Pro Asp Asn His Leu
170 175 180

gca cgg tcc gtg ccc ttt att tgg gcc cag tcg ccc tcg ccc tac ggc 691
Ala Arg Ser Val Pro Phe Ile Trp Ala Gln Ser Pro Ser Pro Tyr Gly
185 190 195

cct gtt gcg ctg agc atc gcg gcg tcg ata agc gtt att act aat gac 739

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Pro Val Ala Leu Ser Ile Ala Ala Ser Ile Ser Val Ile Thr Asn Asp
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agc atc gtt gga ggc gtg ctg gcg cac cgt att gcg tcg ctg ctg ggc   787
Ser Ile Val Gly Gly Val Leu Ala His Arg Ile Ala Ser Leu Leu Gly
    215                 220                 225

gtt gtg gct gca ggc tgg gcg atc acc atg ctg gcc agg cgc tgt cgg   835
Val Val Ala Ala Gly Trp Ala Ile Thr Met Leu Ala Arg Arg Cys Arg
230                 235                 240                 245

gta tct gaa gaa gcg tcc ttt tac ctg ggc gta ctt aat ccg ctg ctg   883
Val Ser Glu Glu Ala Ser Phe Tyr Leu Gly Val Leu Asn Pro Leu Leu
                250                 255                 260

att ctg cac ctg atc ggc ggt att cac aac gaa tcc atc ctg ctg gga   931
Ile Leu His Leu Ile Gly Gly Ile His Asn Glu Ser Ile Leu Leu Gly
            265                 270                 275

ttt tta ctt gtt ggc ctg gaa ctc gga ctg cgt ggc acc gac cgg att   979
Phe Leu Leu Val Gly Leu Glu Leu Gly Leu Arg Gly Thr Asp Arg Ile
        280                 285                 290

caa aca ggg ctg tgg ggg cct gcg tgg aca tat att gca ctg agt ggc   1027
Gln Thr Gly Leu Trp Gly Pro Ala Trp Thr Tyr Ile Ala Leu Ser Gly
    295                 300                 305

gta ttg att tct tgc gca ggc ctg gtc aag gtg acc ggc ttt att ggg   1075
Val Leu Ile Ser Cys Ala Gly Leu Val Lys Val Thr Gly Phe Ile Gly
310                 315                 320                 325

ctc ggt ttt gtg ggc atg gcc ttg gcc agg gcg ttt cat gca cgt gga   1123
Leu Gly Phe Val Gly Met Ala Leu Ala Arg Ala Phe His Ala Arg Gly
                330                 335                 340

cat cga cac gtc gtt gcg atc ggc gtt gca ggc ctc gtt caa gta gca   1171
His Arg His Val Val Ala Ile Gly Val Ala Gly Leu Val Gln Val Ala
            345                 350                 355

gcc ctg gtg atc acc gtg gtt gtt ctc agt gtg att acc gga atc agt   1219
Ala Leu Val Ile Thr Val Val Val Leu Ser Val Ile Thr Gly Ile Ser
        360                 365                 370

ttg ggg tgg atc aca ggt caa ggt ggc gct gcg acg atc cga agc tgg   1267
Leu Gly Trp Ile Thr Gly Gln Gly Gly Ala Ala Thr Ile Arg Ser Trp
    375                 380                 385

atg tct atg acc acc aac att ggc gtt att tct gga ttc atc gga atg   1315
Met Ser Met Thr Thr Asn Ile Gly Val Ile Ser Gly Phe Ile Gly Met
390                 395                 400                 405

aat ttg ggg cta ggc gac cac acc gca gcc atg ctc gtt gtg acc cgt   1363
Asn Leu Gly Leu Gly Asp His Thr Ala Ala Met Leu Val Val Thr Arg
                410                 415                 420

gca gcc gga atc gcg gta gct gcc gcc ttc atg gtt cgt atg ttg ttt   1411
Ala Ala Gly Ile Ala Val Ala Ala Ala Phe Met Val Arg Met Leu Phe
            425                 430                 435

gcc aca tat aga ggt cac att cac gct gtg ggc gga ctg ggc gtg gcg   1459
Ala Thr Tyr Arg Gly His Ile His Ala Val Gly Gly Leu Gly Val Ala
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        440                 445                 450

act ttc gtc ctc gtt atc ctc ttc ccc gtg gtg cat ccg tgg tac atg   1507
Thr Phe Val Leu Val Ile Leu Phe Pro Val Val His Pro Trp Tyr Met
    455                 460                 465

ctg tgg gct atc gtg ccg cta gct tcc tgg gca aat aga ctg ttc ttc   1555
Leu Trp Ala Ile Val Pro Leu Ala Ser Trp Ala Asn Arg Leu Phe Phe
470                 475                 480                 485

cag ctc gga gtg att gcc tac tcc act gcc ttc agt ttc ttt gtg ctg   1603
Gln Leu Gly Val Ile Ala Tyr Ser Thr Ala Phe Ser Phe Phe Val Leu
                490                 495                 500

cct cgc ggg ctt gca ctt cca gtc gga act gtc ttt tcc atc tac ttc   1651
Pro Arg Gly Leu Ala Leu Pro Val Gly Thr Val Phe Ser Ile Tyr Phe
            505                 510                 515

ggc gca gcg ctc gga ttc agc att ctc cta tta gtt gga tgg tgg agt   1699
Gly Ala Ala Leu Gly Phe Ser Ile Leu Leu Leu Val Gly Trp Trp Ser
        520                 525                 530

ttg agg cgg aat cca acc ttt ggt tta cac tgatcaactg tgactactga     1749
Leu Arg Arg Asn Pro Thr Phe Gly Leu His
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ttt                                                               1752


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            20                  25                  30

Glu Pro Glu Lys Ile Arg Arg Phe Ala Trp Leu Arg Leu Ile Gly Thr
        35                  40                  45

Met Gly Ala Leu Met Ile Ala Phe Gly Ala Leu Gly Ala Gly Ala Leu
    50                  55                  60

Pro Val Val Asn Asn Pro Tyr Val Asp Phe Pro Gly Gly Asn Phe Met
65                  70                  75                  80

Ser Arg Met Leu Gln Thr Ser Ser Met Ile Val Leu Ile Gly Val Gly
                85                  90                  95

Phe Leu Val Leu Ala Trp Val Leu Met Ala Pro Leu Val Gly Ile Pro
            100                 105                 110

Phe Lys Arg Ser Gly Asn Arg Thr Ala Ser Val Ser Leu Ser Met Leu
        115                 120                 125

Arg Arg Thr Phe Gly Ala Trp Val Ala Pro Ile Met Leu Thr Ala Pro
    130                 135                 140
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Leu Phe Thr Gln Asp Ile Tyr Ser Tyr Leu Ala Gln Gly Ser Val Thr
145                 150                 155                 160

Ala Gln Gly Met Asp Ala Tyr Ala Gly Gly Pro Leu Glu Leu Leu Gly
                165                 170                 175

Pro Asp Asn His Leu Ala Arg Ser Val Pro Phe Ile Trp Ala Gln Ser
            180                 185                 190

Pro Ser Pro Tyr Gly Pro Val Ala Leu Ser Ile Ala Ala Ser Ile Ser
        195                 200                 205

Val Ile Thr Asn Asp Ser Ile Val Gly Gly Val Leu Ala His Arg Ile
    210                 215                 220

Ala Ser Leu Leu Gly Val Val Ala Ala Gly Trp Ala Ile Thr Met Leu
225                 230                 235                 240

Ala Arg Arg Cys Arg Val Ser Glu Glu Ala Ser Phe Tyr Leu Gly Val
                245                 250                 255

Leu Asn Pro Leu Leu Ile Leu His Leu Ile Gly Gly Ile His Asn Glu
            260                 265                 270

Ser Ile Leu Leu Gly Phe Leu Leu Val Gly Leu Glu Leu Gly Leu Arg
        275                 280                 285

Gly Thr Asp Arg Ile Gln Thr Gly Leu Trp Gly Pro Ala Trp Thr Tyr
    290                 295                 300

Ile Ala Leu Ser Gly Val Leu Ile Ser Cys Ala Gly Leu Val Lys Val
305                 310                 315                 320

Thr Gly Phe Ile Gly Leu Gly Phe Val Gly Met Ala Leu Ala Arg Ala
                325                 330                 335

Phe His Ala Arg Gly His Arg His Val Val Ala Ile Gly Val Ala Gly
            340                 345                 350

Leu Val Gln Val Ala Ala Leu Val Ile Thr Val Val Val Leu Ser Val
        355                 360                 365

Ile Thr Gly Ile Ser Leu Gly Trp Ile Thr Gly Gln Gly Gly Ala Ala
    370                 375                 380

Thr Ile Arg Ser Trp Met Ser Met Thr Thr Asn Ile Gly Val Ile Ser
385                 390                 395                 400

Gly Phe Ile Gly Met Asn Leu Gly Leu Gly Asp His Thr Ala Ala Met
                405                 410                 415

Leu Val Val Thr Arg Ala Ala Gly Ile Ala Val Ala Ala Ala Phe Met
            420                 425                 430

Val Arg Met Leu Phe Ala Thr Tyr Arg Gly His Ile His Ala Val Gly
        435                 440                 445

Gly Leu Gly Val Ala Thr Phe Val Leu Val Ile Leu Phe Pro Val Val
    450                 455                 460
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His Pro Trp Tyr Met Leu Trp Ala Ile Val Pro Leu Ala Ser Trp Ala
465                 470                 475                 480

Asn Arg Leu Phe Phe Gln Leu Gly Val Ile Ala Tyr Ser Thr Ala Phe
                485                 490                 495

Ser Phe Phe Val Leu Pro Arg Gly Leu Ala Leu Pro Val Gly Thr Val
            500                 505                 510

Phe Ser Ile Tyr Phe Gly Ala Ala Leu Gly Phe Ser Ile Leu Leu Leu
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Val Gly Trp Trp Ser Leu Arg Arg Asn Pro Thr Phe Gly Leu His
    530                 535                 540


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atccccttc gggtcaccac cagactctga tgcgaggtaa atg ttc tcc gct ccc   115
                                            Met Phe Ser Ala Pro
                                              1               5

ttg cgt aga atg atg cga gtg acg aag gac gag cag att caa ccc aat   163
Leu Arg Arg Met Met Arg Val Thr Lys Asp Glu Gln Ile Gln Pro Asn
                  10                  15                  20

tcg aac gcc cct gaa aac aga aaa tgg ttt cct cgg gca cct cgt ccc   211
Ser Asn Ala Pro Glu Asn Arg Lys Trp Phe Pro Arg Ala Pro Arg Pro
              25                  30                  35

cta cgc caa ttt ctc gac act ttg ccg cgc atc ggc acc gct ggt tcc   259
Leu Arg Gln Phe Leu Asp Thr Leu Pro Arg Ile Gly Thr Ala Gly Ser
          40                  45                  50

aga tca gcg acc ctc cac gtg gaa gac gag cag agc cct tta ggg gca   307
Arg Ser Ala Thr Leu His Val Glu Asp Glu Gln Ser Pro Leu Gly Ala
      55                  60                  65

acg ctt ttc gac gtc gcg acc ggc gcg agc tcc atc aac gac cgc gat   355
Thr Leu Phe Asp Val Ala Thr Gly Ala Ser Ser Ile Asn Asp Arg Asp
  70                  75                  80                  85

acc gac gcc tca ggg ctt gag cct gaa aag att cgc cga ttt gca tgg   403
Thr Asp Ala Ser Gly Leu Glu Pro Glu Lys Ile Arg Arg Phe Ala Trp
                  90                  95                 100

ctg cgc ctg atc ggc acc atg ggt gcg tta atg atc gcg ttt ggt gcg   451
Leu Arg Leu Ile Gly Thr Met Gly Ala Leu Met Ile Ala Phe Gly Ala
              105                 110                 115
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ctg ggc gcg ggt gca ctt ccg gtg gtg aat aat ccg tat gtg gat ttc   499
Leu Gly Ala Gly Ala Leu Pro Val Val Asn Asn Pro Tyr Val Asp Phe
        120                 125                 130

cct ggc gga aac ttc atg agc cga atg ctg cag acc tct tcc atg atc   547
Pro Gly Gly Asn Phe Met Ser Arg Met Leu Gln Thr Ser Ser Met Ile
    135                 140                 145

gtg ctc atc ggc gtg gga ttt ttg gtg ctg gcg tgg gtg tta atg gca   595
Val Leu Ile Gly Val Gly Phe Leu Val Leu Ala Trp Val Leu Met Ala
150                 155                 160                 165

ccg ctg gtg ggt att cct ttt aaa cgc agc gga aac aga aca gcc agc   643
Pro Leu Val Gly Ile Pro Phe Lys Arg Ser Gly Asn Arg Thr Ala Ser
                170                 175                 180

gtg agt ttg tcc atg ctg cgc cgc aca ttt ggc gcc tgg gta gcg ccc   691
Val Ser Leu Ser Met Leu Arg Arg Thr Phe Gly Ala Trp Val Ala Pro
            185                 190                 195

atc atg ctc acc gcc cca ctg ttt act caa gac att tat tct tat ctg   739
Ile Met Leu Thr Ala Pro Leu Phe Thr Gln Asp Ile Tyr Ser Tyr Leu
        200                 205                 210

gca caa ggc tct gtg acc gcg cag gga atg gat gcc tac gcc ggt gga   787
Ala Gln Gly Ser Val Thr Ala Gln Gly Met Asp Ala Tyr Ala Gly Gly
    215                 220                 225

ccg ctt gaa cta ttg ggg ccc gat aat cat ctg gca cgg tcc gtg ccc   835
Pro Leu Glu Leu Leu Gly Pro Asp Asn His Leu Ala Arg Ser Val Pro
230                 235                 240                 245

ttt att tgg gcc cag tcg ccc tcg ccc tac ggc cct gtt gcg ctg agc   883
Phe Ile Trp Ala Gln Ser Pro Ser Pro Tyr Gly Pro Val Ala Leu Ser
                250                 255                 260

atc gcg gcg tcg ata agc gtt att act aat gac agc atc gtt gga ggc   931
Ile Ala Ala Ser Ile Ser Val Ile Thr Asn Asp Ser Ile Val Gly Gly
            265                 270                 275

gtg ctg gcg cac cgt att gcg tcg ctg ctg ggc gtt gtg gct gca ggc   979
Val Leu Ala His Arg Ile Ala Ser Leu Leu Gly Val Val Ala Ala Gly
        280                 285                 290

tgg gcg atc acc atg ctg gcc agg cgc tgt cgg gta tct gaa gaa gcg   1027
Trp Ala Ile Thr Met Leu Ala Arg Arg Cys Arg Val Ser Glu Glu Ala
    295                 300                 305

tcc ttt tac ctg ggc gta ctt aat ccg ctg ctg att ctg cac ctg atc   1075
Ser Phe Tyr Leu Gly Val Leu Asn Pro Leu Leu Ile Leu His Leu Ile
310                 315                 320                 325

ggc ggt att cac aac gaa tcc atc ctg ctg gga ttt tta ctt gtt ggc   1123
Gly Gly Ile His Asn Glu Ser Ile Leu Leu Gly Phe Leu Leu Val Gly
                330                 335                 340

ctg gaa ctc gga ctg cgt ggc acc gac cgg att caa aca ggg ctg tgg   1171
Leu Glu Leu Gly Leu Arg Gly Thr Asp Arg Ile Gln Thr Gly Leu Trp
            345                 350                 355

ggg cct gcg tgg aca tat att gca ctg agt ggc gta ttg att tct tgc   1219
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Gly Pro Ala Trp Thr Tyr Ile Ala Leu Ser Gly Val Leu Ile Ser Cys
        360                 365                 370

gca ggc ctg gtc aag gtg acc ggc ttt att ggg ctc ggt ttt gtg ggc   1267
Ala Gly Leu Val Lys Val Thr Gly Phe Ile Gly Leu Gly Phe Val Gly
    375                 380                 385

atg gcc ttg gcc agg gcg ttt cat gca cgt gga cat cga cac gtc gtt   1315
Met Ala Leu Ala Arg Ala Phe His Ala Arg Gly His Arg His Val Val
390                 395                 400                 405

gcg atc ggc gtt gca ggc ctc gtt caa gta gca gcc ctg gtg atc acc   1363
Ala Ile Gly Val Ala Gly Leu Val Gln Val Ala Ala Leu Val Ile Thr
                410                 415                 420

gtg gtt gtt ctc agt gtg att acc gga atc agt ttg ggg tgg atc aca   1411
Val Val Val Leu Ser Val Ile Thr Gly Ile Ser Leu Gly Trp Ile Thr
            425                 430                 435

ggt caa ggt ggc gct gcg acg atc cga agc tgg atg tct atg acc acc   1459
Gly Gln Gly Gly Ala Ala Thr Ile Arg Ser Trp Met Ser Met Thr Thr
        440                 445                 450

aac att ggc gtt att tct gga ttc atc gga atg aat ttg ggg cta ggc   1507
Asn Ile Gly Val Ile Ser Gly Phe Ile Gly Met Asn Leu Gly Leu Gly
    455                 460                 465

gac cac acc gca gcc atg ctc gtt gtg acc cgt gca gcc gga atc gcg   1555
Asp His Thr Ala Ala Met Leu Val Val Thr Arg Ala Ala Gly Ile Ala
470                 475                 480                 485

gta gct gcc gcc ttc atg gtt cgt atg ttg ttt gcc aca tat aga ggt   1603
Val Ala Ala Ala Phe Met Val Arg Met Leu Phe Ala Thr Tyr Arg Gly
                490                 495                 500

cac att cac gct gtg ggc gga ctg ggc gtg gcg act ttc gtc ctc gtt   1651
His Ile His Ala Val Gly Gly Leu Gly Val Ala Thr Phe Val Leu Val
            505                 510                 515

atc ctc ttc ccc gtg gtg cat ccg tgg tac atg ctg tgg gct atc gtg   1699
Ile Leu Phe Pro Val Val His Pro Trp Tyr Met Leu Trp Ala Ile Val
        520                 525                 530

ccg cta gct tcc tgg gca aat aga ctg ttc ttc cag ctc gga gtg att   1747
Pro Leu Ala Ser Trp Ala Asn Arg Leu Phe Phe Gln Leu Gly Val Ile
    535                 540                 545

gcc tac tcc act gcc ttc agt ttc ttt gtg ctg cct cgc ggg ctt gca   1795
Ala Tyr Ser Thr Ala Phe Ser Phe Phe Val Leu Pro Arg Gly Leu Ala
550                 555                 560                 565

ctt cca gtc gga act gtc ttt tcc atc tac ttc ggc gca gcg ctc gga   1843
Leu Pro Val Gly Thr Val Phe Ser Ile Tyr Phe Gly Ala Ala Leu Gly
                570                 575                 580

ttc agc att ctc cta tta gtt gga tgg tgg agt ttg agg cgg aat cca   1891
Phe Ser Ile Leu Leu Leu Val Gly Trp Trp Ser Leu Arg Arg Asn Pro
            585                 590                 595

acc ttt ggt tta cac tgatcaactg tgactactga ttt                     1929
Thr Phe Gly Leu His
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Arg Ala Pro Arg Pro Leu Arg Gln Phe Leu Asp Thr Leu Pro Arg Ile
         35                  40                  45

Gly Thr Ala Gly Ser Arg Ser Ala Thr Leu His Val Glu Asp Glu Gln
     50                  55                  60

Ser Pro Leu Gly Ala Thr Leu Phe Asp Val Ala Thr Gly Ala Ser Ser
 65                  70                  75                  80

Ile Asn Asp Arg Asp Thr Asp Ala Ser Gly Leu Glu Pro Glu Lys Ile
                 85                  90                  95

Arg Arg Phe Ala Trp Leu Arg Leu Ile Gly Thr Met Gly Ala Leu Met
            100                 105                 110

Ile Ala Phe Gly Ala Leu Gly Ala Gly Ala Leu Pro Val Val Asn Asn
        115                 120                 125

Pro Tyr Val Asp Phe Pro Gly Gly Asn Phe Met Ser Arg Met Leu Gln
    130                 135                 140

Thr Ser Ser Met Ile Val Leu Ile Gly Val Gly Phe Leu Val Leu Ala
145                 150                 155                 160

Trp Val Leu Met Ala Pro Leu Val Gly Ile Pro Phe Lys Arg Ser Gly
                165                 170                 175

Asn Arg Thr Ala Ser Val Ser Leu Ser Met Leu Arg Arg Thr Phe Gly
            180                 185                 190

Ala Trp Val Ala Pro Ile Met Leu Thr Ala Pro Leu Phe Thr Gln Asp
        195                 200                 205

Ile Tyr Ser Tyr Leu Ala Gln Gly Ser Val Thr Ala Gln Gly Met Asp
    210                 215                 220

Ala Tyr Ala Gly Gly Pro Leu Glu Leu Leu Gly Pro Asp Asn His Leu
225                 230                 235                 240

Ala Arg Ser Val Pro Phe Ile Trp Ala Gln Ser Pro Ser Pro Tyr Gly
                245                 250                 255

Pro Val Ala Leu Ser Ile Ala Ala Ser Ile Ser Val Ile Thr Asn Asp
            260                 265                 270

Ser Ile Val Gly Gly Val Leu Ala His Arg Ile Ala Ser Leu Leu Gly
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        275                 280                 285

Val Val Ala Ala Gly Trp Ala Ile Thr Met Leu Ala Arg Arg Cys Arg
    290                 295                 300

Val Ser Glu Glu Ala Ser Phe Tyr Leu Gly Val Leu Asn Pro Leu Leu
305                 310                 315                 320

Ile Leu His Leu Ile Gly Gly Ile His Asn Glu Ser Ile Leu Leu Gly
                325                 330                 335

Phe Leu Leu Val Gly Leu Glu Leu Gly Leu Arg Gly Thr Asp Arg Ile
            340                 345                 350

Gln Thr Gly Leu Trp Gly Pro Ala Trp Thr Tyr Ile Ala Leu Ser Gly
        355                 360                 365

Val Leu Ile Ser Cys Ala Gly Leu Val Lys Val Thr Gly Phe Ile Gly
    370                 375                 380

Leu Gly Phe Val Gly Met Ala Leu Ala Arg Ala Phe His Ala Arg Gly
385                 390                 395                 400

His Arg His Val Val Ala Ile Gly Val Ala Gly Leu Val Gln Val Ala
                405                 410                 415

Ala Leu Val Ile Thr Val Val Val Leu Ser Val Ile Thr Gly Ile Ser
            420                 425                 430

Leu Gly Trp Ile Thr Gly Gln Gly Gly Ala Ala Thr Ile Arg Ser Trp
        435                 440                 445

Met Ser Met Thr Thr Asn Ile Gly Val Ile Ser Gly Phe Ile Gly Met
    450                 455                 460

Asn Leu Gly Leu Gly Asp His Thr Ala Ala Met Leu Val Val Thr Arg
465                 470                 475                 480

Ala Ala Gly Ile Ala Val Ala Ala Ala Phe Met Val Arg Met Leu Phe
                485                 490                 495

Ala Thr Tyr Arg Gly His Ile His Ala Val Gly Gly Leu Gly Val Ala
            500                 505                 510

Thr Phe Val Leu Val Ile Leu Phe Pro Val Val His Pro Trp Tyr Met
        515                 520                 525

Leu Trp Ala Ile Val Pro Leu Ala Ser Trp Ala Asn Arg Leu Phe Phe
    530                 535                 540

Gln Leu Gly Val Ile Ala Tyr Ser Thr Ala Phe Ser Phe Phe Val Leu
545                 550                 555                 560

Pro Arg Gly Leu Ala Leu Pro Val Gly Thr Val Phe Ser Ile Tyr Phe
                565                 570                 575

Gly Ala Ala Leu Gly Phe Ser Ile Leu Leu Leu Val Gly Trp Trp Ser
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Val Gly Asp Val Val
1 5

aaa ggc aac gac gcg cac acc gga gac ggt gat acg cgc cga aaa att 163
Lys Gly Asn Asp Ala His Thr Gly Asp Gly Asp Thr Arg Arg Lys Ile
10 15 20

ctt ctc atc ctg ttg gaa cgt gca ccg gtg atc gct tca gat att gct 211
Leu Leu Ile Leu Leu Glu Arg Ala Pro Val Ile Ala Ser Asp Ile Ala
25 30 35

gaa cag ctt cag ctt tca act gtg gga gtg cgc agg cac cta gac aac 259
Glu Gln Leu Gln Leu Ser Thr Val Gly Val Arg Arg His Leu Asp Asn
40 45 50

ttg gtt gaa gaa aat ctg gcg gag gcg gca aat ccg cgc cag aac cca 307
Leu Val Glu Glu Asn Leu Ala Glu Ala Ala Asn Pro Arg Gln Asn Pro
55 60 65

tat gag ccc aaa atg cgc ggt agg cca gca aaa act tat cgg ctt act 355
Tyr Glu Pro Lys Met Arg Gly Arg Pro Ala Lys Thr Tyr Arg Leu Thr
70 75 80 85

gat aaa ggt cgc tca atc ttc ggc cac gaa tat gat tcc ctt gct gcg 403
Asp Lys Gly Arg Ser Ile Phe Gly His Glu Tyr Asp Ser Leu Ala Ala
90 95 100

gca gct cta gcc act ctt cga gag gtc ggc gga gat gat gca gta agg 451
Ala Ala Leu Ala Thr Leu Arg Glu Val Gly Gly Asp Asp Ala Val Arg
105 110 115

caa ttt gct aga aag cgg atc gaa aca att gtt gag ggt att acc cca 499
Gln Phe Ala Arg Lys Arg Ile Glu Thr Ile Val Glu Gly Ile Thr Pro
120 125 130

gca gat gtc aca gat caa tca atc gaa gat aca gcc aaa tct tta gtt 547
Ala Asp Val Thr Asp Gln Ser Ile Glu Asp Thr Ala Lys Ser Leu Val
135 140 145

gaa gct ttt agt cgg cat ggt tat gca gca act gtc gat gcc act cga 595
Glu Ala Phe Ser Arg His Gly Tyr Ala Ala Thr Val Asp Ala Thr Arg
150 155 160 165

aac ggg ttg caa ctc tgc cag cat cac tgt cca ata tct aca gtc gcc 643
Asn Gly Leu Gln Leu Cys Gln His His Cys Pro Ile Ser Thr Val Ala

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                170                 175                 180

acg gaa ttt ccg gaa ctg tgt gag gca gag cat caa gca gtc tca gaa   691
Thr Glu Phe Pro Glu Leu Cys Glu Ala Glu His Gln Ala Val Ser Glu
            185                 190                 195

ctt ttg ggg cag cac acg caa cca ttg gca aca atc gcg gac ggc cac   739
Leu Leu Gly Gln His Thr Gln Pro Leu Ala Thr Ile Ala Asp Gly His
        200                 205                 210

ggc atc tgc aca aca aat att gca ttg aca ccc atc aaa cac tcc       784
Gly Ile Cys Thr Thr Asn Ile Ala Leu Thr Pro Ile Lys His Ser
    215                 220                 225

tgatgaaagg agcggatcat gac                                        807


<210> 1202
<211> 228
<212> PRT
<213> Corynebacterium glutamicum

<400> 1202
Val Gly Asp Val Val Lys Gly Asn Asp Ala His Thr Gly Asp Gly Asp
  1               5                  10                  15

Thr Arg Arg Lys Ile Leu Leu Ile Leu Leu Glu Arg Ala Pro Val Ile
             20                  25                  30

Ala Ser Asp Ile Ala Glu Gln Leu Gln Leu Ser Thr Val Gly Val Arg
         35                  40                  45

Arg His Leu Asp Asn Leu Val Glu Glu Asn Leu Ala Glu Ala Ala Asn
     50                  55                  60

Pro Arg Gln Asn Pro Tyr Glu Pro Lys Met Arg Gly Arg Pro Ala Lys
 65                  70                  75                  80

Thr Tyr Arg Leu Thr Asp Lys Gly Arg Ser Ile Phe Gly His Glu Tyr
                 85                  90                  95

Asp Ser Leu Ala Ala Ala Ala Leu Ala Thr Leu Arg Glu Val Gly Gly
            100                 105                 110

Asp Asp Ala Val Arg Gln Phe Ala Arg Lys Arg Ile Glu Thr Ile Val
        115                 120                 125

Glu Gly Ile Thr Pro Ala Asp Val Thr Asp Gln Ser Ile Glu Asp Thr
    130                 135                 140

Ala Lys Ser Leu Val Glu Ala Phe Ser Arg His Gly Tyr Ala Ala Thr
145                 150                 155                 160

Val Asp Ala Thr Arg Asn Gly Leu Gln Leu Cys Gln His His Cys Pro
                165                 170                 175

Ile Ser Thr Val Ala Thr Glu Phe Pro Glu Leu Cys Glu Ala Glu His
            180                 185                 190

Gln Ala Val Ser Glu Leu Leu Gly Gln His Thr Gln Pro Leu Ala Thr
        195                 200                 205
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Ile Ala Asp Gly His Gly Ile Cys Thr Thr Asn Ile Ala Leu Thr Pro
    210                 215                 220

Ile Lys His Ser
225


<210> 1203
<211> 807
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(784)
<223> FRXA02520

<400> 1203
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gtctaaaggt gaaagctaaa tcaagcagga ggtgacacca gtg gga gat gtt gta   115
                                            Val Gly Asp Val Val
                                              1               5

aaa ggc aac gac gcg cac acc gga gac ggt gat acg cgc cga aaa att   163
Lys Gly Asn Asp Ala His Thr Gly Asp Gly Asp Thr Arg Arg Lys Ile
                10                  15                  20

ctt ctc atc ctg ttg gaa cgt gca ccg gtg atc gct tca gat att gct   211
Leu Leu Ile Leu Leu Glu Arg Ala Pro Val Ile Ala Ser Asp Ile Ala
            25                  30                  35

gaa cag ctt cag ctt tca act gtg gga gtg cgc agg cac cta gac aac   259
Glu Gln Leu Gln Leu Ser Thr Val Gly Val Arg Arg His Leu Asp Asn
        40                  45                  50

ttg gtt gaa gaa aat ctg gcg gag gcg gca aat ccg cgc cag aac cca   307
Leu Val Glu Glu Asn Leu Ala Glu Ala Ala Asn Pro Arg Gln Asn Pro
    55                  60                  65

tat gag ccc aaa atg cgc ggt agg cca gca aaa act tat cgg ctt act   355
Tyr Glu Pro Lys Met Arg Gly Arg Pro Ala Lys Thr Tyr Arg Leu Thr
70                  75                  80                  85

gat aaa ggt cgc tca atc ttc ggc cac gaa tat gat tcc ctt gct gcg   403
Asp Lys Gly Arg Ser Ile Phe Gly His Glu Tyr Asp Ser Leu Ala Ala
                90                  95                  100

gca gct cta gcc act ctt cga gag gtc ggc gga gat gat gca gta agg   451
Ala Ala Leu Ala Thr Leu Arg Glu Val Gly Gly Asp Asp Ala Val Arg
            105                 110                 115

caa ttt gct aga aag cgg atc gaa aca att gtt gag ggt att acc cca   499
Gln Phe Ala Arg Lys Arg Ile Glu Thr Ile Val Glu Gly Ile Thr Pro
        120                 125                 130

gca gat gtc aca gat caa tca atc gaa gat aca gcc aaa tct tta gtt   547
Ala Asp Val Thr Asp Gln Ser Ile Glu Asp Thr Ala Lys Ser Leu Val
    135                 140                 145
```

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gaa gct ttt agt cgg cat ggt tat gca gca act gtc gat gcc act cga   595
Glu Ala Phe Ser Arg His Gly Tyr Ala Ala Thr Val Asp Ala Thr Arg
150                 155                 160                 165

aac ggg ttg caa ctc tgc cag cat cac tgt cca ata tct aca gtc gcc   643
Asn Gly Leu Gln Leu Cys Gln His His Cys Pro Ile Ser Thr Val Ala
                170                 175                 180

acg gaa ttt ccg gaa ctg tgt gag gca gag cat caa gca gtc tca gaa   691
Thr Glu Phe Pro Glu Leu Cys Glu Ala Glu His Gln Ala Val Ser Glu
            185                 190                 195

ctt ttg ggg cag cac acg caa cca ttg gca aca atc gcg gac ggc cac   739
Leu Leu Gly Gln His Thr Gln Pro Leu Ala Thr Ile Ala Asp Gly His
        200                 205                 210

ggc atc tgc aca aca aat att gca ttg aca ccc atc aaa cac tcc       784
Gly Ile Cys Thr Thr Asn Ile Ala Leu Thr Pro Ile Lys His Ser
    215                 220                 225

tgatgaaagg agcggatcat gac                                        807
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<210> 1204
<211> 228
<212> PRT
<213> Corynebacterium glutamicum

<400> 1204

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Val Gly Asp Val Val Lys Gly Asn Asp Ala His Thr Gly Asp Gly Asp
  1               5                  10                  15

Thr Arg Arg Lys Ile Leu Leu Ile Leu Leu Glu Arg Ala Pro Val Ile
             20                  25                  30

Ala Ser Asp Ile Ala Glu Gln Leu Gln Leu Ser Thr Val Gly Val Arg
         35                  40                  45

Arg His Leu Asp Asn Leu Val Glu Glu Asn Leu Ala Glu Ala Ala Asn
     50                  55                  60

Pro Arg Gln Asn Pro Tyr Glu Pro Lys Met Arg Gly Arg Pro Ala Lys
 65                  70                  75                  80

Thr Tyr Arg Leu Thr Asp Lys Gly Arg Ser Ile Phe Gly His Glu Tyr
                 85                  90                  95

Asp Ser Leu Ala Ala Ala Ala Leu Ala Thr Leu Arg Glu Val Gly Gly
            100                 105                 110

Asp Asp Ala Val Arg Gln Phe Ala Arg Lys Arg Ile Glu Thr Ile Val
        115                 120                 125

Glu Gly Ile Thr Pro Ala Asp Val Thr Asp Gln Ser Ile Glu Asp Thr
    130                 135                 140

Ala Lys Ser Leu Val Glu Ala Phe Ser Arg His Gly Tyr Ala Ala Thr
145                 150                 155                 160

Val Asp Ala Thr Arg Asn Gly Leu Gln Leu Cys Gln His His Cys Pro
                165                 170                 175
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```
Ile Ser Thr Val Ala Thr Glu Phe Pro Glu Leu Cys Glu Ala Glu His
            180                 185                 190

Gln Ala Val Ser Glu Leu Leu Gly Gln His Thr Gln Pro Leu Ala Thr
        195                 200                 205

Ile Ala Asp Gly His Gly Ile Cys Thr Thr Asn Ile Ala Leu Thr Pro
    210                 215                 220

Ile Lys His Ser
225
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<210> 1205
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> RXN02534

<400> 1205

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ttaccagtaa tctatgcaga tttactgtcc gttggggatc cgcgcctatc ggaagttgcc 60

tacattataa aaactcagat tcaggaatac acagaccatg atg aat tca ccg aac   115
                                          Met Asn Ser Pro Asn
                                            1               5

gcg gac att att tta gta gtt aac aag ctg tcc aag ttt att gat atc   163
Ala Asp Ile Ile Leu Val Val Asn Lys Leu Ser Lys Phe Ile Asp Ile
                10                  15                  20

gaa aat att atg ctc gtt gga gca cga tgt aga gac att cac cag caa   211
Glu Asn Ile Met Leu Val Gly Ala Arg Cys Arg Asp Ile His Gln Gln
            25                  30                  35

aaa tat cgc gat caa aca gcg ggt aga aga act aag gat gtt gac ttc   259
Lys Tyr Arg Asp Gln Thr Ala Gly Arg Arg Thr Lys Asp Val Asp Phe
        40                  45                  50

gct tta gct tta gaa agc tgg gac gac ttc aat cta tta aag caa caa   307
Ala Leu Ala Leu Glu Ser Trp Asp Asp Phe Asn Leu Leu Lys Gln Gln
    55                  60                  65

ttc tca ccg act ggt aac gca tgg caa gga atc acc att gga aat att   355
Phe Ser Pro Thr Gly Asn Ala Trp Gln Gly Ile Thr Ile Gly Asn Ile
70                  75                  80                  85

cca gta gat ctc gtg cca ttc gga aat att gaa aac cca ccc ggt gaa   403
Pro Val Asp Leu Val Pro Phe Gly Asn Ile Glu Asn Pro Pro Gly Glu
                90                  95                  100

gtc ttg tcc aga aaa ggt cat cta ctt aat gtc gct ggg ttc aag gaa   451
Val Leu Ser Arg Lys Gly His Leu Leu Asn Val Ala Gly Phe Lys Glu
            105                 110                 115

gta ttc gag caa gct gag cta tat ccc cta aat gat gcg ata gac att   499
Val Phe Glu Gln Ala Glu Leu Tyr Pro Leu Asn Asp Ala Ile Asp Ile
```

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        120                 125                 130

aag ttg tct aca gtt ccc gga ctt act gcg cta aag cta cat gca tgg   547
Lys Leu Ser Thr Val Pro Gly Leu Thr Ala Leu Lys Leu His Ala Trp
    135                 140                 145

ctc gac cgt aaa gaa aat aac atc aaa gat gca agc gat cta gca tta   595
Leu Asp Arg Lys Glu Asn Asn Ile Lys Asp Ala Ser Asp Leu Ala Leu
150                 155                 160                 165

atc ttg tcg tgg tac gaa gag gat gta gaa act tta tgg aat cgc tat   643
Ile Leu Ser Trp Tyr Glu Glu Asp Val Glu Thr Leu Trp Asn Arg Tyr
                170                 175                 180

ttt gcc ctg gaa aat caa gga tac ata ggt gaa cca gag gca atg gca   691
Phe Ala Leu Glu Asn Gln Gly Tyr Ile Gly Glu Pro Glu Ala Met Ala
            185                 190                 195

gct gaa tta cta gga ctt gac act gga aga ata ctc ggc cac aag gaa   739
Ala Glu Leu Leu Gly Leu Asp Thr Gly Arg Ile Leu Gly His Lys Glu
        200                 205                 210

act caa gcc ctc ctt gat cga ttt aat gaa cag tct cct cct gag cta   787
Thr Gln Ala Leu Leu Asp Arg Phe Asn Glu Gln Ser Pro Pro Glu Leu
    215                 220                 225

aac caa ttt gct gaa tca ctt gaa gcc cct cct gaa cac agt cac cca   835
Asn Gln Phe Ala Glu Ser Leu Glu Ala Pro Pro Glu His Ser His Pro
230                 235                 240                 245

tta gaa cgg cgt cgt atc cag gtc gag gca ctg tta ggt gga ctt aga   883
Leu Glu Arg Arg Arg Ile Gln Val Glu Ala Leu Leu Gly Gly Leu Arg
                250                 255                 260

gat tcc ctc ggt tac gat gaa tagcttccaa tcccgcattg ttc            927
Asp Ser Leu Gly Tyr Asp Glu
            265
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<210> 1206
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 1206

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Met Asn Ser Pro Asn Ala Asp Ile Ile Leu Val Val Asn Lys Leu Ser
  1               5                  10                  15

Lys Phe Ile Asp Ile Glu Asn Ile Met Leu Val Gly Ala Arg Cys Arg
             20                  25                  30

Asp Ile His Gln Gln Lys Tyr Arg Asp Gln Thr Ala Gly Arg Arg Thr
         35                  40                  45

Lys Asp Val Asp Phe Ala Leu Ala Leu Glu Ser Trp Asp Asp Phe Asn
     50                  55                  60

Leu Leu Lys Gln Gln Phe Ser Pro Thr Gly Asn Ala Trp Gln Gly Ile
 65                  70                  75                  80

Thr Ile Gly Asn Ile Pro Val Asp Leu Val Pro Phe Gly Asn Ile Glu
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                85                  90                  95

Asn Pro Pro Gly Glu Val Leu Ser Arg Lys Gly His Leu Leu Asn Val
            100                 105                 110

Ala Gly Phe Lys Glu Val Phe Glu Gln Ala Glu Leu Tyr Pro Leu Asn
        115                 120                 125

Asp Ala Ile Asp Ile Lys Leu Ser Thr Val Pro Gly Leu Thr Ala Leu
    130                 135                 140

Lys Leu His Ala Trp Leu Asp Arg Lys Glu Asn Asn Ile Lys Asp Ala
145                 150                 155                 160

Ser Asp Leu Ala Leu Ile Leu Ser Trp Tyr Glu Glu Asp Val Glu Thr
                165                 170                 175

Leu Trp Asn Arg Tyr Phe Ala Leu Glu Asn Gln Gly Tyr Ile Gly Glu
            180                 185                 190

Pro Glu Ala Met Ala Ala Glu Leu Leu Gly Leu Asp Thr Gly Arg Ile
        195                 200                 205

Leu Gly His Lys Glu Thr Gln Ala Leu Leu Asp Arg Phe Asn Glu Gln
    210                 215                 220

Ser Pro Pro Glu Leu Asn Gln Phe Ala Glu Ser Leu Glu Ala Pro Pro
225                 230                 235                 240

Glu His Ser His Pro Leu Glu Arg Arg Arg Ile Gln Val Glu Ala Leu
                245                 250                 255

Leu Gly Gly Leu Arg Asp Ser Leu Gly Tyr Asp Glu
            260                 265
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20050250 20050250 20050250 20050250

<210> 1207
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> FRXA02534

<400> 1207

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ttaccagtaa tctatgcaga tttactgtcc gttggggatc cgcgcctatc ggaagttgcc 60

tacattataa aaactcagat tcaggaatac acagaccatg atg aat tca ccg aac   115
                                           Met Asn Ser Pro Asn
                                             1               5

gcg gac att att tta gta gtt aac aag ctg tcc aag ttt att gat atc   163
Ala Asp Ile Ile Leu Val Val Asn Lys Leu Ser Lys Phe Ile Asp Ile
                 10                  15                  20

gaa aat att atg ctc gtt gga gca cga tgt aga gac att cac cag caa   211
Glu Asn Ile Met Leu Val Gly Ala Arg Cys Arg Asp Ile His Gln Gln
             25                  30                  35
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```
aaa tat cgc gat caa aca gcg ggt aga aga act aag gat gtt gac ttc   259
Lys Tyr Arg Asp Gln Thr Ala Gly Arg Arg Thr Lys Asp Val Asp Phe
          40                  45                  50

gct tta gct tta gaa agc tgg gac gac ttc aat cta tta aag caa caa   307
Ala Leu Ala Leu Glu Ser Trp Asp Asp Phe Asn Leu Leu Lys Gln Gln
     55                  60                  65

ttc tca ccg act ggt aac gca tgg caa gga atc acc att gga aat att   355
Phe Ser Pro Thr Gly Asn Ala Trp Gln Gly Ile Thr Ile Gly Asn Ile
 70                  75                  80                  85

cca gta gat ctc gtg cca ttc gga aat att gaa aac cca ccc ggt gaa   403
Pro Val Asp Leu Val Pro Phe Gly Asn Ile Glu Asn Pro Pro Gly Glu
                 90                  95                 100

gtc ttg tcc aga aaa ggt cat cta ctt aat gtc gct ggg ttc aag gaa   451
Val Leu Ser Arg Lys Gly His Leu Leu Asn Val Ala Gly Phe Lys Glu
            105                 110                 115

gta ttc gag caa gct gag cta tat ccc cta aat gat gcg ata gac att   499
Val Phe Glu Gln Ala Glu Leu Tyr Pro Leu Asn Asp Ala Ile Asp Ile
        120                 125                 130

aag ttg tct aca gtt ccc gga ctt act gcg cta aag cta cat gca tgg   547
Lys Leu Ser Thr Val Pro Gly Leu Thr Ala Leu Lys Leu His Ala Trp
    135                 140                 145

ctc gac cgt aaa gaa aat aac atc aaa gat gca agc gat cta gca tta   595
Leu Asp Arg Lys Glu Asn Asn Ile Lys Asp Ala Ser Asp Leu Ala Leu
150                 155                 160                 165

atc ttg tcg tgg tac gaa gag gat gta gaa act tta tgg aat cgc tat   643
Ile Leu Ser Trp Tyr Glu Glu Asp Val Glu Thr Leu Trp Asn Arg Tyr
                170                 175                 180

ttt gcc ctg gaa aat caa gga tac ata ggt gaa cca gag gca atg gca   691
Phe Ala Leu Glu Asn Gln Gly Tyr Ile Gly Glu Pro Glu Ala Met Ala
            185                 190                 195

gct gaa tta cta gga ctt gac act gga aga ata ctc ggc cac aag gaa   739
Ala Glu Leu Leu Gly Leu Asp Thr Gly Arg Ile Leu Gly His Lys Glu
        200                 205                 210

act caa gcc ctc ctt gat cga ttt aat gaa cag tct cct cct gag cta   787
Thr Gln Ala Leu Leu Asp Arg Phe Asn Glu Gln Ser Pro Pro Glu Leu
    215                 220                 225

aac caa ttt gct gaa tca ctt gaa gcc cct cct gaa cac agt cac cca   835
Asn Gln Phe Ala Glu Ser Leu Glu Ala Pro Pro Glu His Ser His Pro
230                 235                 240                 245

tta gaa cgg cgt cgt atc cag gtc gag gca ctg tta ggt gga ctt aga   883
Leu Glu Arg Arg Arg Ile Gln Val Glu Ala Leu Leu Gly Gly Leu Arg
                250                 255                 260

gat tcc ctc ggt tac gat gaa tagcttccaa tcccgcattg ttc            927
Asp Ser Leu Gly Tyr Asp Glu
            265
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<210> 1208
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 1208

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Met Asn Ser Pro Asn Ala Asp Ile Ile Leu Val Val Asn Lys Leu Ser
  1               5                  10                  15

Lys Phe Ile Asp Ile Glu Asn Ile Met Leu Val Gly Ala Arg Cys Arg
             20                  25                  30

Asp Ile His Gln Gln Lys Tyr Arg Asp Gln Thr Ala Gly Arg Arg Thr
         35                  40                  45

Lys Asp Val Asp Phe Ala Leu Ala Leu Glu Ser Trp Asp Asp Phe Asn
     50                  55                  60

Leu Leu Lys Gln Gln Phe Ser Pro Thr Gly Asn Ala Trp Gln Gly Ile
 65                  70                  75                  80

Thr Ile Gly Asn Ile Pro Val Asp Leu Val Pro Phe Gly Asn Ile Glu
                 85                  90                  95

Asn Pro Pro Gly Glu Val Leu Ser Arg Lys Gly His Leu Leu Asn Val
            100                 105                 110

Ala Gly Phe Lys Glu Val Phe Glu Gln Ala Glu Leu Tyr Pro Leu Asn
        115                 120                 125

Asp Ala Ile Asp Ile Lys Leu Ser Thr Val Pro Gly Leu Thr Ala Leu
    130                 135                 140

Lys Leu His Ala Trp Leu Asp Arg Lys Glu Asn Asn Ile Lys Asp Ala
145                 150                 155                 160

Ser Asp Leu Ala Leu Ile Leu Ser Trp Tyr Glu Glu Asp Val Glu Thr
                165                 170                 175

Leu Trp Asn Arg Tyr Phe Ala Leu Glu Asn Gln Gly Tyr Ile Gly Glu
            180                 185                 190

Pro Glu Ala Met Ala Ala Glu Leu Leu Gly Leu Asp Thr Gly Arg Ile
        195                 200                 205

Leu Gly His Lys Glu Thr Gln Ala Leu Leu Asp Arg Phe Asn Glu Gln
    210                 215                 220

Ser Pro Pro Glu Leu Asn Gln Phe Ala Glu Ser Leu Glu Ala Pro Pro
225                 230                 235                 240

Glu His Ser His Pro Leu Glu Arg Arg Arg Ile Gln Val Glu Ala Leu
                245                 250                 255

Leu Gly Gly Leu Arg Asp Ser Leu Gly Tyr Asp Glu
            260                 265
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<210> 1209
<211> 585
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> RXN02537

<400> 1209
acctccatct caacaatcat ctttccgata tgcgcactgt cagcgagcag atgctcaaca 60

tagacgtcga tcttggccac acactgaata agttgcactg atg ctc gcc ctc aaa 115
Met Leu Ala Leu Lys
1 5

agt tca gaa tta gaa ggc ata gcc aca tca ctc acc gcc gtg gcg ggt 163
Ser Ser Glu Leu Glu Gly Ile Ala Thr Ser Leu Thr Ala Val Ala Gly
10 15 20

gcg ctc cac gaa tca aac act gac cgg ttg cag tcc tgg cag cag ctc 211
Ala Leu His Glu Ser Asn Thr Asp Arg Leu Gln Ser Trp Gln Gln Leu
25 30 35

gaa acg atg acc tct gcc agc tcc ctt atc cag ggc ttt atc aag ctt 259
Glu Thr Met Thr Ser Ala Ser Ser Leu Ile Gln Gly Phe Ile Lys Leu
40 45 50

gtc gat tac aac cga ccc aca gtg aat atc gtg gaa caa atg cac aaa 307
Val Asp Tyr Asn Arg Pro Thr Val Asn Ile Val Glu Gln Met His Lys
55 60 65

acc gca tcc acg ctt ttc aac acc gct gat ttc cta cgc act ttg gaa 355
Thr Ala Ser Thr Leu Phe Asn Thr Ala Asp Phe Leu Arg Thr Leu Glu
70 75 80 85

ggc tat gtt gat gta ctg gaa aaa caa gcc gat aaa tct ata acg ctc 403
Gly Tyr Val Asp Val Leu Glu Lys Gln Ala Asp Lys Ser Ile Thr Leu
90 95 100

acc gtc atg ctt cga tat att gcc agc ttg agt agc ctt tta gac ctc 451
Thr Val Met Leu Arg Tyr Ile Ala Ser Leu Ser Ser Leu Leu Asp Leu
105 110 115

atg tgt gca cgc gag atc aac gcg ttg tgc aca gcg att act cca gaa 499
Met Cys Ala Arg Glu Ile Asn Ala Leu Cys Thr Ala Ile Thr Pro Glu
120 125 130

cca ttg aag cat ctg ggc gat ttt ggc act cta ccg cct cag caa tcc 547
Pro Leu Lys His Leu Gly Asp Phe Gly Thr Leu Pro Pro Gln Gln Ser
135 140 145

acg agt ttc att tgg tgaatgcccc accagaaatc cgt 585
Thr Ser Phe Ile Trp
150

<210> 1210
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 1210

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Met Leu Ala Leu Lys Ser Ser Glu Leu Glu Gly Ile Ala Thr Ser Leu
  1               5                  10                  15

Thr Ala Val Ala Gly Ala Leu His Glu Ser Asn Thr Asp Arg Leu Gln
             20                  25                  30

Ser Trp Gln Gln Leu Glu Thr Met Thr Ser Ala Ser Ser Leu Ile Gln
         35                  40                  45

Gly Phe Ile Lys Leu Val Asp Tyr Asn Arg Pro Thr Val Asn Ile Val
     50                  55                  60

Glu Gln Met His Lys Thr Ala Ser Thr Leu Phe Asn Thr Ala Asp Phe
 65                  70                  75                  80

Leu Arg Thr Leu Glu Gly Tyr Val Asp Val Leu Glu Lys Gln Ala Asp
                 85                  90                  95

Lys Ser Ile Thr Leu Thr Val Met Leu Arg Tyr Ile Ala Ser Leu Ser
            100                 105                 110

Ser Leu Leu Asp Leu Met Cys Ala Arg Glu Ile Asn Ala Leu Cys Thr
        115                 120                 125

Ala Ile Thr Pro Glu Pro Leu Lys His Leu Gly Asp Phe Gly Thr Leu
    130                 135                 140

Pro Pro Gln Gln Ser Thr Ser Phe Ile Trp
145                 150
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CONFIDENTIAL

<210> 1211
<211> 585
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> FRXA02537

<400> 1211
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tagacgtcga tcttggccac acactgaata agttgcactg atg ctc gcc ctc aaa 115
                                              Met Leu Ala Leu Lys
                                                1   5

agt tca gaa tta gaa ggc ata gcc aca tca ctc acc gcc gtg gcg ggt 163
Ser Ser Glu Leu Glu Gly Ile Ala Thr Ser Leu Thr Ala Val Ala Gly
            10   15   20

gcg ctc cac gaa tca aac act gac cgg ttg cag tcc tgg cag cag ctc 211
Ala Leu His Glu Ser Asn Thr Asp Arg Leu Gln Ser Trp Gln Gln Leu
        25   30   35

gaa acg atg acc tct gcc agc tcc ctt atc cag ggc ttt atc aag ctt 259
Glu Thr Met Thr Ser Ala Ser Ser Leu Ile Gln Gly Phe Ile Lys Leu
    40   45   50

gtc gat tac aac cga ccc aca gtg aat atc gtg gaa caa atg cac aaa 307
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Val Asp Tyr Asn Arg Pro Thr Val Asn Ile Val Glu Gln Met His Lys
     55                  60                  65

acc gca tcc acg ctt ttc aac acc gct gat ttc cta cgc act ttg gaa   355
Thr Ala Ser Thr Leu Phe Asn Thr Ala Asp Phe Leu Arg Thr Leu Glu
 70                  75                  80                  85

ggc tat gtt gat gta ctg gaa aaa caa gcc gat aaa tct ata acg ctc   403
Gly Tyr Val Asp Val Leu Glu Lys Gln Ala Asp Lys Ser Ile Thr Leu
                 90                  95                 100

acc gtc atg ctt cga tat att gcc agc ttg agt agc ctt tta gac ctc   451
Thr Val Met Leu Arg Tyr Ile Ala Ser Leu Ser Ser Leu Leu Asp Leu
            105                 110                 115

atg tgt gca cgc gag atc aac gcg ttg tgc aca gcg att act cca gaa   499
Met Cys Ala Arg Glu Ile Asn Ala Leu Cys Thr Ala Ile Thr Pro Glu
        120                 125                 130

cca ttg aag cat ctg ggc gat ttt ggc act cta ccg cct cag caa tcc   547
Pro Leu Lys His Leu Gly Asp Phe Gly Thr Leu Pro Pro Gln Gln Ser
    135                 140                 145

acg agt ttc att tgg tgaatgcccc accagaaatc cgt                     585
Thr Ser Phe Ile Trp
150
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09/05/2005 09:55:49

<210> 1212
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 1212

```
Met Leu Ala Leu Lys Ser Ser Glu Leu Glu Gly Ile Ala Thr Ser Leu
  1               5                  10                  15

Thr Ala Val Ala Gly Ala Leu His Glu Ser Asn Thr Asp Arg Leu Gln
             20                  25                  30

Ser Trp Gln Gln Leu Glu Thr Met Thr Ser Ala Ser Ser Leu Ile Gln
         35                  40                  45

Gly Phe Ile Lys Leu Val Asp Tyr Asn Arg Pro Thr Val Asn Ile Val
     50                  55                  60

Glu Gln Met His Lys Thr Ala Ser Thr Leu Phe Asn Thr Ala Asp Phe
 65                  70                  75                  80

Leu Arg Thr Leu Glu Gly Tyr Val Asp Val Leu Glu Lys Gln Ala Asp
                 85                  90                  95

Lys Ser Ile Thr Leu Thr Val Met Leu Arg Tyr Ile Ala Ser Leu Ser
            100                 105                 110

Ser Leu Leu Asp Leu Met Cys Ala Arg Glu Ile Asn Ala Leu Cys Thr
        115                 120                 125

Ala Ile Thr Pro Glu Pro Leu Lys His Leu Gly Asp Phe Gly Thr Leu
    130                 135                 140
```

```
Pro Pro Gln Gln Ser Thr Ser Phe Ile Trp
145                 150


<210> 1213
<211> 795
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(772)
<223> RXN02538

<400> 1213
gcgagatcaa cgcgttgtgc acagcgatta ctccagaacc attgaagcat ctgggcgatt 60

ttggcactct accgcctcag caatccacga gtttcatttg gtg aat gcc cca cca   115
                                            Val Asn Ala Pro Pro
                                              1               5

gaa atc cgt gcc tta gcc gaa gcc cat ccc gat atg cag atc cta gaa   163
Glu Ile Arg Ala Leu Ala Glu Ala His Pro Asp Met Gln Ile Leu Glu
                  10                  15                  20

gcc ggc gat ggt tca ttg gta gca tcg ttt ggg gat att gat agg gct   211
Ala Gly Asp Gly Ser Leu Val Ala Ser Phe Gly Asp Ile Asp Arg Ala
              25                  30                  35

acg acc gtg acc acc atc gtg gca ggt gtg ggt tcc tcc aac cca gaa   259
Thr Thr Val Thr Thr Ile Val Ala Gly Val Gly Ser Ser Asn Pro Glu
          40                  45                  50

ggg tgg aat aca tat gtt gac cgt gcc cgc aca gta tct gct tcc acc   307
Gly Trp Asn Thr Tyr Val Asp Arg Ala Arg Thr Val Ser Ala Ser Thr
      55                  60                  65

ggt tcc gca acg gtg ttg tgg ctg gga tat caa gca ccc gct tcg att   355
Gly Ser Ala Thr Val Leu Trp Leu Gly Tyr Gln Ala Pro Ala Ser Ile
  70                  75                  80                  85

cct gct gcg gta tcc ggc gcg gca gcg aat cgc gct gcc gcg gat ctc   403
Pro Ala Ala Val Ser Gly Ala Ala Ala Asn Arg Ala Ala Ala Asp Leu
                  90                  95                 100

cag agg ttt caa gcg gca cta cag tcc cgc aat ccc cac caa aga aaa   451
Gln Arg Phe Gln Ala Ala Leu Gln Ser Arg Asn Pro His Gln Arg Lys
              105                 110                 115

gta gtg atg ggc tac agc tac ggt tcc aca gtg gtg gga aaa gct gcg   499
Val Val Met Gly Tyr Ser Tyr Gly Ser Thr Val Val Gly Lys Ala Ala
          120                 125                 130

tct tcc ggc gag ctc agt gcc gat gcg ttg gta ttg gtt ggc agt ccc   547
Ser Ser Gly Glu Leu Ser Ala Asp Ala Leu Val Leu Val Gly Ser Pro
      135                 140                 145

ggc gcg ggt gtc tcg cac tct tcc cag ctt ggc gca cct gtg tat gcg   595
Gly Ala Gly Val Ser His Ser Ser Gln Leu Gly Ala Pro Val Tyr Ala
150                 155                 160                 165
```

```
gta aca ggg tct gct gat ccc atc ggt ttt gcc ggc acc caa tat gac   643
Val Thr Gly Ser Ala Asp Pro Ile Gly Phe Ala Gly Thr Gln Tyr Asp
                170                 175                 180

ggc atc cac ggc act gat ccc acc gct gcc cta ttc ggt gca aca gtg   691
Gly Ile His Gly Thr Asp Pro Thr Ala Ala Leu Phe Gly Ala Thr Val
            185                 190                 195

tgg gat tcg ccc tca acg cat tcc ggt tat tgg aat gac cag gag ttc   739
Trp Asp Ser Pro Ser Thr His Ser Gly Tyr Trp Asn Asp Gln Glu Phe
        200                 205                 210

ctg ggc aat gtg gcg gag gtg gtt cgc ggc aaa tagaaaagcc gccgcacact 792
Leu Gly Asn Val Ala Glu Val Val Arg Gly Lys
    215                 220

gga                                                               795
```

<210> 1214
<211> 224
<212> PRT
<213> Corynebacterium glutamicum

<400> 1214

```
Val Asn Ala Pro Pro Glu Ile Arg Ala Leu Ala Glu Ala His Pro Asp
  1               5                  10                  15

Met Gln Ile Leu Glu Ala Gly Asp Gly Ser Leu Val Ala Ser Phe Gly
             20                  25                  30

Asp Ile Asp Arg Ala Thr Thr Val Thr Thr Ile Val Ala Gly Val Gly
         35                  40                  45

Ser Ser Asn Pro Glu Gly Trp Asn Thr Tyr Val Asp Arg Ala Arg Thr
     50                  55                  60

Val Ser Ala Ser Thr Gly Ser Ala Thr Val Leu Trp Leu Gly Tyr Gln
 65                  70                  75                  80

Ala Pro Ala Ser Ile Pro Ala Ala Val Ser Gly Ala Ala Ala Asn Arg
                 85                  90                  95

Ala Ala Ala Asp Leu Gln Arg Phe Gln Ala Ala Leu Gln Ser Arg Asn
            100                 105                 110

Pro His Gln Arg Lys Val Val Met Gly Tyr Ser Tyr Gly Ser Thr Val
        115                 120                 125

Val Gly Lys Ala Ala Ser Ser Gly Glu Leu Ser Ala Asp Ala Leu Val
    130                 135                 140

Leu Val Gly Ser Pro Gly Ala Gly Val Ser His Ser Ser Gln Leu Gly
145                 150                 155                 160

Ala Pro Val Tyr Ala Val Thr Gly Ser Ala Asp Pro Ile Gly Phe Ala
                165                 170                 175

Gly Thr Gln Tyr Asp Gly Ile His Gly Thr Asp Pro Thr Ala Ala Leu
            180                 185                 190
```

```
Phe Gly Ala Thr Val Trp Asp Ser Pro Ser Thr His Ser Gly Tyr Trp
        195                 200                 205

Asn Asp Gln Glu Phe Leu Gly Asn Val Ala Glu Val Val Arg Gly Lys
    210                 215                 220
```

<210> 1215
<211> 795
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(772)
<223> FRXA02538

<400> 1215

```
gcgagatcaa cgcgttgtgc acagcgatta ctccagaacc attgaagcat ctgggcgatt 60

ttggcactct accgcctcag caatccacga gtttcatttg gtg aat gcc cca cca   115
                                            Val Asn Ala Pro Pro
                                              1               5

gaa atc cgt gcc tta gcc gaa gcc cat ccc gat atg cag atc cta gaa   163
Glu Ile Arg Ala Leu Ala Glu Ala His Pro Asp Met Gln Ile Leu Glu
                 10                  15                  20

gcc ggc gat ggt tca ttg gta gca tcg ttt ggg gat att gat agg gct   211
Ala Gly Asp Gly Ser Leu Val Ala Ser Phe Gly Asp Ile Asp Arg Ala
             25                  30                  35

acg acc gtg acc acc atc gtg gca ggt gtg ggt tcc tcc aac cca gaa   259
Thr Thr Val Thr Thr Ile Val Ala Gly Val Gly Ser Ser Asn Pro Glu
         40                  45                  50

ggg tgg aat aca tat gtt gac cgt gcc cgc aca gta tct gct tcc acc   307
Gly Trp Asn Thr Tyr Val Asp Arg Ala Arg Thr Val Ser Ala Ser Thr
     55                  60                  65

ggt tcc gca acg gtg ttg tgg ctg gga tat caa gca ccc gct tcg att   355
Gly Ser Ala Thr Val Leu Trp Leu Gly Tyr Gln Ala Pro Ala Ser Ile
 70                  75                  80                  85

cct gct gcg gta tcc ggc gcg gca gcg aat cgc gct gcc gcg gat ctc   403
Pro Ala Ala Val Ser Gly Ala Ala Ala Asn Arg Ala Ala Ala Asp Leu
                 90                  95                 100

cag agg ttt caa gcg gca cta cag tcc cgc aat ccc cac caa aga aaa   451
Gln Arg Phe Gln Ala Ala Leu Gln Ser Arg Asn Pro His Gln Arg Lys
            105                 110                 115

gta gtg atg ggc tac agc tac ggt tcc aca gtg gtg gga aaa gct gcg   499
Val Val Met Gly Tyr Ser Tyr Gly Ser Thr Val Val Gly Lys Ala Ala
        120                 125                 130

tct tcc ggc gag ctc agt gcc gat gcg ttg gta ttg gtt ggc agt ccc   547
Ser Ser Gly Glu Leu Ser Ala Asp Ala Leu Val Leu Val Gly Ser Pro
```

```
    135                 140                 145

ggc gcg ggt gtc tcg cac tct tcc cag ctt ggc gca cct gtg tat gcg   595
Gly Ala Gly Val Ser His Ser Ser Gln Leu Gly Ala Pro Val Tyr Ala
150                 155                 160                 165

gta aca ggg tct gct gat ccc atc ggt ttt gcc ggc acc caa tat gac   643
Val Thr Gly Ser Ala Asp Pro Ile Gly Phe Ala Gly Thr Gln Tyr Asp
                170                 175                 180

ggc atc cac ggc act gat ccc acc gct gcc cta ttc ggt gca aca gtg   691
Gly Ile His Gly Thr Asp Pro Thr Ala Ala Leu Phe Gly Ala Thr Val
            185                 190                 195

tgg gat tcg ccc tca acg cat tcc ggt tat tgg aat gac cag gag ttc   739
Trp Asp Ser Pro Ser Thr His Ser Gly Tyr Trp Asn Asp Gln Glu Phe
        200                 205                 210

ctg ggc aat gtg gcg gag gtg gtt cgc ggc aaa tagaaaagcc gccgcacact 792
Leu Gly Asn Val Ala Glu Val Val Arg Gly Lys
    215                 220

gga                                                               795
```

US20070298030A1

<210> 1216
<211> 224
<212> PRT
<213> Corynebacterium glutamicum

<400> 1216

```
Val Asn Ala Pro Pro Glu Ile Arg Ala Leu Ala Glu Ala His Pro Asp
  1               5                  10                  15

Met Gln Ile Leu Glu Ala Gly Asp Gly Ser Leu Val Ala Ser Phe Gly
             20                  25                  30

Asp Ile Asp Arg Ala Thr Thr Val Thr Thr Ile Val Ala Gly Val Gly
         35                  40                  45

Ser Ser Asn Pro Glu Gly Trp Asn Thr Tyr Val Asp Arg Ala Arg Thr
     50                  55                  60

Val Ser Ala Ser Thr Gly Ser Ala Thr Val Leu Trp Leu Gly Tyr Gln
 65                  70                  75                  80

Ala Pro Ala Ser Ile Pro Ala Ala Val Ser Gly Ala Ala Ala Asn Arg
                 85                  90                  95

Ala Ala Ala Asp Leu Gln Arg Phe Gln Ala Ala Leu Gln Ser Arg Asn
            100                 105                 110

Pro His Gln Arg Lys Val Val Met Gly Tyr Ser Tyr Gly Ser Thr Val
        115                 120                 125

Val Gly Lys Ala Ala Ser Ser Gly Glu Leu Ser Ala Asp Ala Leu Val
    130                 135                 140

Leu Val Gly Ser Pro Gly Ala Gly Val Ser His Ser Ser Gln Leu Gly
145                 150                 155                 160
```

```
Ala Pro Val Tyr Ala Val Thr Gly Ser Ala Asp Pro Ile Gly Phe Ala
               165                 170                 175

Gly Thr Gln Tyr Asp Gly Ile His Gly Thr Asp Pro Thr Ala Ala Leu
            180                 185                 190

Phe Gly Ala Thr Val Trp Asp Ser Pro Ser Thr His Ser Gly Tyr Trp
        195                 200                 205

Asn Asp Gln Glu Phe Leu Gly Asn Val Ala Glu Val Val Arg Gly Lys
    210                 215                 220
```

<210> 1217
<211> 726
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> RXN02555

<400> 1217

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gttttatcgc tatttaatac aggcctaccc ccactacccc cattcagttc agggaatccc 60

cggatttaaa acaattaaaa accctctaga atgagacatt atg ggc gaa caa ttt   115
                                          Met Gly Glu Gln Phe
                                            1               5

cca ggc gat aaa aac atc cga gtc agc gac acc gaa aga tca gca gca   163
Pro Gly Asp Lys Asn Ile Arg Val Ser Asp Thr Glu Arg Ser Ala Ala
                10                  15                  20

cta gca gca ctc ggc cag ttc tac gca gaa ggt cgc ctc tcc cta gaa   211
Leu Ala Ala Leu Gly Gln Phe Tyr Ala Glu Gly Arg Leu Ser Leu Glu
            25                  30                  35

gaa acc gac gac cgc tgc gaa gcc gtc gcc gac gcc aaa acc cgc ggc   259
Glu Thr Asp Asp Arg Cys Glu Ala Val Ala Asp Ala Lys Thr Arg Gly
        40                  45                  50

gac ctc aac gcc atc ttc tac gat ctg ccc aac caa caa atc gca gtc   307
Asp Leu Asn Ala Ile Phe Tyr Asp Leu Pro Asn Gln Gln Ile Ala Val
    55                  60                  65

gtc gac cgc tcc gaa caa acc tac aca gcc acc gaa gtt gcc gaa ctc   355
Val Asp Arg Ser Glu Gln Thr Tyr Thr Ala Thr Glu Val Ala Glu Leu
70                  75                  80                  85

cac cgc aaa ggc gca cgc cca cgc gcc gga atc ctc gga ctc acc aca   403
His Arg Lys Gly Ala Arg Pro Arg Ala Gly Ile Leu Gly Leu Thr Thr
                90                  95                  100

gtt tta gcc atc acc ggt acc gct gct ttc gcc agc acc aca gct ttt   451
Val Leu Ala Ile Thr Gly Thr Ala Ala Phe Ala Ser Thr Thr Ala Phe
            105                 110                 115
```

```
gca aca gta ctt tta gcc ctg att ccg atc gtg ttc atc atg ctg tac   499
Ala Thr Val Leu Leu Ala Leu Ile Pro Ile Val Phe Ile Met Leu Tyr
        120                 125                 130

gtg atg aaa att ggt cct gaa tcc tgg cac gca cca aca cct cgc caa   547
Val Met Lys Ile Gly Pro Glu Ser Trp His Ala Pro Thr Pro Arg Gln
    135                 140                 145

ctt cag cga aag cgc atg atc gaa ctg cgt gaa aag gaa aaa ctc cgc   595
Leu Gln Arg Lys Arg Met Ile Glu Leu Arg Glu Lys Glu Lys Leu Arg
150                 155                 160                 165

gac atg gag ctc aaa gcc cag cgc aag gaa cgc acc cac gca tta acc   643
Asp Met Glu Leu Lys Ala Gln Arg Lys Glu Arg Thr His Ala Leu Thr
                170                 175                 180

aac cgc gcg ttg gat gct gct gaa act gct ttc aac acc aag ccc tgg   691
Asn Arg Ala Leu Asp Ala Ala Glu Thr Ala Phe Asn Thr Lys Pro Trp
            185                 190                 195

aag aag aac aaa tagggctttt gaagtgtgtc gcg                        726
Lys Lys Asn Lys
        200
```

<210> 1218
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 1218

```
Met Gly Glu Gln Phe Pro Gly Asp Lys Asn Ile Arg Val Ser Asp Thr
  1               5                  10                  15

Glu Arg Ser Ala Ala Leu Ala Ala Leu Gly Gln Phe Tyr Ala Glu Gly
             20                  25                  30

Arg Leu Ser Leu Glu Glu Thr Asp Asp Arg Cys Glu Ala Val Ala Asp
         35                  40                  45

Ala Lys Thr Arg Gly Asp Leu Asn Ala Ile Phe Tyr Asp Leu Pro Asn
     50                  55                  60

Gln Gln Ile Ala Val Val Asp Arg Ser Glu Gln Thr Tyr Thr Ala Thr
 65                  70                  75                  80

Glu Val Ala Glu Leu His Arg Lys Gly Ala Arg Pro Arg Ala Gly Ile
                 85                  90                  95

Leu Gly Leu Thr Thr Val Leu Ala Ile Thr Gly Thr Ala Ala Phe Ala
            100                 105                 110

Ser Thr Thr Ala Phe Ala Thr Val Leu Leu Ala Leu Ile Pro Ile Val
        115                 120                 125

Phe Ile Met Leu Tyr Val Met Lys Ile Gly Pro Glu Ser Trp His Ala
    130                 135                 140

Pro Thr Pro Arg Gln Leu Gln Arg Lys Arg Met Ile Glu Leu Arg Glu
145                 150                 155                 160
```

```
Lys Glu Lys Leu Arg Asp Met Glu Leu Lys Ala Gln Arg Lys Glu Arg
                165                 170                 175

Thr His Ala Leu Thr Asn Arg Ala Leu Asp Ala Ala Glu Thr Ala Phe
            180                 185                 190

Asn Thr Lys Pro Trp Lys Lys Asn Lys
        195                 200
```

<210> 1219
<211> 726
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> FRXA02555

<400> 1219

```
gttttatcgc tatttaatac aggcctaccc ccactacccc cattcagttc agggaatccc 60

cggatttaaa acaattaaaa accctctaga atgagacatt atg ggc gaa caa ttt   115
                                            Met Gly Glu Gln Phe
                                              1               5

cca ggc gat aaa aac atc cga gtc agc gac acc gaa aga tca gca gca   163
Pro Gly Asp Lys Asn Ile Arg Val Ser Asp Thr Glu Arg Ser Ala Ala
                10                  15                  20

cta gca gca ctc ggc cag ttc tac gca gaa ggt cgc ctc tcc cta gaa   211
Leu Ala Ala Leu Gly Gln Phe Tyr Ala Glu Gly Arg Leu Ser Leu Glu
            25                  30                  35

gaa acc gac gac cgc tgc gaa gcc gtc gcc gac gcc aaa acc cgc ggc   259
Glu Thr Asp Asp Arg Cys Glu Ala Val Ala Asp Ala Lys Thr Arg Gly
        40                  45                  50

gac ctc aac gcc atc ttc tac gat ctg ccc aac caa caa atc gca gtc   307
Asp Leu Asn Ala Ile Phe Tyr Asp Leu Pro Asn Gln Gln Ile Ala Val
    55                  60                  65

gtc gac cgc tcc gaa caa acc tac aca gcc acc gaa gtt gcc gaa ctc   355
Val Asp Arg Ser Glu Gln Thr Tyr Thr Ala Thr Glu Val Ala Glu Leu
70                  75                  80                  85

cac cgc aaa ggc gca cgc cca cgc gcc gga atc ctc gga ctc acc aca   403
His Arg Lys Gly Ala Arg Pro Arg Ala Gly Ile Leu Gly Leu Thr Thr
                90                  95                  100

gtt tta gcc atc acc ggt acc gct gct ttc gcc agc acc aca gct ttt   451
Val Leu Ala Ile Thr Gly Thr Ala Ala Phe Ala Ser Thr Thr Ala Phe
            105                 110                 115

gca aca gta ctt tta gcc ctg att ccg atc gtg ttc atc atg ctg tac   499
Ala Thr Val Leu Leu Ala Leu Ile Pro Ile Val Phe Ile Met Leu Tyr
        120                 125                 130

gtg atg aaa att ggt cct gaa tcc tgg cac gca cca aca cct cgc caa   547
Val Met Lys Ile Gly Pro Glu Ser Trp His Ala Pro Thr Pro Arg Gln
```

```
    135                 140                 145

ctt cag cga aag cgc atg atc gaa ctg cgt gaa aag gaa aaa ctc cgc   595
Leu Gln Arg Lys Arg Met Ile Glu Leu Arg Glu Lys Glu Lys Leu Arg
150                 155                 160                 165

gac atg gag ctc aaa gcc cag cgc aag gaa cgc acc cac gca tta acc   643
Asp Met Glu Leu Lys Ala Gln Arg Lys Glu Arg Thr His Ala Leu Thr
                170                 175                 180

aac cgc gcg ttg gat gct gct gaa act gct ttc aac acc aag ccc tgg   691
Asn Arg Ala Leu Asp Ala Ala Glu Thr Ala Phe Asn Thr Lys Pro Trp
            185                 190                 195

aag aag aac aaa tagggctttt gaagtgtgtc gcg                        726
Lys Lys Asn Lys
        200
```

<210> 1220
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 1220

```
Met Gly Glu Gln Phe Pro Gly Asp Lys Asn Ile Arg Val Ser Asp Thr
  1               5                  10                  15

Glu Arg Ser Ala Ala Leu Ala Ala Leu Gly Gln Phe Tyr Ala Glu Gly
             20                  25                  30

Arg Leu Ser Leu Glu Glu Thr Asp Asp Arg Cys Glu Ala Val Ala Asp
         35                  40                  45

Ala Lys Thr Arg Gly Asp Leu Asn Ala Ile Phe Tyr Asp Leu Pro Asn
     50                  55                  60

Gln Gln Ile Ala Val Val Asp Arg Ser Glu Gln Thr Tyr Thr Ala Thr
 65                  70                  75                  80

Glu Val Ala Glu Leu His Arg Lys Gly Ala Arg Pro Arg Ala Gly Ile
                 85                  90                  95

Leu Gly Leu Thr Thr Val Leu Ala Ile Thr Gly Thr Ala Ala Phe Ala
            100                 105                 110

Ser Thr Thr Ala Phe Ala Thr Val Leu Leu Ala Leu Ile Pro Ile Val
        115                 120                 125

Phe Ile Met Leu Tyr Val Met Lys Ile Gly Pro Glu Ser Trp His Ala
    130                 135                 140

Pro Thr Pro Arg Gln Leu Gln Arg Lys Arg Met Ile Glu Leu Arg Glu
145                 150                 155                 160

Lys Glu Lys Leu Arg Asp Met Glu Leu Lys Ala Gln Arg Lys Glu Arg
                165                 170                 175

Thr His Ala Leu Thr Asn Arg Ala Leu Asp Ala Ala Glu Thr Ala Phe
            180                 185                 190
```

```
Asn Thr Lys Pro Trp Lys Lys Asn Lys
        195                 200


<210> 1221
<211> 1125
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1102)
<223> RXN02564

<400> 1221
acaccacagt gaagcggtga cgtgaatcac ccaagcactt aggcatcaaa cattcaagag 60

cttgttgtcc aaaagtccga ccgagaggga ttcccccaaa atg gcc gaa gta gga   115
                                            Met Ala Glu Val Gly
                                              1               5

gca gaa ccc gca ggg tct gca caa tcc aaa act aaa caa ttt gtt gta   163
Ala Glu Pro Ala Gly Ser Ala Gln Ser Lys Thr Lys Gln Phe Val Val
                 10                  15                  20

ggt acc gca gcg gtg gtc atc act gca atc gct gcg ttt ttc tcc atc   211
Gly Thr Ala Ala Val Val Ile Thr Ala Ile Ala Ala Phe Phe Ser Ile
             25                  30                  35

cag tct gca tcc ggt ggc gag gat att cgt tcc aac atg acg ctg att   259
Gln Ser Ala Ser Gly Gly Glu Asp Ile Arg Ser Asn Met Thr Leu Ile
         40                  45                  50

gct cct gca gct gca ggt gga ggt tgg gat act ttc caa cgt gag cag   307
Ala Pro Ala Ala Ala Gly Gly Gly Trp Asp Thr Phe Gln Arg Glu Gln
     55                  60                  65

cag cag tct atg cgc gtg aat aag atc gtg aac aat att cag gtg gtc   355
Gln Gln Ser Met Arg Val Asn Lys Ile Val Asn Asn Ile Gln Val Val
 70                  75                  80                  85

aac atc cct gga gct ggt gga acc att gca ctt ggc aaa ctg tct acc   403
Asn Ile Pro Gly Ala Gly Gly Thr Ile Ala Leu Gly Lys Leu Ser Thr
                 90                  95                 100

atg act gca ccg aac acc ttg atg gtg ggt gga acg ggg cat atc gca   451
Met Thr Ala Pro Asn Thr Leu Met Val Gly Gly Thr Gly His Ile Ala
             105                 110                 115

gca caa att caa ttc gat acc cct gcg aaa atc cag gat gtc acc cca   499
Ala Gln Ile Gln Phe Asp Thr Pro Ala Lys Ile Gln Asp Val Thr Pro
         120                 125                 130

att gct cgt gtg gtg gaa gag ttc gac atc atc acc gtg cca gcg gat   547
Ile Ala Arg Val Val Glu Glu Phe Asp Ile Ile Thr Val Pro Ala Asp
     135                 140                 145

tct cca tac aac acc ctt gaa gag ctc att gaa ggt tgg aag gca gat   595
Ser Pro Tyr Asn Thr Leu Glu Glu Leu Ile Glu Gly Trp Lys Ala Asp
150                 155                 160                 165
```

```
cca gca gga gtg tcc tgg acc ggt ggt ggt tcc ttt gac cag ctt gtt   643
Pro Ala Gly Val Ser Trp Thr Gly Gly Gly Ser Phe Asp Gln Leu Val
                170                 175                 180

atg aca gaa att gca ctg tct gca ggt ata gat cct aag caa acc acc   691
Met Thr Glu Ile Ala Leu Ser Ala Gly Ile Asp Pro Lys Gln Thr Thr
            185                 190                 195

ttt att cct tct gat ggt ggt ggc gaa gcg att cag gcg cta ctg aac   739
Phe Ile Pro Ser Asp Gly Gly Gly Glu Ala Ile Gln Ala Leu Leu Asn
        200                 205                 210

gga acc gca aag gca tca act ggt ggt ttt gct gat atg tat ccg cag   787
Gly Thr Ala Lys Ala Ser Thr Gly Gly Phe Ala Asp Met Tyr Pro Gln
    215                 220                 225

gta gaa gcc ggt cga ttg aag gtt ttg gga att gct gca gaa gaa cgc   835
Val Glu Ala Gly Arg Leu Lys Val Leu Gly Ile Ala Ala Glu Glu Arg
230                 235                 240                 245

ctt cca ggt tct gac att cca acg cta gtg gaa caa ggc tat gac gtg   883
Leu Pro Gly Ser Asp Ile Pro Thr Leu Val Glu Gln Gly Tyr Asp Val
                250                 255                 260

acc ttg acc aac tgg cgt gcc atg ttc gct cct cct ggt ttg agc gat   931
Thr Leu Thr Asn Trp Arg Ala Met Phe Ala Pro Pro Gly Leu Ser Asp
            265                 270                 275

gat caa att gcg gaa ctt cga gca atc gtt gcg gag tct gtg gag act   979
Asp Gln Ile Ala Glu Leu Arg Ala Ile Val Ala Glu Ser Val Glu Thr
        280                 285                 290

gct gaa tgg cag tcc gcg gtg gaa cga aac tac tgg atg aac gcc tca   1027
Ala Glu Trp Gln Ser Ala Val Glu Arg Asn Tyr Trp Met Asn Ala Ser
    295                 300                 305

ctt gaa ggc gaa gaa ctc gac cag ttt gtt gaa gat gaa att gac cga   1075
Leu Glu Gly Glu Glu Leu Asp Gln Phe Val Glu Asp Glu Ile Asp Arg
310                 315                 320                 325

att gat cag cta ttc aag gag atg ggc tagtgaacgt cactgaacaa        1122
Ile Asp Gln Leu Phe Lys Glu Met Gly
                330

tcc                                                              1125
```

<210> 1222
<211> 334
<212> PRT
<213> Corynebacterium glutamicum

<400> 1222

```
Met Ala Glu Val Gly Ala Glu Pro Ala Gly Ser Ala Gln Ser Lys Thr
  1               5                  10                  15

Lys Gln Phe Val Val Gly Thr Ala Ala Val Val Ile Thr Ala Ile Ala
             20                  25                  30

Ala Phe Phe Ser Ile Gln Ser Ala Ser Gly Gly Glu Asp Ile Arg Ser
         35                  40                  45
```

```
Asn Met Thr Leu Ile Ala Pro Ala Ala Ala Gly Gly Gly Trp Asp Thr
     50                  55                  60

Phe Gln Arg Glu Gln Gln Gln Ser Met Arg Val Asn Lys Ile Val Asn
 65                  70                  75                  80

Asn Ile Gln Val Val Asn Ile Pro Gly Ala Gly Gly Thr Ile Ala Leu
                 85                  90                  95

Gly Lys Leu Ser Thr Met Thr Ala Pro Asn Thr Leu Met Val Gly Gly
            100                 105                 110

Thr Gly His Ile Ala Ala Gln Ile Gln Phe Asp Thr Pro Ala Lys Ile
        115                 120                 125

Gln Asp Val Thr Pro Ile Ala Arg Val Val Glu Glu Phe Asp Ile Ile
    130                 135                 140

Thr Val Pro Ala Asp Ser Pro Tyr Asn Thr Leu Glu Glu Leu Ile Glu
145                 150                 155                 160

Gly Trp Lys Ala Asp Pro Ala Gly Val Ser Trp Thr Gly Gly Gly Ser
                165                 170                 175

Phe Asp Gln Leu Val Met Thr Glu Ile Ala Leu Ser Ala Gly Ile Asp
            180                 185                 190

Pro Lys Gln Thr Thr Phe Ile Pro Ser Asp Gly Gly Gly Glu Ala Ile
        195                 200                 205

Gln Ala Leu Leu Asn Gly Thr Ala Lys Ala Ser Thr Gly Gly Phe Ala
    210                 215                 220

Asp Met Tyr Pro Gln Val Glu Ala Gly Arg Leu Lys Val Leu Gly Ile
225                 230                 235                 240

Ala Ala Glu Glu Arg Leu Pro Gly Ser Asp Ile Pro Thr Leu Val Glu
                245                 250                 255

Gln Gly Tyr Asp Val Thr Leu Thr Asn Trp Arg Ala Met Phe Ala Pro
            260                 265                 270

Pro Gly Leu Ser Asp Asp Gln Ile Ala Glu Leu Arg Ala Ile Val Ala
        275                 280                 285

Glu Ser Val Glu Thr Ala Glu Trp Gln Ser Ala Val Glu Arg Asn Tyr
    290                 295                 300

Trp Met Asn Ala Ser Leu Glu Gly Glu Glu Leu Asp Gln Phe Val Glu
305                 310                 315                 320

Asp Glu Ile Asp Arg Ile Asp Gln Leu Phe Lys Glu Met Gly
                325                 330
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<210> 1223
<211> 775
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> FRXA02564

<400> 1223
acaccacagt gaagcggtga cgtgaatcac ccaagcactt aggcatcaaa cattcaagag 60

cttgttgtcc aaaagtccga ccgagaggga ttcccccaaa atg gcc gaa gta gga 115
Met Ala Glu Val Gly
1 5

gca gaa ccc gca ggg tct gca caa tcc aaa act aaa caa ttt gtt gta 163
Ala Glu Pro Ala Gly Ser Ala Gln Ser Lys Thr Lys Gln Phe Val Val
10 15 20

ggt acc gca gcg gtg gtc atc act gca atc gct gcg ttt ttc tcc atc 211
Gly Thr Ala Ala Val Val Ile Thr Ala Ile Ala Ala Phe Phe Ser Ile
25 30 35

cag tct gca tcc ggt ggc gag gat att cgt tcc aac atg acg ctg att 259
Gln Ser Ala Ser Gly Gly Glu Asp Ile Arg Ser Asn Met Thr Leu Ile
40 45 50

gct cct gca gct gca ggt gga ggt tgg gat act ttc caa cgt gag cag 307
Ala Pro Ala Ala Ala Gly Gly Gly Trp Asp Thr Phe Gln Arg Glu Gln
55 60 65

cag cag tct atg cgc gtg aat aag atc gtg aac aat att cag gtg gtc 355
Gln Gln Ser Met Arg Val Asn Lys Ile Val Asn Asn Ile Gln Val Val
70 75 80 85

aac atc cct gga gct ggt gga acc att gca ctt ggc aaa ctg tct acc 403
Asn Ile Pro Gly Ala Gly Gly Thr Ile Ala Leu Gly Lys Leu Ser Thr
90 95 100

atg act gca ccg aac acc ttg atg gtg ggt gga acg ggg cat atc gca 451
Met Thr Ala Pro Asn Thr Leu Met Val Gly Gly Thr Gly His Ile Ala
105 110 115

gca caa att caa ttc gat acc cct gcg aaa atc cag gat gtc acc cca 499
Ala Gln Ile Gln Phe Asp Thr Pro Ala Lys Ile Gln Asp Val Thr Pro
120 125 130

att gct cgt gtg gtg gaa gag ttc gac atc atc acc gtg cca gcg gat 547
Ile Ala Arg Val Val Glu Glu Phe Asp Ile Ile Thr Val Pro Ala Asp
135 140 145

tct cca tac aac acc ctt gaa gag ctc att gaa ggt tgg aag gca gat 595
Ser Pro Tyr Asn Thr Leu Glu Glu Leu Ile Glu Gly Trp Lys Ala Asp
150 155 160 165

cca gca gga gtg tcc tgg acc ggt ggt ggt tcc ttt gac cag ctt gtt 643
Pro Ala Gly Val Ser Trp Thr Gly Gly Gly Ser Phe Asp Gln Leu Val
170 175 180

atg aca gaa att gca ctg tct gca ggt ata gat cct aag caa acc acc 691
Met Thr Glu Ile Ala Leu Ser Ala Gly Ile Asp Pro Lys Gln Thr Thr
185 190 195

ttt att cct tct gat ggt ggt ggc gaa gcg att cag gcg cta ctg aac 739

```
Phe Ile Pro Ser Asp Gly Gly Gly Glu Ala Ile Gln Ala Leu Leu Asn
        200                 205                 210

gga acc gca aag gca tca act ggt ggt ttt gct gat                  775
Gly Thr Ala Lys Ala Ser Thr Gly Gly Phe Ala Asp
    215                 220                 225


<210> 1224
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 1224
Met Ala Glu Val Gly Ala Glu Pro Ala Gly Ser Ala Gln Ser Lys Thr
  1               5                  10                  15

Lys Gln Phe Val Val Gly Thr Ala Ala Val Val Ile Thr Ala Ile Ala
             20                  25                  30

Ala Phe Phe Ser Ile Gln Ser Ala Ser Gly Gly Glu Asp Ile Arg Ser
         35                  40                  45

Asn Met Thr Leu Ile Ala Pro Ala Ala Ala Gly Gly Gly Trp Asp Thr
     50                  55                  60

Phe Gln Arg Glu Gln Gln Gln Ser Met Arg Val Asn Lys Ile Val Asn
 65                  70                  75                  80

Asn Ile Gln Val Val Asn Ile Pro Gly Ala Gly Gly Thr Ile Ala Leu
                 85                  90                  95

Gly Lys Leu Ser Thr Met Thr Ala Pro Asn Thr Leu Met Val Gly Gly
            100                 105                 110

Thr Gly His Ile Ala Ala Gln Ile Gln Phe Asp Thr Pro Ala Lys Ile
        115                 120                 125

Gln Asp Val Thr Pro Ile Ala Arg Val Val Glu Glu Phe Asp Ile Ile
    130                 135                 140

Thr Val Pro Ala Asp Ser Pro Tyr Asn Thr Leu Glu Glu Leu Ile Glu
145                 150                 155                 160

Gly Trp Lys Ala Asp Pro Ala Gly Val Ser Trp Thr Gly Gly Gly Ser
                165                 170                 175

Phe Asp Gln Leu Val Met Thr Glu Ile Ala Leu Ser Ala Gly Ile Asp
            180                 185                 190

Pro Lys Gln Thr Thr Phe Ile Pro Ser Asp Gly Gly Gly Glu Ala Ile
        195                 200                 205

Gln Ala Leu Leu Asn Gly Thr Ala Lys Ala Ser Thr Gly Gly Phe Ala
    210                 215                 220

Asp
225


<210> 1225
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<211> 1753
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1753)
<223> RXN02568

<400> 1225

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ccagctacga tatggaattt caccaaatgc gaactaccct aaataccaaa gacagacagt 60

gacagcccct tcgagaatgc agcaagagac gacacctcct atg gac ggc acc tcg   115
                                            Met Asp Gly Thr Ser
                                              1               5

cca cag aac aaa att tcc acc act ccc cca gcg cca gga aat gct att   163
Pro Gln Asn Lys Ile Ser Thr Thr Pro Pro Ala Pro Gly Asn Ala Ile
                 10                  15                  20

cct gca cct gga ggc gcc att cct aca cca gcg aaa act gag cag gac   211
Pro Ala Pro Gly Gly Ala Ile Pro Thr Pro Ala Lys Thr Glu Gln Asp
             25                  30                  35

gca gta cct cca act gtg gcg gcg aaa cta ccc gta cct gga agt tct   259
Ala Val Pro Pro Thr Val Ala Ala Lys Leu Pro Val Pro Gly Ser Ser
         40                  45                  50

att cca gca ccc ggt aga gca ttg cca act cca gtg gct ccg gga ggt   307
Ile Pro Ala Pro Gly Arg Ala Leu Pro Thr Pro Val Ala Pro Gly Gly
     55                  60                  65

tcc gtc cca gct ccg aga gcg tcc gca cct gcg gtt cct aac gtt cct   355
Ser Val Pro Ala Pro Arg Ala Ser Ala Pro Ala Val Pro Asn Val Pro
 70                  75                  80                  85

gca gct ccc ggc gct gct gtt cca gct ccg gga atc tcg atc ccg gca   403
Ala Ala Pro Gly Ala Ala Val Pro Ala Pro Gly Ile Ser Ile Pro Ala
                 90                  95                 100

gca cct agt gcc cca ggc agt gca att cca aca cca ggc aca gca atc   451
Ala Pro Ser Ala Pro Gly Ser Ala Ile Pro Thr Pro Gly Thr Ala Ile
            105                 110                 115

cct gtg cct gga agt gca act cct gtc cca gca cct ggg gtt agt gca   499
Pro Val Pro Gly Ser Ala Thr Pro Val Pro Ala Pro Gly Val Ser Ala
        120                 125                 130

cct ggc gca agc gtt cca agc att cca gta cca gga tct gtc acc cca   547
Pro Gly Ala Ser Val Pro Ser Ile Pro Val Pro Gly Ser Val Thr Pro
    135                 140                 145

cct gca cca gga att tcc gca cct ggc ggt gca ctt ccg act cct ggc   595
Pro Ala Pro Gly Ile Ser Ala Pro Gly Gly Ala Leu Pro Thr Pro Gly
150                 155                 160                 165

agt gcg ccc cca aca cct ggc ggt gcc ctt ccg act cca ggt gag gca   643
Ser Ala Pro Pro Thr Pro Gly Gly Ala Leu Pro Thr Pro Gly Glu Ala
                170                 175                 180

ctt ccc gtt ccc gga gca cct ggt gca ccc gga gca tcc gga atc cca   691
```

```
Leu Pro Val Pro Gly Ala Pro Gly Ala Pro Gly Ala Ser Gly Ile Pro
            185                 190                 195

agt cct ggc ctt cca acc cca ggt gtc cca act ccc gga gct tcc tta   739
Ser Pro Gly Leu Pro Thr Pro Gly Val Pro Thr Pro Gly Ala Ser Leu
        200                 205                 210

cca gtc cca gga gca cca gac gca cct gga acc cca agc att ccc gca   787
Pro Val Pro Gly Ala Pro Asp Ala Pro Gly Thr Pro Ser Ile Pro Ala
    215                 220                 225

gct ccc ggc att caa gca cca gga att cca gca gca cca gga gcc cct   835
Ala Pro Gly Ile Gln Ala Pro Gly Ile Pro Ala Ala Pro Gly Ala Pro
230                 235                 240                 245

gcc caa gct gct gct cac gca aag cca gta ttc caa gat gca gag aaa   883
Ala Gln Ala Ala Ala His Ala Lys Pro Val Phe Gln Asp Ala Glu Lys
                250                 255                 260

cga cct cgc aca gat gaa gct gga aat gcg aag aag gaa ctg ccg ctg   931
Arg Pro Arg Thr Asp Glu Ala Gly Asn Ala Lys Lys Glu Leu Pro Leu
            265                 270                 275

aga gtt cgg ttg gcg cag cca att aca cgt aag cag tgg gca atg act   979
Arg Val Arg Leu Ala Gln Pro Ile Thr Arg Lys Gln Trp Ala Met Thr
        280                 285                 290

ctt ggt gtc ctg gtt ctc gga gca att gtc gtg gct gca atc gcg gtg   1027
Leu Gly Val Leu Val Leu Gly Ala Ile Val Val Ala Ala Ile Ala Val
    295                 300                 305

gtc ctt gcc aaa tgg gcg ttt acc acg gag tgg ttg cag gac ttc gtc   1075
Val Leu Ala Lys Trp Ala Phe Thr Thr Glu Trp Leu Gln Asp Phe Val
310                 315                 320                 325

gag aag tat ccg ggt aaa tat gac aac ccc gaa ggt gcg cca gta gga   1123
Glu Lys Tyr Pro Gly Lys Tyr Asp Asn Pro Glu Gly Ala Pro Val Gly
                330                 335                 340

att cca acg tgg ctg agt tgg cag cac ttc ttc aac atg ttc ttc atg   1171
Ile Pro Thr Trp Leu Ser Trp Gln His Phe Phe Asn Met Phe Phe Met
            345                 350                 355

gtg ttg att atc aag acg ggc att gag atc aat aga acc cgc agg cca   1219
Val Leu Ile Ile Lys Thr Gly Ile Glu Ile Asn Arg Thr Arg Arg Pro
        360                 365                 370

aag ggt tat tgg acg ccg aaa aag ggt ggc aag aag atc tcc ttg acg   1267
Lys Gly Tyr Trp Thr Pro Lys Lys Gly Gly Lys Lys Ile Ser Leu Thr
    375                 380                 385

ttg tgg atc cac ctg gtt ttg gat ttg ttg tgg atc atc aac ggt gcg   1315
Leu Trp Ile His Leu Val Leu Asp Leu Leu Trp Ile Ile Asn Gly Ala
390                 395                 400                 405

gtg ttc atc att ttg ttg ttc gcg acg ggt cag tgg atg cgc att gtt   1363
Val Phe Ile Ile Leu Leu Phe Ala Thr Gly Gln Trp Met Arg Ile Val
                410                 415                 420

cca acc agt tgg gat gtg ttc ccg aac gcg ctg agt gct ggt ttg cag   1411
Pro Thr Ser Trp Asp Val Phe Pro Asn Ala Leu Ser Ala Gly Leu Gln
```

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            425                 430                 435

tat gtg tcg ttg gat tgg ccg act gag aat ggt tgg gcg aat tac aac   1459
Tyr Val Ser Leu Asp Trp Pro Thr Glu Asn Gly Trp Ala Asn Tyr Asn
        440                 445                 450

agt ttg cag gag ctg acg tac ttc ttc act gtc ttt att gcg gca ccg   1507
Ser Leu Gln Glu Leu Thr Tyr Phe Phe Thr Val Phe Ile Ala Ala Pro
    455                 460                 465

ttg tcg att gtg tct ggt ttc cgg atg tcg agt tac tgg cct aag aac   1555
Leu Ser Ile Val Ser Gly Phe Arg Met Ser Ser Tyr Trp Pro Lys Asn
470                 475                 480                 485

aat gcg acg atg aat aag ttg atc ccc atc ggg ttt gct cgt gcg ctg   1603
Asn Ala Thr Met Asn Lys Leu Ile Pro Ile Gly Phe Ala Arg Ala Leu
                490                 495                 500

cac atg cca gtg atg gtg tat tac atc gtg ttc att tgt atc cac gtg   1651
His Met Pro Val Met Val Tyr Tyr Ile Val Phe Ile Cys Ile His Val
            505                 510                 515

ttc ttg gtg ttg gcg acc ggc gcg ttg cgc aat ttc aac cat atg tat   1699
Phe Leu Val Leu Ala Thr Gly Ala Leu Arg Asn Phe Asn His Met Tyr
        520                 525                 530

gca ggt caa gac gtt gtg aac tgg gtt ggt ttt ggt tgg ttc gtg gcg   1747
Ala Gly Gln Asp Val Val Asn Trp Val Gly Phe Gly Trp Phe Val Ala
    535                 540                 545

tcg ttg                                                           1753
Ser Leu
550
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<210> 1226
<211> 551
<212> PRT
<213> Corynebacterium glutamicum

<400> 1226

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Met Asp Gly Thr Ser Pro Gln Asn Lys Ile Ser Thr Thr Pro Pro Ala
  1               5                  10                  15

Pro Gly Asn Ala Ile Pro Ala Pro Gly Gly Ala Ile Pro Thr Pro Ala
             20                  25                  30

Lys Thr Glu Gln Asp Ala Val Pro Pro Thr Val Ala Ala Lys Leu Pro
         35                  40                  45

Val Pro Gly Ser Ser Ile Pro Ala Pro Gly Arg Ala Leu Pro Thr Pro
     50                  55                  60

Val Ala Pro Gly Gly Ser Val Pro Ala Pro Arg Ala Ser Ala Pro Ala
 65                  70                  75                  80

Val Pro Asn Val Pro Ala Ala Pro Gly Ala Ala Val Pro Ala Pro Gly
                 85                  90                  95

Ile Ser Ile Pro Ala Ala Pro Ser Ala Pro Gly Ser Ala Ile Pro Thr
            100                 105                 110
```

```
Pro Gly Thr Ala Ile Pro Val Pro Gly Ser Ala Thr Pro Val Pro Ala
        115                 120                 125

Pro Gly Val Ser Ala Pro Gly Ala Ser Val Pro Ser Ile Pro Val Pro
    130                 135                 140

Gly Ser Val Thr Pro Pro Ala Pro Gly Ile Ser Ala Pro Gly Gly Ala
145                 150                 155                 160

Leu Pro Thr Pro Gly Ser Ala Pro Pro Thr Pro Gly Gly Ala Leu Pro
                165                 170                 175

Thr Pro Gly Glu Ala Leu Pro Val Pro Gly Ala Pro Gly Ala Pro Gly
            180                 185                 190

Ala Ser Gly Ile Pro Ser Pro Gly Leu Pro Thr Pro Gly Val Pro Thr
        195                 200                 205

Pro Gly Ala Ser Leu Pro Val Pro Gly Ala Pro Asp Ala Pro Gly Thr
    210                 215                 220

Pro Ser Ile Pro Ala Ala Pro Gly Ile Gln Ala Pro Gly Ile Pro Ala
225                 230                 235                 240

Ala Pro Gly Ala Pro Ala Gln Ala Ala Ala His Ala Lys Pro Val Phe
                245                 250                 255

Gln Asp Ala Glu Lys Arg Pro Arg Thr Asp Glu Ala Gly Asn Ala Lys
            260                 265                 270

Lys Glu Leu Pro Leu Arg Val Arg Leu Ala Gln Pro Ile Thr Arg Lys
        275                 280                 285

Gln Trp Ala Met Thr Leu Gly Val Leu Val Leu Gly Ala Ile Val Val
    290                 295                 300

Ala Ala Ile Ala Val Val Leu Ala Lys Trp Ala Phe Thr Thr Glu Trp
305                 310                 315                 320

Leu Gln Asp Phe Val Glu Lys Tyr Pro Gly Lys Tyr Asp Asn Pro Glu
                325                 330                 335

Gly Ala Pro Val Gly Ile Pro Thr Trp Leu Ser Trp Gln His Phe Phe
            340                 345                 350

Asn Met Phe Phe Met Val Leu Ile Ile Lys Thr Gly Ile Glu Ile Asn
        355                 360                 365

Arg Thr Arg Arg Pro Lys Gly Tyr Trp Thr Pro Lys Lys Gly Gly Lys
    370                 375                 380

Lys Ile Ser Leu Thr Leu Trp Ile His Leu Val Leu Asp Leu Leu Trp
385                 390                 395                 400

Ile Ile Asn Gly Ala Val Phe Ile Ile Leu Leu Phe Ala Thr Gly Gln
                405                 410                 415

Trp Met Arg Ile Val Pro Thr Ser Trp Asp Val Phe Pro Asn Ala Leu
            420                 425                 430
```

```
Ser Ala Gly Leu Gln Tyr Val Ser Leu Asp Trp Pro Thr Glu Asn Gly
        435                 440                 445

Trp Ala Asn Tyr Asn Ser Leu Gln Glu Leu Thr Tyr Phe Phe Thr Val
    450                 455                 460

Phe Ile Ala Ala Pro Leu Ser Ile Val Ser Gly Phe Arg Met Ser Ser
465                 470                 475                 480

Tyr Trp Pro Lys Asn Asn Ala Thr Met Asn Lys Leu Ile Pro Ile Gly
                485                 490                 495

Phe Ala Arg Ala Leu His Met Pro Val Met Val Tyr Tyr Ile Val Phe
            500                 505                 510

Ile Cys Ile His Val Phe Leu Val Leu Ala Thr Gly Ala Leu Arg Asn
        515                 520                 525

Phe Asn His Met Tyr Ala Gly Gln Asp Val Val Asn Trp Val Gly Phe
    530                 535                 540

Gly Trp Phe Val Ala Ser Leu
545                 550
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5600,5600,5600,5600

<210> 1227
<211> 1359
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1359)
<223> FRXA02568

<400> 1227

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atc ccg gca gca cct agt gcc cca ggc agt gca att cca aca cca ggc   48
Ile Pro Ala Ala Pro Ser Ala Pro Gly Ser Ala Ile Pro Thr Pro Gly
  1               5                  10                  15

aca gca atc cct gtg cct gga agt gca act cct gtc cca gca cct ggg   96
Thr Ala Ile Pro Val Pro Gly Ser Ala Thr Pro Val Pro Ala Pro Gly
            20                  25                  30

gtt agt gca cct ggc gca agc gtt cca agc att cca gta cca gga tct  144
Val Ser Ala Pro Gly Ala Ser Val Pro Ser Ile Pro Val Pro Gly Ser
        35                  40                  45

gtc acc cca cct gca cca gga att tcc gca cct ggc ggt gca ctt ccg  192
Val Thr Pro Pro Ala Pro Gly Ile Ser Ala Pro Gly Gly Ala Leu Pro
    50                  55                  60

act cct ggc agt gcg ccc cca aca cct ggc ggt gcc ctt ccg act cca  240
Thr Pro Gly Ser Ala Pro Pro Thr Pro Gly Gly Ala Leu Pro Thr Pro
65                  70                  75                  80

ggt gag gca ctt ccc gtt ccc gga gca cct ggt gca ccc gga gca tcc  288
Gly Glu Ala Leu Pro Val Pro Gly Ala Pro Gly Ala Pro Gly Ala Ser
                85                  90                  95

gga atc cca agt cct ggc ctt cca acc cca ggt gtc cca act ccc gga  336
```

```
Gly Ile Pro Ser Pro Gly Leu Pro Thr Pro Gly Val Pro Thr Pro Gly
            100                 105                 110

gct tcc tta cca gtc cca gga gca cca gac gca cct gga acc cca agc   384
Ala Ser Leu Pro Val Pro Gly Ala Pro Asp Ala Pro Gly Thr Pro Ser
        115                 120                 125

att ccc gca gct ccc ggc att caa gca cca gga att cca gca gca cca   432
Ile Pro Ala Ala Pro Gly Ile Gln Ala Pro Gly Ile Pro Ala Ala Pro
    130                 135                 140

gga gcc cct gcc caa gct gct gct cac gca aag cca gta ttc caa gat   480
Gly Ala Pro Ala Gln Ala Ala Ala His Ala Lys Pro Val Phe Gln Asp
145                 150                 155                 160

gca gag aaa cga cct cgc aca gat gaa gct gga aat gcg aag aag gaa   528
Ala Glu Lys Arg Pro Arg Thr Asp Glu Ala Gly Asn Ala Lys Lys Glu
                165                 170                 175

ctg ccg ctg aga gtt cgg ttg gcg cag cca att aca cgt aag cag tgg   576
Leu Pro Leu Arg Val Arg Leu Ala Gln Pro Ile Thr Arg Lys Gln Trp
            180                 185                 190

gca atg act ctt ggt gtc ctg gtt ctc gga gca att gtc gtg gct gca   624
Ala Met Thr Leu Gly Val Leu Val Leu Gly Ala Ile Val Val Ala Ala
        195                 200                 205

atc gcg gtg gtc ctt gcc aaa tgg gcg ttt acc acg gag tgg ttg cag   672
Ile Ala Val Val Leu Ala Lys Trp Ala Phe Thr Thr Glu Trp Leu Gln
    210                 215                 220

gac ttc gtc gag aag tat ccg ggt aaa tat gac aac ccc gaa ggt gcg   720
Asp Phe Val Glu Lys Tyr Pro Gly Lys Tyr Asp Asn Pro Glu Gly Ala
225                 230                 235                 240

cca gta gga att cca acg tgg ctg agt tgg cag cac ttc ttc aac atg   768
Pro Val Gly Ile Pro Thr Trp Leu Ser Trp Gln His Phe Phe Asn Met
                245                 250                 255

ttc ttc atg gtg ttg att atc aag acg ggc att gag atc aat aga acc   816
Phe Phe Met Val Leu Ile Ile Lys Thr Gly Ile Glu Ile Asn Arg Thr
            260                 265                 270

cgc agg cca aag ggt tat tgg acg ccg aaa aag ggt ggc aag aag atc   864
Arg Arg Pro Lys Gly Tyr Trp Thr Pro Lys Lys Gly Gly Lys Lys Ile
        275                 280                 285

tcc ttg acg ttg tgg atc cac ctg gtt ttg gat ttg ttg tgg atc atc   912
Ser Leu Thr Leu Trp Ile His Leu Val Leu Asp Leu Leu Trp Ile Ile
    290                 295                 300

aac ggt gcg gtg ttc atc att ttg ttg ttc gcg acg ggt cag tgg atg   960
Asn Gly Ala Val Phe Ile Ile Leu Leu Phe Ala Thr Gly Gln Trp Met
305                 310                 315                 320

cgc att gtt cca acc agt tgg gat gtg ttc ccg aac gcg ctg agt gct  1008
Arg Ile Val Pro Thr Ser Trp Asp Val Phe Pro Asn Ala Leu Ser Ala
                325                 330                 335

ggt ttg cag tat gtg tcg ttg gat tgg ccg act gag aat ggt tgg gcg  1056
Gly Leu Gln Tyr Val Ser Leu Asp Trp Pro Thr Glu Asn Gly Trp Ala
```

```
            340                 345                 350

aat tac aac agt ttg cag gag ctg acg tac ttc ttc act gtc ttt att   1104
Asn Tyr Asn Ser Leu Gln Glu Leu Thr Tyr Phe Phe Thr Val Phe Ile
        355                 360                 365

gcg gca ccg ttg tcg att gtg tct ggt ttc cgg atg tcg agt tac tgg   1152
Ala Ala Pro Leu Ser Ile Val Ser Gly Phe Arg Met Ser Ser Tyr Trp
    370                 375                 380

cct aag aac aat gcg acg atg aat aag ttg atc ccc atc ggg ttt gct   1200
Pro Lys Asn Asn Ala Thr Met Asn Lys Leu Ile Pro Ile Gly Phe Ala
385                 390                 395                 400

cgt gcg ctg cac atg cca gtg atg gtg tat tac atc gtg ttc att tgt   1248
Arg Ala Leu His Met Pro Val Met Val Tyr Tyr Ile Val Phe Ile Cys
                405                 410                 415

atc cac gtg ttc ttg gtg ttg gcg acc ggc gcg ttg cgc aat ttc aac   1296
Ile His Val Phe Leu Val Leu Ala Thr Gly Ala Leu Arg Asn Phe Asn
            420                 425                 430

cat atg tat gca ggt caa gac gtt gtg aac tgg gtt ggt ttt ggt tgg   1344
His Met Tyr Ala Gly Gln Asp Val Val Asn Trp Val Gly Phe Gly Trp
        435                 440                 445

ttc gtg gcg tcg ttg                                             1359
Phe Val Ala Ser Leu
    450


<210> 1228
<211> 453
<212> PRT
<213> Corynebacterium glutamicum

<400> 1228
Ile Pro Ala Ala Pro Ser Ala Pro Gly Ser Ala Ile Pro Thr Pro Gly
  1               5                  10                  15

Thr Ala Ile Pro Val Pro Gly Ser Ala Thr Pro Val Pro Ala Pro Gly
             20                  25                  30

Val Ser Ala Pro Gly Ala Ser Val Pro Ser Ile Pro Val Pro Gly Ser
         35                  40                  45

Val Thr Pro Pro Ala Pro Gly Ile Ser Ala Pro Gly Gly Ala Leu Pro
     50                  55                  60

Thr Pro Gly Ser Ala Pro Pro Thr Pro Gly Gly Ala Leu Pro Thr Pro
 65                  70                  75                  80

Gly Glu Ala Leu Pro Val Pro Gly Ala Pro Gly Ala Pro Gly Ala Ser
                 85                  90                  95

Gly Ile Pro Ser Pro Gly Leu Pro Thr Pro Gly Val Pro Thr Pro Gly
            100                 105                 110

Ala Ser Leu Pro Val Pro Gly Ala Pro Asp Ala Pro Gly Thr Pro Ser
        115                 120                 125
```

```
Ile Pro Ala Ala Pro Gly Ile Gln Ala Pro Gly Ile Pro Ala Ala Pro
    130                 135                 140

Gly Ala Pro Ala Gln Ala Ala Ala His Ala Lys Pro Val Phe Gln Asp
145                 150                 155                 160

Ala Glu Lys Arg Pro Arg Thr Asp Glu Ala Gly Asn Ala Lys Lys Glu
                165                 170                 175

Leu Pro Leu Arg Val Arg Leu Ala Gln Pro Ile Thr Arg Lys Gln Trp
            180                 185                 190

Ala Met Thr Leu Gly Val Leu Val Leu Gly Ala Ile Val Val Ala Ala
        195                 200                 205

Ile Ala Val Val Leu Ala Lys Trp Ala Phe Thr Thr Glu Trp Leu Gln
    210                 215                 220

Asp Phe Val Glu Lys Tyr Pro Gly Lys Tyr Asp Asn Pro Glu Gly Ala
225                 230                 235                 240

Pro Val Gly Ile Pro Thr Trp Leu Ser Trp Gln His Phe Phe Asn Met
                245                 250                 255

Phe Phe Met Val Leu Ile Ile Lys Thr Gly Ile Glu Ile Asn Arg Thr
            260                 265                 270

Arg Arg Pro Lys Gly Tyr Trp Thr Pro Lys Lys Gly Gly Lys Lys Ile
        275                 280                 285

Ser Leu Thr Leu Trp Ile His Leu Val Leu Asp Leu Leu Trp Ile Ile
    290                 295                 300

Asn Gly Ala Val Phe Ile Ile Leu Leu Phe Ala Thr Gly Gln Trp Met
305                 310                 315                 320

Arg Ile Val Pro Thr Ser Trp Asp Val Phe Pro Asn Ala Leu Ser Ala
                325                 330                 335

Gly Leu Gln Tyr Val Ser Leu Asp Trp Pro Thr Glu Asn Gly Trp Ala
            340                 345                 350

Asn Tyr Asn Ser Leu Gln Glu Leu Thr Tyr Phe Phe Thr Val Phe Ile
        355                 360                 365

Ala Ala Pro Leu Ser Ile Val Ser Gly Phe Arg Met Ser Ser Tyr Trp
    370                 375                 380

Pro Lys Asn Asn Ala Thr Met Asn Lys Leu Ile Pro Ile Gly Phe Ala
385                 390                 395                 400

Arg Ala Leu His Met Pro Val Met Val Tyr Tyr Ile Val Phe Ile Cys
                405                 410                 415

Ile His Val Phe Leu Val Leu Ala Thr Gly Ala Leu Arg Asn Phe Asn
            420                 425                 430

His Met Tyr Ala Gly Gln Asp Val Val Asn Trp Val Gly Phe Gly Trp
        435                 440                 445

Phe Val Ala Ser Leu
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450

<210> 1229
<211> 720
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(697)
<223> RXN02593

<400> 1229
gcgttcactt ccgccacctt gaggatgagt ggtatcacgc cagcacaaca aaaggatctt 60

```
catagggtta ttcagtctag ctgcttttaa acaagccata atg gaa gcc atg gcc   115
                                           Met Glu Ala Met Ala
                                             1               5

aca acg atc acc gtt ttc tct ccc acc cac tcc ccc gca caa atc cgc   163
Thr Thr Ile Thr Val Phe Ser Pro Thr His Ser Pro Ala Gln Ile Arg
                 10                  15                  20

gaa acc atc ctc agc gcc gcg aaa gaa gac gac gtg gac ttc ctc gga   211
Glu Thr Ile Leu Ser Ala Ala Lys Glu Asp Asp Val Asp Phe Leu Gly
             25                  30                  35

gtc ccc ttt acc cac ccc aga aac gtc acc atc gaa gtc gac gac gaa   259
Val Pro Phe Thr His Pro Arg Asn Val Thr Ile Glu Val Asp Asp Glu
         40                  45                  50

ctg atc aac gac tgc tta ggc tgg ctc gac gac gtg gca ctc gcc tcc   307
Leu Ile Asn Asp Cys Leu Gly Trp Leu Asp Asp Val Ala Leu Ala Ser
     55                  60                  65

ggc ctg ggc atc caa tac aac gac gaa gtg ctc cgc tac ggc gac gaa   355
Gly Leu Gly Ile Gln Tyr Asn Asp Glu Val Leu Arg Tyr Gly Asp Glu
 70                  75                  80                  85

gac att tcc ttt acc gtc caa acc aaa aat gac gat gac gcc cgc atc   403
Asp Ile Ser Phe Thr Val Gln Thr Lys Asn Asp Asp Asp Ala Arg Ile
                 90                  95                 100

ggc gcc tcc cgc ctt gga ctc gag cac cag ttg aac gtc att gcc ggg   451
Gly Ala Ser Arg Leu Gly Leu Glu His Gln Leu Asn Val Ile Ala Gly
            105                 110                 115

ggc tct gga gat tcc ggg gat tcc ggg gat tat ttg aag att gca cac   499
Gly Ser Gly Asp Ser Gly Asp Ser Gly Asp Tyr Leu Lys Ile Ala His
        120                 125                 130

ttc gac cta gac aac ccc gcc gac gag tcc tcc tac atc ttc gcg cgc   547
Phe Asp Leu Asp Asn Pro Ala Asp Glu Ser Ser Tyr Ile Phe Ala Arg
    135                 140                 145

agc ctc gca gaa gta gac ggc tgg acc cta gaa ttc ggc gtc gca gga   595
Ser Leu Ala Glu Val Asp Gly Trp Thr Leu Glu Phe Gly Val Ala Gly
150                 155                 160                 165

gta aaa aac acc acc att gtt tcc tcc atc gac gat gcc atc acc acc   643
```

```
Val Lys Asn Thr Thr Ile Val Ser Ser Ile Asp Asp Ala Ile Thr Thr
                170                 175                 180

att ttg cga tgg atg aac ggc gaa gac atc cgc gac ctc aac tgg acc   691
Ile Leu Arg Trp Met Asn Gly Glu Asp Ile Arg Asp Leu Asn Trp Thr
            185                 190                 195

cgc gca taaatggcct catttccgga gct                                 720
Arg Ala
```

<210> 1230
<211> 199
<212> PRT
<213> Corynebacterium glutamicum

<400> 1230

```
Met Glu Ala Met Ala Thr Thr Ile Thr Val Phe Ser Pro Thr His Ser
  1               5                  10                  15

Pro Ala Gln Ile Arg Glu Thr Ile Leu Ser Ala Ala Lys Glu Asp Asp
             20                  25                  30

Val Asp Phe Leu Gly Val Pro Phe Thr His Pro Arg Asn Val Thr Ile
         35                  40                  45

Glu Val Asp Asp Glu Leu Ile Asn Asp Cys Leu Gly Trp Leu Asp Asp
     50                  55                  60

Val Ala Leu Ala Ser Gly Leu Gly Ile Gln Tyr Asn Asp Glu Val Leu
 65                  70                  75                  80

Arg Tyr Gly Asp Glu Asp Ile Ser Phe Thr Val Gln Thr Lys Asn Asp
                 85                  90                  95

Asp Asp Ala Arg Ile Gly Ala Ser Arg Leu Gly Leu Glu His Gln Leu
            100                 105                 110

Asn Val Ile Ala Gly Gly Ser Gly Asp Ser Gly Asp Ser Gly Asp Tyr
        115                 120                 125

Leu Lys Ile Ala His Phe Asp Leu Asp Asn Pro Ala Asp Glu Ser Ser
    130                 135                 140

Tyr Ile Phe Ala Arg Ser Leu Ala Glu Val Asp Gly Trp Thr Leu Glu
145                 150                 155                 160

Phe Gly Val Ala Gly Val Lys Asn Thr Thr Ile Val Ser Ser Ile Asp
                165                 170                 175

Asp Ala Ile Thr Thr Ile Leu Arg Trp Met Asn Gly Glu Asp Ile Arg
            180                 185                 190

Asp Leu Asn Trp Thr Arg Ala
        195
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<210> 1231
<211> 336
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> FRXA02593

<400> 1231
tgacgatgac gcccgcatcg gcgcctcccg ccttggactc tagcaccagt tgaacgtcat 60

tgccgggggc tctggagatt ccggggattc cggggattat ttg aag att gca cac 115
Leu Lys Ile Ala His
1 5

ttc gac cta gac aac ccc gcc gac gag tcc tcc tac atc ttc gcg cgc 163
Phe Asp Leu Asp Asn Pro Ala Asp Glu Ser Ser Tyr Ile Phe Ala Arg
10 15 20

agc ctc gca gaa gta gac ggc tgg acc cta gaa ttc ggc gtc gca gga 211
Ser Leu Ala Glu Val Asp Gly Trp Thr Leu Glu Phe Gly Val Ala Gly
25 30 35

gta aaa aac acc acc att gtt tcc tcc atc gac gat gcc atc acc acc 259
Val Lys Asn Thr Thr Ile Val Ser Ser Ile Asp Asp Ala Ile Thr Thr
40 45 50

att ttg cga tgg atg aac ggc gaa gac atc cgc gac ctc aac tgg acc 307
Ile Leu Arg Trp Met Asn Gly Glu Asp Ile Arg Asp Leu Asn Trp Thr
55 60 65

cgc gca taaatggcct catttccgga gct 336
Arg Ala
70

<210> 1232
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 1232
Leu Lys Ile Ala His Phe Asp Leu Asp Asn Pro Ala Asp Glu Ser Ser
1 5 10 15

Tyr Ile Phe Ala Arg Ser Leu Ala Glu Val Asp Gly Trp Thr Leu Glu
20 25 30

Phe Gly Val Ala Gly Val Lys Asn Thr Thr Ile Val Ser Ser Ile Asp
35 40 45

Asp Ala Ile Thr Thr Ile Leu Arg Trp Met Asn Gly Glu Asp Ile Arg
50 55 60

Asp Leu Asn Trp Thr Arg Ala
65 70

<210> 1233
<211> 447
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(424)
<223> FRXA02594

<400> 1233
gcgttcactt ccgccacctt gaggatgagt ggtatcacgc cagcacaaca aaaggatctt 60

catagggtta ttcagtctag ctgcttttaa acaagccata atg gaa gcc atg gcc 115
Met Glu Ala Met Ala
1 5

aca acg atc acc gtt ttc tct ccc acc cac tcc ccc gca caa atc cgc 163
Thr Thr Ile Thr Val Phe Ser Pro Thr His Ser Pro Ala Gln Ile Arg
10 15 20

gaa acc atc ctc agc gcc gcg aaa gaa gac gac gtg gac ttc ctc gga 211
Glu Thr Ile Leu Ser Ala Ala Lys Glu Asp Asp Val Asp Phe Leu Gly
25 30 35

gtc ccc ttt acc cac ccc aga aac gtc acc atc gaa gtc gac gac gaa 259
Val Pro Phe Thr His Pro Arg Asn Val Thr Ile Glu Val Asp Asp Glu
40 45 50

ctg atc aac gac tgc tta ggc tgg ctc gac gac gtg gca ctc gcc tcc 307
Leu Ile Asn Asp Cys Leu Gly Trp Leu Asp Asp Val Ala Leu Ala Ser
55 60 65

ggc ctg ggc atc caa tac aac gac gaa gtg ctc cgc tac ggc gac gaa 355
Gly Leu Gly Ile Gln Tyr Asn Asp Glu Val Leu Arg Tyr Gly Asp Glu
70 75 80 85

gac att tcc ttt acc gtc caa acc aaa aat gac gat gac gcc cgc atc 403
Asp Ile Ser Phe Thr Val Gln Thr Lys Asn Asp Asp Asp Ala Arg Ile
90 95 100

ggc gcc tcc cgc ctt gga ctc tagcaccagt tgaacgtcat tgc 447
Gly Ala Ser Arg Leu Gly Leu
105

<210> 1234
<211> 108
<212> PRT
<213> Corynebacterium glutamicum

<400> 1234
Met Glu Ala Met Ala Thr Thr Ile Thr Val Phe Ser Pro Thr His Ser
1 5 10 15

Pro Ala Gln Ile Arg Glu Thr Ile Leu Ser Ala Ala Lys Glu Asp Asp
20 25 30

Val Asp Phe Leu Gly Val Pro Phe Thr His Pro Arg Asn Val Thr Ile
35 40 45

Glu Val Asp Asp Glu Leu Ile Asn Asp Cys Leu Gly Trp Leu Asp Asp
50 55 60

Val Ala Leu Ala Ser Gly Leu Gly Ile Gln Tyr Asn Asp Glu Val Leu

```
 65                  70                  75                  80

Arg Tyr Gly Asp Glu Asp Ile Ser Phe Thr Val Gln Thr Lys Asn Asp
                 85                  90                  95

Asp Asp Ala Arg Ile Gly Ala Ser Arg Leu Gly Leu
            100                 105


<210> 1235
<211> 1494
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1471)
<223> RXN02606

<400> 1235
agggcgcgga tcacttcgga tctgtggata acttttaagg cccttgtttt ccccttgaag 60

cttcggttgt gtggaaaaca gaaaaggagg ggaaaacaaa atg caa gaa atc cac   115
                                              Met Gln Glu Ile His
                                                1               5

acc atc atg aaa cac atg gac gcg ctc atc gcc gac ccg tcc gcc gcc   163
Thr Ile Met Lys His Met Asp Ala Leu Ile Ala Asp Pro Ser Ala Ala
                10                  15                  20

gca ttc aaa gca aca ctc ccc ttc gcc gaa ctc ctc gaa aag ctc cac   211
Ala Phe Lys Ala Thr Leu Pro Phe Ala Glu Leu Leu Glu Lys Leu His
            25                  30                  35

aac aaa aaa gcg ctt ttc gac gcc gcc ctc gcc aaa tcc gcc gag cgc   259
Asn Lys Lys Ala Leu Phe Asp Ala Ala Leu Ala Lys Ser Ala Glu Arg
        40                  45                  50

gcc gat gcc gga cgc atc atc gga aaa acc tcc cac atc gat gcc ctc   307
Ala Asp Ala Gly Arg Ile Ile Gly Lys Thr Ser His Ile Asp Ala Leu
    55                  60                  65

gcg tac ctt ctc gac atc tcc aaa tcc gaa gca ttc cga cgc aca aaa   355
Ala Tyr Leu Leu Asp Ile Ser Lys Ser Glu Ala Phe Arg Arg Thr Lys
70                  75                  80                  85

cgc gcc gaa gaa cac tac ggc aac cca agc ccg gaa ccc agt tca gaa   403
Arg Ala Glu Glu His Tyr Gly Asn Pro Ser Pro Glu Pro Ser Ser Glu
                90                  95                  100

gaa ctc gcg aaa gaa acc ccc gaa gag aag cta gcc aga gaa gaa aaa   451
Glu Leu Ala Lys Glu Thr Pro Glu Glu Lys Leu Ala Arg Glu Glu Lys
            105                 110                 115

gag aaa caa gac cta gcc gaa caa gca gaa gcc aac cgc atc gcc cgc   499
Glu Lys Gln Asp Leu Ala Glu Gln Ala Glu Ala Asn Arg Ile Ala Arg
        120                 125                 130

gaa cac ggc atc tcc gcc gaa aaa caa gac acc atc cgc tac gaa cta   547
Glu His Gly Ile Ser Ala Glu Lys Gln Asp Thr Ile Arg Tyr Glu Leu
    135                 140                 145
```

```
gaa aaa ctc aac gac aac aca tcc cta tcc cga gcc tca ctc cgc aaa   595
Glu Lys Leu Asn Asp Asn Thr Ser Leu Ser Arg Ala Ser Leu Arg Lys
150                 155                 160                 165

cta gca atg cag gaa gcc acc agc cga acc ccc gaa gac cta cgc aac   643
Leu Ala Met Gln Glu Ala Thr Ser Arg Thr Pro Glu Asp Leu Arg Asn
                170                 175                 180

tgg acc cgc aac aaa gtt atc cgc ata aac ccc acc gcc aaa gac cca   691
Trp Thr Arg Asn Lys Val Ile Arg Ile Asn Pro Thr Ala Lys Asp Pro
            185                 190                 195

ctc gcc gca gta aag aaa cgc tcc tta agc atc gga cgc caa gac cac   739
Leu Ala Ala Val Lys Lys Arg Ser Leu Ser Ile Gly Arg Gln Asp His
        200                 205                 210

gac ggc gga gcc aaa gca tcc ctc tat tta gat gcc aaa ggt cta gcc   787
Asp Gly Gly Ala Lys Ala Ser Leu Tyr Leu Asp Ala Lys Gly Leu Ala
    215                 220                 225

ctg ctc aaa tca ctg atg tct aaa gcc aag ccg ggg cat ttg ctt gaa   835
Leu Leu Lys Ser Leu Met Ser Lys Ala Lys Pro Gly His Leu Leu Glu
230                 235                 240                 245

gac tct ttg gcg gag gat aaa cgt acg aaa ccg caa cgc caa tac gat   883
Asp Ser Leu Ala Glu Asp Lys Arg Thr Lys Pro Gln Arg Gln Tyr Asp
                250                 255                 260

gcc ttc gcc gac atc ctc cac cgc gca cac agc gat ctc ctc ccc gca   931
Ala Phe Ala Asp Ile Leu His Arg Ala His Ser Asp Leu Leu Pro Ala
            265                 270                 275

cga tcc gga gtg ggc acc atc ctc gtc tcc ctc tcc gcc aaa gac gta   979
Arg Ser Gly Val Gly Thr Ile Leu Val Ser Leu Ser Ala Lys Asp Val
        280                 285                 290

aca aac ctc aaa gca tcg ggc ccc gac cac cgc tac ccc acc agc acc   1027
Thr Asn Leu Lys Ala Ser Gly Pro Asp His Arg Tyr Pro Thr Ser Thr
    295                 300                 305

ggc ata aaa ctc aca ccg ctt gag atc ctg cga ctc ggt gca gcc aaa   1075
Gly Ile Lys Leu Thr Pro Leu Glu Ile Leu Arg Leu Gly Ala Ala Lys
310                 315                 320                 325

tat gac ttc gtg acc gtc ctc gac tcc gaa tcc ggc cgt ccg ctg cac   1123
Tyr Asp Phe Val Thr Val Leu Asp Ser Glu Ser Gly Arg Pro Leu His
                330                 335                 340

ctg gca cgc act caa cgc acc gcc agc ctg tat caa cgc cta gcc ctc   1171
Leu Ala Arg Thr Gln Arg Thr Ala Ser Leu Tyr Gln Arg Leu Ala Leu
            345                 350                 355

ttc gcc tcc gaa ctc gtc tgc acc cgc gaa ggc tgc gac tcc ccc ttc   1219
Phe Ala Ser Glu Leu Val Cys Thr Arg Glu Gly Cys Asp Ser Pro Phe
        360                 365                 370

gaa gac aac gaa ata cac cac atc aga tcc tgg cta gac ggc ggc ccc   1267
Glu Asp Asn Glu Ile His His Ile Arg Ser Trp Leu Asp Gly Gly Pro
    375                 380                 385
```

```
aca gac ata gaa aac atc acc aac atc tgc ccc cac gac cac gga aac   1315
Thr Asp Ile Glu Asn Ile Thr Asn Ile Cys Pro His Asp His Gly Asn
390                 395                 400                 405

aac aac gac caa cgc gac ggc aaa gac aac atg ggg cac atg aac ata   1363
Asn Asn Asp Gln Arg Asp Gly Lys Asp Asn Met Gly His Met Asn Ile
                410                 415                 420

gat ccc aca acc ggg cgc gtc gga tat caa ccc gcc gac cgc cga aaa   1411
Asp Pro Thr Thr Gly Arg Val Gly Tyr Gln Pro Ala Asp Arg Arg Lys
            425                 430                 435

ccc atg cgg ttt aac aac acc gca gcc gca gca gaa tca gga gga gca   1459
Pro Met Arg Phe Asn Asn Thr Ala Ala Ala Ala Glu Ser Gly Gly Ala
        440                 445                 450

cag gcc agg acc taagttttta gcgcgccaaa aag                        1494
Gln Ala Arg Thr
    455
```

<210> 1236
<211> 457
<212> PRT
<213> Corynebacterium glutamicum

<400> 1236

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Met Gln Glu Ile His Thr Ile Met Lys His Met Asp Ala Leu Ile Ala
  1               5                  10                  15

Asp Pro Ser Ala Ala Ala Phe Lys Ala Thr Leu Pro Phe Ala Glu Leu
             20                  25                  30

Leu Glu Lys Leu His Asn Lys Lys Ala Leu Phe Asp Ala Ala Leu Ala
         35                  40                  45

Lys Ser Ala Glu Arg Ala Asp Ala Gly Arg Ile Ile Gly Lys Thr Ser
     50                  55                  60

His Ile Asp Ala Leu Ala Tyr Leu Leu Asp Ile Ser Lys Ser Glu Ala
 65                  70                  75                  80

Phe Arg Arg Thr Lys Arg Ala Glu Glu His Tyr Gly Asn Pro Ser Pro
                 85                  90                  95

Glu Pro Ser Ser Glu Glu Leu Ala Lys Glu Thr Pro Glu Glu Lys Leu
            100                 105                 110

Ala Arg Glu Glu Lys Glu Lys Gln Asp Leu Ala Glu Gln Ala Glu Ala
        115                 120                 125

Asn Arg Ile Ala Arg Glu His Gly Ile Ser Ala Glu Lys Gln Asp Thr
    130                 135                 140

Ile Arg Tyr Glu Leu Glu Lys Leu Asn Asp Asn Thr Ser Leu Ser Arg
145                 150                 155                 160

Ala Ser Leu Arg Lys Leu Ala Met Gln Glu Ala Thr Ser Arg Thr Pro
                165                 170                 175

Glu Asp Leu Arg Asn Trp Thr Arg Asn Lys Val Ile Arg Ile Asn Pro
```

```
            180                 185                 190

Thr Ala Lys Asp Pro Leu Ala Ala Val Lys Lys Arg Ser Leu Ser Ile
        195                 200                 205

Gly Arg Gln Asp His Asp Gly Gly Ala Lys Ala Ser Leu Tyr Leu Asp
    210                 215                 220

Ala Lys Gly Leu Ala Leu Leu Lys Ser Leu Met Ser Lys Ala Lys Pro
225                 230                 235                 240

Gly His Leu Leu Glu Asp Ser Leu Ala Glu Asp Lys Arg Thr Lys Pro
                245                 250                 255

Gln Arg Gln Tyr Asp Ala Phe Ala Asp Ile Leu His Arg Ala His Ser
            260                 265                 270

Asp Leu Leu Pro Ala Arg Ser Gly Val Gly Thr Ile Leu Val Ser Leu
        275                 280                 285

Ser Ala Lys Asp Val Thr Asn Leu Lys Ala Ser Gly Pro Asp His Arg
    290                 295                 300

Tyr Pro Thr Ser Thr Gly Ile Lys Leu Thr Pro Leu Glu Ile Leu Arg
305                 310                 315                 320

Leu Gly Ala Ala Lys Tyr Asp Phe Val Thr Val Leu Asp Ser Glu Ser
                325                 330                 335

Gly Arg Pro Leu His Leu Ala Arg Thr Gln Arg Thr Ala Ser Leu Tyr
            340                 345                 350

Gln Arg Leu Ala Leu Phe Ala Ser Glu Leu Val Cys Thr Arg Glu Gly
        355                 360                 365

Cys Asp Ser Pro Phe Glu Asp Asn Glu Ile His His Ile Arg Ser Trp
    370                 375                 380

Leu Asp Gly Gly Pro Thr Asp Ile Glu Asn Ile Thr Asn Ile Cys Pro
385                 390                 395                 400

His Asp His Gly Asn Asn Asn Asp Gln Arg Asp Gly Lys Asp Asn Met
                405                 410                 415

Gly His Met Asn Ile Asp Pro Thr Thr Gly Arg Val Gly Tyr Gln Pro
            420                 425                 430

Ala Asp Arg Arg Lys Pro Met Arg Phe Asn Asn Thr Ala Ala Ala Ala
        435                 440                 445

Glu Ser Gly Gly Ala Gln Ala Arg Thr
    450                 455
```

<210> 1237
<211> 1494
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(1471)
<223> FRXA02606

<400> 1237
agggcgcgga tcacttcgga tctgtggata acttttaagg cccttgtttt ccccttgaag 60

cttcggttgt gtggaaaaca gaaaaggagg ggaaaacaaa atg caa gaa atc cac 115
Met Gln Glu Ile His
1 5

acc atc atg aaa cac atg gac gcg ctc atc gcc gac ccg tcc gcc gcc 163
Thr Ile Met Lys His Met Asp Ala Leu Ile Ala Asp Pro Ser Ala Ala
10 15 20

gca ttc aaa gca aca ctc ccc ttc gcc gaa ctc ctc gaa aag ctc cac 211
Ala Phe Lys Ala Thr Leu Pro Phe Ala Glu Leu Leu Glu Lys Leu His
25 30 35

aac aaa aaa gcg ctt ttc gac gcc gcc ctc gcc aaa tcc gcc gag cgc 259
Asn Lys Lys Ala Leu Phe Asp Ala Ala Leu Ala Lys Ser Ala Glu Arg
40 45 50

gcc gat gcc gga cgc atc atc gga aaa acc tcc cac atc gat gcc ctc 307
Ala Asp Ala Gly Arg Ile Ile Gly Lys Thr Ser His Ile Asp Ala Leu
55 60 65

gcg tac ctt ctc gac atc tcc aaa tcc gaa gca ttc cga cgc aca aaa 355
Ala Tyr Leu Leu Asp Ile Ser Lys Ser Glu Ala Phe Arg Arg Thr Lys
70 75 80 85

cgc gcc gaa gaa cac tac ggc aac cca agc ccg gaa ccc agt tca gaa 403
Arg Ala Glu Glu His Tyr Gly Asn Pro Ser Pro Glu Pro Ser Ser Glu
90 95 100

gaa ctc gcg aaa gaa acc ccc gaa gag aag cta gcc aga gaa gaa aaa 451
Glu Leu Ala Lys Glu Thr Pro Glu Glu Lys Leu Ala Arg Glu Glu Lys
105 110 115

gag aaa caa gac cta gcc gaa caa gca gaa gcc aac cgc atc gcc cgc 499
Glu Lys Gln Asp Leu Ala Glu Gln Ala Glu Ala Asn Arg Ile Ala Arg
120 125 130

gaa cac ggc atc tcc gcc gaa aaa caa gac acc atc cgc tac gaa cta 547
Glu His Gly Ile Ser Ala Glu Lys Gln Asp Thr Ile Arg Tyr Glu Leu
135 140 145

gaa aaa ctc aac gac aac aca tcc cta tcc cga gcc tca ctc cgc aaa 595
Glu Lys Leu Asn Asp Asn Thr Ser Leu Ser Arg Ala Ser Leu Arg Lys
150 155 160 165

cta gca atg cag gaa gcc acc agc cga acc ccc gaa gac cta cgc aac 643
Leu Ala Met Gln Glu Ala Thr Ser Arg Thr Pro Glu Asp Leu Arg Asn
170 175 180

tgg acc cgc aac aaa gtt atc cgc ata aac ccc acc gcc aaa gac cca 691
Trp Thr Arg Asn Lys Val Ile Arg Ile Asn Pro Thr Ala Lys Asp Pro
185 190 195

ctc gcc gca gta aag aaa cgc tcc tta agc atc gga cgc caa gac cac 739
Leu Ala Ala Val Lys Lys Arg Ser Leu Ser Ile Gly Arg Gln Asp His
200 205 210

```
gac ggc gga gcc aaa gca tcc ctc tat tta gat gcc aaa ggt cta gcc   787
Asp Gly Gly Ala Lys Ala Ser Leu Tyr Leu Asp Ala Lys Gly Leu Ala
    215                 220                 225

ctg ctc aaa tca ctg atg tct aaa gcc aag ccg ggg cat ttg ctt gaa   835
Leu Leu Lys Ser Leu Met Ser Lys Ala Lys Pro Gly His Leu Leu Glu
230                 235                 240                 245

gac tct ttg gcg gag gat aaa cgt acg aaa ccg caa cgc caa tac gat   883
Asp Ser Leu Ala Glu Asp Lys Arg Thr Lys Pro Gln Arg Gln Tyr Asp
                250                 255                 260

gcc ttc gcc gac atc ctc cac cgc gca cac agc gat ctc ctc ccc gca   931
Ala Phe Ala Asp Ile Leu His Arg Ala His Ser Asp Leu Leu Pro Ala
            265                 270                 275

cga tcc gga gtg ggc acc atc ctc gtc tcc ctc tcc gcc aaa gac gta   979
Arg Ser Gly Val Gly Thr Ile Leu Val Ser Leu Ser Ala Lys Asp Val
        280                 285                 290

aca aac ctc aaa gca tcg ggc ccc gac cac cgc tac ccc acc agc acc   1027
Thr Asn Leu Lys Ala Ser Gly Pro Asp His Arg Tyr Pro Thr Ser Thr
    295                 300                 305

ggc ata aaa ctc aca ccg ctt gag atc ctg cga ctc ggt gca gcc aaa   1075
Gly Ile Lys Leu Thr Pro Leu Glu Ile Leu Arg Leu Gly Ala Ala Lys
310                 315                 320                 325

tat gac ttc gtg acc gtc ctc gac tcc gaa tcc ggc cgt ccg ctg cac   1123
Tyr Asp Phe Val Thr Val Leu Asp Ser Glu Ser Gly Arg Pro Leu His
                330                 335                 340

ctg gca cgc act caa cgc acc gcc agc ctg tat caa cgc cta gcc ctc   1171
Leu Ala Arg Thr Gln Arg Thr Ala Ser Leu Tyr Gln Arg Leu Ala Leu
            345                 350                 355

ttc gcc tcc gaa ctc gtc tgc acc cgc gaa ggc tgc gac tcc ccc ttc   1219
Phe Ala Ser Glu Leu Val Cys Thr Arg Glu Gly Cys Asp Ser Pro Phe
        360                 365                 370

gaa gac aac gaa ata cac cac atc aga tcc tgg cta gac ggc ggc ccc   1267
Glu Asp Asn Glu Ile His His Ile Arg Ser Trp Leu Asp Gly Gly Pro
    375                 380                 385

aca gac ata gaa aac atc acc aac atc tgc ccc cac gac cac gga aac   1315
Thr Asp Ile Glu Asn Ile Thr Asn Ile Cys Pro His Asp His Gly Asn
390                 395                 400                 405

aac aac gac caa cgc gac ggc aaa gac aac atg ggg cac atg aac ata   1363
Asn Asn Asp Gln Arg Asp Gly Lys Asp Asn Met Gly His Met Asn Ile
                410                 415                 420

gat ccc aca acc ggg cgc gtc gga tat caa ccc gcc gac cgc cga aaa   1411
Asp Pro Thr Thr Gly Arg Val Gly Tyr Gln Pro Ala Asp Arg Arg Lys
            425                 430                 435

ccc atg cgg ttt aac aac acc gca gcc gca gca gaa tca gga gga gca   1459
Pro Met Arg Phe Asn Asn Thr Ala Ala Ala Ala Glu Ser Gly Gly Ala
        440                 445                 450
```

```
cag gcc agg acc taagttttta gcgcgccaaa aag                              1494
Gln Ala Arg Thr
    455
```

<210> 1238
<211> 457
<212> PRT
<213> Corynebacterium glutamicum

<400> 1238

```
Met Gln Glu Ile His Thr Ile Met Lys His Met Asp Ala Leu Ile Ala
  1               5                  10                  15

Asp Pro Ser Ala Ala Ala Phe Lys Ala Thr Leu Pro Phe Ala Glu Leu
             20                  25                  30

Leu Glu Lys Leu His Asn Lys Lys Ala Leu Phe Asp Ala Ala Leu Ala
         35                  40                  45

Lys Ser Ala Glu Arg Ala Asp Ala Gly Arg Ile Ile Gly Lys Thr Ser
     50                  55                  60

His Ile Asp Ala Leu Ala Tyr Leu Leu Asp Ile Ser Lys Ser Glu Ala
 65                  70                  75                  80

Phe Arg Arg Thr Lys Arg Ala Glu Glu His Tyr Gly Asn Pro Ser Pro
                 85                  90                  95

Glu Pro Ser Ser Glu Glu Leu Ala Lys Glu Thr Pro Glu Glu Lys Leu
            100                 105                 110

Ala Arg Glu Glu Lys Glu Lys Gln Asp Leu Ala Glu Gln Ala Glu Ala
        115                 120                 125

Asn Arg Ile Ala Arg Glu His Gly Ile Ser Ala Glu Lys Gln Asp Thr
    130                 135                 140

Ile Arg Tyr Glu Leu Glu Lys Leu Asn Asp Asn Thr Ser Leu Ser Arg
145                 150                 155                 160

Ala Ser Leu Arg Lys Leu Ala Met Gln Glu Ala Thr Ser Arg Thr Pro
                165                 170                 175

Glu Asp Leu Arg Asn Trp Thr Arg Asn Lys Val Ile Arg Ile Asn Pro
            180                 185                 190

Thr Ala Lys Asp Pro Leu Ala Ala Val Lys Lys Arg Ser Leu Ser Ile
        195                 200                 205

Gly Arg Gln Asp His Asp Gly Gly Ala Lys Ala Ser Leu Tyr Leu Asp
    210                 215                 220

Ala Lys Gly Leu Ala Leu Leu Lys Ser Leu Met Ser Lys Ala Lys Pro
225                 230                 235                 240

Gly His Leu Leu Glu Asp Ser Leu Ala Glu Asp Lys Arg Thr Lys Pro
                245                 250                 255

Gln Arg Gln Tyr Asp Ala Phe Ala Asp Ile Leu His Arg Ala His Ser
            260                 265                 270
```

```
Asp Leu Leu Pro Ala Arg Ser Gly Val Gly Thr Ile Leu Val Ser Leu
        275                 280                 285

Ser Ala Lys Asp Val Thr Asn Leu Lys Ala Ser Gly Pro Asp His Arg
    290                 295                 300

Tyr Pro Thr Ser Thr Gly Ile Lys Leu Thr Pro Leu Glu Ile Leu Arg
305                 310                 315                 320

Leu Gly Ala Ala Lys Tyr Asp Phe Val Thr Val Leu Asp Ser Glu Ser
                325                 330                 335

Gly Arg Pro Leu His Leu Ala Arg Thr Gln Arg Thr Ala Ser Leu Tyr
            340                 345                 350

Gln Arg Leu Ala Leu Phe Ala Ser Glu Leu Val Cys Thr Arg Glu Gly
        355                 360                 365

Cys Asp Ser Pro Phe Glu Asp Asn Glu Ile His His Ile Arg Ser Trp
    370                 375                 380

Leu Asp Gly Gly Pro Thr Asp Ile Glu Asn Ile Thr Asn Ile Cys Pro
385                 390                 395                 400

His Asp His Gly Asn Asn Asn Asp Gln Arg Asp Gly Lys Asp Asn Met
                405                 410                 415

Gly His Met Asn Ile Asp Pro Thr Thr Gly Arg Val Gly Tyr Gln Pro
            420                 425                 430

Ala Asp Arg Arg Lys Pro Met Arg Phe Asn Asn Thr Ala Ala Ala Ala
        435                 440                 445

Glu Ser Gly Gly Ala Gln Ala Arg Thr
    450                 455
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US20030148463A1

<210> 1239
<211> 1050
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1027)
<223> RXN02610

<400> 1239

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ccagctcatc gtgcagggac gcaccagcgt gaaggaagat caagcagcgg aaatttctac 60

gctgctgaag gaatctgcgg atcggacgta ttgttaaccg atg agg aaa acc atc   115
                                              Met Arg Lys Thr Ile
                                                1               5

acc gtt att gct gta ttg atc gtc ctc gcc tta atc ggc gtg ggc atc   163
Thr Val Ile Ala Val Leu Ile Val Leu Ala Leu Ile Gly Val Gly Ile
                10                  15                  20

gtg cag tat gtg aac aca tcc gat gac tca gat ttc att ggc cag cct   211
Val Gln Tyr Val Asn Thr Ser Asp Asp Ser Asp Phe Ile Gly Gln Pro
```

```
                25                  30                  35

ggc gag cca acc ggt acc gaa acc acg gaa cca ccg gtt caa cct gat   259
Gly Glu Pro Thr Gly Thr Glu Thr Thr Glu Pro Pro Val Gln Pro Asp
         40                  45                  50

tgg tgc cct gcg gta gaa gtc att gcc gcg ccg ggt acg tgg gag tcg   307
Trp Cys Pro Ala Val Glu Val Ile Ala Ala Pro Gly Thr Trp Glu Ser
     55                  60                  65

gct gct aat gat gat ccg atc aac ccg acc gct aat ccg ctg tca ttc   355
Ala Ala Asn Asp Asp Pro Ile Asn Pro Thr Ala Asn Pro Leu Ser Phe
 70                  75                  80                  85

atg ttg agc atc act cag cca ctg cag gag cgt tat tct gcg gat gac   403
Met Leu Ser Ile Thr Gln Pro Leu Gln Glu Arg Tyr Ser Ala Asp Asp
                 90                  95                 100

gtc aag gtg tgg acg ctg ccg tac act gcg cag ttc cgc aac atc aac   451
Val Lys Val Trp Thr Leu Pro Tyr Thr Ala Gln Phe Arg Asn Ile Asn
            105                 110                 115

tcg caa aat gag atg tcc tat gat gat tcg cgc aat gaa ggc acc gcg   499
Ser Gln Asn Glu Met Ser Tyr Asp Asp Ser Arg Asn Glu Gly Thr Ala
        120                 125                 130

aag atg aat gag gaa ctg atc aac act cac aat gag tgc cct gcc acg   547
Lys Met Asn Glu Glu Leu Ile Asn Thr His Asn Glu Cys Pro Ala Thr
    135                 140                 145

gag ttc atc atc gtt ggt ttc tcc cag ggt gcg gtc att gcg ggc gat   595
Glu Phe Ile Ile Val Gly Phe Ser Gln Gly Ala Val Ile Ala Gly Asp
150                 155                 160                 165

gtg gct gct cag atc ggt tca gag caa ggt gtt att cca gct gac agc   643
Val Ala Ala Gln Ile Gly Ser Glu Gln Gly Val Ile Pro Ala Asp Ser
                170                 175                 180

gtc agg ggt gtc gcc ctg atc gct gac ggt cgc cgg gag cct ggt gtg   691
Val Arg Gly Val Ala Leu Ile Ala Asp Gly Arg Arg Glu Pro Gly Val
            185                 190                 195

ggc cag ttc cca ggc acg ttt gtg gat ggc atc ggc gcg gag gtt act   739
Gly Gln Phe Pro Gly Thr Phe Val Asp Gly Ile Gly Ala Glu Val Thr
        200                 205                 210

ctg cag cct ttg aac ttg ctg gtg cag ccg att gtt ccg ggc gca acc   787
Leu Gln Pro Leu Asn Leu Leu Val Gln Pro Ile Val Pro Gly Ala Thr
    215                 220                 225

atg cgt ggc ggg cgc gcg ggc ggt ttc ggt gtg ctc aac gac cgg gtg   835
Met Arg Gly Gly Arg Ala Gly Gly Phe Gly Val Leu Asn Asp Arg Val
230                 235                 240                 245

cag gat att tgt gct cca aat gat gcg atc tgt gat gct ccg gtg aat   883
Gln Asp Ile Cys Ala Pro Asn Asp Ala Ile Cys Asp Ala Pro Val Asn
                250                 255                 260

gtc ggc aac gcc ctt gat cgt gcg ttg gcc atg gtc tcc gcc aac ggt   931
Val Gly Asn Ala Leu Asp Arg Ala Leu Ala Met Val Ser Ala Asn Gly
            265                 270                 275
```

```
gtg cac gcg ctc tac gcc acc aat ccg gat gtt ttc cca ggc aca acc   979
Val His Ala Leu Tyr Ala Thr Asn Pro Asp Val Phe Pro Gly Thr Thr
        280                 285                 290

acc aat gcg tgg gtt gtg gat tgg gcg acc aac ctc atc gac aac gga   1027
Thr Asn Ala Trp Val Val Asp Trp Ala Thr Asn Leu Ile Asp Asn Gly
    295                 300                 305                 .

taaagctttt tcgcttttcg acg                                       1050


<210> 1240
<211> 309
<212> PRT
<213> Corynebacterium glutamicum

<400> 1240
Met Arg Lys Thr Ile Thr Val Ile Ala Val Leu Ile Val Leu Ala Leu
  1               5                  10                  15

Ile Gly Val Gly Ile Val Gln Tyr Val Asn Thr Ser Asp Asp Ser Asp
             20                  25                  30
.
Phe Ile Gly Gln Pro Gly Glu Pro Thr Gly Thr Glu Thr Thr Glu Pro
         35                  40                  45

Pro Val Gln Pro Asp Trp Cys Pro Ala Val Glu Val Ile Ala Ala Pro
     50                  55                  60

Gly Thr Trp Glu Ser Ala Ala Asn Asp Asp Pro Ile Asn Pro Thr Ala
 65                  70                  75                  80

Asn Pro Leu Ser Phe Met Leu Ser Ile Thr Gln Pro Leu Gln Glu Arg
                 85                  90                  95

Tyr Ser Ala Asp Asp Val Lys Val Trp Thr Leu Pro Tyr Thr Ala Gln
            100                 105                 110

Phe Arg Asn Ile Asn Ser Gln Asn Glu Met Ser Tyr Asp Asp Ser Arg
        115                 120                 125

Asn Glu Gly Thr Ala Lys Met Asn Glu Glu Leu Ile Asn Thr His Asn
    130                 135                 140

Glu Cys Pro Ala Thr Glu Phe Ile Ile Val Gly Phe Ser Gln Gly Ala
145                 150                 155                 160

Val Ile Ala Gly Asp Val Ala Ala Gln Ile Gly Ser Glu Gln Gly Val
                165                 170                 175

Ile Pro Ala Asp Ser Val Arg Gly Val Ala Leu Ile Ala Asp Gly Arg
            180                 185                 190

Arg Glu Pro Gly Val Gly Gln Phe Pro Gly Thr Phe Val Asp Gly Ile
        195                 200                 205

Gly Ala Glu Val Thr Leu Gln Pro Leu Asn Leu Leu Val Gln Pro Ile
    210                 215                 220

Val Pro Gly Ala Thr Met Arg Gly Gly Arg Ala Gly Gly Phe Gly Val
```

```
225                 230                 235                 240

Leu Asn Asp Arg Val Gln Asp Ile Cys Ala Pro Asn Asp Ala Ile Cys
                245                 250                 255

Asp Ala Pro Val Asn Val Gly Asn Ala Leu Asp Arg Ala Leu Ala Met
            260                 265                 270

Val Ser Ala Asn Gly Val His Ala Leu Tyr Ala Thr Asn Pro Asp Val
        275                 280                 285

Phe Pro Gly Thr Thr Thr Asn Ala Trp Val Val Asp Trp Ala Thr Asn
    290                 295                 300

Leu Ile Asp Asn Gly
305
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<210> 1241
<211> 1050
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1027)
<223> FRXA02610

<400> 1241

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ccagctcatc gtgcagggac gcaccagcgt gaaggaagat caagcagcgg aaatttctac 60

gctgctgaag gaatctgcgg atcggacgta ttgttaaccg atg agg aaa acc atc   115
                                            Met Arg Lys Thr Ile
                                              1               5

acc gtt att gct gta ttg atc gtc ctc gcc tta atc ggc gtg ggc atc   163
Thr Val Ile Ala Val Leu Ile Val Leu Ala Leu Ile Gly Val Gly Ile
                  10                  15                  20

gtg cag tat gtg aac aca tcc gat gac tca gat ttc att ggc cag cct   211
Val Gln Tyr Val Asn Thr Ser Asp Asp Ser Asp Phe Ile Gly Gln Pro
              25                  30                  35

ggc gag cca acc ggt acc gaa acc acg gaa cca ccg gtt caa cct gat   259
Gly Glu Pro Thr Gly Thr Glu Thr Thr Glu Pro Pro Val Gln Pro Asp
          40                  45                  50

tgg tgc cct gcg gta gaa gtc att gcc gcg ccg ggt acg tgg gag tcg   307
Trp Cys Pro Ala Val Glu Val Ile Ala Ala Pro Gly Thr Trp Glu Ser
      55                  60                  65

gct gct aat gat gat ccg atc aac ccg acc gct aat ccg ctg tca ttc   355
Ala Ala Asn Asp Asp Pro Ile Asn Pro Thr Ala Asn Pro Leu Ser Phe
  70                  75                  80                  85

atg ttg agc atc act cag cca ctg cag gag cgt tat tct gcg gat gac   403
Met Leu Ser Ile Thr Gln Pro Leu Gln Glu Arg Tyr Ser Ala Asp Asp
                  90                  95                 100

gtc aag gtg tgg acg ctg ccg tac act gcg cag ttc cgc aac atc aac   451
Val Lys Val Trp Thr Leu Pro Tyr Thr Ala Gln Phe Arg Asn Ile Asn
```

```
            105                 110                 115

tcg caa aat gag atg tcc tat gat gat tcg cgc aat gaa ggc acc gcg   499
Ser Gln Asn Glu Met Ser Tyr Asp Asp Ser Arg Asn Glu Gly Thr Ala
        120                 125                 130

aag atg aat gag gaa ctg atc aac act cac aat gag tgc cct gcc acg   547
Lys Met Asn Glu Glu Leu Ile Asn Thr His Asn Glu Cys Pro Ala Thr
    135                 140                 145

gag ttc atc atc gtt ggt ttc tcc cag ggt gcg gtc att gcg ggc gat   595
Glu Phe Ile Ile Val Gly Phe Ser Gln Gly Ala Val Ile Ala Gly Asp
150                 155                 160                 165

gtg gct gct cag atc ggt tca gag caa ggt gtt att cca gct gac agc   643
Val Ala Ala Gln Ile Gly Ser Glu Gln Gly Val Ile Pro Ala Asp Ser
                170                 175                 180

gtc agg ggt gtc gcc ctg atc gct gac ggt cgc cgg gag cct ggt gtg   691
Val Arg Gly Val Ala Leu Ile Ala Asp Gly Arg Arg Glu Pro Gly Val
            185                 190                 195

ggc cag ttc cca ggc acg ttt gtg gat ggc atc ggc gcg gag gtt act   739
Gly Gln Phe Pro Gly Thr Phe Val Asp Gly Ile Gly Ala Glu Val Thr
        200                 205                 210

ctg cag cct ttg aac ttg ctg gtg cag ccg att gtt ccg ggc gca acc   787
Leu Gln Pro Leu Asn Leu Leu Val Gln Pro Ile Val Pro Gly Ala Thr
    215                 220                 225

atg cgt ggc ggg cgc gcg ggc ggt ttc ggt gtg ctc aac gac cgg gtg   835
Met Arg Gly Gly Arg Ala Gly Gly Phe Gly Val Leu Asn Asp Arg Val
230                 235                 240                 245

cag gat att tgt gct cca aat gat gcg atc tgt gat gct ccg gtg aat   883
Gln Asp Ile Cys Ala Pro Asn Asp Ala Ile Cys Asp Ala Pro Val Asn
                250                 255                 260

gtc ggc aac gcc ctt gat cgt gcg ttg gcc atg gtc tcc gcc aac ggt   931
Val Gly Asn Ala Leu Asp Arg Ala Leu Ala Met Val Ser Ala Asn Gly
            265                 270                 275

gtg cac gcg ctc tac gcc acc aat ccg gat gtt ttc cca ggc aca acc   979
Val His Ala Leu Tyr Ala Thr Asn Pro Asp Val Phe Pro Gly Thr Thr
        280                 285                 290

acc aat gcg tgg gtt gtg gat tgg gcg acc aac ctc atc gac aac gga  1027
Thr Asn Ala Trp Val Val Asp Trp Ala Thr Asn Leu Ile Asp Asn Gly
    295                 300                 305

taaagctttt tcgcttttcg acg                                       1050


<210> 1242
<211> 309
<212> PRT
<213> Corynebacterium glutamicum

<400> 1242
Met Arg Lys Thr Ile Thr Val Ile Ala Val Leu Ile Val Leu Ala Leu
  1               5                  10                  15
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Ile Gly Val Gly Ile Val Gln Tyr Val Asn Thr Ser Asp Asp Ser Asp
            20                  25                  30

Phe Ile Gly Gln Pro Gly Glu Pro Thr Gly Thr Glu Thr Thr Glu Pro
        35                  40                  45

Pro Val Gln Pro Asp Trp Cys Pro Ala Val Glu Val Ile Ala Ala Pro
    50                  55                  60

Gly Thr Trp Glu Ser Ala Ala Asn Asp Asp Pro Ile Asn Pro Thr Ala
65                  70                  75                  80

Asn Pro Leu Ser Phe Met Leu Ser Ile Thr Gln Pro Leu Gln Glu Arg
                85                  90                  95

Tyr Ser Ala Asp Asp Val Lys Val Trp Thr Leu Pro Tyr Thr Ala Gln
            100                 105                 110

Phe Arg Asn Ile Asn Ser Gln Asn Glu Met Ser Tyr Asp Asp Ser Arg
        115                 120                 125

Asn Glu Gly Thr Ala Lys Met Asn Glu Glu Leu Ile Asn Thr His Asn
    130                 135                 140

Glu Cys Pro Ala Thr Glu Phe Ile Ile Val Gly Phe Ser Gln Gly Ala
145                 150                 155                 160

Val Ile Ala Gly Asp Val Ala Ala Gln Ile Gly Ser Glu Gln Gly Val
                165                 170                 175

Ile Pro Ala Asp Ser Val Arg Gly Val Ala Leu Ile Ala Asp Gly Arg
            180                 185                 190

Arg Glu Pro Gly Val Gly Gln Phe Pro Gly Thr Phe Val Asp Gly Ile
        195                 200                 205

Gly Ala Glu Val Thr Leu Gln Pro Leu Asn Leu Leu Val Gln Pro Ile
    210                 215                 220

Val Pro Gly Ala Thr Met Arg Gly Gly Arg Ala Gly Gly Phe Gly Val
225                 230                 235                 240

Leu Asn Asp Arg Val Gln Asp Ile Cys Ala Pro Asn Asp Ala Ile Cys
                245                 250                 255

Asp Ala Pro Val Asn Val Gly Asn Ala Leu Asp Arg Ala Leu Ala Met
            260                 265                 270

Val Ser Ala Asn Gly Val His Ala Leu Tyr Ala Thr Asn Pro Asp Val
        275                 280                 285

Phe Pro Gly Thr Thr Thr Asn Ala Trp Val Val Asp Trp Ala Thr Asn
    290                 295                 300

Leu Ile Asp Asn Gly
305
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<210> 1243
<211> 1419

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1396)
<223> RXN02624

<400> 1243
acccggtcag atccgacgtc gccggccaaa accgcaagca cctgcgcaaa cgccacagaa 60

ggcagctcag caatcaaagt tgctgcgttt ccttccaacc gtg ctg att ccg cat 115
Val Leu Ile Pro His
1 5

ggc gtg gcg gtg ctt ttg gtt att att ctc gcc gta gcc tcc cta atg 163
Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala Val Ala Ser Leu Met
10 15 20

ttc acc aat tct tca atg gtg aat ctt tcg gca acg att gca cag ctg 211
Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala Thr Ile Ala Gln Leu
25 30 35

tgg ctt tcc cta aat ctc ggt gcg gtg gac ggc agt ggg gaa gtg atc 259
Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly Ser Gly Glu Val Ile
40 45 50

tca gta ctg ccc acg ctt ccc ggc ttt ata ttc ctc tgg gcc atc gcc 307
Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe Leu Trp Ala Ile Ala
55 60 65

gcg cgc atc cac cgc gca gtc aaa gat cgt gtc agc atc gcc gac tta 355
Ala Arg Ile His Arg Ala Val Lys Asp Arg Val Ser Ile Ala Asp Leu
70 75 80 85

ggc gtc ctc gca gca ctc gtc ctc ggc atc ccg ctt gcg ctc acc gcc 403
Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro Leu Ala Leu Thr Ala
90 95 100

atc gca gcg ttc atg ctt ttc gac gcc tcc agc gtc ctc aac gtc gag 451
Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser Val Leu Asn Val Glu
105 110 115

gtc ccg cca atc acg cgc ctc cta cgc gtg atg ttg ttc cac ctc agc 499
Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met Leu Phe His Leu Ser
120 125 130

gcc ctc ttc ctc ggc atg ggg cca cgc ctg tgg cag gcg ttg gcg cgc 547
Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp Gln Ala Leu Ala Arg
135 140 145

cgc tac ggt gct cca gaa tgg ctt atc gac gcc atc acc caa gct ttc 595
Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala Ile Thr Gln Ala Phe
150 155 160 165

cgc ttc ctc atc gca ttt gga aca gtc tcc ttg gtt tcc gtg ctc gtg 643
Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu Val Ser Val Leu Val
170 175 180

atg acc gcg atc aac cac agt gca ttc acc gcg acc atg cag ggt tac 691
Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala Thr Met Gln Gly Tyr

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                185                 190                 195

gac gac tcc gcc tct gtt gtg gcc ttg atc gtc ctg agc att ctg tat   739
Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val Leu Ser Ile Leu Tyr
        200                 205                 210

ctg ccc aac atg atg atc ttt gcg atg ggc aat ctg atc ggc tca ccc   787
Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn Leu Ile Gly Ser Pro
    215                 220                 225

ctt tac ttc ggt gac gcc tcc atc agc gtc ttc agc gtg cat tcc gtt   835
Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe Ser Val His Ser Val
230                 235                 240                 245

cca ttg cca ccg ctt ccc atc ctc gca gct ctc ccc agc gaa gcc ctc   883
Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser Glu Ala Leu
                250                 255                 260

tca tgg gca gtg gcc tta ctg gtc atc cct gca att att gcc acc tgg   931
Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile Ala Thr Trp
            265                 270                 275

gtc tgc gtg aga aac ccc atg cgc ctt gcc gtg aac aca aca gca gca   979
Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr Thr Ala Ala
        280                 285                 290

gtc att tca gca ctg tgt ttc ctc gtc ctg gca gtt ttc gcc ggc gga  1027
Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe Ala Gly Gly
    295                 300                 305

acc ttg ggc gta tac aac tac gtc gga ctc aac ctc ctg gcg tca gtt  1075
Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu Ala Ser Val
310                 315                 320                 325

ggc cta gtt ttc gtc tat ttc gcc ctc gtt gga ctc ctc atc gcc gga  1123
Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu Ile Ala Gly
                330                 335                 340

atc gac aag ctg cgc aac cct gta gaa gtt aag tct gtt aag gct gtg  1171
Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val Lys Ala Val
            345                 350                 355

gct gtt gtg gag ccc gag cct gaa gaa gtt gaa gag gac gaa gag gag  1219
Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp Glu Glu Glu
        360                 365                 370

cat gtt gaa gaa gaa gta gat gag gag gaa gag gaa gtt gag gaa ggg  1267
His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Glu Val Glu Glu Gly
    375                 380                 385

gta gaa gag gtc gaa gaa gac gac gca gag gat cct gaa gag aat cct  1315
Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu Glu Asn Pro
390                 395                 400                 405

gaa gag gaa gaa tcc gac gaa gaa att gag aca gaa act gag gct gaa  1363
Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr Glu Ala Glu
                410                 415                 420

gaa acc aat gat ggt tcc gag gcc gaa gac cgt taacatatct gttgtgaatt 1416
Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg
            425                 430
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ctg 1419

<210> 1244
<211> 432
<212> PRT
<213> Corynebacterium glutamicum

<400> 1244

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Val Leu Ile Pro His Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala
  1               5                  10                  15

Val Ala Ser Leu Met Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala
             20                  25                  30

Thr Ile Ala Gln Leu Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly
         35                  40                  45

Ser Gly Glu Val Ile Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe
     50                  55                  60

Leu Trp Ala Ile Ala Ala Arg Ile His Arg Ala Val Lys Asp Arg Val
 65                  70                  75                  80

Ser Ile Ala Asp Leu Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro
                 85                  90                  95

Leu Ala Leu Thr Ala Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser
            100                 105                 110

Val Leu Asn Val Glu Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met
        115                 120                 125

Leu Phe His Leu Ser Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp
    130                 135                 140

Gln Ala Leu Ala Arg Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala
145                 150                 155                 160

Ile Thr Gln Ala Phe Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu
                165                 170                 175

Val Ser Val Leu Val Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala
            180                 185                 190

Thr Met Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val
        195                 200                 205

Leu Ser Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn
    210                 215                 220

Leu Ile Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe
225                 230                 235                 240

Ser Val His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu
                245                 250                 255

Pro Ser Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala
            260                 265                 270
```

```
Ile Ile Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val
        275                 280                 285

Asn Thr Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala
    290                 295                 300

Val Phe Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn
305                 310                 315                 320

Leu Leu Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly
                325                 330                 335

Leu Leu Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys
            340                 345                 350

Ser Val Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu
        355                 360                 365

Glu Asp Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu
    370                 375                 380

Glu Val Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp
385                 390                 395                 400

Pro Glu Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr
                405                 410                 415

Glu Thr Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg
            420                 425                 430
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SEQUENCE LISTING

<210> 1245
<211> 737
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(714)
<223> FRXA02624

<400> 1245

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cag ggc tac gac gac tcc gcc tct gtt gtg gcc ttg atc gtc ctg agc   48
Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val Leu Ser
  1               5                  10                  15

att ctg tat ctg ccc aac atg atg atc ttt gcg atg ggc aat ctg atc   96
Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn Leu Ile
            20                  25                  30

ggc tca ccc ctt tac ttc ggt gac gcc tcc atc agc gtc ttc agc gtg   144
Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe Ser Val
        35                  40                  45

cat tcc gtt cca ttg cca ccg ctt ccc atc ctc gca gct ctc ccc agc   192
His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser
    50                  55                  60
```

```
gaa gcc ctc tca tgg gca gtg gcc tta ctg gtc atc cct gca att att   240
Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile
 65                  70                  75                  80

gcc acc tgg gtc tgc gtg aga aac ccc atg cgc ctt gcc gtg aac aca   288
Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr
                85                  90                  95

aca gca gca gtc att tca gca ctg tgt ttc ctc gtc ctg gca gtt ttc   336
Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe
            100                 105                 110

gcc ggc gga acc ttg ggc gta tac aac tac gtc gga ctc aac ctc ctg   384
Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu
        115                 120                 125

gcg tca gtt ggc cta gtt ttc gtc tat ttc gcc ctc gtt gga ctc ctc   432
Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu
    130                 135                 140

atc gcc gga atc gac aag ctg cgc aac cct gta gaa gtt aag tct gtt   480
Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val
145                 150                 155                 160

aag gct gtg gct gtt gtg gag ccc gag cct gaa gaa gtt gaa gag gac   528
Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp
                165                 170                 175

gaa gag gag cat gtt gaa gaa gaa gta gat gag gag gaa gag gaa gtt   576
Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Glu Val
            180                 185                 190

gag gaa ggg gta gaa gag gtc gaa gaa gac gac gca gag gat cct gaa   624
Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu
        195                 200                 205

gag aat cct gaa gag gaa gaa tcc gac gaa gaa att gag aca gaa act   672
Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr
    210                 215                 220

gag gct gaa gaa acc aat gat ggt tcc gag gcc gaa gac cgt           714
Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg
225                 230                 235

taacatatct gttgtgaatt ctg                                        737
```

<210> 1246
<211> 238
<212> PRT
<213> Corynebacterium glutamicum

```
<400> 1246
Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val Leu Ser
  1               5                  10                  15

Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn Leu Ile
             20                  25                  30

Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe Ser Val
         35                  40                  45
```

```
His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser
     50                  55                  60

Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile
 65                  70                  75                  80

Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr
                 85                  90                  95

Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe
            100                 105                 110

Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu
        115                 120                 125

Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu
    130                 135                 140

Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val
145                 150                 155                 160

Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp
                165                 170                 175

Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Glu Val
            180                 185                 190

Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu
        195                 200                 205

Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr
    210                 215                 220

Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg
225                 230                 235
```

20050208030

<210> 1247
<211> 1128
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1105)
<223> RXN02626

<400> 1247

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gtagcggtcg aattatttgc ctgtgggcat aattttgaga caaaataata gaaacgtctc 60

agatgttggg aagttcttca cgctatcagt tagggagcac atg agt act caa gtt   115
                                            Met Ser Thr Gln Val
                                              1               5

gaa ctc aaa aca ccg aaa tcg gaa gac cgg gca gca tat atc gct gca   163
Glu Leu Lys Thr Pro Lys Ser Glu Asp Arg Ala Ala Tyr Ile Ala Ala
                 10                  15                  20

ttg gga ttc ccg gtc ttg gtc atc att ggc ggc atc atc gga ttc aca   211
Leu Gly Phe Pro Val Leu Val Ile Ile Gly Gly Ile Ile Gly Phe Thr
```

```
                25                  30                  35

gcc tcg gat gtt gtg ctc aat att tct tcg tgg gtc aat cct ttg ctg   259
Ala Ser Asp Val Val Leu Asn Ile Ser Ser Trp Val Asn Pro Leu Leu
        40                  45                  50

ggc atc atc atg ttc tcc atg ggc ctg acc ttg aag cca gtt gac ttc   307
Gly Ile Ile Met Phe Ser Met Gly Leu Thr Leu Lys Pro Val Asp Phe
    55                  60                  65

gcc ctt gtt gct aaa cgc cca ctc cca gtt ctt atc ggc gtg atc gcc   355
Ala Leu Val Ala Lys Arg Pro Leu Pro Val Leu Ile Gly Val Ile Ala
70                  75                  80                  85

cag ttt gtc atc atg ccc ctg atc gca ttg ctg gtg gtc tgg gtt ttg   403
Gln Phe Val Ile Met Pro Leu Ile Ala Leu Leu Val Val Trp Val Leu
                90                  95                  100

cag ctg cct gcg gaa att gcg gcc ggt gtc atc ttg gtt ggt tgt gca   451
Gln Leu Pro Ala Glu Ile Ala Ala Gly Val Ile Leu Val Gly Cys Ala
            105                 110                 115

cct ggc gga act tcc tcc aac gtg gtg tct tac ctg tcc cgt ggt gat   499
Pro Gly Gly Thr Ser Ser Asn Val Val Ser Tyr Leu Ser Arg Gly Asp
        120                 125                 130

gtt gcg ctg tct gtc acc atg act tcc atc tcc acg ctg ctt gct cca   547
Val Ala Leu Ser Val Thr Met Thr Ser Ile Ser Thr Leu Leu Ala Pro
    135                 140                 145

att ttc act cca ctg ctt acc ctg tgg ctg gcg ggg caa tac atg cca   595
Ile Phe Thr Pro Leu Leu Thr Leu Trp Leu Ala Gly Gln Tyr Met Pro
150                 155                 160                 165

ctt aat gcc gct gat atg gct gta tcc atc gtc caa gtt gtg ctg atc   643
Leu Asn Ala Ala Asp Met Ala Val Ser Ile Val Gln Val Val Leu Ile
                170                 175                 180

cca gtc gtg ggc gga ctt gtt gtg cgg ttg atc ttc ccg aca ctc att   691
Pro Val Val Gly Gly Leu Val Val Arg Leu Ile Phe Pro Thr Leu Ile
            185                 190                 195

ggc aag gtt ttg cct ctt ttg cca tgg att tca gtc att gcg att tca   739
Gly Lys Val Leu Pro Leu Leu Pro Trp Ile Ser Val Ile Ala Ile Ser
        200                 205                 210

ttg atc gtt gcc atc gtg gtc gct ggt tca agg gat aaa atc ctc gaa   787
Leu Ile Val Ala Ile Val Val Ala Gly Ser Arg Asp Lys Ile Leu Glu
    215                 220                 225

gca gga ctg ctc gtg ctg gct gcc gtg att att cac aac acc ctc ggc   835
Ala Gly Leu Leu Val Leu Ala Ala Val Ile Ile His Asn Thr Leu Gly
230                 235                 240                 245

tac tcc ctg gga tac ctc gct gcg aaa ttc act ggg cag cct gct gca   883
Tyr Ser Leu Gly Tyr Leu Ala Ala Lys Phe Thr Gly Gln Pro Ala Ala
                250                 255                 260

gct cga cgc act acc gcg att gag gtc ggt atg caa aac tcc ggc ctc   931
Ala Arg Arg Thr Thr Ala Ile Glu Val Gly Met Gln Asn Ser Gly Leu
            265                 270                 275
```

```
gca gat gga ctc gca tcc cag tac atg tca cca atg tct gct ctg cca   979
Ala Asp Gly Leu Ala Ser Gln Tyr Met Ser Pro Met Ser Ala Leu Pro
        280                 285                 290

ggc gct atc ttc tct gtc tgg cac aac ctt tcc gga gca ctt ctt gct   1027
Gly Ala Ile Phe Ser Val Trp His Asn Leu Ser Gly Ala Leu Leu Ala
    295                 300                 305

gca ttg tgc agg gcg tcc gat aag agg gct gcg gag aag gtg gct tca   1075
Ala Leu Cys Arg Ala Ser Asp Lys Arg Ala Ala Glu Lys Val Ala Ser
310                 315                 320                 325

gaa aag gct gcc tcg gag aag gcc gct tcc taaaaggctt cgctcctaaa     1125
Glu Lys Ala Ala Ser Glu Lys Ala Ala Ser
                330                 335

act                                                               1128
```

<210> 1248
<211> 335
<212> PRT
<213> Corynebacterium glutamicum

<400> 1248

```
Met Ser Thr Gln Val Glu Leu Lys Thr Pro Lys Ser Glu Asp Arg Ala
  1               5                  10                  15

Ala Tyr Ile Ala Ala Leu Gly Phe Pro Val Leu Val Ile Ile Gly Gly
            20                  25                  30

Ile Ile Gly Phe Thr Ala Ser Asp Val Val Leu Asn Ile Ser Ser Trp
        35                  40                  45

Val Asn Pro Leu Leu Gly Ile Ile Met Phe Ser Met Gly Leu Thr Leu
    50                  55                  60

Lys Pro Val Asp Phe Ala Leu Val Ala Lys Arg Pro Leu Pro Val Leu
65                  70                  75                  80

Ile Gly Val Ile Ala Gln Phe Val Ile Met Pro Leu Ile Ala Leu Leu
                85                  90                  95

Val Val Trp Val Leu Gln Leu Pro Ala Glu Ile Ala Ala Gly Val Ile
            100                 105                 110

Leu Val Gly Cys Ala Pro Gly Gly Thr Ser Ser Asn Val Val Ser Tyr
        115                 120                 125

Leu Ser Arg Gly Asp Val Ala Leu Ser Val Thr Met Thr Ser Ile Ser
    130                 135                 140

Thr Leu Leu Ala Pro Ile Phe Thr Pro Leu Leu Thr Leu Trp Leu Ala
145                 150                 155                 160

Gly Gln Tyr Met Pro Leu Asn Ala Ala Asp Met Ala Val Ser Ile Val
                165                 170                 175

Gln Val Val Leu Ile Pro Val Val Gly Gly Leu Val Val Arg Leu Ile
            180                 185                 190
```

```
Phe Pro Thr Leu Ile Gly Lys Val Leu Pro Leu Leu Pro Trp Ile Ser
        195                 200                 205

Val Ile Ala Ile Ser Leu Ile Val Ala Ile Val Val Ala Gly Ser Arg
    210                 215                 220

Asp Lys Ile Leu Glu Ala Gly Leu Leu Val Leu Ala Ala Val Ile Ile
225                 230                 235                 240

His Asn Thr Leu Gly Tyr Ser Leu Gly Tyr Leu Ala Ala Lys Phe Thr
                245                 250                 255

Gly Gln Pro Ala Ala Ala Arg Arg Thr Thr Ala Ile Glu Val Gly Met
            260                 265                 270

Gln Asn Ser Gly Leu Ala Asp Gly Leu Ala Ser Gln Tyr Met Ser Pro
        275                 280                 285

Met Ser Ala Leu Pro Gly Ala Ile Phe Ser Val Trp His Asn Leu Ser
    290                 295                 300

Gly Ala Leu Leu Ala Ala Leu Cys Arg Ala Ser Asp Lys Arg Ala Ala
305                 310                 315                 320

Glu Lys Val Ala Ser Glu Lys Ala Ala Ser Glu Lys Ala Ala Ser
                325                 330                 335
```

US20050059090A1

<210> 1249
<211> 963
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(940)
<223> RXN02656

<400> 1249

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gccatgtggg acagtctagc catctcctta cacccgtgaa actcctattt cattaacgca 60

ttgatctcgg cttttctaac ctaggtataa ggtaacagct atg att ttc ggc gta   115
                                            Met Ile Phe Gly Val
                                              1               5

ctc gca tac ttg gga tgg ggc atg ttc ccg gcc ttt ttc cca cta ctt   163
Leu Ala Tyr Leu Gly Trp Gly Met Phe Pro Ala Phe Phe Pro Leu Leu
                 10                  15                  20

ctt ccg gca gga ccg ttc gaa att tta gcg cat cgg atc cta tgg act   211
Leu Pro Ala Gly Pro Phe Glu Ile Leu Ala His Arg Ile Leu Trp Thr
             25                  30                  35

gct gta tta atg atg att atc att agt ttc acg tcg gga tgg aaa gag   259
Ala Val Leu Met Met Ile Ile Ile Ser Phe Thr Ser Gly Trp Lys Glu
         40                  45                  50

ctt aag tcc gct gat cgc ggt aca tgg tta cgc att ata ttg tca tcg   307
Leu Lys Ser Ala Asp Arg Gly Thr Trp Leu Arg Ile Ile Leu Ser Ser
     55                  60                  65
```

```
ttg ttt att gcc ggg aac tgg ctg atc tat gtc atc gct gtc aat tct   355
Leu Phe Ile Ala Gly Asn Trp Leu Ile Tyr Val Ile Ala Val Asn Ser
 70                  75                  80                  85

ggg caa gtt act gaa gcc gct ctc gga tac ttt att aac ccc ctg tta   403
Gly Gln Val Thr Glu Ala Ala Leu Gly Tyr Phe Ile Asn Pro Leu Leu
                 90                  95                 100

agt gtc gtg ctt ggc att gtg ttc ttc aaa gaa cag tta cga aaa ctg   451
Ser Val Val Leu Gly Ile Val Phe Phe Lys Glu Gln Leu Arg Lys Leu
            105                 110                 115

caa att agt gcg gtg gtt att gct gct gcg ggg gtt ttg gta cta aca   499
Gln Ile Ser Ala Val Val Ile Ala Ala Ala Gly Val Leu Val Leu Thr
        120                 125                 130

ttt cta ggt gat aag cca ccg tat tta gcg ata aca cta gca ttt aca   547
Phe Leu Gly Asp Lys Pro Pro Tyr Leu Ala Ile Thr Leu Ala Phe Thr
    135                 140                 145

ttc ggc atc tat gga gcg ttg aaa aaa caa gtc aag atg tct gct gct   595
Phe Gly Ile Tyr Gly Ala Leu Lys Lys Gln Val Lys Met Ser Ala Ala
150                 155                 160                 165

agt tct ttg tgc gct gaa act tta gta ctg ctg ccc atc gca gtc ata   643
Ser Ser Leu Cys Ala Glu Thr Leu Val Leu Leu Pro Ile Ala Val Ile
                170                 175                 180

tac ctg att ggg ctc gaa gct tcc ggt cac agt acc ttt ttc aac aat   691
Tyr Leu Ile Gly Leu Glu Ala Ser Gly His Ser Thr Phe Phe Asn Asn
            185                 190                 195

ggc agt ggg cac atg gcg tta tta atc tgc tcg ggt ttg gtc aca gcc   739
Gly Ser Gly His Met Ala Leu Leu Ile Cys Ser Gly Leu Val Thr Ala
        200                 205                 210

gtc ccg ctg ttg atg ttt gca ttg gcc gcc aag gca ata cct ctt tcc   787
Val Pro Leu Leu Met Phe Ala Leu Ala Ala Lys Ala Ile Pro Leu Ser
    215                 220                 225

act gtc ggc atg ctg caa tat ctg acc cca acg atg cag atg ctg tgg   835
Thr Val Gly Met Leu Gln Tyr Leu Thr Pro Thr Met Gln Met Leu Trp
230                 235                 240                 245

gca ttg ttt gtg gtc aac gaa tca gta gaa cca atg cgt tgg ttc gga   883
Ala Leu Phe Val Val Asn Glu Ser Val Glu Pro Met Arg Trp Phe Gly
                250                 255                 260

ttc gtt ttc att tgg atc gca gtt act att tac atc aca gat agc cta   931
Phe Val Phe Ile Trp Ile Ala Val Thr Ile Tyr Ile Thr Asp Ser Leu
            265                 270                 275

ctt aag aag taggtaatag cagtattgat atg                            963
Leu Lys Lys
        280
```

<210> 1250
<211> 280
<212> PRT

<213> Corynebacterium glutamicum

<400> 1250

```
Met Ile Phe Gly Val Leu Ala Tyr Leu Gly Trp Gly Met Phe Pro Ala
  1               5                  10                  15

Phe Phe Pro Leu Leu Leu Pro Ala Gly Pro Phe Glu Ile Leu Ala His
             20                  25                  30

Arg Ile Leu Trp Thr Ala Val Leu Met Met Ile Ile Ile Ser Phe Thr
         35                  40                  45

Ser Gly Trp Lys Glu Leu Lys Ser Ala Asp Arg Gly Thr Trp Leu Arg
     50                  55                  60

Ile Ile Leu Ser Ser Leu Phe Ile Ala Gly Asn Trp Leu Ile Tyr Val
 65                  70                  75                  80

Ile Ala Val Asn Ser Gly Gln Val Thr Glu Ala Ala Leu Gly Tyr Phe
                 85                  90                  95

Ile Asn Pro Leu Leu Ser Val Val Leu Gly Ile Val Phe Phe Lys Glu
            100                 105                 110

Gln Leu Arg Lys Leu Gln Ile Ser Ala Val Val Ile Ala Ala Ala Gly
        115                 120                 125

Val Leu Val Leu Thr Phe Leu Gly Asp Lys Pro Pro Tyr Leu Ala Ile
    130                 135                 140

Thr Leu Ala Phe Thr Phe Gly Ile Tyr Gly Ala Leu Lys Lys Gln Val
145                 150                 155                 160

Lys Met Ser Ala Ala Ser Ser Leu Cys Ala Glu Thr Leu Val Leu Leu
                165                 170                 175

Pro Ile Ala Val Ile Tyr Leu Ile Gly Leu Glu Ala Ser Gly His Ser
            180                 185                 190

Thr Phe Phe Asn Asn Gly Ser Gly His Met Ala Leu Leu Ile Cys Ser
        195                 200                 205

Gly Leu Val Thr Ala Val Pro Leu Leu Met Phe Ala Leu Ala Ala Lys
    210                 215                 220

Ala Ile Pro Leu Ser Thr Val Gly Met Leu Gln Tyr Leu Thr Pro Thr
225                 230                 235                 240

Met Gln Met Leu Trp Ala Leu Phe Val Val Asn Glu Ser Val Glu Pro
                245                 250                 255

Met Arg Trp Phe Gly Phe Val Phe Ile Trp Ile Ala Val Thr Ile Tyr
            260                 265                 270

Ile Thr Asp Ser Leu Leu Lys Lys
        275                 280
```

<210> 1251
<211> 756
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)
<223> RXN02673

<400> 1251
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acgcccaaaa cgctaatccg ctgaacaggc cgatgaaagt aatagagtgt tctgtgtggg 60

aacgccgaga cataatgaag tcatttacaa gcgccgccgc atg gca gcg ctc cta   115
                                            Met Ala Ala Leu Leu
                                              1               5

gtt ctg ctc gtc gtg att gcc ttg att atc tgg gca gtc gtc gcg ctt   163
Val Leu Leu Val Val Ile Ala Leu Ile Ile Trp Ala Val Val Ala Leu
                 10                  15                  20

cga ggt gga tca tcg gag cct gag gaa gag cag cca aat aat gct gta   211
Arg Gly Gly Ser Ser Glu Pro Glu Glu Glu Gln Pro Asn Asn Ala Val
             25                  30                  35

gtg acc tcc tca atg gaa tct tcc gcg acg tct agt tct tct tct aaa   259
Val Thr Ser Ser Met Glu Ser Ser Ala Thr Ser Ser Ser Ser Ser Lys
         40                  45                  50

gaa tcc acg act gaa gcc acc aca gaa gaa gag act tcc agt gct gaa   307
Glu Ser Thr Thr Glu Ala Thr Thr Glu Glu Glu Thr Ser Ser Ala Glu
     55                  60                  65

cca acc gca aca tcc tcc gtt gca gca gat gca aaa aag acc tgt gag   355
Pro Thr Ala Thr Ser Ser Val Ala Ala Asp Ala Lys Lys Thr Cys Glu
 70                  75                  80                  85

ctt agt gac ttg gtg att tcc gca agc act aat cag ccg act ttc tca   403
Leu Ser Asp Leu Val Ile Ser Ala Ser Thr Asn Gln Pro Thr Phe Ser
                 90                  95                 100

ggt tct gcg cag cca gaa tta ttt atg gct gtg cat aat ccg act gct   451
Gly Ser Ala Gln Pro Glu Leu Phe Met Ala Val His Asn Pro Thr Ala
            105                 110                 115

gtt gat tgc gaa att gac ctc gag gag aac aaa ctc cgt ttc gag gta   499
Val Asp Cys Glu Ile Asp Leu Glu Glu Asn Lys Leu Arg Phe Glu Val
        120                 125                 130

tac aat ctc gcg acc aac gca cga atc tgg tct gat gtc gac tgc aac   547
Tyr Asn Leu Ala Thr Asn Ala Arg Ile Trp Ser Asp Val Asp Cys Asn
    135                 140                 145

cct gca gtt gaa gac ggc acg agc gtg ttc cct gcc ggc gag gat cgc   595
Pro Ala Val Glu Asp Gly Thr Ser Val Phe Pro Ala Gly Glu Asp Arg
150                 155                 160                 165

tac ttc cag gca aca tgg tct cgt acc act tca gcg cca aac cag tgc   643
Tyr Phe Gln Ala Thr Trp Ser Arg Thr Thr Ser Ala Pro Asn Gln Cys
                170                 175                 180

aac aac cgc act gat gtc ccc gcc ggt ggc tac tac ttg cac act gtg   691
Asn Asn Arg Thr Asp Val Pro Ala Gly Gly Tyr Tyr Leu His Thr Val
            185                 190                 195
```

```
gtc ggt aat aac cct tca cca gcg gtg acc ttt aac cta act          733
Val Gly Asn Asn Pro Ser Pro Ala Val Thr Phe Asn Leu Thr
        200                 205                 210

taaacggcca agtccgtcgg tga                                       756
```

<210> 1252
<211> 211
<212> PRT
<213> Corynebacterium glutamicum

<400> 1252

```
Met Ala Ala Leu Leu Val Leu Leu Val Val Ile Ala Leu Ile Ile Trp
  1               5                  10                  15

Ala Val Val Ala Leu Arg Gly Gly Ser Ser Glu Pro Glu Glu Glu Gln
             20                  25                  30

Pro Asn Asn Ala Val Val Thr Ser Ser Met Glu Ser Ser Ala Thr Ser
         35                  40                  45

Ser Ser Ser Ser Lys Glu Ser Thr Thr Glu Ala Thr Thr Glu Glu Glu
     50                  55                  60

Thr Ser Ser Ala Glu Pro Thr Ala Thr Ser Ser Val Ala Ala Asp Ala
 65                  70                  75                  80

Lys Lys Thr Cys Glu Leu Ser Asp Leu Val Ile Ser Ala Ser Thr Asn
                 85                  90                  95

Gln Pro Thr Phe Ser Gly Ser Ala Gln Pro Glu Leu Phe Met Ala Val
            100                 105                 110

His Asn Pro Thr Ala Val Asp Cys Glu Ile Asp Leu Glu Glu Asn Lys
        115                 120                 125

Leu Arg Phe Glu Val Tyr Asn Leu Ala Thr Asn Ala Arg Ile Trp Ser
    130                 135                 140

Asp Val Asp Cys Asn Pro Ala Val Glu Asp Gly Thr Ser Val Phe Pro
145                 150                 155                 160

Ala Gly Glu Asp Arg Tyr Phe Gln Ala Thr Trp Ser Arg Thr Thr Ser
                165                 170                 175

Ala Pro Asn Gln Cys Asn Asn Arg Thr Asp Val Pro Ala Gly Gly Tyr
            180                 185                 190

Tyr Leu His Thr Val Val Gly Asn Asn Pro Ser Pro Ala Val Thr Phe
        195                 200                 205

Asn Leu Thr
    210
```

<210> 1253
<211> 756
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)
<223> FRXA02673

<400> 1253
acgcccaaaa cgctaatccg ctgaacaggc cgatgaaagt aatagagtgt tctgtgtggg 60

aacgccgaga cataatgaag tcatttacaa gcgccgccgc atg gca gcg ctc cta 115
Met Ala Ala Leu Leu
1 5

gtt ctg ctc gtc gtg att gcc ttg att atc tgg gca gtc gtc gcg ctt 163
Val Leu Leu Val Val Ile Ala Leu Ile Ile Trp Ala Val Val Ala Leu
10 15 20

cga ggt gga tca tcg gag cct gag gaa gag cag cca aat aat gct gta 211
Arg Gly Gly Ser Ser Glu Pro Glu Glu Glu Gln Pro Asn Asn Ala Val
25 30 35

gtg acc tcc tca atg gaa tct tcc gcg acg tct agt tct tct tct aaa 259
Val Thr Ser Ser Met Glu Ser Ser Ala Thr Ser Ser Ser Ser Ser Lys
40 45 50

gaa tcc acg act gaa gcc acc aca gaa gaa gag act tcc agt gct gaa 307
Glu Ser Thr Thr Glu Ala Thr Thr Glu Glu Glu Thr Ser Ser Ala Glu
55 60 65

cca acc gca aca tcc tcc gtt gca gca gat gca aaa aag acc tgt gag 355
Pro Thr Ala Thr Ser Ser Val Ala Ala Asp Ala Lys Lys Thr Cys Glu
70 75 80 85

ctt agt gac ttg gtg att tcc gca agc act aat cag ccg act ttc tca 403
Leu Ser Asp Leu Val Ile Ser Ala Ser Thr Asn Gln Pro Thr Phe Ser
90 95 100

ggt tct gcg cag cca gaa tta ttt atg gct gtg cat aat ccg act gct 451
Gly Ser Ala Gln Pro Glu Leu Phe Met Ala Val His Asn Pro Thr Ala
105 110 115

gtt gat tgc gaa att gac ctc gag gag aac aaa ctc cgt ttc gag gta 499
Val Asp Cys Glu Ile Asp Leu Glu Glu Asn Lys Leu Arg Phe Glu Val
120 125 130

tac aat ctc gcg acc aac gca cga atc tgg tct gat gtc gac tgc aac 547
Tyr Asn Leu Ala Thr Asn Ala Arg Ile Trp Ser Asp Val Asp Cys Asn
135 140 145

cct gca gtt gaa gac ggc acg agc gtg ttc cct gcc ggc gag gat cgc 595
Pro Ala Val Glu Asp Gly Thr Ser Val Phe Pro Ala Gly Glu Asp Arg
150 155 160 165

tac ttc cag gca aca tgg tct cgt acc act tca gcg cca aac cag tgc 643
Tyr Phe Gln Ala Thr Trp Ser Arg Thr Thr Ser Ala Pro Asn Gln Cys
170 175 180

aac aac cgc act gat gtc ccc gcc ggt ggc tac tac ttg cac act gtg 691
Asn Asn Arg Thr Asp Val Pro Ala Gly Gly Tyr Tyr Leu His Thr Val
185 190 195

```
gtc ggt aat aac cct tca cca gcg gtg acc ttt aac cta act          733
Val Gly Asn Asn Pro Ser Pro Ala Val Thr Phe Asn Leu Thr
        200                 205                 210

taaacggcca agtccgtcgg tga                                       756


<210> 1254
<211> 211
<212> PRT
<213> Corynebacterium glutamicum

<400> 1254
Met Ala Ala Leu Leu Val Leu Leu Val Val Ile Ala Leu Ile Ile Trp
  1               5                  10                  15

Ala Val Val Ala Leu Arg Gly Gly Ser Ser Glu Pro Glu Glu Glu Gln
             20                  25                  30

Pro Asn Asn Ala Val Val Thr Ser Ser Met Glu Ser Ser Ala Thr Ser
         35                  40                  45

Ser Ser Ser Ser Lys Glu Ser Thr Thr Glu Ala Thr Thr Glu Glu Glu
     50                  55                  60

Thr Ser Ser Ala Glu Pro Thr Ala Thr Ser Ser Val Ala Ala Asp Ala
 65                  70                  75                  80

Lys Lys Thr Cys Glu Leu Ser Asp Leu Val Ile Ser Ala Ser Thr Asn
                 85                  90                  95

Gln Pro Thr Phe Ser Gly Ser Ala Gln Pro Glu Leu Phe Met Ala Val
            100                 105                 110

His Asn Pro Thr Ala Val Asp Cys Glu Ile Asp Leu Glu Glu Asn Lys
        115                 120                 125

Leu Arg Phe Glu Val Tyr Asn Leu Ala Thr Asn Ala Arg Ile Trp Ser
    130                 135                 140

Asp Val Asp Cys Asn Pro Ala Val Glu Asp Gly Thr Ser Val Phe Pro
145                 150                 155                 160

Ala Gly Glu Asp Arg Tyr Phe Gln Ala Thr Trp Ser Arg Thr Thr Ser
                165                 170                 175

Ala Pro Asn Gln Cys Asn Asn Arg Thr Asp Val Pro Ala Gly Gly Tyr
            180                 185                 190

Tyr Leu His Thr Val Val Gly Asn Asn Pro Ser Pro Ala Val Thr Phe
        195                 200                 205

Asn Leu Thr
    210


<210> 1255
<211> 1407
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1384)
<223> RXN02680

<400> 1255
aataccaggt caacacacac aggaaccgtt cagaaacctt ccagattgct cacttttaa 60

tttcactttt ttgagaagtt ttacttttat attagttctc atg cgc ctc aac aaa 115
Met Arg Leu Asn Lys
1 5

cga ctc cca gcg gca ctc tcc gga ctg ctc tct gct gcc ctt ctt 163
Arg Leu Pro Ala Ala Leu Ser Gly Leu Leu Ser Ala Ala Leu Leu
10 15 20

gcc gga tgc tcc act tct gga acc gcc gag acc acg aca aca acc gtt 211
Ala Gly Cys Ser Thr Ser Gly Thr Ala Glu Thr Thr Thr Thr Thr Val
25 30 35

tca tct gct gcg gca tca aca acc act tcc acc tcc tct gct tcg tct 259
Ser Ser Ala Ala Ala Ser Thr Thr Thr Ser Thr Ser Ser Ala Ser Ser
40 45 50

tcc tct tcc tcc tcc tct tcc tcc tct tcc tcc gac tca agc acc acc 307
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Thr
55 60 65

gcc gaa acc atc tcc aac acc gcg gaa gct gcc caa gct ttc ttg tcc 355
Ala Glu Thr Ile Ser Asn Thr Ala Glu Ala Ala Gln Ala Phe Leu Ser
70 75 80 85

acc ctg tcc acc gaa gaa caa gac gcc gta ctc tac gac tac gac gcc 403
Thr Leu Ser Thr Glu Glu Gln Asp Ala Val Leu Tyr Asp Tyr Asp Ala
90 95 100

gaa gaa aag tcc acc ggc tgg tct aac ttc cca gtc acc ttc gtg cag 451
Glu Glu Lys Ser Thr Gly Trp Ser Asn Phe Pro Val Thr Phe Val Gln
105 110 115

cgt tcc ggc gtg aac ctc acc gac ctc act gag gaa cag caa gca gct 499
Arg Ser Gly Val Asn Leu Thr Asp Leu Thr Glu Glu Gln Gln Ala Ala
120 125 130

gcc ctc aac gtg ctg aag aac ctg ctc aac gac gac gcc tac caa atg 547
Ala Leu Asn Val Leu Lys Asn Leu Leu Asn Asp Asp Ala Tyr Gln Met
135 140 145

atc gaa gac atc atg gct agc gat cag tac ctc aac gac gaa agc aac 595
Ile Glu Asp Ile Met Ala Ser Asp Gln Tyr Leu Asn Asp Glu Ser Asn
150 155 160 165

acc acc gag gat tcc ctc ggc cag tac tac atc gca ttc ttc ggc gat 643
Thr Thr Glu Asp Ser Leu Gly Gln Tyr Tyr Ile Ala Phe Phe Gly Asp
170 175 180

cca agc agc gac tcc gac tgg tcc atc caa ttc ggc gga cac cac atc 691
Pro Ser Ser Asp Ser Asp Trp Ser Ile Gln Phe Gly Gly His His Ile
185 190 195

ggc atc aac acc acc ttc tcc gac ggt gcc atc acc ttc gcc cca acc 739

```
Gly Ile Asn Thr Thr Phe Ser Asp Gly Ala Ile Thr Phe Ala Pro Thr
        200                 205                 210

cac ctt ggc acc cag cct tcc gag tgg acc aac gag gac ggc gaa acc   787
His Leu Gly Thr Gln Pro Ser Glu Trp Thr Asn Glu Asp Gly Glu Thr
    215                 220                 225

gtt gca gca cta agc aac atg tac gaa acc gcc ttc gcc ttc tac gac   835
Val Ala Ala Leu Ser Asn Met Tyr Glu Thr Ala Phe Ala Phe Tyr Asp
230                 235                 240                 245

agc ctc gcc gaa gag cag caa gca cag ctc tac cag ggt gaa gag ttg   883
Ser Leu Ala Glu Glu Gln Gln Ala Gln Leu Tyr Gln Gly Glu Glu Leu
                250                 255                 260

gat tcc atg gtg tgc gca ccg ggc agc acg tgc gac tac cca acc ggc   931
Asp Ser Met Val Cys Ala Pro Gly Ser Thr Cys Asp Tyr Pro Thr Gly
            265                 270                 275

acc ggc ttg aaa ggc tct gac ctc acc gat gag caa aaa gaa ttg ctc   979
Thr Gly Leu Lys Gly Ser Asp Leu Thr Asp Glu Gln Lys Glu Leu Leu
        280                 285                 290

atc gat gtc atc gca aac tgg gtt ggc ctc gcc gat gag gaa acc acc   1027
Ile Asp Val Ile Ala Asn Trp Val Gly Leu Ala Asp Glu Glu Thr Thr
    295                 300                 305

gaa act gaa ctc gat gcc atc cgc gaa acc ctg gat gac acc tac atc   1075
Glu Thr Glu Leu Asp Ala Ile Arg Glu Thr Leu Asp Asp Thr Tyr Ile
310                 315                 320                 325

aac tgg tcc ggc gcc acc gag tac gac acc tcc acc ggc gac ggc atc   1123
Asn Trp Ser Gly Ala Thr Glu Tyr Asp Thr Ser Thr Gly Asp Gly Ile
                330                 335                 340

tac ttc cag atc agt ggc cca aag gtc tac att gag ttc gct aac cag   1171
Tyr Phe Gln Ile Ser Gly Pro Lys Val Tyr Ile Glu Phe Ala Asn Gln
            345                 350                 355

caa ggt tct gca ggt gcc gac atc gac ggt gtc atc acc gct gga tgg   1219
Gln Gly Ser Ala Gly Ala Asp Ile Asp Gly Val Ile Thr Ala Gly Trp
        360                 365                 370

ggc cac att cac acc atc tac cgc gac cca acc aat gac tac gct aac   1267
Gly His Ile His Thr Ile Tyr Arg Asp Pro Thr Asn Asp Tyr Ala Asn
    375                 380                 385

tcc gta act cag gaa gca gcc agc gga atg atg ggc ggc ggc cct ggt   1315
Ser Val Thr Gln Glu Ala Ala Ser Gly Met Met Gly Gly Gly Pro Gly
390                 395                 400                 405

ggt aat ggt ggc gag atg cct agc ggt gac atg cct act ggt gag atg   1363
Gly Asn Gly Gly Glu Met Pro Ser Gly Asp Met Pro Thr Gly Glu Met
                410                 415                 420

cct tct ggc gct cca tca aac taacgccatt taagaggccg aac            1407
Pro Ser Gly Ala Pro Ser Asn
            425
```

<210> 1256

<211> 428
<212> PRT
<213> Corynebacterium glutamicum

<400> 1256

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Met Arg Leu Asn Lys Arg Leu Pro Ala Ala Leu Ser Gly Leu Leu Leu
  1               5                  10                  15

Ser Ala Ala Leu Leu Ala Gly Cys Ser Thr Ser Gly Thr Ala Glu Thr
             20                  25                  30

Thr Thr Thr Thr Val Ser Ser Ala Ala Ala Ser Thr Thr Thr Ser Thr
         35                  40                  45

Ser Ser Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
     50                  55                  60

Asp Ser Ser Thr Thr Ala Glu Thr Ile Ser Asn Thr Ala Glu Ala Ala
 65                  70                  75                  80

Gln Ala Phe Leu Ser Thr Leu Ser Thr Glu Glu Gln Asp Ala Val Leu
                 85                  90                  95

Tyr Asp Tyr Asp Ala Glu Glu Lys Ser Thr Gly Trp Ser Asn Phe Pro
            100                 105                 110

Val Thr Phe Val Gln Arg Ser Gly Val Asn Leu Thr Asp Leu Thr Glu
        115                 120                 125

Glu Gln Gln Ala Ala Ala Leu Asn Val Leu Lys Asn Leu Leu Asn Asp
    130                 135                 140

Asp Ala Tyr Gln Met Ile Glu Asp Ile Met Ala Ser Asp Gln Tyr Leu
145                 150                 155                 160

Asn Asp Glu Ser Asn Thr Thr Glu Asp Ser Leu Gly Gln Tyr Tyr Ile
                165                 170                 175

Ala Phe Phe Gly Asp Pro Ser Ser Asp Ser Asp Trp Ser Ile Gln Phe
            180                 185                 190

Gly Gly His His Ile Gly Ile Asn Thr Thr Phe Ser Asp Gly Ala Ile
        195                 200                 205

Thr Phe Ala Pro Thr His Leu Gly Thr Gln Pro Ser Glu Trp Thr Asn
    210                 215                 220

Glu Asp Gly Glu Thr Val Ala Ala Leu Ser Asn Met Tyr Glu Thr Ala
225                 230                 235                 240

Phe Ala Phe Tyr Asp Ser Leu Ala Glu Glu Gln Gln Ala Gln Leu Tyr
                245                 250                 255

Gln Gly Glu Glu Leu Asp Ser Met Val Cys Ala Pro Gly Ser Thr Cys
            260                 265                 270

Asp Tyr Pro Thr Gly Thr Gly Leu Lys Gly Ser Asp Leu Thr Asp Glu
        275                 280                 285

Gln Lys Glu Leu Leu Ile Asp Val Ile Ala Asn Trp Val Gly Leu Ala
    290                 295                 300
```

```
Asp Glu Glu Thr Thr Glu Thr Glu Leu Asp Ala Ile Arg Glu Thr Leu
305                 310                 315                 320

Asp Asp Thr Tyr Ile Asn Trp Ser Gly Ala Thr Glu Tyr Asp Thr Ser
                325                 330                 335

Thr Gly Asp Gly Ile Tyr Phe Gln Ile Ser Gly Pro Lys Val Tyr Ile
            340                 345                 350

Glu Phe Ala Asn Gln Gln Gly Ser Ala Gly Ala Asp Ile Asp Gly Val
        355                 360                 365

Ile Thr Ala Gly Trp Gly His Ile His Thr Ile Tyr Arg Asp Pro Thr
    370                 375                 380

Asn Asp Tyr Ala Asn Ser Val Thr Gln Glu Ala Ala Ser Gly Met Met
385                 390                 395                 400

Gly Gly Gly Pro Gly Gly Asn Gly Gly Glu Met Pro Ser Gly Asp Met
                405                 410                 415

Pro Thr Gly Glu Met Pro Ser Gly Ala Pro Ser Asn
            420                 425
```

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<210> 1257
<211> 1407
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1384)
<223> FRXA02680

<400> 1257

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aataccaggt caacacacac aggaaccgtt cagaaacctt ccagattgct cacttttaa 60

tttcactttt ttgagaagtt ttacttttat attagttctc atg cgc ctc aac aaa   115
                                            Met Arg Leu Asn Lys
                                              1               5

cga ctc cca gcg gca ctc tcc gga ctg ctg ctc tct gct gcc ctt ctt   163
Arg Leu Pro Ala Ala Leu Ser Gly Leu Leu Leu Ser Ala Ala Leu Leu
                 10                  15                  20

gcc gga tgc tcc act tct gga acc gcc gag acc acg aca aca acc gtt   211
Ala Gly Cys Ser Thr Ser Gly Thr Ala Glu Thr Thr Thr Thr Thr Val
             25                  30                  35

tca tct gct gcg gca tca aca acc act tcc acc tcc tct gct tcg tct   259
Ser Ser Ala Ala Ala Ser Thr Thr Thr Ser Thr Ser Ser Ala Ser Ser
         40                  45                  50

tcc tct tcc tcc tcc tct tcc tcc tct tcc tcc gac tca agc acc acc   307
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Thr
     55                  60                  65

gcc gaa acc atc tcc aac acc gcg gaa gct gcc caa gct ttc ttg tcc   355
Ala Glu Thr Ile Ser Asn Thr Ala Glu Ala Ala Gln Ala Phe Leu Ser
```

```
 70                  75                  80                  85

acc ctg tcc acc gaa gaa caa gac gcc gta ctc tac gac tac gac gcc   403
Thr Leu Ser Thr Glu Glu Gln Asp Ala Val Leu Tyr Asp Tyr Asp Ala
                 90                  95                 100

gaa gaa aag tcc acc ggc tgg tct aac ttc cca gtc acc ttc gtg cag   451
Glu Glu Lys Ser Thr Gly Trp Ser Asn Phe Pro Val Thr Phe Val Gln
            105                 110                 115

cgt tcc ggc gtg aac ctc acc gac ctc act gag gaa cag caa gca gct   499
Arg Ser Gly Val Asn Leu Thr Asp Leu Thr Glu Glu Gln Gln Ala Ala
        120                 125                 130

gcc ctc aac gtg ctg aag aac ctg ctc aac gac gac gcc tac caa atg   547
Ala Leu Asn Val Leu Lys Asn Leu Leu Asn Asp Asp Ala Tyr Gln Met
    135                 140                 145

atc gaa gac atc atg gct agc gat cag tac ctc aac gac gaa agc aac   595
Ile Glu Asp Ile Met Ala Ser Asp Gln Tyr Leu Asn Asp Glu Ser Asn
150                 155                 160                 165

acc acc gag gat tcc ctc ggc cag tac tac atc gca ttc ttc ggc gat   643
Thr Thr Glu Asp Ser Leu Gly Gln Tyr Tyr Ile Ala Phe Phe Gly Asp
                170                 175                 180

cca agc agc gac tcc gac tgg tcc atc caa ttc ggc gga cac cac atc   691
Pro Ser Ser Asp Ser Asp Trp Ser Ile Gln Phe Gly Gly His His Ile
            185                 190                 195

ggc atc aac acc acc ttc tcc gac ggt gcc atc acc ttc gcc cca acc   739
Gly Ile Asn Thr Thr Phe Ser Asp Gly Ala Ile Thr Phe Ala Pro Thr
        200                 205                 210

cac ctt ggc acc cag cct tcc gag tgg acc aac gag gac ggc gaa acc   787
His Leu Gly Thr Gln Pro Ser Glu Trp Thr Asn Glu Asp Gly Glu Thr
    215                 220                 225

gtt gca gca cta agc aac atg tac gaa acc gcc ttc gcc ttc tac gac   835
Val Ala Ala Leu Ser Asn Met Tyr Glu Thr Ala Phe Ala Phe Tyr Asp
230                 235                 240                 245

agc ctc gcc gaa gag cag caa gca cag ctc tac cag ggt gaa gag ttg   883
Ser Leu Ala Glu Glu Gln Gln Ala Gln Leu Tyr Gln Gly Glu Glu Leu
                250                 255                 260

gat tcc atg gtg tgc gca ccg ggc agc acg tgc gac tac cca acc ggc   931
Asp Ser Met Val Cys Ala Pro Gly Ser Thr Cys Asp Tyr Pro Thr Gly
            265                 270                 275

acc ggc ttg aaa ggc tct gac ctc acc gat gag caa aaa gaa ttg ctc   979
Thr Gly Leu Lys Gly Ser Asp Leu Thr Asp Glu Gln Lys Glu Leu Leu
        280                 285                 290

atc gat gtc atc gca aac tgg gtt ggc ctc gcc gat gag gaa acc acc   1027
Ile Asp Val Ile Ala Asn Trp Val Gly Leu Ala Asp Glu Glu Thr Thr
    295                 300                 305

gaa act gaa ctc gat gcc atc cgc gaa acc ctg gat gac acc tac atc   1075
Glu Thr Glu Leu Asp Ala Ile Arg Glu Thr Leu Asp Asp Thr Tyr Ile
310                 315                 320                 325
```

```
aac tgg tcc ggc gcc acc gag tac gac acc tcc acc ggc gac ggc atc   1123
Asn Trp Ser Gly Ala Thr Glu Tyr Asp Thr Ser Thr Gly Asp Gly Ile
                330                 335                 340

tac ttc cag atc agt ggc cca aag gtc tac att gag ttc gct aac cag   1171
Tyr Phe Gln Ile Ser Gly Pro Lys Val Tyr Ile Glu Phe Ala Asn Gln
            345                 350                 355

caa ggt tct gca ggt gcc gac atc gac ggt gtc atc acc gct gga tgg   1219
Gln Gly Ser Ala Gly Ala Asp Ile Asp Gly Val Ile Thr Ala Gly Trp
        360                 365                 370

ggc cac att cac acc atc tac cgc gac cca acc aat gac tac gct aac   1267
Gly His Ile His Thr Ile Tyr Arg Asp Pro Thr Asn Asp Tyr Ala Asn
    375                 380                 385

tcc gta act cag gaa gca gcc agc gga atg atg ggc ggc ggc cct ggt   1315
Ser Val Thr Gln Glu Ala Ala Ser Gly Met Met Gly Gly Gly Pro Gly
390                 395                 400                 405

ggt aat ggt ggc gag atg cct agc ggt gac atg cct act ggt gag atg   1363
Gly Asn Gly Gly Glu Met Pro Ser Gly Asp Met Pro Thr Gly Glu Met
                410                 415                 420

cct tct ggc gct cca tca aac taacgccatt taagaggccg aac             1407
Pro Ser Gly Ala Pro Ser Asn
            425
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<210> 1258
<211> 428
<212> PRT
<213> Corynebacterium glutamicum

<400> 1258

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Met Arg Leu Asn Lys Arg Leu Pro Ala Ala Leu Ser Gly Leu Leu Leu
  1               5                  10                  15

Ser Ala Ala Leu Leu Ala Gly Cys Ser Thr Ser Gly Thr Ala Glu Thr
             20                  25                  30

Thr Thr Thr Thr Val Ser Ser Ala Ala Ala Ser Thr Thr Thr Ser Thr
         35                  40                  45

Ser Ser Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
     50                  55                  60

Asp Ser Ser Thr Thr Ala Glu Thr Ile Ser Asn Thr Ala Glu Ala Ala
 65                  70                  75                  80

Gln Ala Phe Leu Ser Thr Leu Ser Thr Glu Glu Gln Asp Ala Val Leu
                 85                  90                  95

Tyr Asp Tyr Asp Ala Glu Glu Lys Ser Thr Gly Trp Ser Asn Phe Pro
            100                 105                 110

Val Thr Phe Val Gln Arg Ser Gly Val Asn Leu Thr Asp Leu Thr Glu
        115                 120                 125

Glu Gln Gln Ala Ala Ala Leu Asn Val Leu Lys Asn Leu Leu Asn Asp
```

```
    130                 135                 140

Asp Ala Tyr Gln Met Ile Glu Asp Ile Met Ala Ser Asp Gln Tyr Leu
145                 150                 155                 160

Asn Asp Glu Ser Asn Thr Thr Glu Asp Ser Leu Gly Gln Tyr Tyr Ile
                165                 170                 175

Ala Phe Phe Gly Asp Pro Ser Ser Asp Ser Asp Trp Ser Ile Gln Phe
            180                 185                 190

Gly Gly His His Ile Gly Ile Asn Thr Thr Phe Ser Asp Gly Ala Ile
        195                 200                 205

Thr Phe Ala Pro Thr His Leu Gly Thr Gln Pro Ser Glu Trp Thr Asn
    210                 215                 220

Glu Asp Gly Glu Thr Val Ala Ala Leu Ser Asn Met Tyr Glu Thr Ala
225                 230                 235                 240

Phe Ala Phe Tyr Asp Ser Leu Ala Glu Glu Gln Gln Ala Gln Leu Tyr
                245                 250                 255

Gln Gly Glu Glu Leu Asp Ser Met Val Cys Ala Pro Gly Ser Thr Cys
            260                 265                 270

Asp Tyr Pro Thr Gly Thr Gly Leu Lys Gly Ser Asp Leu Thr Asp Glu
        275                 280                 285

Gln Lys Glu Leu Leu Ile Asp Val Ile Ala Asn Trp Val Gly Leu Ala
    290                 295                 300

Asp Glu Glu Thr Thr Glu Thr Glu Leu Asp Ala Ile Arg Glu Thr Leu
305                 310                 315                 320

Asp Asp Thr Tyr Ile Asn Trp Ser Gly Ala Thr Glu Tyr Asp Thr Ser
                325                 330                 335

Thr Gly Asp Gly Ile Tyr Phe Gln Ile Ser Gly Pro Lys Val Tyr Ile
            340                 345                 350

Glu Phe Ala Asn Gln Gln Gly Ser Ala Gly Ala Asp Ile Asp Gly Val
        355                 360                 365

Ile Thr Ala Gly Trp Gly His Ile His Thr Ile Tyr Arg Asp Pro Thr
    370                 375                 380

Asn Asp Tyr Ala Asn Ser Val Thr Gln Glu Ala Ala Ser Gly Met Met
385                 390                 395                 400

Gly Gly Gly Pro Gly Gly Asn Gly Gly Glu Met Pro Ser Gly Asp Met
                405                 410                 415

Pro Thr Gly Glu Met Pro Ser Gly Ala Pro Ser Asn
            420                 425
```

<210> 1259
<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(526)
<223> FRXA02679

<400> 1259
caccattacc accagggccg ccgcccatca ttccgctggc tgcttcctga gttacggagt 60

tagcgtagtc attggttggg tcgcggtaga tggtgtgaat gtg gcc cca tcc agc 115
Val Ala Pro Ser Ser
1 5

ggt gat gac acc gtc gat gtc ggc acc tgc aga acc ttg ctg gtt agc 163
Gly Asp Asp Thr Val Asp Val Gly Thr Cys Arg Thr Leu Leu Val Ser
10 15 20

gaa ctc aat gta gac ctt tgg gcc act gat ctg gaa gta gat gcc gtc 211
Glu Leu Asn Val Asp Leu Trp Ala Thr Asp Leu Glu Val Asp Ala Val
25 30 35

gcc ggt gga ggt gtc gta ctc ggt ggc gcc gga cca gtt gat gta ggt 259
Ala Gly Gly Gly Val Val Leu Gly Gly Ala Gly Pro Val Asp Val Gly
40 45 50

gtc atc cag ggt ttc gcg gat ggc atc gag ttc agt ttc ggt ggt ttc 307
Val Ile Gln Gly Phe Ala Asp Gly Ile Glu Phe Ser Phe Gly Gly Phe
55 60 65

ctc atc ggc gag gcc aac cca gtt tgc gat gac atc gat gag caa ttc 355
Leu Ile Gly Glu Ala Asn Pro Val Cys Asp Asp Ile Asp Glu Gln Phe
70 75 80 85

ttt ttg ctc atc ggt gag gtc aga gcc ttt caa gcc ggt gcc ggt tgg 403
Phe Leu Leu Ile Gly Glu Val Arg Ala Phe Gln Ala Gly Ala Gly Trp
90 95 100

gta gtc gca cgt gct gcc cgg tgc gca cac cat gga atc caa ctc ttc 451
Val Val Ala Arg Ala Ala Arg Cys Ala His His Gly Ile Gln Leu Phe
105 110 115

acc ctg gta gag ctg tgc ttg ctg ctc ttc ggc gag gct gtc gta gaa 499
Thr Leu Val Glu Leu Cys Leu Leu Leu Phe Gly Glu Ala Val Val Glu
120 125 130

ggc gaa ggc ggt ttc gta cat gtt gct tagtgctgca acggtttcgc 546
Gly Glu Gly Gly Phe Val His Val Ala
135 140

cgt 549

<210> 1260
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 1260
Val Ala Pro Ser Ser Gly Asp Asp Thr Val Asp Val Gly Thr Cys Arg
1 5 10 15

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Thr Leu Leu Val Ser Glu Leu Asn Val Asp Leu Trp Ala Thr Asp Leu
             20                  25                  30

Glu Val Asp Ala Val Ala Gly Gly Gly Val Val Leu Gly Gly Ala Gly
         35                  40                  45

Pro Val Asp Val Gly Val Ile Gln Gly Phe Ala Asp Gly Ile Glu Phe
     50                  55                  60

Ser Phe Gly Gly Phe Leu Ile Gly Glu Ala Asn Pro Val Cys Asp Asp
 65                  70                  75                  80

Ile Asp Glu Gln Phe Phe Leu Leu Ile Gly Glu Val Arg Ala Phe Gln
                 85                  90                  95

Ala Gly Ala Gly Trp Val Val Ala Arg Ala Ala Arg Cys Ala His His
            100                 105                 110

Gly Ile Gln Leu Phe Thr Leu Val Glu Leu Cys Leu Leu Leu Phe Gly
        115                 120                 125

Glu Ala Val Val Glu Gly Glu Gly Gly Phe Val His Val Ala
    130                 135                 140
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<210> 1261
<211> 567
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(544)
<223> FRXA02681

<400> 1261

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cgaggctgtc gtagaaggcg aaggcggttt cgtacatgtt gcttagtgct gcaacggttt 60

cgccgtcctc gttggtccac tcggaaggct gggtgccaag gtg ggt tgg ggc gaa   115
                                            Val Gly Trp Gly Glu
                                              1               5

ggt gat ggc acc gtc gga gaa ggt ggt gtt gat gcc gat gtg gtg tcc   163
Gly Asp Gly Thr Val Gly Glu Gly Gly Val Asp Ala Asp Val Val Ser
                 10                  15                  20

gcc gaa ttg gat gga cca gtc gga gtc gct gct tgg atc gcc gaa gaa   211
Ala Glu Leu Asp Gly Pro Val Gly Val Ala Ala Trp Ile Ala Glu Glu
             25                  30                  35

tgc gat gta gta ctg gcc gag gga atc ctc ggt ggt gtt gct ttc gtc   259
Cys Asp Val Val Leu Ala Glu Gly Ile Leu Gly Gly Val Ala Phe Val
         40                  45                  50

gtt gag gta ctg atc gct agc cat gat gtc ttc gat cat ttg gta ggc   307
Val Glu Val Leu Ile Ala Ser His Asp Val Phe Asp His Leu Val Gly
     55                  60                  65

gtc gtc gtt gag cag gtt ctt cag cac gtt gag ggc agc tgc ttg ctg   355
Val Val Val Glu Gln Val Leu Gln His Val Glu Gly Ser Cys Leu Leu
 70                  75                  80                  85
```

```
ttc ctc agt gag gtc ggt gag gtt cac gcc gga acg ctg cac gaa ggt   403
Phe Leu Ser Glu Val Gly Glu Val His Ala Gly Thr Leu His Glu Gly
                 90                  95                 100

gac tgg gaa gtt aga cca gcc ggt gga ctt ttc ttc ggc gtc gta gtc   451
Asp Trp Glu Val Arg Pro Ala Gly Gly Leu Phe Phe Gly Val Val Val
            105                 110                 115

gta gag tac ggc gtc ttg ttc ttc ggt gga cag ggt gga caa gaa agc   499
Val Glu Tyr Gly Val Leu Phe Phe Gly Gly Gln Gly Gly Gln Glu Ser
        120                 125                 130

ttg ggc agc ttc cgc ggt gtt gga gat ggt ttc ggc ggt ggt gct       544
Leu Gly Ser Phe Arg Gly Val Gly Asp Gly Phe Gly Gly Gly Ala
    135                 140                 145

tgagtcggag gaagaggagg aag                                         567
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<210> 1262
<211> 148
<212> PRT
<213> Corynebacterium glutamicum

<400> 1262

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Val Gly Trp Gly Glu Gly Asp Gly Thr Val Gly Glu Gly Gly Val Asp
  1               5                  10                  15

Ala Asp Val Val Ser Ala Glu Leu Asp Gly Pro Val Gly Val Ala Ala
             20                  25                  30

Trp Ile Ala Glu Glu Cys Asp Val Val Leu Ala Glu Gly Ile Leu Gly
         35                  40                  45

Gly Val Ala Phe Val Val Glu Val Leu Ile Ala Ser His Asp Val Phe
     50                  55                  60

Asp His Leu Val Gly Val Val Val Glu Gln Val Leu Gln His Val Glu
 65                  70                  75                  80

Gly Ser Cys Leu Leu Phe Leu Ser Glu Val Gly Glu Val His Ala Gly
                 85                  90                  95

Thr Leu His Glu Gly Asp Trp Glu Val Arg Pro Ala Gly Gly Leu Phe
            100                 105                 110

Phe Gly Val Val Val Val Glu Tyr Gly Val Leu Phe Phe Gly Gly Gln
        115                 120                 125

Gly Gly Gln Glu Ser Leu Gly Ser Phe Arg Gly Val Gly Asp Gly Phe
    130                 135                 140

Gly Gly Gly Ala
145
```

<210> 1263
<211> 1899
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1876)
<223> RXN02693

<400> 1263
cagaccaagt gttatttttg ttgaaaaaat cacattgtaa atcgagcaaa accaacctat 60

gccctgcaga attgtgcatg ctctgccaag atgactcaat atg gtt tcg ctc ccc 115
Met Val Ser Leu Pro
1 5

aga cta gcg tct ctg ctc acc act cgc ctg gca acg ctt aaa ccc gca 163
Arg Leu Ala Ser Leu Leu Thr Thr Arg Leu Ala Thr Leu Lys Pro Ala
10 15 20

cta aaa cct gcc acc cac ctc gcc tcc ctc ggc gcg cag gtc att gca 211
Leu Lys Pro Ala Thr His Leu Ala Ser Leu Gly Ala Gln Val Ile Ala
25 30 35

gag cta gtt ccg ggg atc cga atg tcg cca aac cgc agg cga atc ctc 259
Glu Leu Val Pro Gly Ile Arg Met Ser Pro Asn Arg Arg Arg Ile Leu
40 45 50

cct gca aat atg ggc gct ggc ttt atc gga gcg gaa atc gca atg tgg 307
Pro Ala Asn Met Gly Ala Gly Phe Ile Gly Ala Glu Ile Ala Met Trp
55 60 65

tgg gct ctc tcg ccg tca ttg ttg ccg aaa ccg tgg tgg gtt acg gct 355
Trp Ala Leu Ser Pro Ser Leu Leu Pro Lys Pro Trp Trp Val Thr Ala
70 75 80 85

gct aac ctg gct gtt tta caa gcg gtg ggg cat gcg gca gcg acg gga 403
Ala Asn Leu Ala Val Leu Gln Ala Val Gly His Ala Ala Ala Thr Gly
90 95 100

atc cac tcg atc ctc ccc aga acc aac cgg cgg gta tcc agg aaa att 451
Ile His Ser Ile Leu Pro Arg Thr Asn Arg Arg Val Ser Arg Lys Ile
105 110 115

tac aac gcc acc cac atc gca act ggt gcc atc acg ttg acc acc acg 499
Tyr Asn Ala Thr His Ile Ala Thr Gly Ala Ile Thr Leu Thr Thr Thr
120 125 130

gtt gtg gga ttg atc agg cat cgc acc caa atc cgg ctg att ggg cag 547
Val Val Gly Leu Ile Arg His Arg Thr Gln Ile Arg Leu Ile Gly Gln
135 140 145

aag aat ttt gga ccg aag gag acg atc gcg ggc att agt gtc ggc acc 595
Lys Asn Phe Gly Pro Lys Glu Thr Ile Ala Gly Ile Ser Val Gly Thr
150 155 160 165

ttg ggg tac ggc gcg ctg ctg atc acc ggc gaa tta acc cag cac agt 643
Leu Gly Tyr Gly Ala Leu Leu Ile Thr Gly Glu Leu Thr Gln His Ser
170 175 180

att aat gag gtc aag ctc cta att gag agg ttt tta ccg ccg tgg ata 691
Ile Asn Glu Val Lys Leu Leu Ile Glu Arg Phe Leu Pro Pro Trp Ile
185 190 195

```
agt ttc atc gca gcg gtt tcg gtc att aca ttg acc act ttg acc ttg   739
Ser Phe Ile Ala Ala Val Ser Val Ile Thr Leu Thr Thr Leu Thr Leu
        200                 205                 210

gcc gat cgc gtt ttg ttg cgg cgc atc ttg cat aat tct gca att caa   787
Ala Asp Arg Val Leu Leu Arg Arg Ile Leu His Asn Ser Ala Ile Gln
    215                 220                 225

gca gcg cac ctt aat cgc atg gtg ttc cca gga act gag cag ccg tgg   835
Ala Ala His Leu Asn Arg Met Val Phe Pro Gly Thr Glu Gln Pro Trp
230                 235                 240                 245

gag ccg gag cgt tcg ggt agc ccg tgg tcg tat gaa aaa tgg ggt gcg   883
Glu Pro Glu Arg Ser Gly Ser Pro Trp Ser Tyr Glu Lys Trp Gly Ala
                250                 255                 260

gtg ggt tcg cag ggc cgt gca gtg ttg tcg gga ggc cca cgc aaa gat   931
Val Gly Ser Gln Gly Arg Ala Val Leu Ser Gly Gly Pro Arg Lys Asp
            265                 270                 275

gac atc atc acg gta acc agg ctt tct gac acg gaa aca cat gaa ccg   979
Asp Ile Ile Thr Val Thr Arg Leu Ser Asp Thr Glu Thr His Glu Pro
        280                 285                 290

att cgt att ttt atc ggt atg gtt ccg gga cga tcc tta agc gat cag   1027
Ile Arg Ile Phe Ile Gly Met Val Pro Gly Arg Ser Leu Ser Asp Gln
    295                 300                 305

gtg gat ctt gtc att cat gaa atg cgc cgc acg gga gcc ctg cgc cgc   1075
Val Asp Leu Val Ile His Glu Met Arg Arg Thr Gly Ala Leu Arg Arg
310                 315                 320                 325

gac cac atc gtg atc aac aat tcc acg ggc acc ggc tgg atc acc gat   1123
Asp His Ile Val Ile Asn Asn Ser Thr Gly Thr Gly Trp Ile Thr Asp
                330                 335                 340

tgg tcc gcc cac acc ttt gag ttc ctc acc ggc gga aac tgc gtg aca   1171
Trp Ser Ala His Thr Phe Glu Phe Leu Thr Gly Gly Asn Cys Val Thr
            345                 350                 355

att tcc atg caa tat tct tat ctt ccc agt gca ctg agc tgg tac aag   1219
Ile Ser Met Gln Tyr Ser Tyr Leu Pro Ser Ala Leu Ser Trp Tyr Lys
        360                 365                 370

gac aac gac ggc ccc att aat gcg gcg aga atg ctt atc gac gcc gtc   1267
Asp Asn Asp Gly Pro Ile Asn Ala Ala Arg Met Leu Ile Asp Ala Val
    375                 380                 385

ctc cac gag cta gac cag ctt ccc acc ggg agt cgc cca aag ctg ttc   1315
Leu His Glu Leu Asp Gln Leu Pro Thr Gly Ser Arg Pro Lys Leu Phe
390                 395                 400                 405

ctc gcg gga gag tca ctg ggg gcg tat ggg ttg gct gag gtg tgg gga   1363
Leu Ala Gly Glu Ser Leu Gly Ala Tyr Gly Leu Ala Glu Val Trp Gly
                410                 415                 420

gac gtc gaa aag ctt ctt gga acc gct gac ggc gtg ctg ctc agt ggg   1411
Asp Val Glu Lys Leu Leu Gly Thr Ala Asp Gly Val Leu Leu Ser Gly
            425                 430                 435

gcg ccg cgt ttt tcg gac gcc atg aat gcg ttg cgc acc cgg cgc gat   1459
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Ala Pro Arg Phe Ser Asp Ala Met Asn Ala Leu Arg Thr Arg Arg Asp
        440                 445                 450

gcg agc agc tcc gag cgg ctg ccc gtg att gat agc ggg cgg cac atc   1507
Ala Ser Ser Ser Glu Arg Leu Pro Val Ile Asp Ser Gly Arg His Ile
    455                 460                 465

cgt ttt gcg ggc gag cct gag cac ctt gat atg ccg gct acc tgg cag   1555
Arg Phe Ala Gly Glu Pro Glu His Leu Asp Met Pro Ala Thr Trp Gln
470                 475                 480                 485

ttt ccg cgc atg atc gtg gcg cag cac gcc tct gat cca att gtg tgg   1603
Phe Pro Arg Met Ile Val Ala Gln His Ala Ser Asp Pro Ile Val Trp
                490                 495                 500

tgg aac gcg gag ctg ttt att cgg cgg ccg gaa tgg ttg aaa act ccc   1651
Trp Asn Ala Glu Leu Phe Ile Arg Arg Pro Glu Trp Leu Lys Thr Pro
            505                 510                 515

aag caa gac cac caa gat gtc ttt ccc cgc ttg cga tgg atg ccg ttt   1699
Lys Gln Asp His Gln Asp Val Phe Pro Arg Leu Arg Trp Met Pro Phe
        520                 525                 530

gta acc ggc tgg cag gtg gct ttg gat ttg ttc act tca acc tcc gtt   1747
Val Thr Gly Trp Gln Val Ala Leu Asp Leu Phe Thr Ser Thr Ser Val
    535                 540                 545

ccc ggc ggg cac ggg cac aat tat cac gag gag ttt att gat tat tgg   1795
Pro Gly Gly His Gly His Asn Tyr His Glu Glu Phe Ile Asp Tyr Trp
550                 555                 560                 565

gca gct ctt ttg gac cgc gaa gtc acc ccc gag ctg cgc cac agc att   1843
Ala Ala Leu Leu Asp Arg Glu Val Thr Pro Glu Leu Arg His Ser Ile
                570                 575                 580

gct tat tgg atc cgc gcg aac cac atc aaa cgc tagagtgatt ccatgacgca 1896
Ala Tyr Trp Ile Arg Ala Asn His Ile Lys Arg
            585                 590

tgc                                                               1899


<210> 1264
<211> 592
<212> PRT
<213> Corynebacterium glutamicum

<400> 1264
Met Val Ser Leu Pro Arg Leu Ala Ser Leu Leu Thr Thr Arg Leu Ala
  1               5                  10                  15

Thr Leu Lys Pro Ala Leu Lys Pro Ala Thr His Leu Ala Ser Leu Gly
             20                  25                  30

Ala Gln Val Ile Ala Glu Leu Val Pro Gly Ile Arg Met Ser Pro Asn
         35                  40                  45

Arg Arg Arg Ile Leu Pro Ala Asn Met Gly Ala Gly Phe Ile Gly Ala
     50                  55                  60

Glu Ile Ala Met Trp Trp Ala Leu Ser Pro Ser Leu Leu Pro Lys Pro
```

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65                  70                  75                  80

Trp Trp Val Thr Ala Ala Asn Leu Ala Val Leu Gln Ala Val Gly His
                85                  90                  95

Ala Ala Ala Thr Gly Ile His Ser Ile Leu Pro Arg Thr Asn Arg Arg
            100                 105                 110

Val Ser Arg Lys Ile Tyr Asn Ala Thr His Ile Ala Thr Gly Ala Ile
        115                 120                 125

Thr Leu Thr Thr Thr Val Val Gly Leu Ile Arg His Arg Thr Gln Ile
    130                 135                 140

Arg Leu Ile Gly Gln Lys Asn Phe Gly Pro Lys Glu Thr Ile Ala Gly
145                 150                 155                 160

Ile Ser Val Gly Thr Leu Gly Tyr Gly Ala Leu Leu Ile Thr Gly Glu
                165                 170                 175

Leu Thr Gln His Ser Ile Asn Glu Val Lys Leu Leu Ile Glu Arg Phe
            180                 185                 190

Leu Pro Pro Trp Ile Ser Phe Ile Ala Ala Val Ser Val Ile Thr Leu
        195                 200                 205

Thr Thr Leu Thr Leu Ala Asp Arg Val Leu Leu Arg Arg Ile Leu His
    210                 215                 220

Asn Ser Ala Ile Gln Ala Ala His Leu Asn Arg Met Val Phe Pro Gly
225                 230                 235                 240

Thr Glu Gln Pro Trp Glu Pro Glu Arg Ser Gly Ser Pro Trp Ser Tyr
                245                 250                 255

Glu Lys Trp Gly Ala Val Gly Ser Gln Gly Arg Ala Val Leu Ser Gly
            260                 265                 270

Gly Pro Arg Lys Asp Asp Ile Ile Thr Val Thr Arg Leu Ser Asp Thr
        275                 280                 285

Glu Thr His Glu Pro Ile Arg Ile Phe Ile Gly Met Val Pro Gly Arg
    290                 295                 300

Ser Leu Ser Asp Gln Val Asp Leu Val Ile His Glu Met Arg Arg Thr
305                 310                 315                 320

Gly Ala Leu Arg Arg Asp His Ile Val Ile Asn Asn Ser Thr Gly Thr
                325                 330                 335

Gly Trp Ile Thr Asp Trp Ser Ala His Thr Phe Glu Phe Leu Thr Gly
            340                 345                 350

Gly Asn Cys Val Thr Ile Ser Met Gln Tyr Ser Tyr Leu Pro Ser Ala
        355                 360                 365

Leu Ser Trp Tyr Lys Asp Asn Asp Gly Pro Ile Asn Ala Ala Arg Met
    370                 375                 380

Leu Ile Asp Ala Val Leu His Glu Leu Asp Gln Leu Pro Thr Gly Ser
385                 390                 395                 400
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Arg Pro Lys Leu Phe Leu Ala Gly Glu Ser Leu Gly Ala Tyr Gly Leu
                405                 410                 415

Ala Glu Val Trp Gly Asp Val Glu Lys Leu Leu Gly Thr Ala Asp Gly
            420                 425                 430

Val Leu Leu Ser Gly Ala Pro Arg Phe Ser Asp Ala Met Asn Ala Leu
        435                 440                 445

Arg Thr Arg Arg Asp Ala Ser Ser Ser Glu Arg Leu Pro Val Ile Asp
    450                 455                 460

Ser Gly Arg His Ile Arg Phe Ala Gly Glu Pro Glu His Leu Asp Met
465                 470                 475                 480

Pro Ala Thr Trp Gln Phe Pro Arg Met Ile Val Ala Gln His Ala Ser
                485                 490                 495

Asp Pro Ile Val Trp Trp Asn Ala Glu Leu Phe Ile Arg Arg Pro Glu
            500                 505                 510

Trp Leu Lys Thr Pro Lys Gln Asp His Gln Asp Val Phe Pro Arg Leu
        515                 520                 525

Arg Trp Met Pro Phe Val Thr Gly Trp Gln Val Ala Leu Asp Leu Phe
    530                 535                 540

Thr Ser Thr Ser Val Pro Gly Gly His Gly His Asn Tyr His Glu Glu
545                 550                 555                 560

Phe Ile Asp Tyr Trp Ala Ala Leu Leu Asp Arg Glu Val Thr Pro Glu
                565                 570                 575

Leu Arg His Ser Ile Ala Tyr Trp Ile Arg Ala Asn His Ile Lys Arg
            580                 585                 590
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<210> 1265
<211> 1747
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1747)
<223> FRXA02693

<400> 1265
cagaccaagt gttatttttg ttgaaaaaat cacattgtaa atcgagcaaa accaacctat 60

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gccctgcaga attgtgcatg ctctgccaag atgactcaat atg gtt tcg ctc ccc   115
                                              Met Val Ser Leu Pro
                                                1               5

aga cta gcg tct ctg ctc acc act cgc ctg gca acg ctt aaa ccc gca   163
Arg Leu Ala Ser Leu Leu Thr Thr Arg Leu Ala Thr Leu Lys Pro Ala
                10                  15                  20
```

```
cta aaa cct gcc acc cac ctc gcc tcc ctc ggc gcg cag gtc att gca   211
Leu Lys Pro Ala Thr His Leu Ala Ser Leu Gly Ala Gln Val Ile Ala
            25                  30                  35

gag cta gtt ccg ggg atc cga atg tcg cca aac cgc agg cga atc ctc   259
Glu Leu Val Pro Gly Ile Arg Met Ser Pro Asn Arg Arg Arg Ile Leu
        40                  45                  50

cct gca aat atg ggc gct ggc ttt atc gga gcg gaa atc gca atg tgg   307
Pro Ala Asn Met Gly Ala Gly Phe Ile Gly Ala Glu Ile Ala Met Trp
    55                  60                  65

tgg gct ctc tcg ccg tca ttg ttg ccg aaa ccg tgg tgg gtt acg gct   355
Trp Ala Leu Ser Pro Ser Leu Leu Pro Lys Pro Trp Trp Val Thr Ala
70                  75                  80                  85

gct aac ctg gct gtt tta caa gcg gtg ggg cat gcg gca gcg acg gga   403
Ala Asn Leu Ala Val Leu Gln Ala Val Gly His Ala Ala Ala Thr Gly
                90                  95                  100

atc cac tcg atc ctc ccc aga acc aac cgg cgg gta tcc agg aaa att   451
Ile His Ser Ile Leu Pro Arg Thr Asn Arg Arg Val Ser Arg Lys Ile
            105                 110                 115

tac aac gcc acc cac atc gca act ggt gcc atc acg ttg acc acc acg   499
Tyr Asn Ala Thr His Ile Ala Thr Gly Ala Ile Thr Leu Thr Thr Thr
        120                 125                 130

gtt gtg gga ttg atc agg cat cgc acc caa atc cgg ctg att ggg cag   547
Val Val Gly Leu Ile Arg His Arg Thr Gln Ile Arg Leu Ile Gly Gln
    135                 140                 145

aag aat ttt gga ccg aag gag acg atc gcg ggc att agt gtc ggc acc   595
Lys Asn Phe Gly Pro Lys Glu Thr Ile Ala Gly Ile Ser Val Gly Thr
150                 155                 160                 165

ttg ggg tac ggc gcg ctg ctg atc acc ggc gaa tta acc cag cac agt   643
Leu Gly Tyr Gly Ala Leu Leu Ile Thr Gly Glu Leu Thr Gln His Ser
                170                 175                 180

att aat gag gtc aag ctc cta att gag agg ttt tta ccg ccg tgg ata   691
Ile Asn Glu Val Lys Leu Leu Ile Glu Arg Phe Leu Pro Pro Trp Ile
            185                 190                 195

agt ttc atc gca gcg gtt tcg gtc att aca ttg acc act ttg acc ttg   739
Ser Phe Ile Ala Ala Val Ser Val Ile Thr Leu Thr Thr Leu Thr Leu
        200                 205                 210

gcc gat cgc gtt ttg ttg cgg cgc atc ttg cat aat tct gca att caa   787
Ala Asp Arg Val Leu Leu Arg Arg Ile Leu His Asn Ser Ala Ile Gln
    215                 220                 225

gca gcg cac ctt aat cgc atg gtg ttc cca gga act gag cag ccg tgg   835
Ala Ala His Leu Asn Arg Met Val Phe Pro Gly Thr Glu Gln Pro Trp
230                 235                 240                 245

gag ccg gag cgt tcg ggt agc ccg tgg tcg tat gaa aaa tgg ggt gcg   883
Glu Pro Glu Arg Ser Gly Ser Pro Trp Ser Tyr Glu Lys Trp Gly Ala
                250                 255                 260
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gtg ggt tcg cag ggc cgt gca gtg ttg tcg gga ggc cca cgc aaa gat   931
Val Gly Ser Gln Gly Arg Ala Val Leu Ser Gly Gly Pro Arg Lys Asp
            265                 270                 275

gac atc atc acg gta acc agg ctt tct gac acg gaa aca cat gaa ccg   979
Asp Ile Ile Thr Val Thr Arg Leu Ser Asp Thr Glu Thr His Glu Pro
        280                 285                 290

att cgt att ttt atc ggt atg gtt ccg gga cga tcc tta agc gat cag   1027
Ile Arg Ile Phe Ile Gly Met Val Pro Gly Arg Ser Leu Ser Asp Gln
    295                 300                 305

gtg gat ctt gtc att cat gaa atg cgc cgc acg gga gcc ctg cgc cgc   1075
Val Asp Leu Val Ile His Glu Met Arg Arg Thr Gly Ala Leu Arg Arg
310                 315                 320                 325

gac cac atc gtg atc aac aat tcc acg ggc acc ggc tgg atc acc gat   1123
Asp His Ile Val Ile Asn Asn Ser Thr Gly Thr Gly Trp Ile Thr Asp
                330                 335                 340

tgg tcc gcc cac acc ttt gag ttc ctc acc ggc gga aac tgc gtg aca   1171
Trp Ser Ala His Thr Phe Glu Phe Leu Thr Gly Gly Asn Cys Val Thr
            345                 350                 355

att tcc atg caa tat tct tat ctt ccc agt gca ctg agc tgg tac aag   1219
Ile Ser Met Gln Tyr Ser Tyr Leu Pro Ser Ala Leu Ser Trp Tyr Lys
        360                 365                 370

gac aac gac ggc ccc att aat gcg gcg aga atg ctt atc gac gcc gtc   1267
Asp Asn Asp Gly Pro Ile Asn Ala Ala Arg Met Leu Ile Asp Ala Val
    375                 380                 385

ctc cac gag cta gac cag ctt ccc acc ggg agt cgc cca aag ctg ttc   1315
Leu His Glu Leu Asp Gln Leu Pro Thr Gly Ser Arg Pro Lys Leu Phe
390                 395                 400                 405

ctc gcg gga gag tca ctg ggg gcg tat ggg ttg gct gag gtg tgg gga   1363
Leu Ala Gly Glu Ser Leu Gly Ala Tyr Gly Leu Ala Glu Val Trp Gly
                410                 415                 420

gac gtc gaa aag ctt ctt gga acc gct gac ggc gtg ctg ctc agt ggg   1411
Asp Val Glu Lys Leu Leu Gly Thr Ala Asp Gly Val Leu Leu Ser Gly
            425                 430                 435

gcg ccg cgt ttt tcg gac gcc atg aat gcg ttg cgc acc cgg cgc gat   1459
Ala Pro Arg Phe Ser Asp Ala Met Asn Ala Leu Arg Thr Arg Arg Asp
        440                 445                 450

gcg agc agc tcc gag cgg ctg ccc gtg att gat agc ggg cgg cac atc   1507
Ala Ser Ser Ser Glu Arg Leu Pro Val Ile Asp Ser Gly Arg His Ile
    455                 460                 465

cgt ttt gcg ggc gag cct gag cac ctt gat atg ccg gct acc tgg cag   1555
Arg Phe Ala Gly Glu Pro Glu His Leu Asp Met Pro Ala Thr Trp Gln
470                 475                 480                 485

ttt ccg cgc atg atc gtg gcg cag cac gcc tct gat cca att gtg tgg   1603
Phe Pro Arg Met Ile Val Ala Gln His Ala Ser Asp Pro Ile Val Trp
                490                 495                 500

tgg aac gcg gag ctg ttt att cgg cgg ccg gaa tgg ttg aaa act ccc   1651
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Trp Asn Ala Glu Leu Phe Ile Arg Arg Pro Glu Trp Leu Lys Thr Pro
            505                 510                 515

aag caa gac cac caa gat gtc ttt aac cgc ttg cga tgg atg ccg ttt   1699
Lys Gln Asp His Gln Asp Val Phe Asn Arg Leu Arg Trp Met Pro Phe
        520                 525                 530

gtt gcc ggc tgg cag gtg gct ttg gat ttg ttc act tca acc tcc gtt   1747
Val Ala Gly Trp Gln Val Ala Leu Asp Leu Phe Thr Ser Thr Ser Val
    535                 540                 545


<210> 1266
<211> 549
<212> PRT
<213> Corynebacterium glutamicum

<400> 1266
Met Val Ser Leu Pro Arg Leu Ala Ser Leu Leu Thr Thr Arg Leu Ala
  1               5                  10                  15

Thr Leu Lys Pro Ala Leu Lys Pro Ala Thr His Leu Ala Ser Leu Gly
             20                  25                  30

Ala Gln Val Ile Ala Glu Leu Val Pro Gly Ile Arg Met Ser Pro Asn
         35                  40                  45

Arg Arg Arg Ile Leu Pro Ala Asn Met Gly Ala Gly Phe Ile Gly Ala
     50                  55                  60

Glu Ile Ala Met Trp Trp Ala Leu Ser Pro Ser Leu Leu Pro Lys Pro
 65                  70                  75                  80

Trp Trp Val Thr Ala Ala Asn Leu Ala Val Leu Gln Ala Val Gly His
                85                  90                  95

Ala Ala Ala Thr Gly Ile His Ser Ile Leu Pro Arg Thr Asn Arg Arg
            100                 105                 110

Val Ser Arg Lys Ile Tyr Asn Ala Thr His Ile Ala Thr Gly Ala Ile
        115                 120                 125

Thr Leu Thr Thr Thr Val Val Gly Leu Ile Arg His Arg Thr Gln Ile
    130                 135                 140

Arg Leu Ile Gly Gln Lys Asn Phe Gly Pro Lys Glu Thr Ile Ala Gly
145                 150                 155                 160

Ile Ser Val Gly Thr Leu Gly Tyr Gly Ala Leu Leu Ile Thr Gly Glu
                165                 170                 175

Leu Thr Gln His Ser Ile Asn Glu Val Lys Leu Leu Ile Glu Arg Phe
            180                 185                 190

Leu Pro Pro Trp Ile Ser Phe Ile Ala Ala Val Ser Val Ile Thr Leu
        195                 200                 205

Thr Thr Leu Thr Leu Ala Asp Arg Val Leu Leu Arg Arg Ile Leu His
    210                 215                 220

Asn Ser Ala Ile Gln Ala Ala His Leu Asn Arg Met Val Phe Pro Gly
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225                 230                 235                 240

Thr Glu Gln Pro Trp Glu Pro Glu Arg Ser Gly Ser Pro Trp Ser Tyr
                245                 250                 255

Glu Lys Trp Gly Ala Val Gly Ser Gln Gly Arg Ala Val Leu Ser Gly
            260                 265                 270

Gly Pro Arg Lys Asp Asp Ile Ile Thr Val Thr Arg Leu Ser Asp Thr
        275                 280                 285

Glu Thr His Glu Pro Ile Arg Ile Phe Ile Gly Met Val Pro Gly Arg
    290                 295                 300

Ser Leu Ser Asp Gln Val Asp Leu Val Ile His Glu Met Arg Arg Thr
305                 310                 315                 320

Gly Ala Leu Arg Arg Asp His Ile Val Ile Asn Asn Ser Thr Gly Thr
                325                 330                 335

Gly Trp Ile Thr Asp Trp Ser Ala His Thr Phe Glu Phe Leu Thr Gly
            340                 345                 350

Gly Asn Cys Val Thr Ile Ser Met Gln Tyr Ser Tyr Leu Pro Ser Ala
        355                 360                 365

Leu Ser Trp Tyr Lys Asp Asn Asp Gly Pro Ile Asn Ala Ala Arg Met
    370                 375                 380

Leu Ile Asp Ala Val Leu His Glu Leu Asp Gln Leu Pro Thr Gly Ser
385                 390                 395                 400

Arg Pro Lys Leu Phe Leu Ala Gly Glu Ser Leu Gly Ala Tyr Gly Leu
                405                 410                 415

Ala Glu Val Trp Gly Asp Val Glu Lys Leu Leu Gly Thr Ala Asp Gly
            420                 425                 430

Val Leu Leu Ser Gly Ala Pro Arg Phe Ser Asp Ala Met Asn Ala Leu
        435                 440                 445

Arg Thr Arg Arg Asp Ala Ser Ser Ser Glu Arg Leu Pro Val Ile Asp
    450                 455                 460

Ser Gly Arg His Ile Arg Phe Ala Gly Glu Pro Glu His Leu Asp Met
465                 470                 475                 480

Pro Ala Thr Trp Gln Phe Pro Arg Met Ile Val Ala Gln His Ala Ser
                485                 490                 495

Asp Pro Ile Val Trp Trp Asn Ala Glu Leu Phe Ile Arg Arg Pro Glu
            500                 505                 510

Trp Leu Lys Thr Pro Lys Gln Asp His Gln Asp Val Phe Asn Arg Leu
        515                 520                 525

Arg Trp Met Pro Phe Val Ala Gly Trp Gln Val Ala Leu Asp Leu Phe
    530                 535                 540

Thr Ser Thr Ser Val
545
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<210> 1267
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXN02696

<400> 1267
cttgggaacc gaccgctagc gtagaaaatc aagttaaggg tgtgacgagc accccagctg 60

cacatgaaat ttaagacatt ccaggtgaag ggaaactgcc atg tcc atg ctc aag 115
Met Ser Met Leu Lys
1 5

aag act aaa gaa ttc ttc gga ctc gct cca tac gaa gcg gag cac gag 163
Lys Thr Lys Glu Phe Phe Gly Leu Ala Pro Tyr Glu Ala Glu His Glu
10 15 20

gat gct tac tat gca gat gaa cca cgt tac gag ggc acc gct gcg tac 211
Asp Ala Tyr Tyr Ala Asp Glu Pro Arg Tyr Glu Gly Thr Ala Ala Tyr
25 30 35

gca cct gaa tac cgt gag cgt gac tac ggc tat gca cca gag gca cca 259
Ala Pro Glu Tyr Arg Glu Arg Asp Tyr Gly Tyr Ala Pro Glu Ala Pro
40 45 50

gcc cct gtt gct cca tcg cca gca cct cgc tct tac cag tcc acc atc 307
Ala Pro Val Ala Pro Ser Pro Ala Pro Arg Ser Tyr Gln Ser Thr Ile
55 60 65

gtt cca gta gag ctt cat tcc ttt gaa gac gct cag gtt att ggt gga 355
Val Pro Val Glu Leu His Ser Phe Glu Asp Ala Gln Val Ile Gly Gly
70 75 80 85

gca ttt cgc gac ggc gac gca gtt gtt ttc gac atg agc ttg ctt tcc 403
Ala Phe Arg Asp Gly Asp Ala Val Val Phe Asp Met Ser Leu Leu Ser
90 95 100

cgt gag gaa gca cgc cgc att gtg gac ttc gct gca ggc ctg tgc ttc 451
Arg Glu Glu Ala Arg Arg Ile Val Asp Phe Ala Ala Gly Leu Cys Phe
105 110 115

gca ttg cgt ggc aag atg cag aag att gac agc gtc acc ttc gct gtc 499
Ala Leu Arg Gly Lys Met Gln Lys Ile Asp Ser Val Thr Phe Ala Val
120 125 130

gtt cca gag ctg tcc aac atc agc act tcc gag ctc gag cgc gcc gca 547
Val Pro Glu Leu Ser Asn Ile Ser Thr Ser Glu Leu Glu Arg Ala Ala
135 140 145

cgc atc cgc taaacacacc ctcgtggtgt gga 579
Arg Ile Arg
150

<210> 1268

<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 1268
Met Ser Met Leu Lys Lys Thr Lys Glu Phe Phe Gly Leu Ala Pro Tyr
1 5 10 15

Glu Ala Glu His Glu Asp Ala Tyr Tyr Ala Asp Glu Pro Arg Tyr Glu
20 25 30

Gly Thr Ala Ala Tyr Ala Pro Glu Tyr Arg Glu Arg Asp Tyr Gly Tyr
35 40 45

Ala Pro Glu Ala Pro Ala Pro Val Ala Pro Ser Pro Ala Pro Arg Ser
50 55 60

Tyr Gln Ser Thr Ile Val Pro Val Glu Leu His Ser Phe Glu Asp Ala
65 70 75 80

Gln Val Ile Gly Gly Ala Phe Arg Asp Gly Asp Ala Val Val Phe Asp
85 90 95

Met Ser Leu Leu Ser Arg Glu Glu Ala Arg Arg Ile Val Asp Phe Ala
100 105 110

Ala Gly Leu Cys Phe Ala Leu Arg Gly Lys Met Gln Lys Ile Asp Ser
115 120 125

Val Thr Phe Ala Val Val Pro Glu Leu Ser Asn Ile Ser Thr Ser Glu
130 135 140

Leu Glu Arg Ala Ala Arg Ile Arg
145 150

<210> 1269
<211> 578
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (100)..(555)
<223> FRXA02696

<400> 1269
ngcttnaaga aataaagccc tncccagtta anggtgngna tgggtaccag ccctgtggac 60

gctgtacatn taagtcattn ctggttnagg tganctgccatg tcc atg ctc aag aag 117
Met Ser Met Leu Lys Lys
1 5

act aaa gaa ttc ttc gga ctc gct cca tac gaa gcg gag cac gag gat 165
Thr Lys Glu Phe Phe Gly Leu Ala Pro Tyr Glu Ala Glu His Glu Asp
10 15 20

gct tac tat gca gat gaa cca cgt tac gag ggc acc gct gcg tac gca 213
Ala Tyr Tyr Ala Asp Glu Pro Arg Tyr Glu Gly Thr Ala Ala Tyr Ala
25 30 35

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cct gaa tac cgt gag cgt gac tac ggc tat gca cca gag gca cca gcc   261
Pro Glu Tyr Arg Glu Arg Asp Tyr Gly Tyr Ala Pro Glu Ala Pro Ala
     40                  45                  50

cct gtt gct cca tcg cca gca cct cgc tct tac cag tcc acc atc gtt   309
Pro Val Ala Pro Ser Pro Ala Pro Arg Ser Tyr Gln Ser Thr Ile Val
 55                  60                  65                  70

cca gta gag ctt cat tcc ttt gaa gac gct cag gtt att ggt gga gca   357
Pro Val Glu Leu His Ser Phe Glu Asp Ala Gln Val Ile Gly Gly Ala
                 75                  80                  85

ttt cgc gac ggc gac gca gtt gtt ttc gac atg agc ttg ctt tcc cgt   405
Phe Arg Asp Gly Asp Ala Val Val Phe Asp Met Ser Leu Leu Ser Arg
             90                  95                 100

gag gaa gca cgc cgc att gtg gac ttc gct gca ggc ctg tgc ttc gca   453
Glu Glu Ala Arg Arg Ile Val Asp Phe Ala Ala Gly Leu Cys Phe Ala
        105                 110                 115

ttg cgt ggc aag atg cag aag att gac agc gtc acc ttc gct gtc gtt   501
Leu Arg Gly Lys Met Gln Lys Ile Asp Ser Val Thr Phe Ala Val Val
    120                 125                 130

cca gag ctg tcc aac atc agc act tcc gag ctc gag cgc gcc gca cgc   549
Pro Glu Leu Ser Asn Ile Ser Thr Ser Glu Leu Glu Arg Ala Ala Arg
135                 140                 145                 150

atc cgc taaacacacc ctcgtggtgt gga                                578
Ile Arg
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09550.0009.CP1.000

<210> 1270
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 1270

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Met Ser Met Leu Lys Lys Thr Lys Glu Phe Phe Gly Leu Ala Pro Tyr
  1               5                  10                  15

Glu Ala Glu His Glu Asp Ala Tyr Tyr Ala Asp Glu Pro Arg Tyr Glu
             20                  25                  30

Gly Thr Ala Ala Tyr Ala Pro Glu Tyr Arg Glu Arg Asp Tyr Gly Tyr
         35                  40                  45

Ala Pro Glu Ala Pro Ala Pro Val Ala Pro Ser Pro Ala Pro Arg Ser
     50                  55                  60

Tyr Gln Ser Thr Ile Val Pro Val Glu Leu His Ser Phe Glu Asp Ala
 65                  70                  75                  80

Gln Val Ile Gly Gly Ala Phe Arg Asp Gly Asp Ala Val Val Phe Asp
                 85                  90                  95

Met Ser Leu Leu Ser Arg Glu Glu Ala Arg Arg Ile Val Asp Phe Ala
            100                 105                 110

Ala Gly Leu Cys Phe Ala Leu Arg Gly Lys Met Gln Lys Ile Asp Ser
```

```
        115                 120                 125

Val Thr Phe Ala Val Val Pro Glu Leu Ser Asn Ile Ser Thr Ser Glu
    130                 135                 140

Leu Glu Arg Ala Ala Arg Ile Arg
145                 150


<210> 1271
<211> 1650
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1627)
<223> RXN02697

<400> 1271
tttggctcac ctcgatgatg tagacatccc cgatgaggtg cgcgcacagt tgcgggcact 60

ggctatccgc tcaaccgaac gtcggatgta gtagacgcgt atg aca ctt ttt caa   115
                                              Met Thr Leu Phe Gln
                                                1               5

cgt tta acc aac cct gta gtg ctc ggc ggc cta gca ggt gtt ttg ctt   163
Arg Leu Thr Asn Pro Val Val Leu Gly Gly Leu Ala Gly Val Leu Leu
                  10                  15                  20

ctg ctc ggc tct ttc ggt ggc ggt gcc att cgg tac cgt ggc gga gtg   211
Leu Leu Gly Ser Phe Gly Gly Gly Ala Ile Arg Tyr Arg Gly Gly Val
              25                  30                  35

ctc gat gcg ttg ggg ctt aac ttc ctt gct ttt ggc cac gcg cag ggt   259
Leu Asp Ala Leu Gly Leu Asn Phe Leu Ala Phe Gly His Ala Gln Gly
          40                  45                  50

att tcc aat acc gtg ttg tgg gtt ggg cag ctg ctg ctg att ggc gcg   307
Ile Ser Asn Thr Val Leu Trp Val Gly Gln Leu Leu Leu Ile Gly Ala
      55                  60                  65

tgg gtt cac ctt gga cgt cgg ttg ttc aag aaa aaa gtc gct gat gac   355
Trp Val His Leu Gly Arg Arg Leu Phe Lys Lys Lys Val Ala Asp Asp
  70                  75                  80                  85

acc gca gac gct gct gac tta ggt ctt gta aag cgc acg ttg tat gcc   403
Thr Ala Asp Ala Ala Asp Leu Gly Leu Val Lys Arg Thr Leu Tyr Ala
                  90                  95                 100

atg gtg gtg ccc ctc att ttt gcg gca cca atg atg tcg cgt gat gtt   451
Met Val Val Pro Leu Ile Phe Ala Ala Pro Met Met Ser Arg Asp Val
              105                 110                 115

tat tcc tat ctc atg cag ggc gcg atg ctg cgt gat ggc ttc gat ccc   499
Tyr Ser Tyr Leu Met Gln Gly Ala Met Leu Arg Asp Gly Phe Asp Pro
          120                 125                 130

tac act gag ggc gct gcg gta aac cct ggc ccc atg ttg ctt gag gtc   547
Tyr Thr Glu Gly Ala Ala Val Asn Pro Gly Pro Met Leu Leu Glu Val
      135                 140                 145
```

```
tct cat gat tgg cgc aac acc acg acg ccg tat ggt cca cta cac ctg   595
Ser His Asp Trp Arg Asn Thr Thr Thr Pro Tyr Gly Pro Leu His Leu
150                 155                 160                 165

tgg att gga gac atg atc acc acg gtt gtg ggc gat aat gtc acc ttg   643
Trp Ile Gly Asp Met Ile Thr Thr Val Val Gly Asp Asn Val Thr Leu
                170                 175                 180

ggc gtc gtc gct tac aag atc ttg tcg atc att ggc ctt gct gtg aca   691
Gly Val Val Ala Tyr Lys Ile Leu Ser Ile Ile Gly Leu Ala Val Thr
            185                 190                 195

ggc tgg agc att gtc cgc att gca caa cat ttt gga gcc aac cca gca   739
Gly Trp Ser Ile Val Arg Ile Ala Gln His Phe Gly Ala Asn Pro Ala
        200                 205                 210

att gca ttg tgg att ggt gtg gcc aat cct gtg atg atc atc cac atg   787
Ile Ala Leu Trp Ile Gly Val Ala Asn Pro Val Met Ile Ile His Met
    215                 220                 225

atc ggc ggc atg cac aat gaa tcc ctc atg gtg gga ttg gtc agc gtc   835
Ile Gly Gly Met His Asn Glu Ser Leu Met Val Gly Leu Val Ser Val
230                 235                 240                 245

ggc ttg ttg cta gca ctg aag aag cgt ttc gtg gca ggt gtg gca ctc   883
Gly Leu Leu Leu Ala Leu Lys Lys Arg Phe Val Ala Gly Val Ala Leu
                250                 255                 260

att gca gtg gct gtg tcg ctg aaa gct aca gcg gcg att gca ctt cct   931
Ile Ala Val Ala Val Ser Leu Lys Ala Thr Ala Ala Ile Ala Leu Pro
            265                 270                 275

ttt gtg gtg tgg atc ggc atg cat cat ttc gca gga ttc tta gcc acc   979
Phe Val Val Trp Ile Gly Met His His Phe Ala Gly Phe Leu Ala Thr
        280                 285                 290

aaa aag ggc aaa gac tcc cct acc ctt aag caa cag gtc ccc gcg ttc  1027
Lys Lys Gly Lys Asp Ser Pro Thr Leu Lys Gln Gln Val Pro Ala Phe
    295                 300                 305

ttt gcc act gga gct gca ggt gtt gct gtc act ggt gtt gtt gtc agt  1075
Phe Ala Thr Gly Ala Ala Gly Val Ala Val Thr Gly Val Val Val Ser
310                 315                 320                 325

gcg atc act tgg gcg tct ggc gct tcg tgg ggc tgg atc agt gag atc  1123
Ala Ile Thr Trp Ala Ser Gly Ala Ser Trp Gly Trp Ile Ser Glu Ile
                330                 335                 340

agt ggc aac agc aag gta atc aac ccg ctg gct ttc cct tct ttg gtg  1171
Ser Gly Asn Ser Lys Val Ile Asn Pro Leu Ala Phe Pro Ser Leu Val
            345                 350                 355

gcc agt gtg atc acc atg gtg gct gaa gtg ttc gtt gac gat ttc gac  1219
Ala Ser Val Ile Thr Met Val Ala Glu Val Phe Val Asp Asp Phe Asp
        360                 365                 370

tac aac gca gtg gtt aat gtt gtg cgc tca atc tcc atg ctg atc atg  1267
Tyr Asn Ala Val Val Asn Val Val Arg Ser Ile Ser Met Leu Ile Met
    375                 380                 385
```

```
ctt ggc ggg ttg gtc gta tgt tgg tgg ctg ttc cgc cag aac gaa cgc   1315
Leu Gly Gly Leu Val Val Cys Trp Trp Leu Phe Arg Gln Asn Glu Arg
390                 395                 400                 405

agg gcg gtc act ggt aca gca gcg gct tat gcc gtg gct ttt gtg ttc   1363
Arg Ala Val Thr Gly Thr Ala Ala Ala Tyr Ala Val Ala Phe Val Phe
                410                 415                 420

aat tct gtg acc ttg ccg tgg tac tac gcc agc ttg atc tct ttg ctc   1411
Asn Ser Val Thr Leu Pro Trp Tyr Tyr Ala Ser Leu Ile Ser Leu Leu
            425                 430                 435

ggc aca ttt aaa cca ccg atg tgg ttg att cgc ttc gca gcg ggt gct   1459
Gly Thr Phe Lys Pro Pro Met Trp Leu Ile Arg Phe Ala Ala Gly Ala
        440                 445                 450

tcg gtg ttt atc gcg ctg atg ttt acc gga agt gga aac cac cag ctg   1507
Ser Val Phe Ile Ala Leu Met Phe Thr Gly Ser Gly Asn His Gln Leu
    455                 460                 465

tac aac atc gtt acg gtg atc atc gca gca att atc gcg tgg ctt gcc   1555
Tyr Asn Ile Val Thr Val Ile Ile Ala Ala Ile Ile Ala Trp Leu Ala
470                 475                 480                 485

acc gtg gtg atc ttt gat gac act gac cct gca aca acg gcc acg gag   1603
Thr Val Val Ile Phe Asp Asp Thr Asp Pro Ala Thr Thr Ala Thr Glu
                490                 495                 500

aaa ccc tcc ccg cat acc gtt tcc tagttgcata aggtaaaccg cca         1650
Lys Pro Ser Pro His Thr Val Ser
            505
```

<210> 1272
<211> 509
<212> PRT
<213> Corynebacterium glutamicum

<400> 1272

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Met Thr Leu Phe Gln Arg Leu Thr Asn Pro Val Val Leu Gly Gly Leu
  1               5                  10                  15

Ala Gly Val Leu Leu Leu Leu Gly Ser Phe Gly Gly Gly Ala Ile Arg
             20                  25                  30

Tyr Arg Gly Gly Val Leu Asp Ala Leu Gly Leu Asn Phe Leu Ala Phe
         35                  40                  45

Gly His Ala Gln Gly Ile Ser Asn Thr Val Leu Trp Val Gly Gln Leu
     50                  55                  60

Leu Leu Ile Gly Ala Trp Val His Leu Gly Arg Arg Leu Phe Lys Lys
 65                  70                  75                  80

Lys Val Ala Asp Asp Thr Ala Asp Ala Ala Asp Leu Gly Leu Val Lys
                 85                  90                  95

Arg Thr Leu Tyr Ala Met Val Val Pro Leu Ile Phe Ala Ala Pro Met
            100                 105                 110

Met Ser Arg Asp Val Tyr Ser Tyr Leu Met Gln Gly Ala Met Leu Arg
```

```
        115                 120                 125

Asp Gly Phe Asp Pro Tyr Thr Glu Gly Ala Ala Val Asn Pro Gly Pro
    130                 135                 140

Met Leu Leu Glu Val Ser His Asp Trp Arg Asn Thr Thr Thr Pro Tyr
145                 150                 155                 160

Gly Pro Leu His Leu Trp Ile Gly Asp Met Ile Thr Thr Val Val Gly
                165                 170                 175

Asp Asn Val Thr Leu Gly Val Val Ala Tyr Lys Ile Leu Ser Ile Ile
            180                 185                 190

Gly Leu Ala Val Thr Gly Trp Ser Ile Val Arg Ile Ala Gln His Phe
        195                 200                 205

Gly Ala Asn Pro Ala Ile Ala Leu Trp Ile Gly Val Ala Asn Pro Val
    210                 215                 220

Met Ile Ile His Met Ile Gly Gly Met His Asn Glu Ser Leu Met Val
225                 230                 235                 240

Gly Leu Val Ser Val Gly Leu Leu Leu Ala Leu Lys Lys Arg Phe Val
                245                 250                 255

Ala Gly Val Ala Leu Ile Ala Val Ala Val Ser Leu Lys Ala Thr Ala
            260                 265                 270

Ala Ile Ala Leu Pro Phe Val Val Trp Ile Gly Met His His Phe Ala
        275                 280                 285

Gly Phe Leu Ala Thr Lys Lys Gly Lys Asp Ser Pro Thr Leu Lys Gln
    290                 295                 300

Gln Val Pro Ala Phe Phe Ala Thr Gly Ala Ala Gly Val Ala Val Thr
305                 310                 315                 320

Gly Val Val Val Ser Ala Ile Thr Trp Ala Ser Gly Ala Ser Trp Gly
                325                 330                 335

Trp Ile Ser Glu Ile Ser Gly Asn Ser Lys Val Ile Asn Pro Leu Ala
            340                 345                 350

Phe Pro Ser Leu Val Ala Ser Val Ile Thr Met Val Ala Glu Val Phe
        355                 360                 365

Val Asp Asp Phe Asp Tyr Asn Ala Val Val Asn Val Val Arg Ser Ile
    370                 375                 380

Ser Met Leu Ile Met Leu Gly Gly Leu Val Val Cys Trp Trp Leu Phe
385                 390                 395                 400

Arg Gln Asn Glu Arg Arg Ala Val Thr Gly Thr Ala Ala Ala Tyr Ala
                405                 410                 415

Val Ala Phe Val Phe Asn Ser Val Thr Leu Pro Trp Tyr Tyr Ala Ser
            420                 425                 430

Leu Ile Ser Leu Leu Gly Thr Phe Lys Pro Pro Met Trp Leu Ile Arg
        435                 440                 445
```

```
Phe Ala Ala Gly Ala Ser Val Phe Ile Ala Leu Met Phe Thr Gly Ser
    450                 455                 460

Gly Asn His Gln Leu Tyr Asn Ile Val Thr Val Ile Ile Ala Ala Ile
465                 470                 475                 480

Ile Ala Trp Leu Ala Thr Val Val Ile Phe Asp Asp Thr Asp Pro Ala
                485                 490                 495

Thr Thr Ala Thr Glu Lys Pro Ser Pro His Thr Val Ser
            500                 505
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<210> 1273
<211> 722
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(699)
<223> FRXA02697

<400> 1273

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cct ttt gtg gtg tgg atc ggc atg cat cat ttc gca gga ttc tta gcc   48
Pro Phe Val Val Trp Ile Gly Met His His Phe Ala Gly Phe Leu Ala
  1               5                  10                  15

acc aaa aag ggc aaa gac tcc cct acc ctt aag caa cag gtc ccc gcg   96
Thr Lys Lys Gly Lys Asp Ser Pro Thr Leu Lys Gln Gln Val Pro Ala
            20                  25                  30

ttc ttt gcc act gga gct gca ggt gtt gct gtc act ggt gtt gtt gtc   144
Phe Phe Ala Thr Gly Ala Ala Gly Val Ala Val Thr Gly Val Val Val
        35                  40                  45

agt gcg atc act tgg gcg tct ggc gct tcg tgg ggc tgg atc agt gag   192
Ser Ala Ile Thr Trp Ala Ser Gly Ala Ser Trp Gly Trp Ile Ser Glu
    50                  55                  60

atc agt ggc aac agc aag gta atc aac ccg ctg gct ttc cct tct ttg   240
Ile Ser Gly Asn Ser Lys Val Ile Asn Pro Leu Ala Phe Pro Ser Leu
65                  70                  75                  80

gtg gcc agt gtg atc acc atg gtg gct gaa gtg ttc gtt gac gat ttc   288
Val Ala Ser Val Ile Thr Met Val Ala Glu Val Phe Val Asp Asp Phe
                85                  90                  95

gac tac aac gca gtg gtt aat gtt gtg cgc tca atc tcc atg ctg atc   336
Asp Tyr Asn Ala Val Val Asn Val Val Arg Ser Ile Ser Met Leu Ile
            100                 105                 110

atg ctt ggc ggg ttg gtc gta tgt tgg tgg ctg ttc cgc cag aac gaa   384
Met Leu Gly Gly Leu Val Val Cys Trp Trp Leu Phe Arg Gln Asn Glu
        115                 120                 125

cgc agg gcg gtc act ggt aca gcg gcg gct tat gcc gtg gct ttt gtg   432
Arg Arg Ala Val Thr Gly Thr Ala Ala Ala Tyr Ala Val Ala Phe Val
    130                 135                 140
```

```
ttc aat tct gtg acc ttg ccg tgg tac tac gcc agc ttg atc tct ttg   480
Phe Asn Ser Val Thr Leu Pro Trp Tyr Tyr Ala Ser Leu Ile Ser Leu
145                 150                 155                 160

ctc ggc aca ttt aaa cca ccg atg tgg ttg att cgc ttc gca gcg ggt   528
Leu Gly Thr Phe Lys Pro Pro Met Trp Leu Ile Arg Phe Ala Ala Gly
                165                 170                 175

gct tcg gtg ttt atc gcg ctg atg ttt acc gga agt gga aac cac cag   576
Ala Ser Val Phe Ile Ala Leu Met Phe Thr Gly Ser Gly Asn His Gln
            180                 185                 190

ctg tac aac atc gtt acg gtg atc atc gca gca att atc gcg tgg ctt   624
Leu Tyr Asn Ile Val Thr Val Ile Ile Ala Ala Ile Ile Ala Trp Leu
        195                 200                 205

gcc acc gtg gtg atc ttt gat gac act gac cct gca aca acg gcc acg   672
Ala Thr Val Val Ile Phe Asp Asp Thr Asp Pro Ala Thr Thr Ala Thr
    210                 215                 220

gag aaa ccc tcc ccg cat acc gtt tcc tagttgcata aggtaaaccg         719
Glu Lys Pro Ser Pro His Thr Val Ser
225                 230

cca                                                               722


<210> 1274
<211> 233
<212> PRT
<213> Corynebacterium glutamicum

<400> 1274
Pro Phe Val Val Trp Ile Gly Met His His Phe Ala Gly Phe Leu Ala
  1               5                  10                  15

Thr Lys Lys Gly Lys Asp Ser Pro Thr Leu Lys Gln Gln Val Pro Ala
             20                  25                  30

Phe Phe Ala Thr Gly Ala Ala Gly Val Ala Val Thr Gly Val Val Val
         35                  40                  45

Ser Ala Ile Thr Trp Ala Ser Gly Ala Ser Trp Gly Trp Ile Ser Glu
     50                  55                  60

Ile Ser Gly Asn Ser Lys Val Ile Asn Pro Leu Ala Phe Pro Ser Leu
 65                  70                  75                  80

Val Ala Ser Val Ile Thr Met Val Ala Glu Val Phe Val Asp Asp Phe
                 85                  90                  95

Asp Tyr Asn Ala Val Val Asn Val Val Arg Ser Ile Ser Met Leu Ile
            100                 105                 110

Met Leu Gly Gly Leu Val Val Cys Trp Trp Leu Phe Arg Gln Asn Glu
        115                 120                 125

Arg Arg Ala Val Thr Gly Thr Ala Ala Ala Tyr Ala Val Ala Phe Val
    130                 135                 140

Phe Asn Ser Val Thr Leu Pro Trp Tyr Tyr Ala Ser Leu Ile Ser Leu
```

```
145                 150                 155                 160

Leu Gly Thr Phe Lys Pro Pro Met Trp Leu Ile Arg Phe Ala Ala Gly
                165                 170                 175

Ala Ser Val Phe Ile Ala Leu Met Phe Thr Gly Ser Gly Asn His Gln
            180                 185                 190

Leu Tyr Asn Ile Val Thr Val Ile Ile Ala Ala Ile Ile Ala Trp Leu
        195                 200                 205

Ala Thr Val Val Ile Phe Asp Asp Thr Asp Pro Ala Thr Thr Ala Thr
    210                 215                 220

Glu Lys Pro Ser Pro His Thr Val Ser
225                 230
```

<210> 1275
<211> 748
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> FRXA02719

<400> 1275

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tttggctcac ctcgatgatg tagacatccc cgatgaggtg cgcgcacagt tgcgggcact 60

ggctatccgc tcaaccgaac gtcggatgta gtagacgcgt atg aca ctt ttt caa   115
                                              Met Thr Leu Phe Gln
                                                1               5

cgt tta acc aac cct gta gtg ctc ggc ggc cta gca ggt gtt ttg ctt   163
Arg Leu Thr Asn Pro Val Val Leu Gly Gly Leu Ala Gly Val Leu Leu
                10                  15                  20

ctg ctc ggc tct ttc ggt ggc ggt gcc att cgg tac cgt ggc gga gtg   211
Leu Leu Gly Ser Phe Gly Gly Gly Ala Ile Arg Tyr Arg Gly Gly Val
            25                  30                  35

ctc gat gcg ttg ggg ctt aac ttc ctt gct ttt ggc cac gcg cag ggt   259
Leu Asp Ala Leu Gly Leu Asn Phe Leu Ala Phe Gly His Ala Gln Gly
        40                  45                  50

att tcc aat acc gtg ttg tgg gtt ggg cag ctg ctg ctg att ggc gcg   307
Ile Ser Asn Thr Val Leu Trp Val Gly Gln Leu Leu Leu Ile Gly Ala
    55                  60                  65

tgg gtt cac ctt gga cgt cgg ttg ttc aag aaa aaa gtc gct gat gac   355
Trp Val His Leu Gly Arg Arg Leu Phe Lys Lys Lys Val Ala Asp Asp
70                  75                  80                  85

acc gca gac gct gct gac tta ggt ctt gta aag cgc acg ttg tat gcc   403
Thr Ala Asp Ala Ala Asp Leu Gly Leu Val Lys Arg Thr Leu Tyr Ala
                90                  95                  100

atg gtg gtg ccc ctc att ttt gcg gca cca atg atg tcg cgt gat gtt   451
Met Val Val Pro Leu Ile Phe Ala Ala Pro Met Met Ser Arg Asp Val
```

```
            105                 110                 115

tat tcc tat ctc atg cag ggc gcg atg ctg cgt gat ggc ttc gat ccc   499
Tyr Ser Tyr Leu Met Gln Gly Ala Met Leu Arg Asp Gly Phe Asp Pro
        120                 125                 130

tac act gag ggc gct gcg gta aac cct ggc ccc atg ttg ctt gag gtc   547
Tyr Thr Glu Gly Ala Ala Val Asn Pro Gly Pro Met Leu Leu Glu Val
    135                 140                 145

tct cat gat tgg cgc aac acc acg acg ccg tat ggt cca cta cac ctg   595
Ser His Asp Trp Arg Asn Thr Thr Thr Pro Tyr Gly Pro Leu His Leu
150                 155                 160                 165

tgg att gga gac atg atc acc acg gtt gtg ggc gat aat gtc acc ttg   643
Trp Ile Gly Asp Met Ile Thr Thr Val Val Gly Asp Asn Val Thr Leu
                170                 175                 180

ggc gtc gtc gct tac aag atc ttg tcg atc att ggc ctt gct gtg aca   691
Gly Val Val Ala Tyr Lys Ile Leu Ser Ile Ile Gly Leu Ala Val Thr
            185                 190                 195

ggc tgg agc att gtc cgc att gca caa cat ttt gga gcc aac cca gca   739
Gly Trp Ser Ile Val Arg Ile Ala Gln His Phe Gly Ala Asn Pro Ala
        200                 205                 210

att gca ttg                                                       748
Ile Ala Leu
    215
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EP2270150A1

<210> 1276
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 1276

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Met Thr Leu Phe Gln Arg Leu Thr Asn Pro Val Val Leu Gly Gly Leu
  1               5                  10                  15

Ala Gly Val Leu Leu Leu Leu Gly Ser Phe Gly Gly Gly Ala Ile Arg
             20                  25                  30

Tyr Arg Gly Gly Val Leu Asp Ala Leu Gly Leu Asn Phe Leu Ala Phe
         35                  40                  45

Gly His Ala Gln Gly Ile Ser Asn Thr Val Leu Trp Val Gly Gln Leu
     50                  55                  60

Leu Leu Ile Gly Ala Trp Val His Leu Gly Arg Arg Leu Phe Lys Lys
 65                  70                  75                  80

Lys Val Ala Asp Asp Thr Ala Asp Ala Ala Asp Leu Gly Leu Val Lys
                 85                  90                  95

Arg Thr Leu Tyr Ala Met Val Val Pro Leu Ile Phe Ala Ala Pro Met
            100                 105                 110

Met Ser Arg Asp Val Tyr Ser Tyr Leu Met Gln Gly Ala Met Leu Arg
        115                 120                 125
```

```
Asp Gly Phe Asp Pro Tyr Thr Glu Gly Ala Ala Val Asn Pro Gly Pro
    130                 135                 140

Met Leu Leu Glu Val Ser His Asp Trp Arg Asn Thr Thr Thr Pro Tyr
145                 150                 155                 160

Gly Pro Leu His Leu Trp Ile Gly Asp Met Ile Thr Thr Val Val Gly
                165                 170                 175

Asp Asn Val Thr Leu Gly Val Val Ala Tyr Lys Ile Leu Ser Ile Ile
            180                 185                 190

Gly Leu Ala Val Thr Gly Trp Ser Ile Val Arg Ile Ala Gln His Phe
        195                 200                 205

Gly Ala Asn Pro Ala Ile Ala Leu
    210                 215


<210> 1277
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> RXN02720

<400> 1277
ccacgctgca ccatcgaaga cgaagatctg ttttcttacc gccgcgaagg cacgacaggc 60

cgccaggccg gcgtggtgtg gctgccaaag gaggcataaa ttg gag cgc cgc gaa   115
                                              Leu Glu Arg Arg Glu
                                                1               5

gag ctg cag gta cga ctg cag cag gtg caa gcg cgt atc gac gcg acc   163
Glu Leu Gln Val Arg Leu Gln Gln Val Gln Ala Arg Ile Asp Ala Thr
                10                  15                  20

ctc aac gaa cac aac cgc ccc gag ggc agt gta cgt ctg ttg ccg gtc   211
Leu Asn Glu His Asn Arg Pro Glu Gly Ser Val Arg Leu Leu Pro Val
            25                  30                  35

acc aaa ttc cac ccc gtg gaa gac atc aag atc tta caa gag ttt ggt   259
Thr Lys Phe His Pro Val Glu Asp Ile Lys Ile Leu Gln Glu Phe Gly
        40                  45                  50

gtc acc gca gtg gga gag aac cgc gaa caa gaa gca cgc gcc aaa gca   307
Val Thr Ala Val Gly Glu Asn Arg Glu Gln Glu Ala Arg Ala Lys Ala
    55                  60                  65

ctc gaa ctt ccc gac atg gac ttt cat atg att ggc caa atc caa tca   355
Leu Glu Leu Pro Asp Met Asp Phe His Met Ile Gly Gln Ile Gln Ser
70                  75                  80                  85

aag aaa gcc aac tcg atc gcc agg tgg gca gct gca gtg cac tcc gtt   403
Lys Lys Ala Asn Ser Ile Ala Arg Trp Ala Ala Ala Val His Ser Val
                90                  95                  100

gat agc gag aaa atc gcc gaa gca ttg ggc agg gga gta gcc ctt gca   451
```

```
Asp Ser Glu Lys Ile Ala Glu Ala Leu Gly Arg Gly Val Ala Leu Ala
            105                 110                 115

ttg gat aga ggc gac cgc acc agt gac gag ctt ccg tgt ttt att caa   499
Leu Asp Arg Gly Asp Arg Thr Ser Asp Glu Leu Pro Cys Phe Ile Gln
        120                 125                 130

ctg agt ttg gat ggt gac ccg agc cga ggt gga act cca ttg agc cag   547
Leu Ser Leu Asp Gly Asp Pro Ser Arg Gly Gly Thr Pro Leu Ser Gln
    135                 140                 145

gtc aca caa ctt gcc gat tgc atc agt gac acc aca cat ctg cgt ttt   595
Val Thr Gln Leu Ala Asp Cys Ile Ser Asp Thr Thr His Leu Arg Phe
150                 155                 160                 165

gag ggc ctc atg tgc gtc cca ccg ctt ggt tgg ggc cct gaa aaa gct   643
Glu Gly Leu Met Cys Val Pro Pro Leu Gly Trp Gly Pro Glu Lys Ala
                170                 175                 180

ttt tcc cag gca aga gac gta ctt tca ggt tta gag gaa cac ttt gac   691
Phe Ser Gln Ala Arg Asp Val Leu Ser Gly Leu Glu Glu His Phe Asp
            185                 190                 195

agg tct ttg gaa ttt tcg gca ggt atg tct gga gac cta gtt gct gcg   739
Arg Ser Leu Glu Phe Ser Ala Gly Met Ser Gly Asp Leu Val Ala Ala
        200                 205                 210

att aaa cac ggc tca aca atc gtg cgt gtc gga act gaa att ctt ggg   787
Ile Lys His Gly Ser Thr Ile Val Arg Val Gly Thr Glu Ile Leu Gly
    215                 220                 225

aac cga ccg cta gcg tagaaaatca agttaagggt gtg                    825
Asn Arg Pro Leu Ala
230
```

<210> 1278
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 1278

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Leu Glu Arg Arg Glu Glu Leu Gln Val Arg Leu Gln Gln Val Gln Ala
  1               5                  10                  15

Arg Ile Asp Ala Thr Leu Asn Glu His Asn Arg Pro Glu Gly Ser Val
             20                  25                  30

Arg Leu Leu Pro Val Thr Lys Phe His Pro Val Glu Asp Ile Lys Ile
         35                  40                  45

Leu Gln Glu Phe Gly Val Thr Ala Val Gly Glu Asn Arg Glu Gln Glu
     50                  55                  60

Ala Arg Ala Lys Ala Leu Glu Leu Pro Asp Met Asp Phe His Met Ile
 65                  70                  75                  80

Gly Gln Ile Gln Ser Lys Lys Ala Asn Ser Ile Ala Arg Trp Ala Ala
                 85                  90                  95

Ala Val His Ser Val Asp Ser Glu Lys Ile Ala Glu Ala Leu Gly Arg
```

```
            100                 105                 110

Gly Val Ala Leu Ala Leu Asp Arg Gly Asp Arg Thr Ser Asp Glu Leu
        115                 120                 125

Pro Cys Phe Ile Gln Leu Ser Leu Asp Gly Asp Pro Ser Arg Gly Gly
    130                 135                 140

Thr Pro Leu Ser Gln Val Thr Gln Leu Ala Asp Cys Ile Ser Asp Thr
145                 150                 155                 160

Thr His Leu Arg Phe Glu Gly Leu Met Cys Val Pro Pro Leu Gly Trp
                165                 170                 175

Gly Pro Glu Lys Ala Phe Ser Gln Ala Arg Asp Val Leu Ser Gly Leu
            180                 185                 190

Glu Glu His Phe Asp Arg Ser Leu Glu Phe Ser Ala Gly Met Ser Gly
        195                 200                 205

Asp Leu Val Ala Ala Ile Lys His Gly Ser Thr Ile Val Arg Val Gly
    210                 215                 220

Thr Glu Ile Leu Gly Asn Arg Pro Leu Ala
225                 230


<210> 1279
<211> 727
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(727)
<223> FRXA02720

<400> 1279
ccacgctgca ccatcgaaga cgaagatctg ttttcttacc gccgcgaagg cacgacaggc 60

cgccaggccg gcgtggtgtg gctgccaaag gaggcataaa ttg gag cgc cgc gaa   115
                                              Leu Glu Arg Arg Glu
                                                1               5

gag ctg cag gta cga ctg cag cag gtg caa gcg cgt atc gac gcg acc   163
Glu Leu Gln Val Arg Leu Gln Gln Val Gln Ala Arg Ile Asp Ala Thr
                10                  15                  20

ctc aac gaa cac aac cgc ccc gag ggc agt gta cgt ctg ttg ccg gtc   211
Leu Asn Glu His Asn Arg Pro Glu Gly Ser Val Arg Leu Leu Pro Val
            25                  30                  35

acc aaa ttc cac ccc gtg gaa gac atc aag atc tta caa gag ttt ggt   259
Thr Lys Phe His Pro Val Glu Asp Ile Lys Ile Leu Gln Glu Phe Gly
        40                  45                  50

gtc acc gca gtg gga gag aac cgc gaa caa gaa gca cgc gcc aaa gca   307
Val Thr Ala Val Gly Glu Asn Arg Glu Gln Glu Ala Arg Ala Lys Ala
    55                  60                  65

ctc gaa ctt ccc gac atg gac ttt cat atg att ggc caa atc caa tca   355
```

```
Leu Glu Leu Pro Asp Met Asp Phe His Met Ile Gly Gln Ile Gln Ser
 70                  75                  80                  85

aag aaa gcc aac tcg atc gcc agg tgg gca gct gca gtg cac tcc gtt   403
Lys Lys Ala Asn Ser Ile Ala Arg Trp Ala Ala Ala Val His Ser Val
                 90                  95                 100

gat agc gag aaa atc gcc gaa gca ttg ggc agg gga gta gcc ctt gca   451
Asp Ser Glu Lys Ile Ala Glu Ala Leu Gly Arg Gly Val Ala Leu Ala
            105                 110                 115

ttg gat aga ggc gac cgc acc agt gac gag ctt ccg tgt ttt att caa   499
Leu Asp Arg Gly Asp Arg Thr Ser Asp Glu Leu Pro Cys Phe Ile Gln
        120                 125                 130

ctg agt ttg gat ggt gac ccg agc cga ggt gga act cca ttg agc cag   547
Leu Ser Leu Asp Gly Asp Pro Ser Arg Gly Gly Thr Pro Leu Ser Gln
    135                 140                 145

gtc aca caa ctt gcc gat tgc atc agt gac acc aca cat ctg cgt ttt   595
Val Thr Gln Leu Ala Asp Cys Ile Ser Asp Thr Thr His Leu Arg Phe
150                 155                 160                 165

gag ggc ctc atg tgc gtc cca ccg ctt ggt tgg ggc cct gaa aaa gct   643
Glu Gly Leu Met Cys Val Pro Pro Leu Gly Trp Gly Pro Glu Lys Ala
                170                 175                 180

ttt tcc cag gca aga gac gta ctt tca ggt tta gag gaa cac ttt gac   691
Phe Ser Gln Ala Arg Asp Val Leu Ser Gly Leu Glu Glu His Phe Asp
            185                 190                 195

agg tct ttg gaa ttt tcg gca ggt atg tct gga gac                   727
Arg Ser Leu Glu Phe Ser Ala Gly Met Ser Gly Asp
        200                 205


<210> 1280
<211> 209
<212> PRT
<213> Corynebacterium,glutamicum

<400> 1280
Leu Glu Arg Arg Glu Glu Leu Gln Val Arg Leu Gln Gln Val Gln Ala
  1               5                  10                  15

Arg Ile Asp Ala Thr Leu Asn Glu His Asn Arg Pro Glu Gly Ser Val
             20                  25                  30

Arg Leu Leu Pro Val Thr Lys Phe His Pro Val Glu Asp Ile Lys Ile
         35                  40                  45

Leu Gln Glu Phe Gly Val Thr Ala Val Gly Glu Asn Arg Glu Gln Glu
     50                  55                  60

Ala Arg Ala Lys Ala Leu Glu Leu Pro Asp Met Asp Phe His Met Ile
 65                  70                  75                  80

Gly Gln Ile Gln Ser Lys Lys Ala Asn Ser Ile Ala Arg Trp Ala Ala
                 85                  90                  95

Ala Val His Ser Val Asp Ser Glu Lys Ile Ala Glu Ala Leu Gly Arg
```

```
            100                 105                 110

Gly Val Ala Leu Ala Leu Asp Arg Gly Asp Arg Thr Ser Asp Glu Leu
        115                 120                 125

Pro Cys Phe Ile Gln Leu Ser Leu Asp Gly Asp Pro Ser Arg Gly Gly
    130                 135                 140

Thr Pro Leu Ser Gln Val Thr Gln Leu Ala Asp Cys Ile Ser Asp Thr
145                 150                 155                 160

Thr His Leu Arg Phe Glu Gly Leu Met Cys Val Pro Pro Leu Gly Trp
                165                 170                 175

Gly Pro Glu Lys Ala Phe Ser Gln Ala Arg Asp Val Leu Ser Gly Leu
            180                 185                 190

Glu Glu His Phe Asp Arg Ser Leu Glu Phe Ser Ala Gly Met Ser Gly
        195                 200                 205

Asp
```

20050250150

```
<210> 1281
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> RXN02744

<400> 1281
gccaaaacgt catgattcgc tctttggata cgggacaccg ctcattggaa gatgtcttcc 60

tggacatcac cggaaaagaa ctgaggagtt aacgcacacc atg tct aaa cct ttt   115
                                               Met Ser Lys Pro Phe
                                                 1               5

gaa aac tct gcg ctc cgc ggt tct tct cga ttc cca gct gga acg ttc   163
Glu Asn Ser Ala Leu Arg Gly Ser Ser Arg Phe Pro Ala Gly Thr Phe
                10                  15                  20

acc cct gct ccc aaa cga gcc acc ccg gca aaa atg ttg gct gct cag   211
Thr Pro Ala Pro Lys Arg Ala Thr Pro Ala Lys Met Leu Ala Ala Gln
            25                  30                  35

ggc aag atg gaa tcc ctg ctg ttt ctt cgc cac ggc gaa cag caa ctg   259
Gly Lys Met Glu Ser Leu Leu Phe Leu Arg His Gly Glu Gln Gln Leu
        40                  45                  50

ctc agc atc atc att ccc ttg gtc gcg ctc atc gca cta gcg aat ttt   307
Leu Ser Ile Ile Ile Pro Leu Val Ala Leu Ile Ala Leu Ala Asn Phe
    55                  60                  65

gat ttc atc cct ggt gag aac tcc ctc gac aag act ttc ccc ttc gcg   355
Asp Phe Ile Pro Gly Glu Asn Ser Leu Asp Lys Thr Phe Pro Phe Ala
70                  75                  80                  85
```

```
ctg gcc aca gca gcc atg agc gct ggt ttt aca ggt caa gcc atc agc   403
Leu Ala Thr Ala Ala Met Ser Ala Gly Phe Thr Gly Gln Ala Ile Ser
                 90                  95                 100

cta gct ttt gac cgc cgc tat ggt gcc ctc aag cgc acc ggc gcc agc   451
Leu Ala Phe Asp Arg Arg Tyr Gly Ala Leu Lys Arg Thr Gly Ala Ser
            105                 110                 115

ggt gtt ccc gcc tgg acg att att ttt ggc aaa gtc atc gca gtc att   499
Gly Val Pro Ala Trp Thr Ile Ile Phe Gly Lys Val Ile Ala Val Ile
        120                 125                 130

gca gtc acc att gtg cag atc atc ttt ctc ggt gtg act gca ctg ctg   547
Ala Val Thr Ile Val Gln Ile Ile Phe Leu Gly Val Thr Ala Leu Leu
    135                 140                 145

ttg ggc tgg tcc gca cct gtc ggt ggt gtg ctc ttt ggc atc gtg acc   595
Leu Gly Trp Ser Ala Pro Val Gly Gly Val Leu Phe Gly Ile Val Thr
150                 155                 160                 165

cta ttt gtg ggt gtt tcc agc ttc acc gcg ctc ggc atg ctg atg ggc   643
Leu Phe Val Gly Val Ser Ser Phe Thr Ala Leu Gly Met Leu Met Gly
                170                 175                 180

gga acg ttg tcc tcc gaa ttg gta ttg gca ctg gct aac ttg att tgg   691
Gly Thr Leu Ser Ser Glu Leu Val Leu Ala Leu Ala Asn Leu Ile Trp
            185                 190                 195

att gta ctg tcc ggc ctt gca gca tgg gcg gtc ttt tcc cct tcc gtc   739
Ile Val Leu Ser Gly Leu Ala Ala Trp Ala Val Phe Ser Pro Ser Val
        200                 205                 210

aac gct gaa gga gtg ctg tcc atc atc cca tcc gtt gcg ctg tcc caa   787
Asn Ala Glu Gly Val Leu Ser Ile Ile Pro Ser Val Ala Leu Ser Gln
    215                 220                 225

ggt atg gtt gac gca ttc aac ggc gaa ctt ccg tgg ctc cag cta gga   835
Gly Met Val Asp Ala Phe Asn Gly Glu Leu Pro Trp Leu Gln Leu Gly
230                 235                 240                 245

att ttg gtg ggc tgg cta att atc acc ggc gtg gcc gca aac aag cta   883
Ile Leu Val Gly Trp Leu Ile Ile Thr Gly Val Ala Ala Asn Lys Leu
                250                 255                 260

ttt aac ttc tct gcg agc cgc tagatatacc cttagtcgga aaa             927
Phe Asn Phe Ser Ala Ser Arg
            265
```

<210> 1282
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 1282

```
Met Ser Lys Pro Phe Glu Asn Ser Ala Leu Arg Gly Ser Ser Arg Phe
  1               5                  10                  15

Pro Ala Gly Thr Phe Thr Pro Ala Pro Lys Arg Ala Thr Pro Ala Lys
             20                  25                  30
```

```
Met Leu Ala Ala Gln Gly Lys Met Glu Ser Leu Leu Phe Leu Arg His
         35                  40                  45

Gly Glu Gln Gln Leu Leu Ser Ile Ile Ile Pro Leu Val Ala Leu Ile
     50                  55                  60

Ala Leu Ala Asn Phe Asp Phe Ile Pro Gly Glu Asn Ser Leu Asp Lys
 65                  70                  75                  80

Thr Phe Pro Phe Ala Leu Ala Thr Ala Ala Met Ser Ala Gly Phe Thr
                 85                  90                  95

Gly Gln Ala Ile Ser Leu Ala Phe Asp Arg Arg Tyr Gly Ala Leu Lys
            100                 105                 110

Arg Thr Gly Ala Ser Gly Val Pro Ala Trp Thr Ile Ile Phe Gly Lys
        115                 120                 125

Val Ile Ala Val Ile Ala Val Thr Ile Val Gln Ile Ile Phe Leu Gly
    130                 135                 140

Val Thr Ala Leu Leu Leu Gly Trp Ser Ala Pro Val Gly Gly Val Leu
145                 150                 155                 160

Phe Gly Ile Val Thr Leu Phe Val Gly Val Ser Ser Phe Thr Ala Leu
                165                 170                 175

Gly Met Leu Met Gly Gly Thr Leu Ser Ser Glu Leu Val Leu Ala Leu
            180                 185                 190

Ala Asn Leu Ile Trp Ile Val Leu Ser Gly Leu Ala Ala Trp Ala Val
        195                 200                 205

Phe Ser Pro Ser Val Asn Ala Glu Gly Val Leu Ser Ile Ile Pro Ser
    210                 215                 220

Val Ala Leu Ser Gln Gly Met Val Asp Ala Phe Asn Gly Glu Leu Pro
225                 230                 235                 240

Trp Leu Gln Leu Gly Ile Leu Val Gly Trp Leu Ile Ile Thr Gly Val
                245                 250                 255

Ala Ala Asn Lys Leu Phe Asn Phe Ser Ala Ser Arg
            260                 265
```

<210> 1283
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> FRXA02744

<400> 1283
gccaaaacgt catgattcgc tctttggata cgggacaccg ctcattggaa gatgtcttcc 60

tggacatcac cggaaaagaa ctgaggagtt aacgcacacc atg tct aaa cct ttt 115
Met Ser Lys Pro Phe

```
                                                    1               5

gaa aac tct gcg ctc cgc ggt tct tct cga ttc cca gct gga acg ttc   163
Glu Asn Ser Ala Leu Arg Gly Ser Ser Arg Phe Pro Ala Gly Thr Phe
                  10                  15                  20

acc cct gct ccc aaa cga gcc acc ccg gca aaa atg ttg gct gct cag   211
Thr Pro Ala Pro Lys Arg Ala Thr Pro Ala Lys Met Leu Ala Ala Gln
              25                  30                  35

ggc aag atg gaa tcc ctg ctg ttt ctt cgc cac ggc gaa cag caa ctg   259
Gly Lys Met Glu Ser Leu Leu Phe Leu Arg His Gly Glu Gln Gln Leu
          40                  45                  50

ctc agc atc atc att ccc ttg gtc gcg ctc atc gca cta gcg aat ttt   307
Leu Ser Ile Ile Ile Pro Leu Val Ala Leu Ile Ala Leu Ala Asn Phe
      55                  60                  65

gat ttc atc cct ggt gag aac tcc ctc gac aag act ttc ccc ttc gcg   355
Asp Phe Ile Pro Gly Glu Asn Ser Leu Asp Lys Thr Phe Pro Phe Ala
  70                  75                  80                  85

ctg gcc aca gca gcc atg agc gct ggt ttt aca ggt caa gcc atc agc   403
Leu Ala Thr Ala Ala Met Ser Ala Gly Phe Thr Gly Gln Ala Ile Ser
                  90                  95                 100

cta gct ttt gac cgc cgc tat ggt gcc ctc aag cgc acc ggc gcc agc   451
Leu Ala Phe Asp Arg Arg Tyr Gly Ala Leu Lys Arg Thr Gly Ala Ser
              105                 110                 115

ggt gtt ccc gcc tgg acg att att ttt ggc aaa gtc atc gca gtc att   499
Gly Val Pro Ala Trp Thr Ile Ile Phe Gly Lys Val Ile Ala Val Ile
          120                 125                 130

gca gtc acc att gtg cag atc atc ttt ctc ggt gtg act gca ctg ctg   547
Ala Val Thr Ile Val Gln Ile Ile Phe Leu Gly Val Thr Ala Leu Leu
      135                 140                 145

ttg ggc tgg tcc gca cct gtc ggt ggt gtg ctc ttt ggc atc gtg acc   595
Leu Gly Trp Ser Ala Pro Val Gly Gly Val Leu Phe Gly Ile Val Thr
150                 155                 160                 165

cta ttt gtg ggt gtt tcc agc ttc acc gcg ctc ggc atg ctg atg ggc   643
Leu Phe Val Gly Val Ser Ser Phe Thr Ala Leu Gly Met Leu Met Gly
                  170                 175                 180

gga acg ttg tcc tcc gaa ttg gta ttg gca ctg gct aac ttg att tgg   691
Gly Thr Leu Ser Ser Glu Leu Val Leu Ala Leu Ala Asn Leu Ile Trp
              185                 190                 195

att gta ctg tcc ggc ctt gca gca tgg gcg gtc ttt tcc cct tcc gtc   739
Ile Val Leu Ser Gly Leu Ala Ala Trp Ala Val Phe Ser Pro Ser Val
          200                 205                 210

aac gct gaa gga gtg ctg tcc atc atc cca tcc gtt gcg ctg tcc caa   787
Asn Ala Glu Gly Val Leu Ser Ile Ile Pro Ser Val Ala Leu Ser Gln
      215                 220                 225

ggt atg gtt gac gca ttc aac ggc gaa ctt ccg tgg ctc cag cta gga   835
Gly Met Val Asp Ala Phe Asn Gly Glu Leu Pro Trp Leu Gln Leu Gly
230                 235                 240                 245
```

```
att ttg gtg ggc tgg cta att atc acc ggc gtg gcc gca aac aag cta   883
Ile Leu Val Gly Trp Leu Ile Ile Thr Gly Val Ala Ala Asn Lys Leu
                250                 255                 260

ttt aac ttc tct gcg agc cgc tagatatacc cttagtcgga aaa             927
Phe Asn Phe Ser Ala Ser Arg
            265
```

<210> 1284
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 1284

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Met Ser Lys Pro Phe Glu Asn Ser Ala Leu Arg Gly Ser Ser Arg Phe
  1               5                  10                  15

Pro Ala Gly Thr Phe Thr Pro Ala Pro Lys Arg Ala Thr Pro Ala Lys
             20                  25                  30

Met Leu Ala Ala Gln Gly Lys Met Glu Ser Leu Leu Phe Leu Arg His
         35                  40                  45

Gly Glu Gln Gln Leu Leu Ser Ile Ile Ile Pro Leu Val Ala Leu Ile
     50                  55                  60

Ala Leu Ala Asn Phe Asp Phe Ile Pro Gly Glu Asn Ser Leu Asp Lys
 65                  70                  75                  80

Thr Phe Pro Phe Ala Leu Ala Thr Ala Ala Met Ser Ala Gly Phe Thr
                 85                  90                  95

Gly Gln Ala Ile Ser Leu Ala Phe Asp Arg Arg Tyr Gly Ala Leu Lys
            100                 105                 110

Arg Thr Gly Ala Ser Gly Val Pro Ala Trp Thr Ile Ile Phe Gly Lys
        115                 120                 125

Val Ile Ala Val Ile Ala Val Thr Ile Val Gln Ile Ile Phe Leu Gly
    130                 135                 140

Val Thr Ala Leu Leu Leu Gly Trp Ser Ala Pro Val Gly Gly Val Leu
145                 150                 155                 160

Phe Gly Ile Val Thr Leu Phe Val Gly Val Ser Ser Phe Thr Ala Leu
                165                 170                 175

Gly Met Leu Met Gly Gly Thr Leu Ser Ser Glu Leu Val Leu Ala Leu
            180                 185                 190

Ala Asn Leu Ile Trp Ile Val Leu Ser Gly Leu Ala Ala Trp Ala Val
        195                 200                 205

Phe Ser Pro Ser Val Asn Ala Glu Gly Val Leu Ser Ile Ile Pro Ser
    210                 215                 220

Val Ala Leu Ser Gln Gly Met Val Asp Ala Phe Asn Gly Glu Leu Pro
225                 230                 235                 240
```

```
Trp Leu Gln Leu Gly Ile Leu Val Gly Trp Leu Ile Ile Thr Gly Val
                245                 250                 255

Ala Ala Asn Lys Leu Phe Asn Phe Ser Ala Ser Arg
            260                 265


<210> 1285
<211> 1689
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1666)
<223> RXN02770

<400> 1285
tcgccggggc aaaaaccgta taattacagt cctattacga ttcggggaaa ggctgggtac 60

ttcacacatg ttgtttcgga agtcacgcag cgcggtaatc atg ttg gtt gca gcg   115
                                            Met Leu Val Ala Ala
                                              1               5

tta gtg atg aca agc tgt ggt gat ggg gaa ccg gaa cca acc agc cac   163
Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro Glu Pro Thr Ser His
                  10                  15                  20

caa aca agc ctt ttc ggc tac gca gtt aac tct tcg ctg gct aca acc   211
Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser Ser Leu Ala Thr Thr
              25                  30                  35

aac gcg gcg tcg ctg ttg gga gtg gct aat gat gct ggt ctt ttg gct   259
Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp Ala Gly Leu Leu Ala
          40                  45                  50

gcc aga gtg tat ccg ggt gtg tat gtt cag ggt cct tct ggg cag atg   307
Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly Pro Ser Gly Gln Met
      55                  60                  65

att ccc aac act gat ctt gct tcc acg cag gta ttg ccg ggt att aac   355
Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val Leu Pro Gly Ile Asn
  70                  75                  80                  85

cgc cag gtg att tac act atc aat gaa gat gcc acc tac tca gat ggt   403
Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr Ser Asp Gly
                  90                  95                 100

cag cct gtg gtg tgt gat gat ttt ctg ctc tct gcg aca gct ggg cag   451
Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr Ala Gly Gln
              105                 110                 115

atg ccg gaa ctg ttc cag tcc cat gtg cca ttg acc tcg cag att gag   499
Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser Gln Ile Glu
          120                 125                 130

cga gtg gac tgt gta tct ggt tct aaa gta gcc acc gtg gtg ttc aag   547
Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val Val Phe Lys
      135                 140                 145

gaa gac ctc ggt gag cgt tgg cgt tat ctt ttt gag cag ggc gat ttg   595
```

```
Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln Gly Asp Leu
150                 155                 160                 165

ttg cca gcc cat gcc gtt gct tcc aaa gca ggt atg acc ttg gag gag   643
Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr Leu Glu Glu
                170                 175                 180

ctt aat cag gcg ttg aag gat aag gat cct gaa gcg ttg act gaa cct   691
Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu Thr Glu Pro
            185                 190                 195

gct cgt gtg tgg agc gaa ggt ttc cag ctg tcc cag ttt gat cca gag   739
Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe Asp Pro Glu
        200                 205                 210

ctg cag acg gct ttt ggc ccg tac aag gtg gat tct gtg ggt gaa ttc   787
Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val Gly Glu Phe
    215                 220                 225

ggc gaa gtc aag ctg gta cgc aat gag ttt tac agt ggc gac cag gcg   835
Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly Asp Gln Ala
230                 235                 240                 245

gtt gaa gca gaa atc acg atg tgg cct aaa ggc tcg gat ctc agc gcc   883
Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp Leu Ser Ala
                250                 255                 260

att gcg gat aat gga aac ctt cag atc gca cat gtt gtg gcg tgg gag   931
Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val Ala Trp Glu
            265                 270                 275

agc gag ccg tgg gta aat cgc gat gac cca ttg aat cct tat gac att   979
Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro Tyr Asp Ile
        280                 285                 290

aag gaa gag gtc ggt gtt ttg act gag cag ctc acc ttg gcc agt gcc   1027
Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu Ala Ser Ala
    295                 300                 305

ggt gtg ttt tac gct gcg gag gcc cgg cag gcg ttt gcg gcc tgc gtt   1075
Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala Ala Cys Val
310                 315                 320                 325

gac cag gaa gcg gtg gct gcg gcg tcg tca agc atc tct gga atc gat   1123
Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser Gly Ile Asp
                330                 335                 340

gtg cct gcc gta ggt gtg cac tcg gtg cgt cac caa aat ccg gtc gtg   1171
Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn Pro Val Val
            345                 350                 355

cac caa atc ggt gat ctg cca gca cag cac atg gcg gtg gat att aat   1219
His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val Asp Ile Asn
        360                 365                 370

gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc tac gac gga   1267
Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly Tyr Asp Gly
    375                 380                 385

ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc caa agt tgt   1315
Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg Gln Ser Cys
```

```
390                 395                 400                 405

gag cct gcc ggt atc acc gtt atc gat gcg tcg cag gag gct gtt agt   1363
Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu Ala Val Ser
                410                 415                 420

ctt aat gat ctc agt cga acc gaa gtc agt gaa tgg ggc tat gag cag   1411
Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly Tyr Glu Gln
            425                 430                 435

tac ttc gaa ggg aca ctt gac gct gtt ctg cgt aca gtg gat cca cat   1459
Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val Asp Pro His
        440                 445                 450

cgg gag tat gaa aat gcc aat acc att gga act gat gcg gag tcg acg   1507
Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala Glu Ser Thr
    455                 460                 465

agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca att cca cta   1555
Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser Ile Pro Leu
470                 475                 480                 485

gca gcg caa ccc cga gtg ttt gtg ata gat cgc aca gtc ggt aac gtt   1603
Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val Gly Asn Val
                490                 495                 500

gtt gtt aat aca gac cta gcc ggt atc gga tgg aac atg gac cgt tgg   1651
Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met Asp Arg Trp
            505                 510                 515

tcc aga agt gag gaa taagtagtga gcgaacaagc tct                    1689
Ser Arg Ser Glu Glu
        520


<210> 1286
<211> 522
<212> PRT
<213> Corynebacterium glutamicum

<400> 1286
Met Leu Val Ala Ala Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro
  1               5                  10                  15

Glu Pro Thr Ser His Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser
             20                  25                  30

Ser Leu Ala Thr Thr Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp
         35                  40                  45

Ala Gly Leu Leu Ala Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly
     50                  55                  60

Pro Ser Gly Gln Met Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val
 65                  70                  75                  80

Leu Pro Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala
                 85                  90                  95

Thr Tyr Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser
            100                 105                 110
```

```
Ala Thr Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu
        115                 120                 125

Thr Ser Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala
    130                 135                 140

Thr Val Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe
145                 150                 155                 160

Glu Gln Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly
                165                 170                 175

Met Thr Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu
            180                 185                 190

Ala Leu Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser
        195                 200                 205

Gln Phe Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp
    210                 215                 220

Ser Val Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr
225                 230                 235                 240

Ser Gly Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly
                245                 250                 255

Ser Asp Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His
            260                 265                 270

Val Val Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu
        275                 280                 285

Asn Pro Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu
    290                 295                 300

Thr Leu Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala
305                 310                 315                 320

Phe Ala Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser
                325                 330                 335

Ile Ser Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His
            340                 345                 350

Gln Asn Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met
        355                 360                 365

Ala Val Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg
    370                 375                 380

Ile Gly Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala
385                 390                 395                 400

Ile Arg Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser
                405                 410                 415

Gln Glu Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu
            420                 425                 430
```

```
Trp Gly Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg
        435                 440                 445

Thr Val Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr
    450                 455                 460

Asp Ala Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val
465                 470                 475                 480

Pro Ser Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg
                485                 490                 495

Thr Val Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp
            500                 505                 510

Asn Met Asp Arg Trp Ser Arg Ser Glu Glu
        515                 520


<210> 1287
<211> 1343
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1320)
<223> FRXA02770

<400> 1287
ggt att aac cgc cag gtg att tac act atc aat gaa gat gcc acc tac   48
Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr
  1               5                  10                  15

tca gat ggt cag cct gtg gtg tgt gat gat ttt ctg ctc tct gcg aca   96
Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr
            20                  25                  30

gct ggg cag atg ccg gaa ctg ttc cag tcc cat gtg cca ttg acc tcg   144
Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser
        35                  40                  45

cag att gag cga gtg gac tgt gta tct ggt tct aaa gta gcc acc gtg   192
Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val
    50                  55                  60

gtg ttc aag gaa gac ctc ggt gag cgt tgg cgt tat ctt ttt gag cag   240
Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln
65                  70                  75                  80

ggc gat ttg ttg cca gcc cat gcc gtt gct tcc aaa gca ggt atg acc   288
Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr
                85                  90                  95

ttg gag gag ctt aat cag gcg ttg aag gat aag gat cct gaa gcg ttg   336
Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu
            100                 105                 110

act gaa cct gct cgt gtg tgg agc gaa ggt ttc cag ctg tcc cag ttt   384
Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe
        115                 120                 125
```

```
gat cca gag ctg cag acg gct ttt ggc ccg tac aag gtg gat tct gtg   432
Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val
    130                 135                 140

ggt gaa ttc ggc gaa gtc aag ctg gta cgc aat gag ttt tac agt ggc   480
Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly
145                 150                 155                 160

gac cag gcg gtt gaa gca gaa atc acg atg tgg cct aaa ggc tcg gat   528
Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp
                165                 170                 175

ctc agc gcc att gcg gat aat gga aac ctt cag atc gca cat gtt gtg   576
Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val
            180                 185                 190

gcg tgg gag agc gag ccg tgg gta aat cgc gat gac cca ttg aat cct   624
Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro
        195                 200                 205

tat gac att aag gaa gag gtc ggt gtt ttg act gag cag ctc acc ttg   672
Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu
    210                 215                 220

gcc agt gcc ggt gtg ttt tac gct gcg gag gcc cgg cag gcg ttt gcg   720
Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala
225                 230                 235                 240

gcc tgc gtt gac cag gaa gcg gtg gct gcg gcg tcg tca agc atc tct   768
Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser
                245                 250                 255

gga atc gat gtg cct gcc gta ggt gtg cac tcg gtg cgt cac caa aat   816
Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn
            260                 265                 270

ccg gtc gtg cac caa atc ggt gat ctg cca gca cag cac atg gcg gtg   864
Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val
        275                 280                 285

gat att aat gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc   912
Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly
    290                 295                 300

tac gac gga ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc   960
Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg
305                 310                 315                 320

caa agt tgt gag cct gcc ggt atc acc gtt atc gat gcg tcg cag gag  1008
Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu
                325                 330                 335

gct gtt agt ctt aat gat ctc agt cga acc gaa gtc agt gaa tgg ggc  1056
Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly
            340                 345                 350

tat gag cag tac ttc gaa ggg aca ctt gac gct gtt ctg cgt aca gtg  1104
Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val
        355                 360                 365
```

```
gat cca cat cgg gag tat gaa aat gcc aat acc att gga act gat gcg   1152
Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala
    370                 375                 380

gag tcg acg agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca   1200
Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser
385                 390                 395                 400

att cca cta gca gcg caa ccc cga gtg ttt gtg ata gat cgc aca gtc   1248
Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val
                405                 410                 415

ggt aac gtt gtt gtt aat aca gac cta gcc ggt atc gga tgg aac atg   1296
Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met
            420                 425                 430

gac cgt tgg tcc aga agt gag gaa taagtagtga gcgaacaagc tct         1343
Asp Arg Trp Ser Arg Ser Glu Glu
        435                 440
```

<210> 1288
<211> 440
<212> PRT
<213> Corynebacterium glutamicum

<400> 1288

```
Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr
  1               5                  10                  15

Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr
             20                  25                  30

Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser
         35                  40                  45

Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val
     50                  55                  60

Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln
 65                  70                  75                  80

Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr
                 85                  90                  95

Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu
            100                 105                 110

Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe
        115                 120                 125

Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val
    130                 135                 140

Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly
145                 150                 155                 160

Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp
                165                 170                 175

Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val
```

```
            180                 185                 190

Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro
        195                 200                 205

Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu
    210                 215                 220

Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala
225                 230                 235                 240

Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser
                245                 250                 255

Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn
            260                 265                 270

Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val
        275                 280                 285

Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly
    290                 295                 300

Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg
305                 310                 315                 320

Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu
                325                 330                 335

Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly
            340                 345                 350

Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val
        355                 360                 365

Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala
    370                 375                 380

Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser
385                 390                 395                 400

Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val
                405                 410                 415

Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met
            420                 425                 430

Asp Arg Trp Ser Arg Ser Glu Glu
        435                 440
```

<210> 1289
<211> 1314
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1291)
<223> RXN02781

<400> 1289
ctccgagagt ttccgcatcc gcggttcgat cccggacgtt ccccgggaga cgcggtggga 60

ccggctgtgg cggcccttct gggcgatacc ggctgccagc gtg gtc gcg gcc ctg 115
Val Val Ala Ala Leu
1 5

gtt ttc ggt ttc ctg ctt ccc acg tgg gaa cgt ggg ttg tcc gac gcc 163
Val Phe Gly Phe Leu Leu Pro Thr Trp Glu Arg Gly Leu Ser Asp Ala
10 15 20

gcg ctc aaa ttc gtt ttt gag ggt ggg cct gat gcc gcc cgc gag gtg 211
Ala Leu Lys Phe Val Phe Glu Gly Gly Pro Asp Ala Ala Arg Glu Val
25 30 35

ctg ggc acc atc gcc gcc tcc acg atc tca gtg acc ggt ctc atc ttc 259
Leu Gly Thr Ile Ala Ala Ser Thr Ile Ser Val Thr Gly Leu Ile Phe
40 45 50

tcc atc act ctc gtt gtt ctg cag ctg gtg agc agc cag ttc agc ccg 307
Ser Ile Thr Leu Val Val Leu Gln Leu Val Ser Ser Gln Phe Ser Pro
55 60 65

cga atg ctc aac ggc ttt ctg cgc aac cgc atc gtg cag gcc acc ctg 355
Arg Met Leu Asn Gly Phe Leu Arg Asn Arg Ile Val Gln Ala Thr Leu
70 75 80 85

gcg atg ttc ctg ggg acg ttc gtg ttc tcc ctg acg gtc atc cgg tac 403
Ala Met Phe Leu Gly Thr Phe Val Phe Ser Leu Thr Val Ile Arg Tyr
90 95 100

gtg tgg agc gag gac gag gac atc acc gga ttc gtc ccc cgt gct tca 451
Val Trp Ser Glu Asp Glu Asp Ile Thr Gly Phe Val Pro Arg Ala Ser
105 110 115

gtg tcg gtt gcc ttc ctg ctg gtg ctc ggg tgt ctg gga ctg ttc ctg 499
Val Ser Val Ala Phe Leu Leu Val Leu Gly Cys Leu Gly Leu Phe Leu
120 125 130

gcg ttc atc cgg ctc atc acc ttc tcg atg cgg gtg gcc aac gcc atc 547
Ala Phe Ile Arg Leu Ile Thr Phe Ser Met Arg Val Ala Asn Ala Ile
135 140 145

tcc gag atc ggg gag gag acg atg gct ctg gcc gca cgt atc tat ccc 595
Ser Glu Ile Gly Glu Glu Thr Met Ala Leu Ala Ala Arg Ile Tyr Pro
150 155 160 165

gtg cag agc gac gac gca ggc cca gtc cag ggg ccg ggc tgg tca ccg 643
Val Gln Ser Asp Asp Ala Gly Pro Val Gln Gly Pro Gly Trp Ser Pro
170 175 180

cgg ccc ggt gac ccc cgg gaa gaa atc cgg gtg ggc aac cat ggt tcg 691
Arg Pro Gly Asp Pro Arg Glu Glu Ile Arg Val Gly Asn His Gly Ser
185 190 195

ctg gtg tgg atc gac tac cgg aag ctg gtg tcc tgg tcg acg gaa cac 739
Leu Val Trp Ile Asp Tyr Arg Lys Leu Val Ser Trp Ser Thr Glu His
200 205 210

cag gcg gtg atc acg gtc gac cgg ccg gtg ggg gac ttc ctc gtc gag 787
Gln Ala Val Ile Thr Val Asp Arg Pro Val Gly Asp Phe Leu Val Glu

```
    215                 220                 225

ggc cag ccg ctg ctg cgg gtc tgg tgg gac ggg gaa ctc agc gac cgg   835
Gly Gln Pro Leu Leu Arg Val Trp Trp Asp Gly Glu Leu Ser Asp Arg
230                 235                 240                 245

gac cga cgc gtt ctg cac tcg gcc atc gag gtg cgg acc gag cgg gaa   883
Asp Arg Arg Val Leu His Ser Ala Ile Glu Val Arg Thr Glu Arg Glu
                250                 255                 260

ctt cac cag gat gtg gcg ttc gga ctg cgt caa ctg gtc gac att gcc   931
Leu His Gln Asp Val Ala Phe Gly Leu Arg Gln Leu Val Asp Ile Ala
            265                 270                 275

gat cgt gcg ttg tcc ccg ggc atc aat gat ccg gcc acg gcg gcc cag   979
Asp Arg Ala Leu Ser Pro Gly Ile Asn Asp Pro Ala Thr Ala Ala Gln
        280                 285                 290

tgt gtc cag gag atc cac cgg atc ttc cgc tat ttg gtc acc gtc atc   1027
Cys Val Gln Glu Ile His Arg Ile Phe Arg Tyr Leu Val Thr Val Ile
    295                 300                 305

gag ccc agc ccc tac atc gcc gat gac gac ggt cgg gtc cgt gtg gtg   1075
Glu Pro Ser Pro Tyr Ile Ala Asp Asp Asp Gly Arg Val Arg Val Val
310                 315                 320                 325

cac cag ccg caa cgt atc gcg gac atg ctc tat gag gtg atc cgt gag   1123
His Gln Pro Gln Arg Ile Ala Asp Met Leu Tyr Glu Val Ile Arg Glu
                330                 335                 340

atc cat ctc tac ggg gcg gat tct gcg atg att ccg agg ctg ctg cgc   1171
Ile His Leu Tyr Gly Ala Asp Ser Ala Met Ile Pro Arg Leu Leu Arg
            345                 350                 355

acc atg gtc gag gac ctg gtg acg gcc gct gcc gat cat tcc ctg cct   1219
Thr Met Val Glu Asp Leu Val Thr Ala Ala Ala Asp His Ser Leu Pro
        360                 365                 370

gcc gtc gag cgt gcc cgc ggc atc ctg gac gat gag acg gac gag gac   1267
Ala Val Glu Arg Ala Arg Gly Ile Leu Asp Asp Glu Thr Asp Glu Asp
    375                 380                 385

cgc gac agt gac acc gcg aac gtc tgatccggga tcaggtggcg gtg         1314
Arg Asp Ser Asp Thr Ala Asn Val
390                 395
```

<210> 1290
<211> 397
<212> PRT
<213> Corynebacterium glutamicum

<400> 1290

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Val Val Ala Ala Leu Val Phe Gly Phe Leu Leu Pro Thr Trp Glu Arg
  1               5                  10                  15

Gly Leu Ser Asp Ala Ala Leu Lys Phe Val Phe Glu Gly Gly Pro Asp
             20                  25                  30

Ala Ala Arg Glu Val Leu Gly Thr Ile Ala Ala Ser Thr Ile Ser Val
         35                  40                  45
```

```
Thr Gly Leu Ile Phe Ser Ile Thr Leu Val Val Leu Gln Leu Val Ser
     50                  55                  60

Ser Gln Phe Ser Pro Arg Met Leu Asn Gly Phe Leu Arg Asn Arg Ile
 65                  70                  75                  80

Val Gln Ala Thr Leu Ala Met Phe Leu Gly Thr Phe Val Phe Ser Leu
                 85                  90                  95

Thr Val Ile Arg Tyr Val Trp Ser Glu Asp Glu Asp Ile Thr Gly Phe
            100                 105                 110

Val Pro Arg Ala Ser Val Ser Val Ala Phe Leu Leu Val Leu Gly Cys
        115                 120                 125

Leu Gly Leu Phe Leu Ala Phe Ile Arg Leu Ile Thr Phe Ser Met Arg
    130                 135                 140

Val Ala Asn Ala Ile Ser Glu Ile Gly Glu Glu Thr Met Ala Leu Ala
145                 150                 155                 160

Ala Arg Ile Tyr Pro Val Gln Ser Asp Asp Ala Gly Pro Val Gln Gly
                165                 170                 175

Pro Gly Trp Ser Pro Arg Pro Gly Asp Pro Arg Glu Glu Ile Arg Val
            180                 185                 190

Gly Asn His Gly Ser Leu Val Trp Ile Asp Tyr Arg Lys Leu Val Ser
        195                 200                 205

Trp Ser Thr Glu His Gln Ala Val Ile Thr Val Asp Arg Pro Val Gly
    210                 215                 220

Asp Phe Leu Val Glu Gly Gln Pro Leu Leu Arg Val Trp Trp Asp Gly
225                 230                 235                 240

Glu Leu Ser Asp Arg Asp Arg Arg Val Leu His Ser Ala Ile Glu Val
                245                 250                 255

Arg Thr Glu Arg Glu Leu His Gln Asp Val Ala Phe Gly Leu Arg Gln
            260                 265                 270

Leu Val Asp Ile Ala Asp Arg Ala Leu Ser Pro Gly Ile Asn Asp Pro
        275                 280                 285

Ala Thr Ala Ala Gln Cys Val Gln Glu Ile His Arg Ile Phe Arg Tyr
    290                 295                 300

Leu Val Thr Val Ile Glu Pro Ser Pro Tyr Ile Ala Asp Asp Asp Gly
305                 310                 315                 320

Arg Val Arg Val Val His Gln Pro Gln Arg Ile Ala Asp Met Leu Tyr
                325                 330                 335

Glu Val Ile Arg Glu Ile His Leu Tyr Gly Ala Asp Ser Ala Met Ile
            340                 345                 350

Pro Arg Leu Leu Arg Thr Met Val Glu Asp Leu Val Thr Ala Ala Ala
        355                 360                 365
```

```
Asp His Ser Leu Pro Ala Val Glu Arg Ala Arg Gly Ile Leu Asp Asp
    370                 375                 380

Glu Thr Asp Glu Asp Arg Asp Ser Asp Thr Ala Asn Val
385                 390                 395


<210> 1291
<211> 1314
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1291)
<223> FRXA02781

<400> 1291
ctccgagagt ttccgcatcc gcggttcgat cccggacgtt ccccgggaga cgcggtggga 60

ccggctgtgg cggcccttct gggcgatacc ggctgccagc gtg gtc gcg gcc ctg   115
                                            Val Val Ala Ala Leu
                                              1               5

gtt ttc ggt ttc ctg ctt ccc acg tgg gaa cgt ggg ttg tcc gac gcc   163
Val Phe Gly Phe Leu Leu Pro Thr Trp Glu Arg Gly Leu Ser Asp Ala
                 10                  15                  20

gcg ctc aaa ttc gtt ttt gag ggt ggg cct gat gcc gcc cgc gag gtg   211
Ala Leu Lys Phe Val Phe Glu Gly Gly Pro Asp Ala Ala Arg Glu Val
             25                  30                  35

ctg ggc acc atc gcc gcc tcc acg atc tca gtg acc ggt ctc atc ttc   259
Leu Gly Thr Ile Ala Ala Ser Thr Ile Ser Val Thr Gly Leu Ile Phe
         40                  45                  50

tcc atc act ctc gtt gtt ctg cag ctg gtg agc agc cag ttc agc ccg   307
Ser Ile Thr Leu Val Val Leu Gln Leu Val Ser Ser Gln Phe Ser Pro
     55                  60                  65

cga atg ctc aac ggc ttt ctg cgc aac cgc atc gtg cag gcc acc ctg   355
Arg Met Leu Asn Gly Phe Leu Arg Asn Arg Ile Val Gln Ala Thr Leu
 70                  75                  80                  85

gcg atg ttc ctg ggg acg ttc gtg ttc tcc ctg acg gtc atc cgg tac   403
Ala Met Phe Leu Gly Thr Phe Val Phe Ser Leu Thr Val Ile Arg Tyr
                 90                  95                 100

gtg tgg agc gag gac gag gac atc acc gga ttc gtc ccc cgt gct tca   451
Val Trp Ser Glu Asp Glu Asp Ile Thr Gly Phe Val Pro Arg Ala Ser
            105                 110                 115

gtg tcg gtt gcc ttc ctg ctg gtg ctc ggg tgt ctg gga ctg ttc ctg   499
Val Ser Val Ala Phe Leu Leu Val Leu Gly Cys Leu Gly Leu Phe Leu
        120                 125                 130

gcg ttc atc cgg ctc atc acc ttc tcg atg cgg gtg gcc aac gcc atc   547
Ala Phe Ile Arg Leu Ile Thr Phe Ser Met Arg Val Ala Asn Ala Ile
    135                 140                 145

tcc gag atc ggg gag gag acg atg gct ctg gcc gca cgt atc tat ccc   595
```

```
Ser Glu Ile Gly Glu Glu Thr Met Ala Leu Ala Ala Arg Ile Tyr Pro
150                 155                 160                 165

gtg cag agc gac gac gca ggc cca gtc cag ggg ccg ggc tgg tca ccg   643
Val Gln Ser Asp Asp Ala Gly Pro Val Gln Gly Pro Gly Trp Ser Pro
                170                 175                 180

cgg ccc ggt gac ccc cgg gaa gaa atc cgg gtg ggc aac cat ggt tcg   691
Arg Pro Gly Asp Pro Arg Glu Glu Ile Arg Val Gly Asn His Gly Ser
            185                 190                 195

ctg gtg tgg atc gac tac cgg aag ctg gtg tcc tgg tcg acg gaa cac   739
Leu Val Trp Ile Asp Tyr Arg Lys Leu Val Ser Trp Ser Thr Glu His
        200                 205                 210

cag gcg gtg atc acg gtc gac cgg ccg gtg ggg gac ttc ctc gtc gag   787
Gln Ala Val Ile Thr Val Asp Arg Pro Val Gly Asp Phe Leu Val Glu
    215                 220                 225

ggc cag ccg ctg ctg cgg gtc tgg tgg gac ggg gaa ctc agc gac cgg   835
Gly Gln Pro Leu Leu Arg Val Trp Trp Asp Gly Glu Leu Ser Asp Arg
230                 235                 240                 245

gac cga cgc gtt ctg cac tcg gcc atc gag gtg cgg acc gag cgg gaa   883
Asp Arg Arg Val Leu His Ser Ala Ile Glu Val Arg Thr Glu Arg Glu
                250                 255                 260

ctt cac cag gat gtg gcg ttc gga ctg cgt caa ctg gtc gac att gcc   931
Leu His Gln Asp Val Ala Phe Gly Leu Arg Gln Leu Val Asp Ile Ala
            265                 270                 275

gat cgt gcg ttg tcc ccg ggc atc aat gat ccg gcc acg gcg gcc cag   979
Asp Arg Ala Leu Ser Pro Gly Ile Asn Asp Pro Ala Thr Ala Ala Gln
        280                 285                 290

tgt gtc cag gag atc cac cgg atc ttc cgc tat ttg gtc acc gtc atc  1027
Cys Val Gln Glu Ile His Arg Ile Phe Arg Tyr Leu Val Thr Val Ile
    295                 300                 305

gag ccc agc ccc tac atc gcc gat gac gac ggt cgg gtc cgt gtg gtg  1075
Glu Pro Ser Pro Tyr Ile Ala Asp Asp Asp Gly Arg Val Arg Val Val
310                 315                 320                 325

cac cag ccg caa cgt atc gcg gac atg ctc tat gag gtg atc cgt gag  1123
His Gln Pro Gln Arg Ile Ala Asp Met Leu Tyr Glu Val Ile Arg Glu
                330                 335                 340

atc cat ctc tac ggg gcg gat tct gcg atg att ccg agg ctg ctg cgc  1171
Ile His Leu Tyr Gly Ala Asp Ser Ala Met Ile Pro Arg Leu Leu Arg
            345                 350                 355

acc atg gtc gag gac ctg gtg acg gcc gct gcc gat cat tcc ctg cct  1219
Thr Met Val Glu Asp Leu Val Thr Ala Ala Ala Asp His Ser Leu Pro
        360                 365                 370

gcc gtc gag cgt gcc cgc ggc atc ctg gac gat gag acg gac gag gac  1267
Ala Val Glu Arg Ala Arg Gly Ile Leu Asp Asp Glu Thr Asp Glu Asp
    375                 380                 385

cgc gac agt gac acc gcg aac gtc tgatccggga tcaggtggcg gtg        1314
Arg Asp Ser Asp Thr Ala Asn Val
```

390 395

<210> 1292
<211> 397
<212> PRT
<213> Corynebacterium glutamicum

<400> 1292

```
Val Val Ala Ala Leu Val Phe Gly Phe Leu Leu Pro Thr Trp Glu Arg
  1               5                  10                  15

Gly Leu Ser Asp Ala Ala Leu Lys Phe Val Phe Glu Gly Gly Pro Asp
             20                  25                  30

Ala Ala Arg Glu Val Leu Gly Thr Ile Ala Ala Ser Thr Ile Ser Val
         35                  40                  45

Thr Gly Leu Ile Phe Ser Ile Thr Leu Val Val Leu Gln Leu Val Ser
     50                  55                  60

Ser Gln Phe Ser Pro Arg Met Leu Asn Gly Phe Leu Arg Asn Arg Ile
 65                  70                  75                  80

Val Gln Ala Thr Leu Ala Met Phe Leu Gly Thr Phe Val Phe Ser Leu
                 85                  90                  95

Thr Val Ile Arg Tyr Val Trp Ser Glu Asp Glu Asp Ile Thr Gly Phe
            100                 105                 110

Val Pro Arg Ala Ser Val Ser Val Ala Phe Leu Leu Val Leu Gly Cys
        115                 120                 125

Leu Gly Leu Phe Leu Ala Phe Ile Arg Leu Ile Thr Phe Ser Met Arg
    130                 135                 140

Val Ala Asn Ala Ile Ser Glu Ile Gly Glu Glu Thr Met Ala Leu Ala
145                 150                 155                 160

Ala Arg Ile Tyr Pro Val Gln Ser Asp Asp Ala Gly Pro Val Gln Gly
                165                 170                 175

Pro Gly Trp Ser Pro Arg Pro Gly Asp Pro Arg Glu Glu Ile Arg Val
            180                 185                 190

Gly Asn His Gly Ser Leu Val Trp Ile Asp Tyr Arg Lys Leu Val Ser
        195                 200                 205

Trp Ser Thr Glu His Gln Ala Val Ile Thr Val Asp Arg Pro Val Gly
    210                 215                 220

Asp Phe Leu Val Glu Gly Gln Pro Leu Leu Arg Val Trp Trp Asp Gly
225                 230                 235                 240

Glu Leu Ser Asp Arg Asp Arg Arg Val Leu His Ser Ala Ile Glu Val
                245                 250                 255

Arg Thr Glu Arg Glu Leu His Gln Asp Val Ala Phe Gly Leu Arg Gln
            260                 265                 270

Leu Val Asp Ile Ala Asp Arg Ala Leu Ser Pro Gly Ile Asn Asp Pro
```

```
        275                 280                 285

Ala Thr Ala Ala Gln Cys Val Gln Glu Ile His Arg Ile Phe Arg Tyr
    290                 295                 300

Leu Val Thr Val Ile Glu Pro Ser Pro Tyr Ile Ala Asp Asp Asp Gly
305                 310                 315                 320

Arg Val Arg Val Val His Gln Pro Gln Arg Ile Ala Asp Met Leu Tyr
                325                 330                 335

Glu Val Ile Arg Glu Ile His Leu Tyr Gly Ala Asp Ser Ala Met Ile
            340                 345                 350

Pro Arg Leu Leu Arg Thr Met Val Glu Asp Leu Val Thr Ala Ala Ala
        355                 360                 365

Asp His Ser Leu Pro Ala Val Glu Arg Ala Arg Gly Ile Leu Asp Asp
    370                 375                 380

Glu Thr Asp Glu Asp Arg Asp Ser Asp Thr Ala Asn Val
385                 390                 395


<210> 1293
<211> 1422
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1399)
<223> RXN02782

<400> 1293
accccacccg gtccccctttt tttcctcact gacaccggag ccgcctcaag caccacgctg 60

caatcacaga agctagttga gcatattgta gaatataact atg cca aca ctg ctt   115
                                            Met Pro Thr Leu Leu
                                              1               5

att gac acc cat ccg cat ctt gca gcg caa ctt ctt gac cct ggt tta   163
Ile Asp Thr His Pro His Leu Ala Ala Gln Leu Leu Asp Pro Gly Leu
                 10                  15                  20

ggt gaa ctt ctt aca gcc ggt tcc aac aaa aaa gtg cag tgg cag tgc   211
Gly Glu Leu Leu Thr Ala Gly Ser Asn Lys Lys Val Gln Trp Gln Cys
             25                  30                  35

cct aag cac tcc aat cac atc tgg acg gcc tcg gtt aat aac cgc acc   259
Pro Lys His Ser Asn His Ile Trp Thr Ala Ser Val Asn Asn Arg Thr
         40                  45                  50

aat gca aag aac ccg cgc tgc ccc tat tgt gcc gga aca cga gtg ttg   307
Asn Ala Lys Asn Pro Arg Cys Pro Tyr Cys Ala Gly Thr Arg Val Leu
     55                  60                  65

gca ggt ttt aat gat ctc gcc acc act cac ccg cat ctt gct gta cag   355
Ala Gly Phe Asn Asp Leu Ala Thr Thr His Pro His Leu Ala Val Gln
 70                  75                  80                  85
```

```
ctg gtt gac caa gat att gcc gtc acc att tcc gct ggt tct ggc aaa   403
Leu Val Asp Gln Asp Ile Ala Val Thr Ile Ser Ala Gly Ser Gly Lys
                 90                  95                 100

aga caa ctg tgg cag tgt gta gta aac cca aaa cac cag tgg ttg gct   451
Arg Gln Leu Trp Gln Cys Val Val Asn Pro Lys His Gln Trp Leu Ala
            105                 110                 115

acg cca aat aat cgc acg agt act aaa tct gcg agt tct ggt tgc ccc   499
Thr Pro Asn Asn Arg Thr Ser Thr Lys Ser Ala Ser Ser Gly Cys Pro
        120                 125                 130

tac tgt gcc aac cga gcg gta tta gtc ggt gac aat gac ttt gca aca   547
Tyr Cys Ala Asn Arg Ala Val Leu Val Gly Asp Asn Asp Phe Ala Thr
    135                 140                 145

acc tac ccc gaa ctt gca gcg caa tta gta gat caa tct gca gcg aca   595
Thr Tyr Pro Glu Leu Ala Ala Gln Leu Val Asp Gln Ser Ala Ala Thr
150                 155                 160                 165

acc ttt aca gcc ggc cac aac aag cct gtt gag tgg atc tgt tgc aag   643
Thr Phe Thr Ala Gly His Asn Lys Pro Val Glu Trp Ile Cys Cys Lys
                170                 175                 180

cat gaa cca cca ttt atc tgg aaa acc tca cca att ttg cgt gta cga   691
His Glu Pro Pro Phe Ile Trp Lys Thr Ser Pro Ile Leu Arg Val Arg
            185                 190                 195

cag aac acc cag tgc cct gtg tgc tca gag cga act gtg gcg ccg gcg   739
Gln Asn Thr Gln Cys Pro Val Cys Ser Glu Arg Thr Val Ala Pro Ala
        200                 205                 210

ctt aat gat ctt gca acc act cac cct aaa ctt gcc gag caa att gca   787
Leu Asn Asp Leu Ala Thr Thr His Pro Lys Leu Ala Glu Gln Ile Ala
    215                 220                 225

gat cct caa cca agt ggt gtg agc gcc gcg gcc att atc ccc acc att   835
Asp Pro Gln Pro Ser Gly Val Ser Ala Ala Ala Ile Ile Pro Thr Ile
230                 235                 240                 245

agc agg ggt tcc cat acg caa tta aca tgg caa tgt tct aaa aat cat   883
Ser Arg Gly Ser His Thr Gln Leu Thr Trp Gln Cys Ser Lys Asn His
                250                 255                 260

gac cac caa tgg gtc gcc aca gta aag gat cgt gtt cgc gga aca gac   931
Asp His Gln Trp Val Ala Thr Val Lys Asp Arg Val Arg Gly Thr Asp
            265                 270                 275

tgc ccc acc tgc gca aat aca gga act tca cgc aaa gag gct gaa ctt   979
Cys Pro Thr Cys Ala Asn Thr Gly Thr Ser Arg Lys Glu Ala Glu Leu
        280                 285                 290

att gag gtc atc cgt gca tta ttc cca aac act gat gtc cag caa ggt   1027
Ile Glu Val Ile Arg Ala Leu Phe Pro Asn Thr Asp Val Gln Gln Gly
    295                 300                 305

gcg ctc att aat gga cgt acc ggt aat caa ggt gca tcg ccg tca acc   1075
Ala Leu Ile Asn Gly Arg Thr Gly Asn Gln Gly Ala Ser Pro Ser Thr
310                 315                 320                 325

gat gta ctc ata ccg tcc aaa aat ctc gct atc gag ttc aac ggc ctg   1123
```

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Asp Val Leu Ile Pro Ser Lys Asn Leu Ala Ile Glu Phe Asn Gly Leu
                330                 335                 340

tac tgg cac tct gag ctt ttc atc aaa gat aag cat tat cat gcg aac   1171
Tyr Trp His Ser Glu Leu Phe Ile Lys Asp Lys His Tyr His Ala Asn
            345                 350                 355

aaa tca gct ctc gca gaa caa gcc ggt gtg cag ctc att cat gtg tgg   1219
Lys Ser Ala Leu Ala Glu Gln Ala Gly Val Gln Leu Ile His Val Trp
        360                 365                 370

gag gac gac tgg aat ctt cgc cgc gac att gtg atc cgc atg atc gca   1267
Glu Asp Asp Trp Asn Leu Arg Arg Asp Ile Val Ile Arg Met Ile Ala
    375                 380                 385

cac aag ctt cat gca acc cat aac ctc agt gct gtt ttg cct acc gaa   1315
His Lys Leu His Ala Thr His Asn Leu Ser Ala Val Leu Pro Thr Glu
390                 395                 400                 405

act act gac tca cgt gtg gca acc acc gct ttc gcc gta cac tca cac   1363
Thr Thr Asp Ser Arg Val Ala Thr Thr Ala Phe Ala Val His Ser His
                410                 415                 420

tgt cgg tgg tct ctg gtt cac gcg ctg ctg cat tct tgaacagcaa        1409
Cys Arg Trp Ser Leu Val His Ala Leu Leu His Ser
            425                 430

ccatattcag ggt                                                   1422


<210> 1294
<211> 433
<212> PRT
<213> Corynebacterium glutamicum

<400> 1294
Met Pro Thr Leu Leu Ile Asp Thr His Pro His Leu Ala Ala Gln Leu
  1               5                  10                  15

Leu Asp Pro Gly Leu Gly Glu Leu Leu Thr Ala Gly Ser Asn Lys Lys
             20                  25                  30

Val Gln Trp Gln Cys Pro Lys His Ser Asn His Ile Trp Thr Ala Ser
         35                  40                  45

Val Asn Asn Arg Thr Asn Ala Lys Asn Pro Arg Cys Pro Tyr Cys Ala
     50                  55                  60

Gly Thr Arg Val Leu Ala Gly Phe Asn Asp Leu Ala Thr Thr His Pro
 65                  70                  75                  80

His Leu Ala Val Gln Leu Val Asp Gln Asp Ile Ala Val Thr Ile Ser
                 85                  90                  95

Ala Gly Ser Gly Lys Arg Gln Leu Trp Gln Cys Val Val Asn Pro Lys
            100                 105                 110

His Gln Trp Leu Ala Thr Pro Asn Asn Arg Thr Ser Thr Lys Ser Ala
        115                 120                 125

Ser Ser Gly Cys Pro Tyr Cys Ala Asn Arg Ala Val Leu Val Gly Asp
```

```
    130                 135                 140

Asn Asp Phe Ala Thr Thr Tyr Pro Glu Leu Ala Ala Gln Leu Val Asp
145                 150                 155                 160

Gln Ser Ala Ala Thr Thr Phe Thr Ala Gly His Asn Lys Pro Val Glu
                165                 170                 175

Trp Ile Cys Cys Lys His Glu Pro Pro Phe Ile Trp Lys Thr Ser Pro
            180                 185                 190

Ile Leu Arg Val Arg Gln Asn Thr Gln Cys Pro Val Cys Ser Glu Arg
        195                 200                 205

Thr Val Ala Pro Ala Leu Asn Asp Leu Ala Thr Thr His Pro Lys Leu
    210                 215                 220

Ala Glu Gln Ile Ala Asp Pro Gln Pro Ser Gly Val Ser Ala Ala Ala
225                 230                 235                 240

Ile Ile Pro Thr Ile Ser Arg Gly Ser His Thr Gln Leu Thr Trp Gln
                245                 250                 255

Cys Ser Lys Asn His Asp His Gln Trp Val Ala Thr Val Lys Asp Arg
            260                 265                 270

Val Arg Gly Thr Asp Cys Pro Thr Cys Ala Asn Thr Gly Thr Ser Arg
        275                 280                 285

Lys Glu Ala Glu Leu Ile Glu Val Ile Arg Ala Leu Phe Pro Asn Thr
    290                 295                 300

Asp Val Gln Gln Gly Ala Leu Ile Asn Gly Arg Thr Gly Asn Gln Gly
305                 310                 315                 320

Ala Ser Pro Ser Thr Asp Val Leu Ile Pro Ser Lys Asn Leu Ala Ile
                325                 330                 335

Glu Phe Asn Gly Leu Tyr Trp His Ser Glu Leu Phe Ile Lys Asp Lys
            340                 345                 350

His Tyr His Ala Asn Lys Ser Ala Leu Ala Glu Gln Ala Gly Val Gln
        355                 360                 365

Leu Ile His Val Trp Glu Asp Asp Trp Asn Leu Arg Arg Asp Ile Val
    370                 375                 380

Ile Arg Met Ile Ala His Lys Leu His Ala Thr His Asn Leu Ser Ala
385                 390                 395                 400

Val Leu Pro Thr Glu Thr Thr Asp Ser Arg Val Ala Thr Thr Ala Phe
                405                 410                 415

Ala Val His Ser His Cys Arg Trp Ser Leu Val His Ala Leu Leu His
            420                 425                 430

Ser
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<210> 1295

<211> 795
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(772)
<223> FRXA02782

<400> 1295
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acgacagaac acccagtgcc ctgtgtgctc agagcgaact gtg gcg ccg gcg ctt   115
                                               Val Ala Pro Ala Leu
                                                 1               5

aat gat ctt gca acc act cac cct aaa ctt gcc gag caa att gca gat   163
Asn Asp Leu Ala Thr Thr His Pro Lys Leu Ala Glu Gln Ile Ala Asp
                10                  15                  20

cct caa cca agt ggt gtg agc gcc gcg gcc att atc ccc acc att agc   211
Pro Gln Pro Ser Gly Val Ser Ala Ala Ala Ile Ile Pro Thr Ile Ser
            25                  30                  35

agg ggt tcc cat acg caa tta aca tgg caa tgt tct aaa aat cat gac   259
Arg Gly Ser His Thr Gln Leu Thr Trp Gln Cys Ser Lys Asn His Asp
        40                  45                  50

cac caa tgg gtc gcc aca gta aag gat cgt gtt cgc gga aca gac tgc   307
His Gln Trp Val Ala Thr Val Lys Asp Arg Val Arg Gly Thr Asp Cys
    55                  60                  65

ccc acc tgc gca aat aca gga act tca cgc aaa gag gct gaa ctt att   355
Pro Thr Cys Ala Asn Thr Gly Thr Ser Arg Lys Glu Ala Glu Leu Ile
70                  75                  80                  85

gag gtc atc cgt gca tta ttc cca aac act gat gtc cag caa ggt gcg   403
Glu Val Ile Arg Ala Leu Phe Pro Asn Thr Asp Val Gln Gln Gly Ala
                90                  95                 100

ctc att aat gga cgt acc ggt aat caa ggt gca tcg ccg tca acc gat   451
Leu Ile Asn Gly Arg Thr Gly Asn Gln Gly Ala Ser Pro Ser Thr Asp
            105                 110                 115

gta ctc ata ccg tcc aaa aat ctc gct atc gag ttc aac ggc ctg tac   499
Val Leu Ile Pro Ser Lys Asn Leu Ala Ile Glu Phe Asn Gly Leu Tyr
        120                 125                 130

tgg cac tct gag ctt ttc atc aaa gat aag cat tat cat gcg aac aaa   547
Trp His Ser Glu Leu Phe Ile Lys Asp Lys His Tyr His Ala Asn Lys
    135                 140                 145

tca gct ctc gca gaa caa gcc ggt gtg cag ctc att cat gtg tgg gag   595
Ser Ala Leu Ala Glu Gln Ala Gly Val Gln Leu Ile His Val Trp Glu
150                 155                 160                 165

gac gac tgg aat ctt cgc cgc gac att gtg atc cgc atg atc gca cac   643
Asp Asp Trp Asn Leu Arg Arg Asp Ile Val Ile Arg Met Ile Ala His
                170                 175                 180

aag ctt cat gca acc cat aac ctc agt gct gtt ttg cct acc gaa act   691
```

```
Lys Leu His Ala Thr His Asn Leu Ser Ala Val Leu Pro Thr Glu Thr
            185                 190                 195

act gac tca cgt gtg gca acc acc gct ttc gcc gta cac tca cac tgt   739
Thr Asp Ser Arg Val Ala Thr Thr Ala Phe Ala Val His Ser His Cys
        200                 205                 210

cgg tgg tct ctg gtt cac gcg ctg ctg cat tct tgaacagcaa ccatattcag 792
Arg Trp Ser Leu Val His Ala Leu Leu His Ser
    215                 220

ggt                                                               795


<210> 1296
<211> 224
<212> PRT
<213> Corynebacterium glutamicum

<400> 1296
Val Ala Pro Ala Leu Asn Asp Leu Ala Thr Thr His Pro Lys Leu Ala
  1               5                  10                  15

Glu Gln Ile Ala Asp Pro Gln Pro Ser Gly Val Ser Ala Ala Ala Ile
             20                  25                  30

Ile Pro Thr Ile Ser Arg Gly Ser His Thr Gln Leu Thr Trp Gln Cys
         35                  40                  45

Ser Lys Asn His Asp His Gln Trp Val Ala Thr Val Lys Asp Arg Val
     50                  55                  60

Arg Gly Thr Asp Cys Pro Thr Cys Ala Asn Thr Gly Thr Ser Arg Lys
 65                  70                  75                  80

Glu Ala Glu Leu Ile Glu Val Ile Arg Ala Leu Phe Pro Asn Thr Asp
                 85                  90                  95

Val Gln Gln Gly Ala Leu Ile Asn Gly Arg Thr Gly Asn Gln Gly Ala
            100                 105                 110

Ser Pro Ser Thr Asp Val Leu Ile Pro Ser Lys Asn Leu Ala Ile Glu
        115                 120                 125

Phe Asn Gly Leu Tyr Trp His Ser Glu Leu Phe Ile Lys Asp Lys His
    130                 135                 140

Tyr His Ala Asn Lys Ser Ala Leu Ala Glu Gln Ala Gly Val Gln Leu
145                 150                 155                 160

Ile His Val Trp Glu Asp Asp Trp Asn Leu Arg Arg Asp Ile Val Ile
                165                 170                 175

Arg Met Ile Ala His Lys Leu His Ala Thr His Asn Leu Ser Ala Val
            180                 185                 190

Leu Pro Thr Glu Thr Thr Asp Ser Arg Val Ala Thr Thr Ala Phe Ala
        195                 200                 205

Val His Ser His Cys Arg Trp Ser Leu Val His Ala Leu Leu His Ser
    210                 215                 220
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<210> 1297
<211> 439
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(439)
<223> RXN02812

<400> 1297
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gggctacacc tttgaagcag tagacagcgc agaagtacct gtg tgg gct gtt gcc 115
Val Trp Ala Val Ala
1 5

atc aac gct gga aac ggt atc tct gaa gac caa gcc cgc gcc gcc tct 163
Ile Asn Ala Gly Asn Gly Ile Ser Glu Asp Gln Ala Arg Ala Ala Ser
10 15 20

gat ttc agt agc ttc agc ttc gac acc ggc aac gcc gat aac tcc gcg 211
Asp Phe Ser Ser Phe Ser Phe Asp Thr Gly Asn Ala Asp Asn Ser Ala
25 30 35

ctt gaa agt gtt ctc acc caa gct tca agc gaa tcc gcg gca gaa act 259
Leu Glu Ser Val Leu Thr Gln Ala Ser Ser Glu Ser Ala Ala Glu Thr
40 45 50

act gag gcg caa cca agc gag acc ccg gtc gag ccc gcc gct gct tcc 307
Thr Glu Ala Gln Pro Ser Glu Thr Pro Val Glu Pro Ala Ala Ala Ser
55 60 65

cca tcc gat acc atc atc aac ctg gat acc tca tcc aac atg gat cga 355
Pro Ser Asp Thr Ile Ile Asn Leu Asp Thr Ser Ser Asn Met Asp Arg
70 75 80 85

gtt gtt gac ggc agc cag gaa acc tac cac acg gtt act tcc cgg act 403
Val Val Asp Gly Ser Gln Glu Thr Tyr His Thr Val Thr Ser Arg Thr
90 95 100

ctg gcc aac ctc gcc cgc gaa act ggt gca cag ggc 439
Leu Ala Asn Leu Ala Arg Glu Thr Gly Ala Gln Gly
105 110

<210> 1298
<211> 113
<212> PRT
<213> Corynebacterium glutamicum

<400> 1298
Val Trp Ala Val Ala Ile Asn Ala Gly Asn Gly Ile Ser Glu Asp Gln
1 5 10 15

Ala Arg Ala Ala Ser Asp Phe Ser Ser Phe Ser Phe Asp Thr Gly Asn

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            20                  25                  30

Ala Asp Asn Ser Ala Leu Glu Ser Val Leu Thr Gln Ala Ser Ser Glu
         35                  40                  45

Ser Ala Ala Glu Thr Thr Glu Ala Gln Pro Ser Glu Thr Pro Val Glu
     50                  55                  60

Pro Ala Ala Ala Ser Pro Ser Asp Thr Ile Ile Asn Leu Asp Thr Ser
 65                  70                  75                  80

Ser Asn Met Asp Arg Val Val Asp Gly Ser Gln Glu Thr Tyr His Thr
                 85                  90                  95

Val Thr Ser Arg Thr Leu Ala Asn Leu Ala Arg Glu Thr Gly Ala Gln
            100                 105                 110

Gly
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<210> 1299
<211> 567
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(567)
<223> FRXA02812

<400> 1299

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gct tca ggc acc gac gcc tca aca atc acc ctt gac cag gta gct ctt   48
Ala Ser Gly Thr Asp Ala Ser Thr Ile Thr Leu Asp Gln Val Ala Leu
  1               5                  10                  15

ccc gtt gcc act aac tcc gga gca tcc gca gcc gta gcg ctg gcg ctg   96
Pro Val Ala Thr Asn Ser Gly Ala Ser Ala Ala Val Ala Leu Ala Leu
             20                  25                  30

gct gaa acc cca gaa gct gcc gct gct gcg ctc aac cgt gac gcc gat   144
Ala Glu Thr Pro Glu Ala Ala Ala Ala Ala Leu Asn Arg Asp Ala Asp
         35                  40                  45

gtc acc gca act gga gct gcc gac tcc cct gcg ttt gcc acc gtt gaa   192
Val Thr Ala Thr Gly Ala Ala Asp Ser Pro Ala Phe Ala Thr Val Glu
     50                  55                  60

gga gca gaa ctt cca gag ggc tac acc ttt gaa gca gta gac agc gca   240
Gly Ala Glu Leu Pro Glu Gly Tyr Thr Phe Glu Ala Val Asp Ser Ala
 65                  70                  75                  80

gaa gta cct gtg tgg gct gtt gcc atc aac gct gga aac ggt atc tct   288
Glu Val Pro Val Trp Ala Val Ala Ile Asn Ala Gly Asn Gly Ile Ser
                 85                  90                  95

gaa gac caa gcc cgc gcc gcc tct gat ttc agt agc ttc agc ttc gac   336
Glu Asp Gln Ala Arg Ala Ala Ser Asp Phe Ser Ser Phe Ser Phe Asp
            100                 105                 110

acc ggc aac gcc gat aac tcc gcg ctt gaa agt gtt ctc acc caa gct   384
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```
Thr Gly Asn Ala Asp Asn Ser Ala Leu Glu Ser Val Leu Thr Gln Ala
        115                 120                 125

tca agc gaa tcc gcg gca gaa act act gag gcg caa cca agc gag acc   432
Ser Ser Glu Ser Ala Ala Glu Thr Thr Glu Ala Gln Pro Ser Glu Thr
    130                 135                 140

ccg gtc gag ccc gcc gct gct tcc cca tcc gat acc atc atc aac ctg   480
Pro Val Glu Pro Ala Ala Ala Ser Pro Ser Asp Thr Ile Ile Asn Leu
145                 150                 155                 160

gat acc tca tcc aac atg gat cga gtt gtt gac ggc agc cag gaa acc   528
Asp Thr Ser Ser Asn Met Asp Arg Val Val Asp Gly Ser Gln Glu Thr
                165                 170                 175

tac cac acg gtt act tcc cgg act ctg gcc aac ctc gcc               567
Tyr His Thr Val Thr Ser Arg Thr Leu Ala Asn Leu Ala
            180                 185


<210> 1300
<211> 189
<212> PRT
<213> Corynebacterium glutamicum

<400> 1300
Ala Ser Gly Thr Asp Ala Ser Thr Ile Thr Leu Asp Gln Val Ala Leu
  1               5                  10                  15

Pro Val Ala Thr Asn Ser Gly Ala Ser Ala Ala Val Ala Leu Ala Leu
             20                  25                  30

Ala Glu Thr Pro Glu Ala Ala Ala Ala Ala Leu Asn Arg Asp Ala Asp
         35                  40                  45

Val Thr Ala Thr Gly Ala Ala Asp Ser Pro Ala Phe Ala Thr Val Glu
     50                  55                  60

Gly Ala Glu Leu Pro Glu Gly Tyr Thr Phe Glu Ala Val Asp Ser Ala
 65                  70                  75                  80

Glu Val Pro Val Trp Ala Val Ala Ile Asn Ala Gly Asn Gly Ile Ser
                 85                  90                  95

Glu Asp Gln Ala Arg Ala Ala Ser Asp Phe Ser Ser Phe Ser Phe Asp
            100                 105                 110

Thr Gly Asn Ala Asp Asn Ser Ala Leu Glu Ser Val Leu Thr Gln Ala
        115                 120                 125

Ser Ser Glu Ser Ala Ala Glu Thr Thr Glu Ala Gln Pro Ser Glu Thr
    130                 135                 140

Pro Val Glu Pro Ala Ala Ala Ser Pro Ser Asp Thr Ile Ile Asn Leu
145                 150                 155                 160

Asp Thr Ser Ser Asn Met Asp Arg Val Val Asp Gly Ser Gln Glu Thr
                165                 170                 175

Tyr His Thr Val Thr Ser Arg Thr Leu Ala Asn Leu Ala
            180                 185
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<210> 1301
<211> 499
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(499)
<223> RXN02817

<400> 1301
aaaattccca cccccaaaac tcccccactt cggttaagga atcaggattc tcacaaagtt 60

caggcaggct cccgctactt ttcagcgcta atcttggctc atg att tta ggc gta 115
Met Ile Leu Gly Val
1 5

ccc att caa tat ttg ctc tat tca ttg tgg aat tgg att gtc gat acc 163
Pro Ile Gln Tyr Leu Leu Tyr Ser Leu Trp Asn Trp Ile Val Asp Thr
10 15 20

ggt ttt gat gta gca att atc ctg gtc ttg gcg ttt ttg att cca cgt 211
Gly Phe Asp Val Ala Ile Ile Leu Val Leu Ala Phe Leu Ile Pro Arg
25 30 35

atc ggc cga ctg gcc atg cgt att atc aag cgc cga gtg gag tct gca 259
Ile Gly Arg Leu Ala Met Arg Ile Ile Lys Arg Arg Val Glu Ser Ala
40 45 50

gcc gat gcg gac acc act aag aac cag ctc gcg ttc gcc ggc gtt ggc 307
Ala Asp Ala Asp Thr Thr Lys Asn Gln Leu Ala Phe Ala Gly Val Gly
55 60 65

gtt tat atc gcg caa att gtg gcg ttt ttc atg ctt gcc gtc tcc gcg 355
Val Tyr Ile Ala Gln Ile Val Ala Phe Phe Met Leu Ala Val Ser Ala
70 75 80 85

atg cag gct ttt ggt ttc tct ctc gcg ggc gct gcg att ccg gca acc 403
Met Gln Ala Phe Gly Phe Ser Leu Ala Gly Ala Ala Ile Pro Ala Thr
90 95 100

att gcg tca gct gcc att ggc ctt ggt gcg cag tcg att gtt gcg gac 451
Ile Ala Ser Ala Ala Ile Gly Leu Gly Ala Gln Ser Ile Val Ala Asp
105 110 115

ttc ttg gcc gga ttt ttc atc ctg acg gaa aag caa ttc ggc gtg ggt 499
Phe Leu Ala Gly Phe Phe Ile Leu Thr Glu Lys Gln Phe Gly Val Gly
120 125 130

<210> 1302
<211> 133
<212> PRT
<213> Corynebacterium glutamicum

<400> 1302
Met Ile Leu Gly Val Pro Ile Gln Tyr Leu Leu Tyr Ser Leu Trp Asn
1 5 10 15

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Trp Ile Val Asp Thr Gly Phe Asp Val Ala Ile Ile Leu Val Leu Ala
            20                  25                  30

Phe Leu Ile Pro Arg Ile Gly Arg Leu Ala Met Arg Ile Ile Lys Arg
        35                  40                  45

Arg Val Glu Ser Ala Ala Asp Ala Asp Thr Thr Lys Asn Gln Leu Ala
    50                  55                  60

Phe Ala Gly Val Gly Val Tyr Ile Ala Gln Ile Val Ala Phe Phe Met
65                  70                  75                  80

Leu Ala Val Ser Ala Met Gln Ala Phe Gly Phe Ser Leu Ala Gly Ala
                85                  90                  95

Ala Ile Pro Ala Thr Ile Ala Ser Ala Ala Ile Gly Leu Gly Ala Gln
            100                 105                 110

Ser Ile Val Ala Asp Phe Leu Ala Gly Phe Phe Ile Leu Thr Glu Lys
        115                 120                 125

Gln Phe Gly Val Gly
    130
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EFS-Web 2.2.0.0 - Sequence Listing

<210> 1303
<211> 499
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(499)
<223> FRXA02817

<400> 1303

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aaaattccca cccccaaaac tcccccactt cggttaagga atcaggattc tcacaaagtt 60

caggcaggct cccgctactt ttcagcgcta atcttggctc atg att tta ggc gta   115
                                            Met Ile Leu Gly Val
                                              1               5

ccc att caa tat ttg ctc tat tca ttg tgg aat tgg att gtc gat acc   163
Pro Ile Gln Tyr Leu Leu Tyr Ser Leu Trp Asn Trp Ile Val Asp Thr
                10                  15                  20

ggt ttt gat gta gca att atc ctg gtc ttg gcg ttt ttg att cca cgt   211
Gly Phe Asp Val Ala Ile Ile Leu Val Leu Ala Phe Leu Ile Pro Arg
            25                  30                  35

atc ggc cga ctg gcc atg cgt att atc aag cgc cga gtg gag tct gca   259
Ile Gly Arg Leu Ala Met Arg Ile Ile Lys Arg Arg Val Glu Ser Ala
        40                  45                  50

gcc gat gcg gac acc act aag aac cag ctc gcg ttc gcc ggc gtt ggc   307
Ala Asp Ala Asp Thr Thr Lys Asn Gln Leu Ala Phe Ala Gly Val Gly
    55                  60                  65

gtt tat atc gcg caa att gtg gcg ttt ttc atg ctt gcc gtc tcc gcg   355
Val Tyr Ile Ala Gln Ile Val Ala Phe Phe Met Leu Ala Val Ser Ala
70                  75                  80                  85
```

```
atg cag gct ttt ggt ttc tct ctc gcg ggc gct gcg att ccg gca acc   403
Met Gln Ala Phe Gly Phe Ser Leu Ala Gly Ala Ala Ile Pro Ala Thr
                 90                  95                 100

att gcg tca gct gcc att ggc ctt ggt gcg cag tcg att gtt gcg gac   451
Ile Ala Ser Ala Ala Ile Gly Leu Gly Ala Gln Ser Ile Val Ala Asp
            105                 110                 115

ttc ttg gcc gga ttt ttc atc ctg acg gaa aag caa ttc ggc gtg ggt   499
Phe Leu Ala Gly Phe Phe Ile Leu Thr Glu Lys Gln Phe Gly Val Gly
        120                 125                 130
```

<210> 1304
<211> 133
<212> PRT
<213> Corynebacterium glutamicum

<400> 1304

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Met Ile Leu Gly Val Pro Ile Gln Tyr Leu Leu Tyr Ser Leu Trp Asn
  1               5                  10                  15

Trp Ile Val Asp Thr Gly Phe Asp Val Ala Ile Ile Leu Val Leu Ala
             20                  25                  30

Phe Leu Ile Pro Arg Ile Gly Arg Leu Ala Met Arg Ile Ile Lys Arg
         35                  40                  45

Arg Val Glu Ser Ala Ala Asp Ala Asp Thr Thr Lys Asn Gln Leu Ala
     50                  55                  60

Phe Ala Gly Val Gly Val Tyr Ile Ala Gln Ile Val Ala Phe Phe Met
 65                  70                  75                  80

Leu Ala Val Ser Ala Met Gln Ala Phe Gly Phe Ser Leu Ala Gly Ala
                 85                  90                  95

Ala Ile Pro Ala Thr Ile Ala Ser Ala Ala Ile Gly Leu Gly Ala Gln
            100                 105                 110

Ser Ile Val Ala Asp Phe Leu Ala Gly Phe Phe Ile Leu Thr Glu Lys
        115                 120                 125

Gln Phe Gly Val Gly
    130
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<210> 1305
<211> 606
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(606)
<223> RXN02818

<400> 1305

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tcc tat tcc cgg aag ttt ttg acc cag gtg tgg att cga gac aat gtc   48
Ser Tyr Ser Arg Lys Phe Leu Thr Gln Val Trp Ile Arg Asp Asn Val
```

```
  1               5                  10                  15

ggc gat tat aaa ggc ctt acc gat acg gcg ttc cgt aag aag ctg cag   96
Gly Asp Tyr Lys Gly Leu Thr Asp Thr Ala Phe Arg Lys Lys Leu Gln
            20                  25                  30

cgc gat ctt gcc tac ctg cgc aga gtt ggc gtt ccg att gag cag ttc   144
Arg Asp Leu Ala Tyr Leu Arg Arg Val Gly Val Pro Ile Glu Gln Phe
        35                  40                  45

acg gtc acc tca ggc ata gct gaa ggc cag cag gcg tac cgt ctg gcc   192
Thr Val Thr Ser Gly Ile Ala Glu Gly Gln Gln Ala Tyr Arg Leu Ala
    50                  55                  60

cag gat tct tat aag ctc ccc gag gtc gaa ttc acc cca gat gag gcc   240
Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala
65                  70                  75                  80

gcc gtg ctg ggc atg gca ggg gag atg ggc cat aat cag gaa ctc ggc   288
Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly
                85                  90                  95

gcc ttc gcg cgt tcg ggg tgg acc aaa ttg gcg gcc ggc ggc gcg cag   336
Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln
            100                 105                 110

cgt gat ctg tcc acg tcc aca gcc ttg acc aat gcg ggc gat tta ggt   384
Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly
        115                 120                 125

tcc ttg tct gca aaa acc ctc gat gcg atc atc aaa gcc cgc caa ttg   432
Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu
    130                 135                 140

ggc aag caa atc agc ttc gaa tac cgg cgc gcc ccc aaa gac gcc ccc   480
Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro
145                 150                 155                 160

tcg ctt cga cac atg gat cct tgg ggt ctg gtc cct gag cgc gac cgc   528
Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg
                165                 170                 175

atc tac ctg gtc gga ttc gac ctc gac cgc caa gaa gca cgc acc ttc   576
Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe
            180                 185                 190

cgc atc acc cgc gtc cgc aac atc aaa ctc                          606
Arg Ile Thr Arg Val Arg Asn Ile Lys Leu
        195                 200
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<210> 1306
<211> 202
<212> PRT
<213> Corynebacterium glutamicum

<400> 1306

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Ser Tyr Ser Arg Lys Phe Leu Thr Gln Val Trp Ile Arg Asp Asn Val
  1               5                  10                  15

Gly Asp Tyr Lys Gly Leu Thr Asp Thr Ala Phe Arg Lys Lys Leu Gln
```

```
            20                  25                  30

Arg Asp Leu Ala Tyr Leu Arg Arg Val Gly Val Pro Ile Glu Gln Phe
         35                  40                  45

Thr Val Thr Ser Gly Ile Ala Glu Gly Gln Gln Ala Tyr Arg Leu Ala
     50                  55                  60

Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala
 65                  70                  75                  80

Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly
                 85                  90                  95

Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln
            100                 105                 110

Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly
        115                 120                 125

Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu
    130                 135                 140

Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro
145                 150                 155                 160

Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg
                165                 170                 175

Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe
            180                 185                 190

Arg Ile Thr Arg Val Arg Asn Ile Lys Leu
        195                 200


<210> 1307
<211> 606
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(606)
<223> FRXA02818

<400> 1307
tcc tat tcc cgg aag ttt ttg acc cag gtg tgg att cga gac aat gtc   48
Ser Tyr Ser Arg Lys Phe Leu Thr Gln Val Trp Ile Arg Asp Asn Val
  1               5                  10                  15

ggc gat tat aaa ggc ctt acc gat acg gcg ttc cgt aag aag ctg cag   96
Gly Asp Tyr Lys Gly Leu Thr Asp Thr Ala Phe Arg Lys Lys Leu Gln
             20                  25                  30

cgc gat ctt gcc tac ctg cgc aga gtt ggc gtt ccg att gag cag ttc   144
Arg Asp Leu Ala Tyr Leu Arg Arg Val Gly Val Pro Ile Glu Gln Phe
         35                  40                  45

acg gtc acc tca ggc ata gct gaa ggc cag cag gcg tac cgt ctg gcc   192
Thr Val Thr Ser Gly Ile Ala Glu Gly Gln Gln Ala Tyr Arg Leu Ala
```

```
     50                  55                  60

cag gat tct tat aag ctc ccc gag gtc gaa ttc acc cca gat gag gcc   240
Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala
 65                  70                  75                  80

gcc gtg ctg ggc atg gca ggg gag atg ggc cat aat cag gaa ctc ggc   288
Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly
                 85                  90                  95

gcc ttc gcg cgt tcg ggg tgg acc aaa ttg gcg gcc ggc ggc gcg cag   336
Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln
            100                 105                 110

cgt gat ctg tcc acg tcc aca gcc ttg acc aat gcg ggc gat tta ggt   384
Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly
        115                 120                 125

tcc ttg tct gca aaa acc ctc gat gcg atc atc aaa gcc cgc caa ttg   432
Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu
    130                 135                 140

ggc aag caa atc agc ttc gaa tac cgg cgc gcc ccc aaa gac gcc ccc   480
Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro
145                 150                 155                 160

tcg ctt cga cac atg gat cct tgg ggt ctg gtc cct gag cgc gac cgc   528
Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg
                165                 170                 175

atc tac ctg gtc gga ttc gac ctc gac cgc caa gaa gca cgc acc ttc   576
Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe
            180                 185                 190

cgc atc acc cgc gtc cgc aac atc aaa ctc                          606
Arg Ile Thr Arg Val Arg Asn Ile Lys Leu
        195                 200
```

US20090269340A1

<210> 1308
<211> 202
<212> PRT
<213> Corynebacterium glutamicum

<400> 1308

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Ser Tyr Ser Arg Lys Phe Leu Thr Gln Val Trp Ile Arg Asp Asn Val
  1               5                  10                  15

Gly Asp Tyr Lys Gly Leu Thr Asp Thr Ala Phe Arg Lys Lys Leu Gln
             20                  25                  30

Arg Asp Leu Ala Tyr Leu Arg Arg Val Gly Val Pro Ile Glu Gln Phe
         35                  40                  45

Thr Val Thr Ser Gly Ile Ala Glu Gly Gln Gln Ala Tyr Arg Leu Ala
     50                  55                  60

Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala
 65                  70                  75                  80

Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly
```

```
                85                  90                  95

Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln
            100                 105                 110

Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly
        115                 120                 125

Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu
    130                 135                 140

Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro
145                 150                 155                 160

Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg
                165                 170                 175

Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe
            180                 185                 190

Arg Ile Thr Arg Val Arg Asn Ile Lys Leu
        195                 200
```

<210> 1309
<211> 1962
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1939)
<223> RXN02825

<400> 1309

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tggcctgccc ctgaaacttt tacggctttc agagcgcagg gcatcatttt cttgtgtcgc 60

caacacttga gaaaaattgc ggaaaaggac actgctgttc atg aaa ctt gca cct   115
                                            Met Lys Leu Ala Pro
                                              1               5

cgt atg cgg atg agg agc ccc aaa act ttc gcg gcc ctc gcc tca ctt   163
Arg Met Arg Met Arg Ser Pro Lys Thr Phe Ala Ala Leu Ala Ser Leu
                10                  15                  20

gct tta gtc ata ggt ctc ggc cag gta ccg atc gcc caa gct caa acc   211
Ala Leu Val Ile Gly Leu Gly Gln Val Pro Ile Ala Gln Ala Gln Thr
            25                  30                  35

gag tat cga acc gcc tcc gac ggt tcc ctg aac tgg gga ttt agg caa   259
Glu Tyr Arg Thr Ala Ser Asp Gly Ser Leu Asn Trp Gly Phe Arg Gln
        40                  45                  50

tcg ttc cgc aat tac atc caa acc ggc gtg gcc aaa ggt tcc atc acg   307
Ser Phe Arg Asn Tyr Ile Gln Thr Gly Val Ala Lys Gly Ser Ile Thr
    55                  60                  65

ctt ggc gac ggc gca tcc gac aac ggt ggc aac ttc gca ttc acc cca   355
Leu Gly Asp Gly Ala Ser Asp Asn Gly Gly Asn Phe Ala Phe Thr Pro
70                  75                  80                  85
```

```
cgc acc aac ggc acc acc gtg acc agc gat tcc caa ggc acc gtg gaa   403
Arg Thr Asn Gly Thr Thr Val Thr Ser Asp Ser Gln Gly Thr Val Glu
                 90                  95                 100

ttc aac ggc tcc gtg cac ttc ctc gga cac cag gca gag gac aaa tgg   451
Phe Asn Gly Ser Val His Phe Leu Gly His Gln Ala Glu Asp Lys Trp
            105                 110                 115

atc ctg gac acc acc atg tct gac atc aaa atg gtg ttc aac gga tcc   499
Ile Leu Asp Thr Thr Met Ser Asp Ile Lys Met Val Phe Asn Gly Ser
        120                 125                 130

tcc gcg cag cta gtt gtg gat ttg gtt gcc cgc gaa ttc aag ggc acc   547
Ser Ala Gln Leu Val Val Asp Leu Val Ala Arg Glu Phe Lys Gly Thr
    135                 140                 145

acc tac gat gac atc ggc gaa tac atc atc tcc gac gac atc gtg ctt   595
Thr Tyr Asp Asp Ile Gly Glu Tyr Ile Ile Ser Asp Asp Ile Val Leu
150                 155                 160                 165

gcc gac gtc tcc ctc aac tcc gcc gcc gac ttc tcc caa gat tcc atc   643
Ala Asp Val Ser Leu Asn Ser Ala Ala Asp Phe Ser Gln Asp Ser Ile
                170                 175                 180

gac ctg tcc ggc acc acc gac ctc acc gca gct ggc gcc caa gct ttc   691
Asp Leu Ser Gly Thr Thr Asp Leu Thr Ala Ala Gly Ala Gln Ala Phe
            185                 190                 195

gga gga ttc tac gaa acc ggc gaa gcc ctc gac ccg acc ggc ggc agc   739
Gly Gly Phe Tyr Glu Thr Gly Glu Ala Leu Asp Pro Thr Gly Gly Ser
        200                 205                 210

ctg acc att tcc tcc acc acc acc gcg cca tcg acc agc acg acc tcc   787
Leu Thr Ile Ser Ser Thr Thr Thr Ala Pro Ser Thr Ser Thr Thr Ser
    215                 220                 225

acc tct gcc tca act tcc ggt gga acc gcc gac tgt tcc tcc ggc gca   835
Thr Ser Ala Ser Thr Ser Gly Gly Thr Ala Asp Cys Ser Ser Gly Ala
230                 235                 240                 245

ttg ggt gtt gtc acc acc gga acc aac gac ggc atg ctg ggc acc atc   883
Leu Gly Val Val Thr Thr Gly Thr Asn Asp Gly Met Leu Gly Thr Ile
                250                 255                 260

cag gaa gta aac aac acc ttc gcg att tgg aac aac ctc atc gtc aac   931
Gln Glu Val Asn Asn Thr Phe Ala Ile Trp Asn Asn Leu Ile Val Asn
            265                 270                 275

acc gag cgc atg ttc tgc aac att gat acc ctc aag gcg cgc ttc gac   979
Thr Glu Arg Met Phe Cys Asn Ile Asp Thr Leu Lys Ala Arg Phe Asp
        280                 285                 290

acg gat gat tcc agc gat tca gcg acc tct gcg act tct ggg act act  1027
Thr Asp Asp Ser Ser Asp Ser Ala Thr Ser Ala Thr Ser Gly Thr Thr
    295                 300                 305

gcg tcc acc ggc acc acc gct gca act acc gcg gga acc acg ggt acc  1075
Ala Ser Thr Gly Thr Thr Ala Ala Thr Thr Ala Gly Thr Thr Gly Thr
310                 315                 320                 325

act gga act gcc agc acc gct tcc gga act tcc gga act tcc gga acc  1123
```

```
Thr Gly Thr Ala Ser Thr Ala Ser Gly Thr Ser Gly Thr Ser Gly Thr
                330                 335                 340

tcc ggc acc gca gca act gtc gct ggc acc acc cca act gac aat ggc   1171
Ser Gly Thr Ala Ala Thr Val Ala Gly Thr Thr Pro Thr Asp Asn Gly
            345                 350                 355

gtt tgc acc gct tcc gga tct ttg ggc gtg acc caa gca tct gcg cag   1219
Val Cys Thr Ala Ser Gly Ser Leu Gly Val Thr Gln Ala Ser Ala Gln
        360                 365                 370

tgg ggt gtg aag gcg tcc ttc cag aac tac att cgc gga tcg atc gcc   1267
Trp Gly Val Lys Ala Ser Phe Gln Asn Tyr Ile Arg Gly Ser Ile Ala
    375                 380                 385

aac ggt agc tgg act ctc aac ggc gtt ggt ttt gat aat cag cag ttc   1315
Asn Gly Ser Trp Thr Leu Asn Gly Val Gly Phe Asp Asn Gln Gln Phe
390                 395                 400                 405

caa ttc tct gga aat tcc gga gca gtc gac gcg gaa aac aag acc ggc   1363
Gln Phe Ser Gly Asn Ser Gly Ala Val Asp Ala Glu Asn Lys Thr Gly
                410                 415                 420

agc atc aat ttc cct ggt tcc atc cac ttc acg ggt cac ggc gga atc   1411
Ser Ile Asn Phe Pro Gly Ser Ile His Phe Thr Gly His Gly Gly Ile
            425                 430                 435

ttg gac atg cag atc gca aac att gag atc agc ttc aac ggc aac tcc   1459
Leu Asp Met Gln Ile Ala Asn Ile Glu Ile Ser Phe Asn Gly Asn Ser
        440                 445                 450

ggc gag ctg att gcg gat gtc gtt tcc tct gac atg gat gga aat tcc   1507
Gly Glu Leu Ile Ala Asp Val Val Ser Ser Asp Met Asp Gly Asn Ser
    455                 460                 465

acc aac tac ggt cgc act gtc gtg ggc acc ctg aac ttc tct gcg ttg   1555
Thr Asn Tyr Gly Arg Thr Val Val Gly Thr Leu Asn Phe Ser Ala Leu
470                 475                 480                 485

aat gtt tct gca acg gaa gct tcc ggt tcc gct tcg gtg tcc ctg tca   1603
Asn Val Ser Ala Thr Glu Ala Ser Gly Ser Ala Ser Val Ser Leu Ser
                490                 495                 500

cag tcg ggt tcg cag gcg ttc gct gat ttc tac acc cca ggc acc cag   1651
Gln Ser Gly Ser Gln Ala Phe Ala Asp Phe Tyr Thr Pro Gly Thr Gln
            505                 510                 515

ttg gat ccg atc agt ttc agc gca act ttg ggc ggc gac gcc agc tgc   1699
Leu Asp Pro Ile Ser Phe Ser Ala Thr Leu Gly Gly Asp Ala Ser Cys
        520                 525                 530

gcc acc gga tcc acc tcg acc aca ggc gct gct gcc acc gcg aac act   1747
Ala Thr Gly Ser Thr Ser Thr Thr Gly Ala Ala Ala Thr Ala Asn Thr
    535                 540                 545

gac aac acc gaa ggt gtt gcc ggc gag gaa tcc acc acc ccc gct aac   1795
Asp Asn Thr Glu Gly Val Ala Gly Glu Glu Ser Thr Thr Pro Ala Asn
550                 555                 560                 565

caa aac agc cag ttc caa atc cgc cag gcc gct gca gat tcc acc gga   1843
Gln Asn Ser Gln Phe Gln Ile Arg Gln Ala Ala Ala Asp Ser Thr Gly
```

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                570                 575                 580

ctg gat acc acc acc aca atg ttg ctc atc ctc gcg gcg ttc gtt gtc   1891
Leu Asp Thr Thr Thr Thr Met Leu Leu Ile Leu Ala Ala Phe Val Val
            585                 590                 595

gca ggt ggc tcc atg act cgc ttc acc gtc ggc aac ccg act gga aaa   1939
Ala Gly Gly Ser Met Thr Arg Phe Thr Val Gly Asn Pro Thr Gly Lys
        600                 605                 610

taaggcttca catgaataac gct                                         1962


<210> 1310
<211> 613
<212> PRT
<213> Corynebacterium glutamicum

<400> 1310
Met Lys Leu Ala Pro Arg Met Arg Met Arg Ser Pro Lys Thr Phe Ala
  1               5                  10                  15

Ala Leu Ala Ser Leu Ala Leu Val Ile Gly Leu Gly Gln Val Pro Ile
             20                  25                  30

Ala Gln Ala Gln Thr Glu Tyr Arg Thr Ala Ser Asp Gly Ser Leu Asn
         35                  40                  45

Trp Gly Phe Arg Gln Ser Phe Arg Asn Tyr Ile Gln Thr Gly Val Ala
     50                  55                  60

Lys Gly Ser Ile Thr Leu Gly Asp Gly Ala Ser Asp Asn Gly Gly Asn
 65                  70                  75                  80

Phe Ala Phe Thr Pro Arg Thr Asn Gly Thr Thr Val Thr Ser Asp Ser
                 85                  90                  95

Gln Gly Thr Val Glu Phe Asn Gly Ser Val His Phe Leu Gly His Gln
            100                 105                 110

Ala Glu Asp Lys Trp Ile Leu Asp Thr Thr Met Ser Asp Ile Lys Met
        115                 120                 125

Val Phe Asn Gly Ser Ser Ala Gln Leu Val Val Asp Leu Val Ala Arg
    130                 135                 140

Glu Phe Lys Gly Thr Thr Tyr Asp Asp Ile Gly Glu Tyr Ile Ile Ser
145                 150                 155                 160

Asp Asp Ile Val Leu Ala Asp Val Ser Leu Asn Ser Ala Ala Asp Phe
                165                 170                 175

Ser Gln Asp Ser Ile Asp Leu Ser Gly Thr Thr Asp Leu Thr Ala Ala
            180                 185                 190

Gly Ala Gln Ala Phe Gly Gly Phe Tyr Glu Thr Gly Glu Ala Leu Asp
        195                 200                 205

Pro Thr Gly Gly Ser Leu Thr Ile Ser Ser Thr Thr Thr Ala Pro Ser
    210                 215                 220
```

```
Thr Ser Thr Thr Ser Thr Ser Ala Ser Thr Ser Gly Gly Thr Ala Asp
225                 230                 235                 240

Cys Ser Ser Gly Ala Leu Gly Val Val Thr Thr Gly Thr Asn Asp Gly
                245                 250                 255

Met Leu Gly Thr Ile Gln Glu Val Asn Asn Thr Phe Ala Ile Trp Asn
            260                 265                 270

Asn Leu Ile Val Asn Thr Glu Arg Met Phe Cys Asn Ile Asp Thr Leu
        275                 280                 285

Lys Ala Arg Phe Asp Thr Asp Asp Ser Ser Asp Ser Ala Thr Ser Ala
    290                 295                 300

Thr Ser Gly Thr Thr Ala Ser Thr Gly Thr Thr Ala Ala Thr Thr Ala
305                 310                 315                 320

Gly Thr Thr Gly Thr Thr Gly Thr Ala Ser Thr Ala Ser Gly Thr Ser
                325                 330                 335

Gly Thr Ser Gly Thr Ser Gly Thr Ala Ala Thr Val Ala Gly Thr Thr
            340                 345                 350

Pro Thr Asp Asn Gly Val Cys Thr Ala Ser Gly Ser Leu Gly Val Thr
        355                 360                 365

Gln Ala Ser Ala Gln Trp Gly Val Lys Ala Ser Phe Gln Asn Tyr Ile
    370                 375                 380

Arg Gly Ser Ile Ala Asn Gly Ser Trp Thr Leu Asn Gly Val Gly Phe
385                 390                 395                 400

Asp Asn Gln Gln Phe Gln Phe Ser Gly Asn Ser Gly Ala Val Asp Ala
                405                 410                 415

Glu Asn Lys Thr Gly Ser Ile Asn Phe Pro Gly Ser Ile His Phe Thr
            420                 425                 430

Gly His Gly Gly Ile Leu Asp Met Gln Ile Ala Asn Ile Glu Ile Ser
        435                 440                 445

Phe Asn Gly Asn Ser Gly Glu Leu Ile Ala Asp Val Val Ser Ser Asp
    450                 455                 460

Met Asp Gly Asn Ser Thr Asn Tyr Gly Arg Thr Val Val Gly Thr Leu
465                 470                 475                 480

Asn Phe Ser Ala Leu Asn Val Ser Ala Thr Glu Ala Ser Gly Ser Ala
                485                 490                 495

Ser Val Ser Leu Ser Gln Ser Gly Ser Gln Ala Phe Ala Asp Phe Tyr
            500                 505                 510

Thr Pro Gly Thr Gln Leu Asp Pro Ile Ser Phe Ser Ala Thr Leu Gly
        515                 520                 525

Gly Asp Ala Ser Cys Ala Thr Gly Ser Thr Ser Thr Thr Gly Ala Ala
    530                 535                 540

Ala Thr Ala Asn Thr Asp Asn Thr Glu Gly Val Ala Gly Glu Glu Ser
```

```
545                 550                 555                 560

Thr Thr Pro Ala Asn Gln Asn Ser Gln Phe Gln Ile Arg Gln Ala Ala
                565                 570                 575

Ala Asp Ser Thr Gly Leu Asp Thr Thr Thr Thr Met Leu Leu Ile Leu
            580                 585                 590

Ala Ala Phe Val Val Ala Gly Gly Ser Met Thr Arg Phe Thr Val Gly
        595                 600                 605

Asn Pro Thr Gly Lys
    610
```

<210> 1311
<211> 538
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(538)
<223> FRXA01322

<400> 1311

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tggcctgccc ctgaaacttt tacggctttc agagcgcagg gcatcatttt cttgtgtcgc 60

caacacttga gaaaaattgc ggaaaaggac actgctgttc atg aaa ctt gca cct   115
                                            Met Lys Leu Ala Pro
                                              1               5

cgt atg cgg atg agg agc ccc aaa act ttc gcg gcc ctc gcc tca ctt   163
Arg Met Arg Met Arg Ser Pro Lys Thr Phe Ala Ala Leu Ala Ser Leu
                 10                  15                  20

gct tta gtc ata ggt ctc ggc cag gta ccg atc gcc caa gct caa acc   211
Ala Leu Val Ile Gly Leu Gly Gln Val Pro Ile Ala Gln Ala Gln Thr
             25                  30                  35

gag tat cga acc gcc tcc gac ggt tcc ctg aac tgg gga ttt agg caa   259
Glu Tyr Arg Thr Ala Ser Asp Gly Ser Leu Asn Trp Gly Phe Arg Gln
         40                  45                  50

tcg ttc cgc aat tac atc caa acc ggc gtg gcc aaa ggt tcc atc acg   307
Ser Phe Arg Asn Tyr Ile Gln Thr Gly Val Ala Lys Gly Ser Ile Thr
     55                  60                  65

ctt ggc gac ggc gca tcc gac aac ggt ggc aac ttc gca ttc acc cca   355
Leu Gly Asp Gly Ala Ser Asp Asn Gly Gly Asn Phe Ala Phe Thr Pro
 70                  75                  80                  85

cgc acc aac ggc acc acc gtg acc agc gat tcc caa ggc acc gtg gaa   403
Arg Thr Asn Gly Thr Thr Val Thr Ser Asp Ser Gln Gly Thr Val Glu
                 90                  95                 100

ttc aac ggc tcc gtg cac ttc ctc gga cac cag gca gag gac aaa tgg   451
Phe Asn Gly Ser Val His Phe Leu Gly His Gln Ala Glu Asp Lys Trp
            105                 110                 115

atc ctg gac acc acc atg tct gac atc aaa atg gtg ttc aac gga tcc   499
```

```
Ile Leu Asp Thr Thr Met Ser Asp Ile Lys Met Val Phe Asn Gly Ser
        120                 125                 130

tcc gcg cag cta gtt gtg gat ttg gtt gcc cgc gaa ttc              538
Ser Ala Gln Leu Val Val Asp Leu Val Ala Arg Glu Phe
    135                 140                 145


<210> 1312
<211> 146
<212> PRT
<213> Corynebacterium glutamicum

<400> 1312
Met Lys Leu Ala Pro Arg Met Arg Met Arg Ser Pro Lys Thr Phe Ala
  1               5                  10                  15

Ala Leu Ala Ser Leu Ala Leu Val Ile Gly Leu Gly Gln Val Pro Ile
             20                  25                  30

Ala Gln Ala Gln Thr Glu Tyr Arg Thr Ala Ser Asp Gly Ser Leu Asn
         35                  40                  45

Trp Gly Phe Arg Gln Ser Phe Arg Asn Tyr Ile Gln Thr Gly Val Ala
     50                  55                  60

Lys Gly Ser Ile Thr Leu Gly Asp Gly Ala Ser Asp Asn Gly Gly Asn
 65                  70                  75                  80

Phe Ala Phe Thr Pro Arg Thr Asn Gly Thr Thr Val Thr Ser Asp Ser
                 85                  90                  95

Gln Gly Thr Val Glu Phe Asn Gly Ser Val His Phe Leu Gly His Gln
            100                 105                 110

Ala Glu Asp Lys Trp Ile Leu Asp Thr Thr Met Ser Asp Ile Lys Met
        115                 120                 125

Val Phe Asn Gly Ser Ser Ala Gln Leu Val Val Asp Leu Val Ala Arg
    130                 135                 140

Glu Phe
145


<210> 1313
<211> 528
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(528)
<223> FRXA02824

<400> 1313
ttc tac gaa acc ggc gaa gcc ctc gac ccg acc ggc gac agc ctg acc    48
Phe Tyr Glu Thr Gly Glu Ala Leu Asp Pro Thr Gly Asp Ser Leu Thr
  1               5                  10                  15

att tcc tcc acc acc acc gcg cca tcg acc agc acg acc tcc acc tct    96
```

```
Ile Ser Ser Thr Thr Thr Ala Pro Ser Thr Ser Thr Thr Ser Thr Ser
             20                  25                  30

gcc tca act tcc ggt gga acc gcc gac tgt tcc tcc ggc gca ttg ggt   144
Ala Ser Thr Ser Gly Gly Thr Ala Asp Cys Ser Ser Gly Ala Leu Gly
         35                  40                  45

gtt gtc acc acc gga acc aac gac ggc atg ctg ggc acc atc cag gaa   192
Val Val Thr Thr Gly Thr Asn Asp Gly Met Leu Gly Thr Ile Gln Glu
     50                  55                  60

gta aac aac acc ttc gcg att tgg aac aac ctc atc gtc aac acc gag   240
Val Asn Asn Thr Phe Ala Ile Trp Asn Asn Leu Ile Val Asn Thr Glu
 65                  70                  75                  80

cgc atg ttc tgc aac att gat acc ctc aag gcg cgc ttc gac acg gat   288
Arg Met Phe Cys Asn Ile Asp Thr Leu Lys Ala Arg Phe Asp Thr Asp
                 85                  90                  95

gat tcc agc gat tca gcg acc tct gcg act tct ggg act act gcg tcc   336
Asp Ser Ser Asp Ser Ala Thr Ser Ala Thr Ser Gly Thr Thr Ala Ser
            100                 105                 110

acc ggc acc acc gct gca act acc gcg gga acc acg ggt acc act gga   384
Thr Gly Thr Thr Ala Ala Thr Thr Ala Gly Thr Thr Gly Thr Thr Gly
        115                 120                 125

act gcc agc acc gct tcc gga act tcc gga act tcc gga acc tcc ggc   432
Thr Ala Ser Thr Ala Ser Gly Thr Ser Gly Thr Ser Gly Thr Ser Gly
    130                 135                 140

acc gca gca act gtc gct ggc acc acc cca act gac aat ggc gtt tgc   480
Thr Ala Ala Thr Val Ala Gly Thr Thr Pro Thr Asp Asn Gly Val Cys
145                 150                 155                 160

acc gct tcc gga tct ttg ggc gtg acc caa gca tct gcg cag tgg ggt   528
Thr Ala Ser Gly Ser Leu Gly Val Thr Gln Ala Ser Ala Gln Trp Gly
                165                 170                 175
```

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<210> 1314
<211> 176
<212> PRT
<213> Corynebacterium glutamicum

<400> 1314

```
Phe Tyr Glu Thr Gly Glu Ala Leu Asp Pro Thr Gly Asp Ser Leu Thr
  1               5                  10                  15

Ile Ser Ser Thr Thr Thr Ala Pro Ser Thr Ser Thr Thr Ser Thr Ser
             20                  25                  30

Ala Ser Thr Ser Gly Gly Thr Ala Asp Cys Ser Ser Gly Ala Leu Gly
         35                  40                  45

Val Val Thr Thr Gly Thr Asn Asp Gly Met Leu Gly Thr Ile Gln Glu
     50                  55                  60

Val Asn Asn Thr Phe Ala Ile Trp Asn Asn Leu Ile Val Asn Thr Glu
 65                  70                  75                  80
```

```
Arg Met Phe Cys Asn Ile Asp Thr Leu Lys Ala Arg Phe Asp Thr Asp
                 85                  90                  95

Asp Ser Ser Asp Ser Ala Thr Ser Ala Thr Ser Gly Thr Thr Ala Ser
            100                 105                 110

Thr Gly Thr Thr Ala Ala Thr Thr Ala Gly Thr Thr Gly Thr Thr Gly
        115                 120                 125

Thr Ala Ser Thr Ala Ser Gly Thr Ser Gly Thr Ser Gly Thr Ser Gly
    130                 135                 140

Thr Ala Ala Thr Val Ala Gly Thr Thr Pro Thr Asp Asn Gly Val Cys
145                 150                 155                 160

Thr Ala Ser Gly Ser Leu Gly Val Thr Gln Ala Ser Ala Gln Trp Gly
                165                 170                 175
```

<210> 1315
<211> 407
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(384)
<223> FRXA02825

<400> 1315

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aat gtt tct gca acg gaa gct tcc ggt tcc gct tcg gtg tcc ctg tca   48
Asn Val Ser Ala Thr Glu Ala Ser Gly Ser Ala Ser Val Ser Leu Ser
  1               5                  10                  15

cag tcg ggt tcg cag gcg ttc gct gat ttc tac acc cca ggc acc cag   96
Gln Ser Gly Ser Gln Ala Phe Ala Asp Phe Tyr Thr Pro Gly Thr Gln
             20                  25                  30

ttg gat ccg atc agt ttc agc gca act ttg ggc ggc gac gcc agc tgc   144
Leu Asp Pro Ile Ser Phe Ser Ala Thr Leu Gly Gly Asp Ala Ser Cys
         35                  40                  45

gcc acc gga tcc acc tcg acc aca ggc gct gct gcc acc gcg aac act   192
Ala Thr Gly Ser Thr Ser Thr Thr Gly Ala Ala Ala Thr Ala Asn Thr
     50                  55                  60

gac aac acc gaa ggt gtt gcc ggc gag gaa tcc acc acc ccc gct aac   240
Asp Asn Thr Glu Gly Val Ala Gly Glu Glu Ser Thr Thr Pro Ala Asn
 65                  70                  75                  80

caa aac agc cag ttc caa atc cgc cag gcc gct gca gat tcc acc gga   288
Gln Asn Ser Gln Phe Gln Ile Arg Gln Ala Ala Ala Asp Ser Thr Gly
                85                  90                  95

ctg gat acc acc acc aca atg ttg ctc atc ctc gcg gcg ttc gtt gtc   336
Leu Asp Thr Thr Thr Thr Met Leu Leu Ile Leu Ala Ala Phe Val Val
            100                 105                 110
```

```
gca ggt ggc tcc atg act cgc ttc acc gtc ggc aac ccg act gga aaa   384
Ala Gly Gly Ser Met Thr Arg Phe Thr Val Gly Asn Pro Thr Gly Lys
        115                 120                 125

taaggcttca catgaataac gct                                       407


<210> 1316
<211> 128
<212> PRT
<213> Corynebacterium glutamicum

<400> 1316
Asn Val Ser Ala Thr Glu Ala Ser Gly Ser Ala Ser Val Ser Leu Ser
  1               5                  10                  15

Gln Ser Gly Ser Gln Ala Phe Ala Asp Phe Tyr Thr Pro Gly Thr Gln
             20                  25                  30

Leu Asp Pro Ile Ser Phe Ser Ala Thr Leu Gly Gly Asp Ala Ser Cys
         35                  40                  45

Ala Thr Gly Ser Thr Ser Thr Thr Gly Ala Ala Ala Thr Ala Asn Thr
     50                  55                  60

Asp Asn Thr Glu Gly Val Ala Gly Glu Glu Ser Thr Thr Pro Ala Asn
 65                  70                  75                  80

Gln Asn Ser Gln Phe Gln Ile Arg Gln Ala Ala Ala Asp Ser Thr Gly
                 85                  90                  95

Leu Asp Thr Thr Thr Thr Met Leu Leu Ile Leu Ala Ala Phe Val Val
            100                 105                 110

Ala Gly Gly Ser Met Thr Arg Phe Thr Val Gly Asn Pro Thr Gly Lys
        115                 120                 125




<210> 1317
<211> 528
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(528)
<223> RXN02838

<400> 1317
aac acg ggc aag ggc ggg ggg ctg acg gtg ccg ctg ggc gac ggg cag   48
Asn Thr Gly Lys Gly Gly Gly Leu Thr Val Pro Leu Gly Asp Gly Gln
  1               5                  10                  15

ggg cgg tat atc gcg aag ttc ccc tcg acc gcg ttt gtg ggg gtg tcg   96
Gly Arg Tyr Ile Ala Lys Phe Pro Ser Thr Ala Phe Val Gly Val Ser
             20                  25                  30

gag aac gaa ttt gcc aat ctg gct ttg gcc gag gcg atc ggg atg gag   144
```

```
Glu Asn Glu Phe Ala Asn Leu Ala Leu Ala Glu Ala Ile Gly Met Glu
          35                  40                  45

gtg ccc gcg cgc gag ttg gtg ggg cgt gcg cag ttt gaa ggc gtg ccc   192
Val Pro Ala Arg Glu Leu Val Gly Arg Ala Gln Phe Glu Gly Val Pro
     50                  55                  60

ccc gag ttt gag gcc atg acc gac ggg ttg gtt ttg ctg gtg cgg cgg   240
Pro Glu Phe Glu Ala Met Thr Asp Gly Leu Val Leu Leu Val Arg Arg
 65                  70                  75                  80

ttt gat cgc gcg ggc gat ggc gtg cgc gtg cat atg gag gat ttc gca   288
Phe Asp Arg Ala Gly Asp Gly Val Arg Val His Met Glu Asp Phe Ala
                 85                  90                  95

cag gtg ttc ggc cta tac ccc gcg cgc aag tat gat ggg gcg gcc agt   336
Gln Val Phe Gly Leu Tyr Pro Ala Arg Lys Tyr Asp Gly Ala Ala Ser
            100                 105                 110

cac gat att gcg gcg gtg ctg ggc agt gcg gtg tcg atc gcg gcg ggg   384
His Asp Ile Ala Ala Val Leu Gly Ser Ala Val Ser Ile Ala Ala Gly
        115                 120                 125

ttg gag ttc gtg cgg cgg ctg gcg ctc tcg gtt gtg atg ggc aac ggc   432
Leu Glu Phe Val Arg Arg Leu Ala Leu Ser Val Val Met Gly Asn Gly
    130                 135                 140

gat atg cat ttg aag aac tgg tcg ctg atc tat cgc ggg cgg ggc gat   480
Asp Met His Leu Lys Asn Trp Ser Leu Ile Tyr Arg Gly Arg Gly Asp
145                 150                 155                 160

gtg ccg gcg ttg gcg cct gtg tat tat atg atg tcg acc gtg acc tat   528
Val Pro Ala Leu Ala Pro Val Tyr Tyr Met Met Ser Thr Val Thr Tyr
                165                 170                 175


<210> 1318
<211> 176
<212> PRT
<213> Corynebacterium glutamicum

<400> 1318
Asn Thr Gly Lys Gly Gly Gly Leu Thr Val Pro Leu Gly Asp Gly Gln
  1               5                  10                  15

Gly Arg Tyr Ile Ala Lys Phe Pro Ser Thr Ala Phe Val Gly Val Ser
             20                  25                  30

Glu Asn Glu Phe Ala Asn Leu Ala Leu Ala Glu Ala Ile Gly Met Glu
         35                  40                  45

Val Pro Ala Arg Glu Leu Val Gly Arg Ala Gln Phe Glu Gly Val Pro
     50                  55                  60

Pro Glu Phe Glu Ala Met Thr Asp Gly Leu Val Leu Leu Val Arg Arg
 65                  70                  75                  80

Phe Asp Arg Ala Gly Asp Gly Val Arg Val His Met Glu Asp Phe Ala
                 85                  90                  95

Gln Val Phe Gly Leu Tyr Pro Ala Arg Lys Tyr Asp Gly Ala Ala Ser
```

```
            100                 105                 110

His Asp Ile Ala Ala Val Leu Gly Ser Ala Val Ser Ile Ala Ala Gly
       115                 120                 125

Leu Glu Phe Val Arg Arg Leu Ala Leu Ser Val Val Met Gly Asn Gly
    130                 135                 140

Asp Met His Leu Lys Asn Trp Ser Leu Ile Tyr Arg Gly Arg Gly Asp
145                 150                 155                 160

Val Pro Ala Leu Ala Pro Val Tyr Tyr Met Met Ser Thr Val Thr Tyr
                165                 170                 175
```

<210> 1319
<211> 462
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(462)
<223> FRXA02838

<400> 1319

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acc gtg ccg ctg ggc gac ggg cag ggg cgg tat atc gcg aag atc ccc   48
Thr Val Pro Leu Gly Asp Gly Gln Gly Arg Tyr Ile Ala Lys Ile Pro
  1               5                  10                  15

tcg acc gcg ttt gtg ggg gtg tcg gag aac aaa ttt gcc aat ctg gct   96
Ser Thr Ala Phe Val Gly Val Ser Glu Asn Lys Phe Ala Asn Leu Ala
             20                  25                  30

ttg gcc gag gcg atc ggg atg gag gtg ccc gcg cgc gag ttg gtg ggg   144
Leu Ala Glu Ala Ile Gly Met Glu Val Pro Ala Arg Glu Leu Val Gly
         35                  40                  45

cgt gcg cag ttt gaa ggc gtg ccc ccc gag ttt gag gcc atg acc gac   192
Arg Ala Gln Phe Glu Gly Val Pro Pro Glu Phe Glu Ala Met Thr Asp
     50                  55                  60

ggg ttg gtt ttg ctg gtg cgg cgg ttt gat cgc gcg ggc gat ggc gtg   240
Gly Leu Val Leu Leu Val Arg Arg Phe Asp Arg Ala Gly Asp Gly Val
 65                  70                  75                  80

cgc gtg cat atg gag gat ttc gca cag gtg ttc ggc cta tac ccc gcg   288
Arg Val His Met Glu Asp Phe Ala Gln Val Phe Gly Leu Tyr Pro Ala
                 85                  90                  95

cgc aag tat gat ggg gcg gcc agt cac gat att gcg gcg gtg ctg ggc   336
Arg Lys Tyr Asp Gly Ala Ala Ser His Asp Ile Ala Ala Val Leu Gly
            100                 105                 110

agt gcg gtg tcg atc gcg gcg ggg ttg gag ttc gtg cgg cgg ctg gcg   384
Ser Ala Val Ser Ile Ala Ala Gly Leu Glu Phe Val Arg Arg Leu Ala
        115                 120                 125
```

```
ctc tct gtt gtg atg ggc aac ggc gat atg cat ttg aag aac tgg tcg   432
Leu Ser Val Val Met Gly Asn Gly Asp Met His Leu Lys Asn Trp Ser
    130                 135                 140

ctg atc tat cac ggg cgg ggc gat gtg ccg                          462
Leu Ile Tyr His Gly Arg Gly Asp Val Pro
145                 150
```

<210> 1320
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 1320

```
Thr Val Pro Leu Gly Asp Gly Gln Gly Arg Tyr Ile Ala Lys Ile Pro
  1               5                  10                  15

Ser Thr Ala Phe Val Gly Val Ser Glu Asn Lys Phe Ala Asn Leu Ala
             20                  25                  30

Leu Ala Glu Ala Ile Gly Met Glu Val Pro Ala Arg Glu Leu Val Gly
         35                  40                  45

Arg Ala Gln Phe Glu Gly Val Pro Pro Glu Phe Glu Ala Met Thr Asp
     50                  55                  60

Gly Leu Val Leu Leu Val Arg Arg Phe Asp Arg Ala Gly Asp Gly Val
 65                  70                  75                  80

Arg Val His Met Glu Asp Phe Ala Gln Val Phe Gly Leu Tyr Pro Ala
                 85                  90                  95

Arg Lys Tyr Asp Gly Ala Ala Ser His Asp Ile Ala Ala Val Leu Gly
            100                 105                 110

Ser Ala Val Ser Ile Ala Ala Gly Leu Glu Phe Val Arg Arg Leu Ala
        115                 120                 125

Leu Ser Val Val Met Gly Asn Gly Asp Met His Leu Lys Asn Trp Ser
    130                 135                 140

Leu Ile Tyr His Gly Arg Gly Asp Val Pro
145                 150
```

<210> 1321
<211> 273
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(250)
<223> RXN02840

<400> 1321

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aagtgaaatc aatcggcttt tccagcagca gcactggtcg cgccagcgtg ggtgttatgg 60

tgaaggcgaa tacaccttca gcaccgctga gccggaagag atg acg gta atc agt   115
                                              Met Thr Val Ile Ser
```

```
                                                  1               5

ggc gcg ctg aat gtg tta ctg cct gac gcg acc gac tgg cag gtg tat   163
Gly Ala Leu Asn Val Leu Leu Pro Asp Ala Thr Asp Trp Gln Val Tyr
                 10                  15                  20

gaa gcc ggt tcg gtg ttt aat gtt ccc ggt cac agt gag ttt cat ctg   211
Glu Ala Gly Ser Val Phe Asn Val Pro Gly His Ser Glu Phe His Leu
             25                  30                  35

caa gtt gcc gaa ccc acc tct tat ctg tgc cgc tat ctg taattcctcg    260
Gln Val Ala Glu Pro Thr Ser Tyr Leu Cys Arg Tyr Leu
         40                  45                  50

ccttccccct gaa                                                   273


<210> 1322
<211> 50
<212> PRT
<213> Corynebacterium glutamicum

<400> 1322
Met Thr Val Ile Ser Gly Ala Leu Asn Val Leu Leu Pro Asp Ala Thr
  1               5                  10                  15

Asp Trp Gln Val Tyr Glu Ala Gly Ser Val Phe Asn Val Pro Gly His
             20                  25                  30

Ser Glu Phe His Leu Gln Val Ala Glu Pro Thr Ser Tyr Leu Cys Arg
         35                  40                  45

Tyr Leu
     50


<210> 1323
<211> 273
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(250)
<223> FRXA02840

<400> 1323
aagtgaaatc aatcggcttt tccagcagca gcactggtcg cgccagcgtg ggtgttatgg 60

tgaaggcgaa tacaccttca gcaccgctga gccggaagag atg acg gta atc agt   115
                                              Met Thr Val Ile Ser
                                                1               5

ggc gcg ctg aat gtg tta ctg cct gac gcg acc gac tgg cag gtg tat   163
Gly Ala Leu Asn Val Leu Leu Pro Asp Ala Thr Asp Trp Gln Val Tyr
                 10                  15                  20

gaa gcc ggt tcg gtg ttt aat gtt ccc ggt cac agt gag ttt cat ctg   211
Glu Ala Gly Ser Val Phe Asn Val Pro Gly His Ser Glu Phe His Leu
             25                  30                  35
```

```
caa gtt gcc gaa ccc acc tct tat ctg tgc cgc tat ctg taattcctcg    260
Gln Val Ala Glu Pro Thr Ser Tyr Leu Cys Arg Tyr Leu
         40                  45                  50

ccttcccctt gaa                                                   273


<210> 1324
<211> 50
<212> PRT
<213> Corynebacterium glutamicum

<400> 1324
Met Thr Val Ile Ser Gly Ala Leu Asn Val Leu Leu Pro Asp Ala Thr
  1               5                  10                  15

Asp Trp Gln Val Tyr Glu Ala Gly Ser Val Phe Asn Val Pro Gly His
             20                  25                  30

Ser Glu Phe His Leu Gln Val Ala Glu Pro Thr Ser Tyr Leu Cys Arg
         35                  40                  45

Tyr Leu
     50


<210> 1325
<211> 558
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(535)
<223> RXN02841

<400> 1325
ctcacataac tttacgccac cccataccct ttaacccctg cactgctcat ccacaagcac 60

tgtgcagggg ttgtgttttc taacaagaaa agagaccacc atg ttc aca gct ttt   115
                                          Met Phe Thr Ala Phe
                                            1               5

aaa agc aat cct acg acc att aaa aag ctg gtt tct gag ctc att aat   163
Lys Ser Asn Pro Thr Thr Ile Lys Lys Leu Val Ser Glu Leu Ile Asn
                 10                  15                  20

ggc gac gat gca gcg ctc aac gaa cta gag cga cac gtc act aat gaa   211
Gly Asp Asp Ala Ala Leu Asn Glu Leu Glu Arg His Val Thr Asn Glu
             25                  30                  35

tca gtc cgt gct cgc gaa ctc cct aat gtc cag tac aaa gcc act gcg   259
Ser Val Arg Ala Arg Glu Leu Pro Asn Val Gln Tyr Lys Ala Thr Ala
         40                  45                  50

ggg cgc aac ttc gcc ata tcc aag ctg gtc caa aat ttg cgt cgc atc   307
Gly Arg Asn Phe Ala Ile Ser Lys Leu Val Gln Asn Leu Arg Arg Ile
     55                  60                  65

aac aag gca caa aac aat cca cgt ggt gtg ccc act cat gcc acc gtg   355
Asn Lys Ala Gln Asn Asn Pro Arg Gly Val Pro Thr His Ala Thr Val
```

```
 70                  75                  80                  85

att ctg ctt aag gaa gac ggc agc tac gac ggt gaa gaa cag tgg cgc   403
Ile Leu Leu Lys Glu Asp Gly Ser Tyr Asp Gly Glu Glu Gln Trp Arg
                 90                  95                 100

att cca gaa aag gcg atc act ccg ttc gac atg cta cgt tcg cct gac   451
Ile Pro Glu Lys Ala Ile Thr Pro Phe Asp Met Leu Arg Ser Pro Asp
            105                 110                 115

ttc aac cac aac agg ctg aag aac cgg ccg ctc atg gtc gag tcc caa   499
Phe Asn His Asn Arg Leu Lys Asn Arg Pro Leu Met Val Glu Ser Gln
        120                 125                 130

tac ccc tgg ggc gtc ccc gga ctc att aaa atg aac tgatcaatcc        545
Tyr Pro Trp Gly Val Pro Gly Leu Ile Lys Met Asn
    135                 140                 145

ctgacacagc cat                                                   558


<210> 1326
<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 1326
Met Phe Thr Ala Phe Lys Ser Asn Pro Thr Thr Ile Lys Lys Leu Val
  1               5                  10                  15

Ser Glu Leu Ile Asn Gly Asp Asp Ala Ala Leu Asn Glu Leu Glu Arg
             20                  25                  30

His Val Thr Asn Glu Ser Val Arg Ala Arg Glu Leu Pro Asn Val Gln
         35                  40                  45

Tyr Lys Ala Thr Ala Gly Arg Asn Phe Ala Ile Ser Lys Leu Val Gln
     50                  55                  60

Asn Leu Arg Arg Ile Asn Lys Ala Gln Asn Asn Pro Arg Gly Val Pro
 65                  70                  75                  80

Thr His Ala Thr Val Ile Leu Leu Lys Glu Asp Gly Ser Tyr Asp Gly
                 85                  90                  95

Glu Glu Gln Trp Arg Ile Pro Glu Lys Ala Ile Thr Pro Phe Asp Met
            100                 105                 110

Leu Arg Ser Pro Asp Phe Asn His Asn Arg Leu Lys Asn Arg Pro Leu
        115                 120                 125

Met Val Glu Ser Gln Tyr Pro Trp Gly Val Pro Gly Leu Ile Lys Met
    130                 135                 140

Asn
145


<210> 1327
<211> 285
<212> DNA
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<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (7)..(285)
<223> FRXA02841

<400> 1327
accaccatg ttc gca gct ttt aaa agc aat ctt ccg acc att aaa aag ctg 51
Met Phe Ala Ala Phe Lys Ser Asn Leu Pro Thr Ile Lys Lys Leu
1 5 10 15

gtt tat gag gtc att aat ggc gtc gat gca gcg ctc aac gaa cta gag 99
Val Tyr Glu Val Ile Asn Gly Val Asp Ala Ala Leu Asn Glu Leu Glu
20 25 30

cga cac gtc act aat gaa tca gtc cgt gct cgc gaa ctc cct aat gtc 147
Arg His Val Thr Asn Glu Ser Val Arg Ala Arg Glu Leu Pro Asn Val
35 40 45

cag tac aaa gcc act gcg ggg cgc aac ttc gcc ata tcc aag ctg gtc 195
Gln Tyr Lys Ala Thr Ala Gly Arg Asn Phe Ala Ile Ser Lys Leu Val
50 55 60

caa aat ttg cgt cgc atc aac aag gca caa aac aat cca cgt ggt gtg 243
Gln Asn Leu Arg Arg Ile Asn Lys Ala Gln Asn Asn Pro Arg Gly Val
65 70 75

ccc act cat gcc acc gtg att ctg ctt aag gga gac ggc agc 285
Pro Thr His Ala Thr Val Ile Leu Leu Lys Gly Asp Gly Ser
80 85 90

<210> 1328
<211> 93
<212> PRT
<213> Corynebacterium glutamicum

<400> 1328
Met Phe Ala Ala Phe Lys Ser Asn Leu Pro Thr Ile Lys Lys Leu Val
1 5 10 15

Tyr Glu Val Ile Asn Gly Val Asp Ala Ala Leu Asn Glu Leu Glu Arg
20 25 30

His Val Thr Asn Glu Ser Val Arg Ala Arg Glu Leu Pro Asn Val Gln
35 40 45

Tyr Lys Ala Thr Ala Gly Arg Asn Phe Ala Ile Ser Lys Leu Val Gln
50 55 60

Asn Leu Arg Arg Ile Asn Lys Ala Gln Asn Asn Pro Arg Gly Val Pro
65 70 75 80

Thr His Ala Thr Val Ile Leu Leu Lys Gly Asp Gly Ser
85 90

<210> 1329
<211> 873
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(850)
<223> RXN02846

<400> 1329
tacaagcgct gaacgttgag tttgagtttg gtccattgag gggtaaaggc ttacctctcg 60

```
actaggtggg gtgggcgtag agcgcctatt ctgattgatc gtg tta acc atc gct   115
                                              Val Leu Thr Ile Ala
                                                1               5

att gta ctt ctc gcg tca gtc ctc atc ggt gct ctt ctc caa cgc atg   163
Ile Val Leu Leu Ala Ser Val Leu Ile Gly Ala Leu Leu Gln Arg Met
                10                  15                  20

aca gga ttg ggc gtc ggt cta gtt acc ggc cca gtc ctg act tct ttg   211
Thr Gly Leu Gly Val Gly Leu Val Thr Gly Pro Val Leu Thr Ser Leu
            25                  30                  35

tta ggg ccg cta gca ggc gtg acc atg gtg aat ggt ctg tcc atc atc   259
Leu Gly Pro Leu Ala Gly Val Thr Met Val Asn Gly Leu Ser Ile Ile
        40                  45                  50

aac gcg gtg aat aat gcg tgg tcg gtg cgc aaa cgc act gac tgg gcc   307
Asn Ala Val Asn Asn Ala Trp Ser Val Arg Lys Arg Thr Asp Trp Ala
    55                  60                  65

aaa ttc cga att ctt gcc ggc gct ttg gtg ctt ggt tct gtt cct gct   355
Lys Phe Arg Ile Leu Ala Gly Ala Leu Val Leu Gly Ser Val Pro Ala
70                  75                  80                  85

gtt gca gtg gtg tat ttc ctt aac gga cca tgg ctg ttg att ttc gtt   403
Val Ala Val Val Tyr Phe Leu Asn Gly Pro Trp Leu Leu Ile Phe Val
                90                  95                  100

ggt gcg atg gtg ctg ctc gcg ttg ggt gtt tcc ctg ttc cca aca gag   451
Gly Ala Met Val Leu Leu Ala Leu Gly Val Ser Leu Phe Pro Thr Glu
            105                 110                 115

aaa ttc gca ctc aag caa gaa gct aaa ctg cct atg gtc atc ttc ggc   499
Lys Phe Ala Leu Lys Gln Glu Ala Lys Leu Pro Met Val Ile Phe Gly
        120                 125                 130

atg att ggt gga ttc atg tcc act gtt gca ggc atc gca ggg cca tcc   547
Met Ile Gly Gly Phe Met Ser Thr Val Ala Gly Ile Ala Gly Pro Ser
    135                 140                 145

ctg act gtt tat gcg cgc ctg agc cgc tgg gat tac cgc gac ttt gtg   595
Leu Thr Val Tyr Ala Arg Leu Ser Arg Trp Asp Tyr Arg Asp Phe Val
150                 155                 160                 165

gcc acc ttg cac cca gtt cta ctc gtg gcc aac acc gta tcg ttc ctg   643
Ala Thr Leu His Pro Val Leu Leu Val Ala Asn Thr Val Ser Phe Leu
                170                 175                 180

ctc aag gtt atc ttg atc ggt gga ctc gat ttc ggt ggc gca ccc gca   691
Leu Lys Val Ile Leu Ile Gly Gly Leu Asp Phe Gly Gly Ala Pro Ala
            185                 190                 195
```

```
tgg ctc tgg atc ggt gcc gta gcg atg atc ttt gtc ggt gct tgg ttg   739
Trp Leu Trp Ile Gly Ala Val Ala Met Ile Phe Val Gly Ala Trp Leu
        200                 205                 210

ggt gaa atc gtc aac gct aag gtg tcc acc cca atg gcc aag cgc atc   787
Gly Glu Ile Val Asn Ala Lys Val Ser Thr Pro Met Ala Lys Arg Ile
    215                 220                 225

gct acg ctc ctg gca gca gct ggt gcc gca gtg gtg ttg ttc cga ggc   835
Ala Thr Leu Leu Ala Ala Ala Gly Ala Ala Val Val Leu Phe Arg Gly
230                 235                 240                 245

atc atg gaa ttg gtt tagcggtctt aattggtggg aag                    873
Ile Met Glu Leu Val
                250
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<210> 1330
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 1330

```
Val Leu Thr Ile Ala Ile Val Leu Leu Ala Ser Val Leu Ile Gly Ala
  1               5                  10                  15

Leu Leu Gln Arg Met Thr Gly Leu Gly Val Gly Leu Val Thr Gly Pro
             20                  25                  30

Val Leu Thr Ser Leu Leu Gly Pro Leu Ala Gly Val Thr Met Val Asn
         35                  40                  45

Gly Leu Ser Ile Ile Asn Ala Val Asn Asn Ala Trp Ser Val Arg Lys
     50                  55                  60

Arg Thr Asp Trp Ala Lys Phe Arg Ile Leu Ala Gly Ala Leu Val Leu
 65                  70                  75                  80

Gly Ser Val Pro Ala Val Ala Val Val Tyr Phe Leu Asn Gly Pro Trp
                 85                  90                  95

Leu Leu Ile Phe Val Gly Ala Met Val Leu Leu Ala Leu Gly Val Ser
            100                 105                 110

Leu Phe Pro Thr Glu Lys Phe Ala Leu Lys Gln Glu Ala Lys Leu Pro
        115                 120                 125

Met Val Ile Phe Gly Met Ile Gly Gly Phe Met Ser Thr Val Ala Gly
    130                 135                 140

Ile Ala Gly Pro Ser Leu Thr Val Tyr Ala Arg Leu Ser Arg Trp Asp
145                 150                 155                 160

Tyr Arg Asp Phe Val Ala Thr Leu His Pro Val Leu Leu Val Ala Asn
                165                 170                 175

Thr Val Ser Phe Leu Leu Lys Val Ile Leu Ile Gly Gly Leu Asp Phe
            180                 185                 190

Gly Gly Ala Pro Ala Trp Leu Trp Ile Gly Ala Val Ala Met Ile Phe
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        195                 200                 205

Val Gly Ala Trp Leu Gly Glu Ile Val Asn Ala Lys Val Ser Thr Pro
    210                 215                 220

Met Ala Lys Arg Ile Ala Thr Leu Leu Ala Ala Ala Gly Ala Ala Val
225                 230                 235                 240

Val Leu Phe Arg Gly Ile Met Glu Leu Val
                245                 250


<210> 1331
<211> 573
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(573)
<223> FRXA02846

<400> 1331
gtg aat ggt ctg tcc atc atc aac gcg gtg aat aat gcg tgg tcg gtg   48
Val Asn Gly Leu Ser Ile Ile Asn Ala Val Asn Asn Ala Trp Ser Val
  1               5                  10                  15

cgc aaa cgc act gac tgg gcc aaa ttc cga att ctt gcc ggc gct ttg   96
Arg Lys Arg Thr Asp Trp Ala Lys Phe Arg Ile Leu Ala Gly Ala Leu
             20                  25                  30

gtg ctt ggt tct gtt cct gct gtt gca gtg gtg tat ttc ctt aac gga   144
Val Leu Gly Ser Val Pro Ala Val Ala Val Val Tyr Phe Leu Asn Gly
         35                  40                  45

cca tgg ctg ttg att ttc gtt ggt gcg atg gtg ctg ctc gcg ttg ggt   192
Pro Trp Leu Leu Ile Phe Val Gly Ala Met Val Leu Leu Ala Leu Gly
     50                  55                  60

gtt tcc ctg ttc cca aca gag aaa ttc gca ctc aag caa gaa gct aaa   240
Val Ser Leu Phe Pro Thr Glu Lys Phe Ala Leu Lys Gln Glu Ala Lys
 65                  70                  75                  80

ctg cct atg gtc atc ttc ggc atg att ggt gga ttc atg tcc act gtt   288
Leu Pro Met Val Ile Phe Gly Met Ile Gly Gly Phe Met Ser Thr Val
                 85                  90                  95

gca ggc atc gca ggg cca tcc ctg act gtt tat gcg cgc ctg agc cgc   336
Ala Gly Ile Ala Gly Pro Ser Leu Thr Val Tyr Ala Arg Leu Ser Arg
            100                 105                 110

tgg gat tac cga gac ttt gtg gcc acc ttg cac cca gtt cta ctc gtg   384
Trp Asp Tyr Arg Asp Phe Val Ala Thr Leu His Pro Val Leu Leu Val
        115                 120                 125

gcc aac acc gta tcg ttc ctg ctc aag gtt atc ttg atc ggt gga ctc   432
Ala Asn Thr Val Ser Phe Leu Leu Lys Val Ile Leu Ile Gly Gly Leu
    130                 135                 140

gat ttc ggt ggc gca ccc gca tgg ctc tgg atc ggt gcc gta gcg atg   480
Asp Phe Gly Gly Ala Pro Ala Trp Leu Trp Ile Gly Ala Val Ala Met
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145                 150                 155                 160

atc ttt gtc ggt gct tgg ttg ggt gaa atc gtc aac gct aag gtg tcc   528
Ile Phe Val Gly Ala Trp Leu Gly Glu Ile Val Asn Ala Lys Val Ser
                165                 170                 175

acc cca atg gcc aag cgc atc gct acg ctc ctg gca gca gct ggt       573
Thr Pro Met Ala Lys Arg Ile Ala Thr Leu Leu Ala Ala Ala Gly
            180                 185                 190


<210> 1332
<211> 191
<212> PRT
<213> Corynebacterium glutamicum

<400> 1332
Val Asn Gly Leu Ser Ile Ile Asn Ala Val Asn Asn Ala Trp Ser Val
  1               5                  10                  15

Arg Lys Arg Thr Asp Trp Ala Lys Phe Arg Ile Leu Ala Gly Ala Leu
             20                  25                  30

Val Leu Gly Ser Val Pro Ala Val Ala Val Val Tyr Phe Leu Asn Gly
         35                  40                  45

Pro Trp Leu Leu Ile Phe Val Gly Ala Met Val Leu Leu Ala Leu Gly
     50                  55                  60

Val Ser Leu Phe Pro Thr Glu Lys Phe Ala Leu Lys Gln Glu Ala Lys
 65                  70                  75                  80

Leu Pro Met Val Ile Phe Gly Met Ile Gly Gly Phe Met Ser Thr Val
                85                  90                  95

Ala Gly Ile Ala Gly Pro Ser Leu Thr Val Tyr Ala Arg Leu Ser Arg
            100                 105                 110

Trp Asp Tyr Arg Asp Phe Val Ala Thr Leu His Pro Val Leu Leu Val
        115                 120                 125

Ala Asn Thr Val Ser Phe Leu Leu Lys Val Ile Leu Ile Gly Gly Leu
    130                 135                 140

Asp Phe Gly Gly Ala Pro Ala Trp Leu Trp Ile Gly Ala Val Ala Met
145                 150                 155                 160

Ile Phe Val Gly Ala Trp Leu Gly Glu Ile Val Asn Ala Lys Val Ser
                165                 170                 175

Thr Pro Met Ala Lys Arg Ile Ala Thr Leu Leu Ala Ala Ala Gly
            180                 185                 190


<210> 1333
<211> 1135
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
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<222> (47)..(1135)
<223> RXN02847

<400> 1333
atatcgcagc agcctcgatg gtcaacgccc atatgatggg aagttgttg gcg cta acc 58
Leu Ala Leu Thr
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gcc aga ggc ttt ctc aat tct gaa aga agc cag aca agg tgg aaa acc 106
Ala Arg Gly Phe Leu Asn Ser Glu Arg Ser Gln Thr Arg Trp Lys Thr
5 10 15 20

cac ttc acc acc cag aaa gtt cca cgc tcc ggc tac aga tat gac ctc 154
His Phe Thr Thr Gln Lys Val Pro Arg Ser Gly Tyr Arg Tyr Asp Leu
25 30 35

gat ggg ctc cgc ggc atc gcg atc gcc ttc gta gtt ttg ttc cat gtt 202
Asp Gly Leu Arg Gly Ile Ala Ile Ala Phe Val Val Leu Phe His Val
40 45 50

ttc gtc gga aaa gtc tcc ggc ggt gtg gat gtc ttc ctg ctg ctg tct 250
Phe Val Gly Lys Val Ser Gly Gly Val Asp Val Phe Leu Leu Leu Ser
55 60 65

ggc tat ttc ttc tta ggg tcg caa ttg cgt tat gca gat cgt cca gat 298
Gly Tyr Phe Phe Leu Gly Ser Gln Leu Arg Tyr Ala Asp Arg Pro Asp
70 75 80

tct tcc atc aac ccc tgg tgg ccg att tgg cgc acg cta cgc aga tta 346
Ser Ser Ile Asn Pro Trp Trp Pro Ile Trp Arg Thr Leu Arg Arg Leu
85 90 95 100

ctt cct gcg tta gtg ctg gtg ttg ggc gtt tcc atg gtc ctc atc ttg 394
Leu Pro Ala Leu Val Leu Val Leu Gly Val Ser Met Val Leu Ile Leu
105 110 115

gcg tgg gtg ccc aga ctg caa cca ata gaa ata gcc aac caa gca gta 442
Ala Trp Val Pro Arg Leu Gln Pro Ile Glu Ile Ala Asn Gln Ala Val
120 125 130

gcc agc ctc ttc tat gtc caa aac tgg gag ctc gca tcc caa ggt gct 490
Ala Ser Leu Phe Tyr Val Gln Asn Trp Glu Leu Ala Ser Gln Gly Ala
135 140 145

gcc tac gga gca gcc tct gca gaa gtc agt cct ttc cag cac ttg tgg 538
Ala Tyr Gly Ala Ala Ser Ala Glu Val Ser Pro Phe Gln His Leu Trp
150 155 160

tcc atg gct gtg caa ggg cag ttc tac ctc ttt gcc atc ttg ttg agc 586
Ser Met Ala Val Gln Gly Gln Phe Tyr Leu Phe Ala Ile Leu Leu Ser
165 170 175 180

atg gcg atc atc ctg att cgt cga tac cgc ccc gaa tac tcc gca gtg 634
Met Ala Ile Ile Leu Ile Arg Arg Tyr Arg Pro Glu Tyr Ser Ala Val
185 190 195

cga cta gcg act cct gtg ctg gca gtg ctc aca tcc gta tca ttt ttc 682
Arg Leu Ala Thr Pro Val Leu Ala Val Leu Thr Ser Val Ser Phe Phe
200 205 210

agt gca atc ctg tgg cat ttc att gat caa tca gtc aac tac tat tcc 730

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Ser Ala Ile Leu Trp His Phe Ile Asp Gln Ser Val Asn Tyr Tyr Ser
        215                 220                 225

acc ttc acc agg ttc tgg gag ctc ggc ctt ggt gca cta ttg gtg ctg   778
Thr Phe Thr Arg Phe Trp Glu Leu Gly Leu Gly Ala Leu Leu Val Leu
    230                 235                 240

cat gcg cct cga att ttg att tct gcg aag act aaa tca ata ctc gca   826
His Ala Pro Arg Ile Leu Ile Ser Ala Lys Thr Lys Ser Ile Leu Ala
245                 250                 255                 260

gcc gtc ggt ttg ttt atg gtg cta tcc act gga ttc ttc atg gat ggc   874
Ala Val Gly Leu Phe Met Val Leu Ser Thr Gly Phe Phe Met Asp Gly
                265                 270                 275

gca gag act ttc cct gga ttc ccc gcg ctg tat ccc atc ttg ggt gct   922
Ala Glu Thr Phe Pro Gly Phe Pro Ala Leu Tyr Pro Ile Leu Gly Ala
            280                 285                 290

tgc tta gtc atc ctt ggc gac ggt aaa atc tcg gtc ttt ctc tcc cga   970
Cys Leu Val Ile Leu Gly Asp Gly Lys Ile Ser Val Phe Leu Ser Arg
        295                 300                 305

aaa tgg atg ctt tgg ctc ggc gat atc gcc tac ccg ctc tac ttg tgg   1018
Lys Trp Met Leu Trp Leu Gly Asp Ile Ala Tyr Pro Leu Tyr Leu Trp
    310                 315                 320

cac tgg cct ctg ctg atc att ttc acc gct ttg ttc aac caa gaa gag   1066
His Trp Pro Leu Leu Ile Ile Phe Thr Ala Leu Phe Asn Gln Glu Glu
325                 330                 335                 340

cca tcc atc tgg ctg ggt atc gcc gtg att atg ctg tcc ctt ggc ttg   1114
Pro Ser Ile Trp Leu Gly Ile Ala Val Ile Met Leu Ser Leu Gly Leu
                345                 350                 355

gcg cag ctg act aac aaa tac                                      1135
Ala Gln Leu Thr Asn Lys Tyr
            360
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<210> 1334
<211> 363
<212> PRT
<213> Corynebacterium glutamicum

<400> 1334

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Leu Ala Leu Thr Ala Arg Gly Phe Leu Asn Ser Glu Arg Ser Gln Thr
  1               5                  10                  15

Arg Trp Lys Thr His Phe Thr Thr Gln Lys Val Pro Arg Ser Gly Tyr
             20                  25                  30

Arg Tyr Asp Leu Asp Gly Leu Arg Gly Ile Ala Ile Ala Phe Val Val
         35                  40                  45

Leu Phe His Val Phe Val Gly Lys Val Ser Gly Gly Val Asp Val Phe
     50                  55                  60

Leu Leu Leu Ser Gly Tyr Phe Phe Leu Gly Ser Gln Leu Arg Tyr Ala
 65                  70                  75                  80
```

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Asp Arg Pro Asp Ser Ser Ile Asn Pro Trp Trp Pro Ile Trp Arg Thr
                 85                  90                  95

Leu Arg Arg Leu Leu Pro Ala Leu Val Leu Val Leu Gly Val Ser Met
            100                 105                 110

Val Leu Ile Leu Ala Trp Val Pro Arg Leu Gln Pro Ile Glu Ile Ala
        115                 120                 125

Asn Gln Ala Val Ala Ser Leu Phe Tyr Val Gln Asn Trp Glu Leu Ala
    130                 135                 140

Ser Gln Gly Ala Ala Tyr Gly Ala Ala Ser Ala Glu Val Ser Pro Phe
145                 150                 155                 160

Gln His Leu Trp Ser Met Ala Val Gln Gly Gln Phe Tyr Leu Phe Ala
                165                 170                 175

Ile Leu Leu Ser Met Ala Ile Ile Leu Ile Arg Arg Tyr Arg Pro Glu
            180                 185                 190

Tyr Ser Ala Val Arg Leu Ala Thr Pro Val Leu Ala Val Leu Thr Ser
        195                 200                 205

Val Ser Phe Phe Ser Ala Ile Leu Trp His Phe Ile Asp Gln Ser Val
    210                 215                 220

Asn Tyr Tyr Ser Thr Phe Thr Arg Phe Trp Glu Leu Gly Leu Gly Ala
225                 230                 235                 240

Leu Leu Val Leu His Ala Pro Arg Ile Leu Ile Ser Ala Lys Thr Lys
                245                 250                 255

Ser Ile Leu Ala Ala Val Gly Leu Phe Met Val Leu Ser Thr Gly Phe
            260                 265                 270

Phe Met Asp Gly Ala Glu Thr Phe Pro Gly Phe Pro Ala Leu Tyr Pro
        275                 280                 285

Ile Leu Gly Ala Cys Leu Val Ile Leu Gly Asp Gly Lys Ile Ser Val
    290                 295                 300

Phe Leu Ser Arg Lys Trp Met Leu Trp Leu Gly Asp Ile Ala Tyr Pro
305                 310                 315                 320

Leu Tyr Leu Trp His Trp Pro Leu Leu Ile Ile Phe Thr Ala Leu Phe
                325                 330                 335

Asn Gln Glu Glu Pro Ser Ile Trp Leu Gly Ile Ala Val Ile Met Leu
            340                 345                 350

Ser Leu Gly Leu Ala Gln Leu Thr Asn Lys Tyr
        355                 360
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<210> 1335
<211> 694
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(694)
<223> FRXA02847

<400> 1335
ccagcctctt ctatgtccaa aaactgggag ctcgcatccc aagggtgctg cctacggagc 60

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agcctctgca gaagtcagtc ctttccagca cttgtggtcc atg gct gtg caa ggg   115
                                            Met Ala Val Gln Gly
                                              1               5

cag ttc tac ctc ttt gcc atc ttg ttg agc atg gcg atc atc ctg att   163
Gln Phe Tyr Leu Phe Ala Ile Leu Leu Ser Met Ala Ile Ile Leu Ile
                 10                  15                  20

cgt cga tac cgc ccc gaa tac tcc gca gtg cga cta gcg act cct gtg   211
Arg Arg Tyr Arg Pro Glu Tyr Ser Ala Val Arg Leu Ala Thr Pro Val
             25                  30                  35

ctg gca gtg ctc aca tcc gta tca ttt ttc agt gca atc ctg tgg cat   259
Leu Ala Val Leu Thr Ser Val Ser Phe Phe Ser Ala Ile Leu Trp His
         40                  45                  50

ttc att gat caa tca gtc aac tac tat tcc acc ttc acc agg ttc tgg   307
Phe Ile Asp Gln Ser Val Asn Tyr Tyr Ser Thr Phe Thr Arg Phe Trp
     55                  60                  65

gag ctc ggc ctt ggt gca cta ttg gtg ctg cat gcg cct cga att ttg   355
Glu Leu Gly Leu Gly Ala Leu Leu Val Leu His Ala Pro Arg Ile Leu
 70                  75                  80                  85

att tct gcg aag act aaa tca ata ctc gca gcc gtc ggt ttg ttt atg   403
Ile Ser Ala Lys Thr Lys Ser Ile Leu Ala Ala Val Gly Leu Phe Met
                 90                  95                 100

gtg cta tcc act gga ttc ttc atg gat ggc gca gag act ttc cct gga   451
Val Leu Ser Thr Gly Phe Phe Met Asp Gly Ala Glu Thr Phe Pro Gly
            105                 110                 115

ttc ccc gcg ctg tat ccc atc ttg ggt gct tgc tta gtc atc ctt ggc   499
Phe Pro Ala Leu Tyr Pro Ile Leu Gly Ala Cys Leu Val Ile Leu Gly
        120                 125                 130

gac ggt aaa atc tcg gtc ttt ctc tcc cga aaa tgg atg ctt tgg ctc   547
Asp Gly Lys Ile Ser Val Phe Leu Ser Arg Lys Trp Met Leu Trp Leu
    135                 140                 145

ggc gat atc gcc tac ccg ctc tac ttg tgg cac tgg cct ctg ctg atc   595
Gly Asp Ile Ala Tyr Pro Leu Tyr Leu Trp His Trp Pro Leu Leu Ile
150                 155                 160                 165

att ttc acc gct ttg ttc aac caa gaa gag cca tcc atc tgg ctg ggt   643
Ile Phe Thr Ala Leu Phe Asn Gln Glu Glu Pro Ser Ile Trp Leu Gly
                170                 175                 180

atc gcc gtg att atg ctg tcc ctt ggc ttg gcg cag ctg act aac aaa   691
Ile Ala Val Ile Met Leu Ser Leu Gly Leu Ala Gln Leu Thr Asn Lys
            185                 190                 195

tac                                                               694
Tyr
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<210> 1336
<211> 198
<212> PRT
<213> Corynebacterium glutamicum

<400> 1336
Met Ala Val Gln Gly Gln Phe Tyr Leu Phe Ala Ile Leu Leu Ser Met
1 5 10 15

Ala Ile Ile Leu Ile Arg Arg Tyr Arg Pro Glu Tyr Ser Ala Val Arg
20 25 30

Leu Ala Thr Pro Val Leu Ala Val Leu Thr Ser Val Ser Phe Phe Ser
35 40 45

Ala Ile Leu Trp His Phe Ile Asp Gln Ser Val Asn Tyr Tyr Ser Thr
50 55 60

Phe Thr Arg Phe Trp Glu Leu Gly Leu Gly Ala Leu Leu Val Leu His
65 70 75 80

Ala Pro Arg Ile Leu Ile Ser Ala Lys Thr Lys Ser Ile Leu Ala Ala
85 90 95

Val Gly Leu Phe Met Val Leu Ser Thr Gly Phe Phe Met Asp Gly Ala
100 105 110

Glu Thr Phe Pro Gly Phe Pro Ala Leu Tyr Pro Ile Leu Gly Ala Cys
115 120 125

Leu Val Ile Leu Gly Asp Gly Lys Ile Ser Val Phe Leu Ser Arg Lys
130 135 140

Trp Met Leu Trp Leu Gly Asp Ile Ala Tyr Pro Leu Tyr Leu Trp His
145 150 155 160

Trp Pro Leu Leu Ile Ile Phe Thr Ala Leu Phe Asn Gln Glu Glu Pro
165 170 175

Ser Ile Trp Leu Gly Ile Ala Val Ile Met Leu Ser Leu Gly Leu Ala
180 185 190

Gln Leu Thr Asn Lys Tyr
195

<210> 1337
<211> 305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(282)
<223> RXN02849

<400> 1337
tcc cca tac ccc gtc atg atc agc acc tct gcc gac gcc tca aac gtg 48

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Ser Pro Tyr Pro Val Met Ile Ser Thr Ser Ala Asp Ala Ser Asn Val
  1               5                  10                  15

acc gtg cgc atc atg ggt gtg gac acc acc tcc gtg gaa tcc atc aac   96
Thr Val Arg Ile Met Gly Val Asp Thr Thr Ser Val Glu Ser Ile Asn
             20                  25                  30

aac gga cgt tgg tcc acc acc cag ccc aac aca gtt cga gta tcg ggt   144
Asn Gly Arg Trp Ser Thr Thr Gln Pro Asn Thr Val Arg Val Ser Gly
         35                  40                  45

tca gat tgt gtg cca tca acc ggt gca cca gga ttt acc acc tca gac   192
Ser Asp Cys Val Pro Ser Thr Gly Ala Pro Gly Phe Thr Thr Ser Asp
     50                  55                  60

acc cga atc atc agc gat ctt tct ggc aac gaa atc acc aga gaa acc   240
Thr Arg Ile Ile Ser Asp Leu Ser Gly Asn Glu Ile Thr Arg Glu Thr
 65                  70                  75                  80

gtc acc acg gtt tac gat cct tca cca aac gtg gtc tgc tcc           282
Val Thr Thr Val Tyr Asp Pro Ser Pro Asn Val Val Cys Ser
                 85                  90

taaaacaaaa tgccccacca gat                                        305


<210> 1338
<211> 94
<212> PRT
<213> Corynebacterium glutamicum

<400> 1338
Ser Pro Tyr Pro Val Met Ile Ser Thr Ser Ala Asp Ala Ser Asn Val
  1               5                  10                  15

Thr Val Arg Ile Met Gly Val Asp Thr Thr Ser Val Glu Ser Ile Asn
             20                  25                  30

Asn Gly Arg Trp Ser Thr Thr Gln Pro Asn Thr Val Arg Val Ser Gly
         35                  40                  45

Ser Asp Cys Val Pro Ser Thr Gly Ala Pro Gly Phe Thr Thr Ser Asp
     50                  55                  60

Thr Arg Ile Ile Ser Asp Leu Ser Gly Asn Glu Ile Thr Arg Glu Thr
 65                  70                  75                  80

Val Thr Thr Val Tyr Asp Pro Ser Pro Asn Val Val Cys Ser
                 85                  90


<210> 1339
<211> 305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(282)
<223> FRXA02849
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<400> 1339
tcc cca tac ccc gtc atg atc agc acc tct gcc gac gcc tca aac gtg 48
Ser Pro Tyr Pro Val Met Ile Ser Thr Ser Ala Asp Ala Ser Asn Val
1 5 10 15

acc gtg cgc atc atg ggt gtg gac acc acc tcc gtg gaa tcc atc aac 96
Thr Val Arg Ile Met Gly Val Asp Thr Thr Ser Val Glu Ser Ile Asn
20 25 30

aac gga cgt tgg tcc acc acc cag ccc aac aca gtt cga gta tcg ggt 144
Asn Gly Arg Trp Ser Thr Thr Gln Pro Asn Thr Val Arg Val Ser Gly
35 40 45

tca gat tgt gtg cca tca acc ggt gca cca gga ttt acc acc tca gac 192
Ser Asp Cys Val Pro Ser Thr Gly Ala Pro Gly Phe Thr Thr Ser Asp
50 55 60

acc cga atc atc agc gat ctt tct ggc aac gaa atc acc aga gaa ccc 240
Thr Arg Ile Ile Ser Asp Leu Ser Gly Asn Glu Ile Thr Arg Glu Pro
65 70 75 80

gtc acc acg gtt tac gat cct tca cca aac gtg gtc tgc tcc 282
Val Thr Thr Val Tyr Asp Pro Ser Pro Asn Val Val Cys Ser
85 90

taaaacaaaa tgccccacca gat 305

<210> 1340
<211> 94
<212> PRT
<213> Corynebacterium glutamicum

<400> 1340
Ser Pro Tyr Pro Val Met Ile Ser Thr Ser Ala Asp Ala Ser Asn Val
1 5 10 15

Thr Val Arg Ile Met Gly Val Asp Thr Thr Ser Val Glu Ser Ile Asn
20 25 30

Asn Gly Arg Trp Ser Thr Thr Gln Pro Asn Thr Val Arg Val Ser Gly
35 40 45

Ser Asp Cys Val Pro Ser Thr Gly Ala Pro Gly Phe Thr Thr Ser Asp
50 55 60

Thr Arg Ile Ile Ser Asp Leu Ser Gly Asn Glu Ile Thr Arg Glu Pro
65 70 75 80

Val Thr Thr Val Tyr Asp Pro Ser Pro Asn Val Val Cys Ser
85 90

<210> 1341
<211> 582
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(559)

<223> RXN02911

<400> 1341
accgcataca ttaacgtgtt gatcattgcc ctagtatgcg cagtagcggc tgctctgatc 60

agcagttacc ttttccgcgg aaatccgaag ggagccaata atg cgc act agt aaa 115
Met Arg Thr Ser Lys
1 5

aaa gag atg att ctg cgc acg gcc atc gat tat atc ggc gag tac agc 163
Lys Glu Met Ile Leu Arg Thr Ala Ile Asp Tyr Ile Gly Glu Tyr Ser
10 15 20

ctc gag acg ctg agt tac gat tcg ctc gcc gag gcg acc ggt ctg tcc 211
Leu Glu Thr Leu Ser Tyr Asp Ser Leu Ala Glu Ala Thr Gly Leu Ser
25 30 35

aag tcg ggc ttg att tat cat ttc ccc agc cgc cat gcg ctg ctt tta 259
Lys Ser Gly Leu Ile Tyr His Phe Pro Ser Arg His Ala Leu Leu Leu
40 45 50

ggc atg cac gag ttg ctt gcc gac gac tgg gac aag gaa ttg cgc gac 307
Gly Met His Glu Leu Leu Ala Asp Asp Trp Asp Lys Glu Leu Arg Asp
55 60 65

ata acc cgc gac cca gag gat cca ctt gag cga ttg cgc gcc gtc gtg 355
Ile Thr Arg Asp Pro Glu Asp Pro Leu Glu Arg Leu Arg Ala Val Val
70 75 80 85

gtt acg ctt gct gaa aac gtt tcg cgc ccc gag ctg gtt ttg ctt atg 403
Val Thr Leu Ala Glu Asn Val Ser Arg Pro Glu Leu Val Leu Leu Met
90 95 100

gac gcc ccc tcc cac ccg gga ttt ctt aac gcc tgg cgc act gta aat 451
Asp Ala Pro Ser His Pro Gly Phe Leu Asn Ala Trp Arg Thr Val Asn
105 110 115

cat caa tgg atc ccc gac acc gat gat ctg gaa aac gat gcc cac aaa 499
His Gln Trp Ile Pro Asp Thr Asp Asp Leu Glu Asn Asp Ala His Lys
120 125 130

cgc gcc gtc tac tct ggt gca gct cgc agc cga tgg cct ctt cgt gca 547
Arg Ala Val Tyr Ser Gly Ala Ala Arg Ser Arg Trp Pro Leu Arg Ala
135 140 145

cga tta cat tca tgatgatgtc ctcagcaagt cca 582
Arg Leu His Ser
150

<210> 1342
<211> 153
<212> PRT
<213> Corynebacterium glutamicum

<400> 1342
Met Arg Thr Ser Lys Lys Glu Met Ile Leu Arg Thr Ala Ile Asp Tyr
1 5 10 15

Ile Gly Glu Tyr Ser Leu Glu Thr Leu Ser Tyr Asp Ser Leu Ala Glu
20 25 30

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Ala Thr Gly Leu Ser Lys Ser Gly Leu Ile Tyr His Phe Pro Ser Arg
          35                  40                  45

His Ala Leu Leu Leu Gly Met His Glu Leu Leu Ala Asp Asp Trp Asp
      50                  55                  60

Lys Glu Leu Arg Asp Ile Thr Arg Asp Pro Glu Asp Pro Leu Glu Arg
 65                  70                  75                  80

Leu Arg Ala Val Val Val Thr Leu Ala Glu Asn Val Ser Arg Pro Glu
                 85                  90                  95

Leu Val Leu Leu Met Asp Ala Pro Ser His Pro Gly Phe Leu Asn Ala
            100                 105                 110

Trp Arg Thr Val Asn His Gln Trp Ile Pro Asp Thr Asp Asp Leu Glu
        115                 120                 125

Asn Asp Ala His Lys Arg Ala Val Tyr Ser Gly Ala Ala Arg Ser Arg
    130                 135                 140

Trp Pro Leu Arg Ala Arg Leu His Ser
145                 150


<210> 1343
<211> 666
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(643)
<223> RXN02914

<400> 1343
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caaaaaccgc cgtgatggcg tactgactgc cgtaggcatc atg gtg gga aac tcc   115
                                              Met Val Gly Asn Ser
                                                1               5

atc tgg atc ata gcc agc ctc ctt ggg ctc tcg gca ctg atc tcc acg   163
Ile Trp Ile Ile Ala Ser Leu Leu Gly Leu Ser Ala Leu Ile Ser Thr
                10                  15                  20

tat cca gca att ttg aac ctg ttg cag ctc gtc ggt ggc ggt tat ttg   211
Tyr Pro Ala Ile Leu Asn Leu Leu Gln Leu Val Gly Gly Gly Tyr Leu
            25                  30                  35

acc tgg atg ggc atc ggg gcg gtg agg tca tgg tgg acg aaa cgc tcc   259
Thr Trp Met Gly Ile Gly Ala Val Arg Ser Trp Trp Thr Lys Arg Ser
        40                  45                  50

aca cag caa gct gca gcg gat tct caa gct gta gag aat acg ttg gtg   307
Thr Gln Gln Ala Ala Ala Asp Ser Gln Ala Val Glu Asn Thr Leu Val
    55                  60                  65

aca gcc acg gct gca tct gtc gga gtg tgg cca gct att cga tct ggc   355
Thr Ala Thr Ala Ala Ser Val Gly Val Trp Pro Ala Ile Arg Ser Gly
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```
 70                  75                  80                  85

att gct acc aac ttg tcc aac ccc aaa gct gtg ctg ttt ttt ggt tcc   403
Ile Ala Thr Asn Leu Ser Asn Pro Lys Ala Val Leu Phe Phe Gly Ser
                 90                  95                 100

gtt ttc gcc caa ttt gtt aga cct gac atg gga atc ggg tgg agt att   451
Val Phe Ala Gln Phe Val Arg Pro Asp Met Gly Ile Gly Trp Ser Ile
            105                 110                 115

ttc att gga gtc ttc ctc acc ctc act ggc ctg ctg tgg ttt gtg ggg   499
Phe Ile Gly Val Phe Leu Thr Leu Thr Gly Leu Leu Trp Phe Val Gly
        120                 125                 130

ttc gcc gtc ttg gtc cgc aaa cta gcc gct ggc ctc acc cga aat gga   547
Phe Ala Val Leu Val Arg Lys Leu Ala Ala Gly Leu Thr Arg Asn Gly
    135                 140                 145

gcc atc atc gac ctg cta acg ggg gtg att ttc atc ggg ctg gga atg   595
Ala Ile Ile Asp Leu Leu Thr Gly Val Ile Phe Ile Gly Leu Gly Met
150                 155                 160                 165

ttc atg atc ttc gag ggg gtt gta gga atc ggt ggc agg gta gtg ggt   643
Phe Met Ile Phe Glu Gly Val Val Gly Ile Gly Gly Arg Val Val Gly
                170                 175                 180

tagccccgcc cccaggacgt cac                                        666


<210> 1344
<211> 181
<212> PRT
<213> Corynebacterium glutamicum

<400> 1344
Met Val Gly Asn Ser Ile Trp Ile Ile Ala Ser Leu Leu Gly Leu Ser
  1               5                  10                  15

Ala Leu Ile Ser Thr Tyr Pro Ala Ile Leu Asn Leu Leu Gln Leu Val
             20                  25                  30

Gly Gly Gly Tyr Leu Thr Trp Met Gly Ile Gly Ala Val Arg Ser Trp
         35                  40                  45

Trp Thr Lys Arg Ser Thr Gln Gln Ala Ala Ala Asp Ser Gln Ala Val
     50                  55                  60

Glu Asn Thr Leu Val Thr Ala Thr Ala Ala Ser Val Gly Val Trp Pro
 65                  70                  75                  80

Ala Ile Arg Ser Gly Ile Ala Thr Asn Leu Ser Asn Pro Lys Ala Val
                 85                  90                  95

Leu Phe Phe Gly Ser Val Phe Ala Gln Phe Val Arg Pro Asp Met Gly
            100                 105                 110

Ile Gly Trp Ser Ile Phe Ile Gly Val Phe Leu Thr Leu Thr Gly Leu
        115                 120                 125

Leu Trp Phe Val Gly Phe Ala Val Leu Val Arg Lys Leu Ala Ala Gly
    130                 135                 140
```

```
Leu Thr Arg Asn Gly Ala Ile Ile Asp Leu Leu Thr Gly Val Ile Phe
145                 150                 155                 160

Ile Gly Leu Gly Met Phe Met Ile Phe Glu Gly Val Val Gly Ile Gly
                165                 170                 175

Gly Arg Val Val Gly
            180
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<210> 1345
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXN02921

<400> 1345

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tggaaaactg ggaagggttg acgttgcgga atctctccgc agcgtcggtt cggaccctaa 60

aaaagggtga ggaaccacat gagctgtttt aaggaatttt gtg tct gca ctt gaa   115
                                              Val Ser Ala Leu Glu
                                                1               5

gag tcg atc cgc atc gcg acc atc gcg gcg aaa gca gcg gat gaa aag   163
Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys Ala Ala Asp Glu Lys
                  10                  15                  20

aag gcc gat gac atc gct gtc atc gat gtc tct gac atg atc gca atc   211
Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser Asp Met Ile Ala Ile
              25                  30                  35

acc gat tgc ttt gtt gtt gca tct gct gac aat gag cgc cag gtg ggc   259
Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn Glu Arg Gln Val Gly
          40                  45                  50

gcc att gtt gag gag atc gaa gat gag atg acc aag gct ggt ttc gag   307
Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr Lys Ala Gly Phe Glu
      55                  60                  65

cct aag cgc cgt gaa ggc aac cgc gaa aac cgt tgg gtt ctc ctt gac   355
Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg Trp Val Leu Leu Asp
  70                  75                  80                  85

tac gga ttg gtt gtt atc cac gtt cag cga cag gca gag cgc gag ttc   403
Tyr Gly Leu Val Val Ile His Val Gln Arg Gln Ala Glu Arg Glu Phe
                  90                  95                 100

tac gga ctg gat cgt ctg tac cgc gac tgc cca ctc att gaa att gaa   451
Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro Leu Ile Glu Ile Glu
              105                 110                 115

gga ctt gaa acc ttc aag cgt gaa tcc tcc tgg tct gat gag gcg gat   499
Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp Ser Asp Glu Ala Asp
          120                 125                 130

atc cgc aac atc gac agc att gat gaa ctc cca cct ttg cca gct gaa   547
```

```
Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro Pro Leu Pro Ala Glu
    135                 140                 145

tac gag cct ggc tac gag gac gat taagaggtag tcctgtgact cgt        594
Tyr Glu Pro Gly Tyr Glu Asp Asp
150                 155


<210> 1346
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 1346
Val Ser Ala Leu Glu Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys
  1               5                  10                  15

Ala Ala Asp Glu Lys Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser
             20                  25                  30

Asp Met Ile Ala Ile Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn
         35                  40                  45

Glu Arg Gln Val Gly Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr
     50                  55                  60

Lys Ala Gly Phe Glu Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg
 65                  70                  75                  80

Trp Val Leu Leu Asp Tyr Gly Leu Val Val Ile His Val Gln Arg Gln
                 85                  90                  95

Ala Glu Arg Glu Phe Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro
            100                 105                 110

Leu Ile Glu Ile Glu Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp
        115                 120                 125

Ser Asp Glu Ala Asp Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro
    130                 135                 140

Pro Leu Pro Ala Glu Tyr Glu Pro Gly Tyr Glu Asp Asp
145                 150                 155


<210> 1347
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
<223> RXN02924

<400> 1347
ctaggcaggt gtgcgatcaa accacactgt cagaatcaaa tctgctggac gctatgccag 60

cggattgttg atcacgaaaa agcatgtcac agacaccttt gtg cct tct gta gca   115
                                              Val Pro Ser Val Ala
                                                1               5
```

```
tcc atc tca gag cgc gcc acg ttt att ctc acc gcc gat cac ttt ttg   163
Ser Ile Ser Glu Arg Ala Thr Phe Ile Leu Thr Ala Asp His Phe Leu
                 10                  15                  20

cgc agc tgc tcg aaa gta att tat gtc cgg ggc gaa aat ttc acc gcc   211
Arg Ser Cys Ser Lys Val Ile Tyr Val Arg Gly Glu Asn Phe Thr Ala
             25                  30                  35

aca gca acc acc agc ctg tct gta ttt ggc aca gat ctg ggt ttg atc   259
Thr Ala Thr Thr Ser Leu Ser Val Phe Gly Thr Asp Leu Gly Leu Ile
         40                  45                  50

aaa tta gac ggc aaa gcc ccc acc atg cca ctt cca ctt ttc gca gat   307
Lys Leu Asp Gly Lys Ala Pro Thr Met Pro Leu Pro Leu Phe Ala Asp
     55                  60                  65

aag cca ctt cgc gtg ggc atg aaa acc acc acg ttc gga ttc ggc ggt   355
Lys Pro Leu Arg Val Gly Met Lys Thr Thr Thr Phe Gly Phe Gly Gly
 70                  75                  80                  85

ctg cca tca gcc acc gtt gct aaa gaa atc cac ggg cgc gtt atc tct   403
Leu Pro Ser Ala Thr Val Ala Lys Glu Ile His Gly Arg Val Ile Ser
                 90                  95                 100

gcc atc ccc cat ggc gta tca aga aac cgc atc acc cga gtc cat cac   451
Ala Ile Pro His Gly Val Ser Arg Asn Arg Ile Thr Arg Val His His
            105                 110                 115

ggt gcc ttg atc ttt aac tcc cca gaa aag gca gta aag gga gac tcc   499
Gly Ala Leu Ile Phe Asn Ser Pro Glu Lys Ala Val Lys Gly Asp Ser
        120                 125                 130

ggc gga cct gtg ctg gtt aat gga cga gta gcc gga atc caa tca atg   547
Gly Gly Pro Val Leu Val Asn Gly Arg Val Ala Gly Ile Gln Ser Met
    135                 140                 145

atc tct gac ccc ggt gga ttt aac acc ggg gtc gcc act gcc gca tcc   595
Ile Ser Asp Pro Gly Gly Phe Asn Thr Gly Val Ala Thr Ala Ala Ser
150                 155                 160                 165

ctt atc cag cac atg cct gcc cta gct caa gcg ctt gaa ctg ctc gaa   643
Leu Ile Gln His Met Pro Ala Leu Ala Gln Ala Leu Glu Leu Leu Glu
                170                 175                 180

cat agc tagctcgcta ggaaccgatc gcc                                672
His Ser
```

<210> 1348
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 1348

```
Val Pro Ser Val Ala Ser Ile Ser Glu Arg Ala Thr Phe Ile Leu Thr
  1               5                  10                  15

Ala Asp His Phe Leu Arg Ser Cys Ser Lys Val Ile Tyr Val Arg Gly
             20                  25                  30
```

```
Glu Asn Phe Thr Ala Thr Ala Thr Thr Ser Leu Ser Val Phe Gly Thr
          35                  40                  45

Asp Leu Gly Leu Ile Lys Leu Asp Gly Lys Ala Pro Thr Met Pro Leu
      50                  55                  60

Pro Leu Phe Ala Asp Lys Pro Leu Arg Val Gly Met Lys Thr Thr Thr
 65                  70                  75                  80

Phe Gly Phe Gly Gly Leu Pro Ser Ala Thr Val Ala Lys Glu Ile His
                 85                  90                  95

Gly Arg Val Ile Ser Ala Ile Pro His Gly Val Ser Arg Asn Arg Ile
            100                 105                 110

Thr Arg Val His His Gly Ala Leu Ile Phe Asn Ser Pro Glu Lys Ala
        115                 120                 125

Val Lys Gly Asp Ser Gly Gly Pro Val Leu Val Asn Gly Arg Val Ala
    130                 135                 140

Gly Ile Gln Ser Met Ile Ser Asp Pro Gly Gly Phe Asn Thr Gly Val
145                 150                 155                 160

Ala Thr Ala Ala Ser Leu Ile Gln His Met Pro Ala Leu Ala Gln Ala
                165                 170                 175

Leu Glu Leu Leu Glu His Ser
            180
```

<210> 1349
<211> 591
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(568)
<223> RXN02927

<400> 1349

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tccgcagttg ggcctgcttg acgccagatc tcaagtgtaa gtttcattac ttgtagttcc 60

ttgtctgcag tgggacagat tcgaagaaca gtggttctgc gtg gca gac gaa ggt   115
                                              Val Ala Asp Glu Gly
                                                1               5

tcc att ctc gcc tgg ttc cca tgc gga gac gaa gca cca gtt ttg gtc   163
Ser Ile Leu Ala Trp Phe Pro Cys Gly Asp Glu Ala Pro Val Leu Val
                10                  15                  20

gtc acg ttg tgc ttc gcc atc ttc gga gag gtg gtc gtc gcg gaa gtg   211
Val Thr Leu Cys Phe Ala Ile Phe Gly Glu Val Val Val Ala Glu Val
            25                  30                  35

agc gcc aca gga ctc gtc gcg gtc gag ggc gtc gac aca cat gag ttc   259
Ser Ala Thr Gly Leu Val Ala Val Glu Gly Val Asp Thr His Glu Phe
        40                  45                  50
```

```
gcc gag gtc gat gta gtc ggc tac gcg tgc tgc gta ttc gag aac ctg   307
Ala Glu Val Asp Val Val Gly Tyr Ala Cys Cys Val Phe Glu Asn Leu
     55                  60                  65

gtt cat ctc atc ggt gct gcc ggt gat gcg cat gtt ctt cca gaa gtc   355
Val His Leu Ile Gly Ala Ala Gly Asp Ala His Val Leu Pro Glu Val
 70                  75                  80                  85

atc gcg gag ggc acg gat ctt gtt gat gcc atc ctg gag gtc ttc tac   403
Ile Ala Glu Gly Thr Asp Leu Val Asp Ala Ile Leu Glu Val Phe Tyr
                 90                  95                 100

gtt tcg gga aac gcc aca gga gaa gta cag gat atc gcc aag ctg gcg   451
Val Ser Gly Asn Ala Thr Gly Glu Val Gln Asp Ile Ala Lys Leu Ala
            105                 110                 115

gtg gta gta ctc agg tcc gtg aac gtt gtc acc gac cca ctc tgg gcg   499
Val Val Val Leu Arg Ser Val Asn Val Val Thr Asp Pro Leu Trp Ala
        120                 125                 130

gtt gcc cat gag gcg gtc aat gcg agc ctg tgc acg cgc aat cgc tgc   547
Val Ala His Glu Ala Val Asn Ala Ser Leu Cys Thr Arg Asn Arg Cys
    135                 140                 145

ctg tgc ttc tgg tgc atc ctc tgacagacgc tcggagccaa gca            591
Leu Cys Phe Trp Cys Ile Leu
150                 155
```

<210> 1350
<211> 156
<212> PRT
<213> Corynebacterium glutamicum

<400> 1350

```
Val Ala Asp Glu Gly Ser Ile Leu Ala Trp Phe Pro Cys Gly Asp Glu
  1               5                  10                  15

Ala Pro Val Leu Val Val Thr Leu Cys Phe Ala Ile Phe Gly Glu Val
            20                  25                  30

Val Val Ala Glu Val Ser Ala Thr Gly Leu Val Ala Val Glu Gly Val
        35                  40                  45

Asp Thr His Glu Phe Ala Glu Val Asp Val Val Gly Tyr Ala Cys Cys
    50                  55                  60

Val Phe Glu Asn Leu Val His Leu Ile Gly Ala Ala Gly Asp Ala His
65                  70                  75                  80

Val Leu Pro Glu Val Ile Ala Glu Gly Thr Asp Leu Val Asp Ala Ile
                85                  90                  95

Leu Glu Val Phe Tyr Val Ser Gly Asn Ala Thr Gly Glu Val Gln Asp
            100                 105                 110

Ile Ala Lys Leu Ala Val Val Val Leu Arg Ser Val Asn Val Val Thr
        115                 120                 125

Asp Pro Leu Trp Ala Val Ala His Glu Ala Val Asn Ala Ser Leu Cys
    130                 135                 140
```

```
Thr Arg Asn Arg Cys Leu Cys Phe Trp Cys Ile Leu
145                 150                 155


<210> 1351
<211> 816
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> RXN02928

<400> 1351
ggtttgcacc gtggtaggtc caggatgctt cgcctgcgca gaacagacct gggagtgacg 60

tcatttcgtt gaagtcagtc cagaggccac ccatggtgaa gtg gca ggt cgg tgc   115
                                              Val Ala Gly Arg Cys
                                                1               5

aat acg cat tgg gct gga gta tgg gtc ctc gcc aat tgc ctc ttc gta   163
Asn Thr His Trp Ala Gly Val Trp Val Leu Ala Asn Cys Leu Phe Val
               10                  15                  20

cat ggt gaa gag gtt gga gta acg ctc gcg gat ggt gtc ctg tcc gag   211
His Gly Glu Glu Val Gly Val Thr Leu Ala Asp Gly Val Leu Ser Glu
           25                  30                  35

gcg ctc ggt ggc gtc gcg gaa gtc cag gta tgc agc gtt gtt cag agg   259
Ala Leu Gly Gly Val Ala Glu Val Gln Val Cys Ser Val Val Gln Arg
       40                  45                  50

tcc aac acc gag acc agc att gat ctg ctg gga gat cgc acg gga agc   307
Ser Asn Thr Glu Thr Ser Ile Asp Leu Leu Gly Asp Arg Thr Gly Ser
   55                  60                  65

aac gtc acg tgg gac gag gtt acc gaa tgc tgg gta gcg gcg ctc cag   355
Asn Val Thr Trp Asp Glu Val Thr Glu Cys Trp Val Ala Ala Leu Gln
70                  75                  80                  85

gaa gta gtc gcg ctc atc ctc agg gat ggt gtt tgg atc gcg gtt atc   403
Glu Val Val Ala Leu Ile Leu Arg Asp Gly Val Trp Ile Ala Val Ile
               90                  95                 100

gtt cgg ttc ctt agg gga cca gat gcg gcc gtc gtt acg cag cga ctc   451
Val Arg Phe Leu Arg Gly Pro Asp Ala Ala Val Val Thr Gln Arg Leu
           105                 110                 115

gga cat cag aat ggt ctt gga ctg cca ggt gga gtt cac agg cag gcc   499
Gly His Gln Asn Gly Leu Gly Leu Pro Gly Gly Val His Arg Gln Ala
       120                 125                 130

ggt tgg gtg gaa ctg gat gaa cga tgg gga cgc gaa gta tgc gcc ggc   547
Gly Trp Val Glu Leu Asp Glu Arg Trp Gly Arg Glu Val Cys Ala Gly
   135                 140                 145

ttc gta tgc acg cat gat ggc cga ggc gtt gga gtt ctt ggc cag ggt   595
Phe Val Cys Thr His Asp Gly Arg Gly Val Gly Val Leu Gly Gln Gly
150                 155                 160                 165
```

```
gga cat gtg gta cac gtt gcc gta gcc acc ggt tgc cag gat aac ggc   643
Gly His Val Val His Val Ala Val Ala Thr Gly Cys Gln Asp Asn Gly
                170                 175                 180

atg gcc ggt gtg tgc ggt gag ctc gcc ggt gat cag gtt gcg cat gat   691
Met Ala Gly Val Cys Gly Glu Leu Ala Gly Asp Gln Val Ala His Asp
            185                 190                 195

cag gcc ttc gca gcg ctt ttc acc gtt acg ttc ggt gac aat gac gtc   739
Gln Ala Phe Ala Ala Leu Phe Thr Val Thr Phe Gly Asp Asn Asp Val
        200                 205                 210

aac cat ttc gtt atg ggt gaa gat ttc tac gga gcc gag gtg gat ctg   787
Asn His Phe Val Met Gly Glu Asp Phe Tyr Gly Ala Glu Val Asp Leu
    215                 220                 225

gcg ctg tagtgcggat gcggtggaga act                                816
Ala Leu
230
```

<210> 1352
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 1352

```
Val Ala Gly Arg Cys Asn Thr His Trp Ala Gly Val Trp Val Leu Ala
  1               5                  10                  15

Asn Cys Leu Phe Val His Gly Glu Glu Val Gly Val Thr Leu Ala Asp
             20                  25                  30

Gly Val Leu Ser Glu Ala Leu Gly Gly Val Ala Glu Val Gln Val Cys
         35                  40                  45

Ser Val Val Gln Arg Ser Asn Thr Glu Thr Ser Ile Asp Leu Leu Gly
     50                  55                  60

Asp Arg Thr Gly Ser Asn Val Thr Trp Asp Glu Val Thr Glu Cys Trp
 65                  70                  75                  80

Val Ala Ala Leu Gln Glu Val Val Ala Leu Ile Leu Arg Asp Gly Val
                 85                  90                  95

Trp Ile Ala Val Ile Val Arg Phe Leu Arg Gly Pro Asp Ala Ala Val
            100                 105                 110

Val Thr Gln Arg Leu Gly His Gln Asn Gly Leu Gly Leu Pro Gly Gly
        115                 120                 125

Val His Arg Gln Ala Gly Trp Val Glu Leu Asp Glu Arg Trp Gly Arg
    130                 135                 140

Glu Val Cys Ala Gly Phe Val Cys Thr His Asp Gly Arg Gly Val Gly
145                 150                 155                 160

Val Leu Gly Gln Gly Gly His Val Val His Val Ala Val Ala Thr Gly
                165                 170                 175
```

```
Cys Gln Asp Asn Gly Met Ala Gly Val Cys Gly Glu Leu Ala Gly Asp
            180                 185                 190

Gln Val Ala His Asp Gln Ala Phe Ala Ala Leu Phe Thr Val Thr Phe
        195                 200                 205

Gly Asp Asn Asp Val Asn His Phe Val Met Gly Glu Asp Phe Tyr Gly
    210                 215                 220

Ala Glu Val Asp Leu Ala Leu
225                 230
```

<210> 1353
<211> 348
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(325)
<223> RXN02931

<400> 1353

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gatgggtgca gaaattgaat tgaaagaatc cgggcacatg tgggtggaat ccccgagtga 60

ctagtgcggt gtaagagcac tagactgttc aactatgagc atg caa cca tac ccc   115
                                           Met Gln Pro Tyr Pro
                                             1               5

cgc aac cca atc gaa aaa cgt aag caa gaa gta cgc aag aac tcc cgc   163
Arg Asn Pro Ile Glu Lys Arg Lys Gln Glu Val Arg Lys Asn Ser Arg
                 10                  15                  20

aac gca gtt gtc agt gtt ggc ggt ggc atc gta ggc ggt gcg gct ctg   211
Asn Ala Val Val Ser Val Gly Gly Gly Ile Val Gly Gly Ala Ala Leu
             25                  30                  35

tgg cta gtg ttc ggc tct gca ttc ttt atg gga ctt gga ttg atc atc   259
Trp Leu Val Phe Gly Ser Ala Phe Phe Met Gly Leu Gly Leu Ile Ile
         40                  45                  50

gcc gtg gtc ggc ggt ttt tat tac tac aac aag gtc caa aag atc att   307
Ala Val Val Gly Gly Phe Tyr Tyr Tyr Asn Lys Val Gln Lys Ile Ile
     55                  60                  65

aac gaa aaa gac cgt tac tagttagaaa tctatgtcag aca                 348
Asn Glu Lys Asp Arg Tyr
 70                  75
```

<210> 1354
<211> 75
<212> PRT
<213> Corynebacterium glutamicum

<400> 1354

```
Met Gln Pro Tyr Pro Arg Asn Pro Ile Glu Lys Arg Lys Gln Glu Val
  1               5                  10                  15

Arg Lys Asn Ser Arg Asn Ala Val Val Ser Val Gly Gly Gly Ile Val
```

```
            20                  25                  30

Gly Gly Ala Ala Leu Trp Leu Val Phe Gly Ser Ala Phe Phe Met Gly
         35                  40                  45

Leu Gly Leu Ile Ile Ala Val Val Gly Gly Phe Tyr Tyr Tyr Asn Lys
     50                  55                  60

Val Gln Lys Ile Ile Asn Glu Lys Asp Arg Tyr
 65                  70                  75


<210> 1355
<211> 1095
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1072)
<223> RXN02932

<400> 1355
cactactgcg ttaaggtatg aaagttcgca caccagcgat ttaattctgt gcccaccact 60

agcacgacca tttcagtttt aactttcttg gagttttcta gtg tcc aaa aca gaa   115
                                            Val Ser Lys Thr Glu
                                              1               5

gaa ggc cgt tca gcg gcc ata att att tac gcg ttt cca act ttc att   163
Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala Phe Pro Thr Phe Ile
                 10                  15                  20

ctg ctg ggc gcg atc att gcg ttt atc ttc ccg gaa cca ttc att ccg   211
Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro Glu Pro Phe Ile Pro
             25                  30                  35

ctg aca aac tac att aat atc ttc ctc acg atc atc atg ttc acc atg   259
Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile Ile Met Phe Thr Met
         40                  45                  50

ggt ttg acc ttg acg gtg ccc gat ttt cag atg gtg ctt aaa cgt cca   307
Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met Val Leu Lys Arg Pro
     55                  60                  65

ctg cct atc ttg atc ggt gta gta gcg cag ttt gtc atc atg cca ttc   355
Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe Val Ile Met Pro Phe
 70                  75                  80                  85

ctg gcg atc gtg gtt gcg aaa atg ttc aac ctc aac cca gca ctc gcc   403
Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu Asn Pro Ala Leu Ala
                 90                  95                 100

gtt ggc ctt ctc atg ctg gga tcc gtt ccg ggt ggc acc tcc tcc aat   451
Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly Gly Thr Ser Ser Asn
            105                 110                 115

gtg att gcg ttt ctc gcc cga gga gat gtc gcg cta tcg gtc acc atg   499
Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala Leu Ser Val Thr Met
        120                 125                 130
```

```
acc tct gtg tcc acc att gtt tcc cca atc atg acg cct ttc ctc atg   547
Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met Thr Pro Phe Leu Met
    135                 140                 145

ctc atg ctg gca ggt act gaa acc gcc gtc gat ggt gga ggc atg gcg   595
Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp Gly Gly Gly Met Ala
150                 155                 160                 165

tgg act ttg gta caa aca gtg ctg ctg cct gtg atc atc ggc cta gtt   643
Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val Ile Ile Gly Leu Val
                170                 175                 180

ctg cgt gtc ttc ttg aac aag tgg atc gac aag att ttg ccg atc ctt   691
Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys Ile Leu Pro Ile Leu
            185                 190                 195

cct tat ctc tcc atc ctc ggt atc ggt ggc gtg gtg ttc ggc gca gtc   739
Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val Val Phe Gly Ala Val
        200                 205                 210

gca gcc aac gcg gaa cga ctc gtg tct gtc gga ctc atc gtg ttc gtt   787
Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly Leu Ile Val Phe Val
    215                 220                 225

gca gtt atc gtg cac aac gta ctt gga tac gtt gtg gga tac ctc acc   835
Ala Val Ile Val His Asn Val Leu Gly Tyr Val Val Gly Tyr Leu Thr
230                 235                 240                 245

ggc cgt gta ttc aaa ttc cca gaa gca gca aac cgc acc atg gcg att   883
Gly Arg Val Phe Lys Phe Pro Glu Ala Ala Asn Arg Thr Met Ala Ile
                250                 255                 260

gaa atc gga acc caa tcc gca ggc ctc gca tcg gga atg gca gga cga   931
Glu Ile Gly Thr Gln Ser Ala Gly Leu Ala Ser Gly Met Ala Gly Arg
            265                 270                 275

ttc ttc acc cca gaa gca gcc ctt cca ggt gct gtc gct gcc ttg gtc   979
Phe Phe Thr Pro Glu Ala Ala Leu Pro Gly Ala Val Ala Ala Leu Val
        280                 285                 290

cac aac atc acc ggc gca gtt tat gtt ggg ctg gta cga aac agg cct   1027
His Asn Ile Thr Gly Ala Val Tyr Val Gly Leu Val Arg Asn Arg Pro
    295                 300                 305

ttg act aag gca tca agg aag aag gaa tcc gtc gcg gtt tcc agc       1072
Leu Thr Lys Ala Ser Arg Lys Lys Glu Ser Val Ala Val Ser Ser
310                 315                 320

taacttattt gctgcccgtt aga                                        1095
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<210> 1356
<211> 324
<212> PRT
<213> Corynebacterium glutamicum

<400> 1356

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Val Ser Lys Thr Glu Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala
  1               5                  10                  15

Phe Pro Thr Phe Ile Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro
```

```
            20                  25                  30

Glu Pro Phe Ile Pro Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile
         35                  40                  45

Ile Met Phe Thr Met Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met
     50                  55                  60

Val Leu Lys Arg Pro Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe
 65                  70                  75                  80

Val Ile Met Pro Phe Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu
                 85                  90                  95

Asn Pro Ala Leu Ala Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly
            100                 105                 110

Gly Thr Ser Ser Asn Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala
        115                 120                 125

Leu Ser Val Thr Met Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met
    130                 135                 140

Thr Pro Phe Leu Met Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp
145                 150                 155                 160

Gly Gly Gly Met Ala Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val
                165                 170                 175

Ile Ile Gly Leu Val Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys
            180                 185                 190

Ile Leu Pro Ile Leu Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val
        195                 200                 205

Val Phe Gly Ala Val Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly
    210                 215                 220

Leu Ile Val Phe Val Ala Val Ile Val His Asn Val Leu Gly Tyr Val
225                 230                 235                 240

Val Gly Tyr Leu Thr Gly Arg Val Phe Lys Phe Pro Glu Ala Ala Asn
                245                 250                 255

Arg Thr Met Ala Ile Glu Ile Gly Thr Gln Ser Ala Gly Leu Ala Ser
            260                 265                 270

Gly Met Ala Gly Arg Phe Phe Thr Pro Glu Ala Ala Leu Pro Gly Ala
        275                 280                 285

Val Ala Ala Leu Val His Asn Ile Thr Gly Ala Val Tyr Val Gly Leu
    290                 295                 300

Val Arg Asn Arg Pro Leu Thr Lys Ala Ser Arg Lys Lys Glu Ser Val
305                 310                 315                 320

Ala Val Ser Ser
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<210> 1357

<211> 429
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(406)
<223> RXN02934

<400> 1357
tggatgggcc ggtggcggtg accatggtag atgcggattc aagctgccag gcgcgctcat 60

tgagtggctg gccgtagtag atttctacaa ctccgccggc gtg ggt gca gac gaa 115
Val Gly Ala Asp Glu
1 5

ttc gat ttc atc ttt gag att gat gcg cca gaa gcc gga ttc gcg ctg 163
Phe Asp Phe Ile Phe Glu Ile Asp Ala Pro Glu Ala Gly Phe Ala Leu
10 15 20

gtc gac gcc ggt ggg gtt tcc ttc ttc gtc gag ttt cca cat gcg gga 211
Val Asp Ala Gly Gly Val Ser Phe Phe Val Glu Phe Pro His Ala Gly
25 30 35

ttc gaa gga gag gta gtt ttc acc gtc gtg ggc gaa ggt gat ttg ctg 259
Phe Glu Gly Glu Val Val Phe Thr Val Val Gly Glu Gly Asp Leu Leu
40 45 50

gcc gaa tgc gta ttg tcc gtc ttc tgc ggt gtc ggc ttg gcc ttc gcc 307
Ala Glu Cys Val Leu Ser Val Phe Cys Gly Val Gly Leu Ala Phe Ala
55 60 65

gcg cca gac gcc gac gag agg gag gag cgc gag gag tcc gtc gtg gag 355
Ala Pro Asp Ala Asp Glu Arg Glu Glu Arg Glu Glu Ser Val Val Glu
70 75 80 85

gtt ggg gcc ttc gcg gag gtt agc ggt gtc gtc agg gat agg aag gtc 403
Val Gly Ala Phe Ala Glu Val Ser Gly Val Val Arg Asp Arg Lys Val
90 95 100

acc taggcctggg atgttgcggt gag 429
Thr

<210> 1358
<211> 102
<212> PRT
<213> Corynebacterium glutamicum

<400> 1358
Val Gly Ala Asp Glu Phe Asp Phe Ile Phe Glu Ile Asp Ala Pro Glu
1 5 10 15

Ala Gly Phe Ala Leu Val Asp Ala Gly Gly Val Ser Phe Phe Val Glu
20 25 30

Phe Pro His Ala Gly Phe Glu Gly Glu Val Val Phe Thr Val Val Gly
35 40 45

Glu Gly Asp Leu Leu Ala Glu Cys Val Leu Ser Val Phe Cys Gly Val

```
     50                  55                  60

Gly Leu Ala Phe Ala Ala Pro Asp Ala Asp Glu Arg Glu Glu Arg Glu
 65                  70                  75                  80

Glu Ser Val Val Glu Val Gly Ala Phe Ala Glu Val Ser Gly Val Val
                 85                  90                  95

Arg Asp Arg Lys Val Thr
            100


<210> 1359
<211> 321
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(298)
<223> RXN02936

<400> 1359
accaagttca gacagctctg ggttggacct accggagtaa aggcgtgcca ctgacatagc 60

agtttggccg tggcgaagca acaagaaacg agtgggatct gtg gtt gcg ccg ttc   115
                                            Val Val Ala Pro Phe
                                              1               5

cag ttg gtg ggt ttg gtt tcg gtg cag ttg agg tct tct ttc tct gag   163
Gln Leu Val Gly Leu Val Ser Val Gln Leu Arg Ser Ser Phe Ser Glu
                 10                  15                  20

ccc gca acc gaa gaa gca gaa gat aca gaa gca gaa tcc cct aca aca   211
Pro Ala Thr Glu Glu Ala Glu Asp Thr Glu Ala Glu Ser Pro Thr Thr
             25                  30                  35

cct acc ggc tta cct gcc gct gca gca tcc atc gcc acg ttg gac aat   259
Pro Thr Gly Leu Pro Ala Ala Ala Ala Ser Ile Ala Thr Leu Asp Asn
         40                  45                  50

gcg tca gct cgt ttg ttt ttc tca cgc gga atc cac gta taagaaacgg    308
Ala Ser Ala Arg Leu Phe Phe Ser Arg Gly Ile His Val
     55                  60                  65

acccgatttc gga                                                   321


<210> 1360
<211> 66
<212> PRT
<213> Corynebacterium glutamicum

<400> 1360
Val Val Ala Pro Phe Gln Leu Val Gly Leu Val Ser Val Gln Leu Arg
  1               5                  10                  15

Ser Ser Phe Ser Glu Pro Ala Thr Glu Glu Ala Glu Asp Thr Glu Ala
             20                  25                  30

Glu Ser Pro Thr Thr Pro Thr Gly Leu Pro Ala Ala Ala Ala Ser Ile
```

```
         35                  40                  45

Ala Thr Leu Asp Asn Ala Ser Ala Arg Leu Phe Phe Ser Arg Gly Ile
     50                  55                  60

His Val
 65


<210> 1361
<211> 1725
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1702)
<223> RXN02939

<400> 1361
cttcgaagaa gacgatatcc cctacgaagt cgacgtggat gacttattta tcctcggtgg 60

cttagacaac ttcataaatc cccttggagt gattgagata atg aat ctc cac tcc   115
                                            Met Asn Leu His Ser
                                              1               5

tta gag att cgc caa att tca tcc ggc aca att tca gaa cga aaa act   163
Leu Glu Ile Arg Gln Ile Ser Ser Gly Thr Ile Ser Glu Arg Lys Thr
                 10                  15                  20

tgg atc ttt ccc act gct gct cgc tca ttc aat caa aat cta gta cac   211
Trp Ile Phe Pro Thr Ala Ala Arg Ser Phe Asn Gln Asn Leu Val His
             25                  30                  35

ccg caa agc att gaa atc gat gca caa acc ggc gtt att ttg gct atg   259
Pro Gln Ser Ile Glu Ile Asp Ala Gln Thr Gly Val Ile Leu Ala Met
         40                  45                  50

gaa aac cga cta caa cgt acc gaa gtt gaa tca gta gag tac cca acg   307
Glu Asn Arg Leu Gln Arg Thr Glu Val Glu Ser Val Glu Tyr Pro Thr
     55                  60                  65

gat ctt cct aat cct gca tgg aca ggt cca gcc att tct tgg cca cta   355
Asp Leu Pro Asn Pro Ala Trp Thr Gly Pro Ala Ile Ser Trp Pro Leu
 70                  75                  80                  85

aaa gac cca tca atc gat ttc cct gac ccg ctc ccc cac agc att tcc   403
Lys Asp Pro Ser Ile Asp Phe Pro Asp Pro Leu Pro His Ser Ile Ser
                 90                  95                 100

gaa tta cca cct caa tcc gat aat cct cgg cat ttg cga gta tcc atc   451
Glu Leu Pro Pro Gln Ser Asp Asn Pro Arg His Leu Arg Val Ser Ile
            105                 110                 115

agc tta gat gca gtg gaa ggt gct ttt ccg cgc tac cgg atc gga gat   499
Ser Leu Asp Ala Val Glu Gly Ala Phe Pro Arg Tyr Arg Ile Gly Asp
        120                 125                 130

tca ata cgt att ccg ctt gtc ttt gcc cgg gac acg ccc ttc atg tcc   547
Ser Ile Arg Ile Pro Leu Val Phe Ala Arg Asp Thr Pro Phe Met Ser
    135                 140                 145
```

```
ggc tta gaa aca aca cgt cgc gcc tgg att gag gcg gcc acg gaa atg   595
Gly Leu Glu Thr Thr Arg Arg Ala Trp Ile Glu Ala Ala Thr Glu Met
150                 155                 160                 165

gac atc cat aac aca tgg ccc ata atc ctc acc ggt gac ggc tgg act   643
Asp Ile His Asn Thr Trp Pro Ile Ile Leu Thr Gly Asp Gly Trp Thr
                170                 175                 180

gca ctc tct cat tca gac aaa cca ata cgc cac gaa gcc gag tta aag   691
Ala Leu Ser His Ser Asp Lys Pro Ile Arg His Glu Ala Glu Leu Lys
            185                 190                 195

gga tgg ttt ttc cac agt ttg ttc ggc agt gaa atg ccc ttg act gat   739
Gly Trp Phe Phe His Ser Leu Phe Gly Ser Glu Met Pro Leu Thr Asp
        200                 205                 210

ctg aag att gaa cga atc tac gga ggc ctg ggt act ttc gac agc gga   787
Leu Lys Ile Glu Arg Ile Tyr Gly Gly Leu Gly Thr Phe Asp Ser Gly
    215                 220                 225

gcc acc cgg tgg caa gaa ctc aca gac aca gat gat gcc tac aca gaa   835
Ala Thr Arg Trp Gln Glu Leu Thr Asp Thr Asp Asp Ala Tyr Thr Glu
230                 235                 240                 245

aat ggc agc tgg ctg ttg gaa gtt atc gtc gat gcc acc ctt gac ggt   883
Asn Gly Ser Trp Leu Leu Glu Val Ile Val Asp Ala Thr Leu Asp Gly
                250                 255                 260

gca att cca cca cca ctt cag cca caa cag ttt gaa gca tcc atc act   931
Ala Ile Pro Pro Pro Leu Gln Pro Gln Gln Phe Glu Ala Ser Ile Thr
            265                 270                 275

cac atc gtc gat gag caa cta tgg gtc ctt ggg cag atg ctt cca gtt   979
His Ile Val Asp Glu Gln Leu Trp Val Leu Gly Gln Met Leu Pro Val
        280                 285                 290

cta cga tgc tgg gat ctt gaa acc gga aaa tac ctg ggg caa acc tat  1027
Leu Arg Cys Trp Asp Leu Glu Thr Gly Lys Tyr Leu Gly Gln Thr Tyr
    295                 300                 305

gta cct att tcg gtt tct cat agt tct cgg ctt cag ttt tcg gaa ggg  1075
Val Pro Ile Ser Val Ser His Ser Ser Arg Leu Gln Phe Ser Glu Gly
310                 315                 320                 325

ttg att cac gat tat gaa aat gcc tgg tcg ctg aat cct ggg gtg cgc  1123
Leu Ile His Asp Tyr Glu Asn Ala Trp Ser Leu Asn Pro Gly Val Arg
                330                 335                 340

atg ctt gcg gag cca cag ccg tgg ata gag cct gtc att gaa ctc gac  1171
Met Leu Ala Glu Pro Gln Pro Trp Ile Glu Pro Val Ile Glu Leu Asp
            345                 350                 355

gtt cca gcg cca tgg gaa tta caa gaa agc ttc ccc gat ggg ctt tac  1219
Val Pro Ala Pro Trp Glu Leu Gln Glu Ser Phe Pro Asp Gly Leu Tyr
        360                 365                 370

tcc cta act gat gga gag caa aca gca ctg ggt cga agc act cca gca  1267
Ser Leu Thr Asp Gly Glu Gln Thr Ala Leu Gly Arg Ser Thr Pro Ala
    375                 380                 385
```

```
gga caa ttg gaa atc tgt gta atc agc aat gac gga tcc agg atc tta   1315
Gly Gln Leu Glu Ile Cys Val Ile Ser Asn Asp Gly Ser Arg Ile Leu
390                 395                 400                 405

aac gca ggc cga gta gaa gac ctg tac ttt gtg caa ttc tgg ggc atg   1363
Asn Ala Gly Arg Val Glu Asp Leu Tyr Phe Val Gln Phe Trp Gly Met
                410                 415                 420

acc gtc ttt ttg aat tcc aac ttt caa gtg caa agt gcc gaa gaa cat   1411
Thr Val Phe Leu Asn Ser Asn Phe Gln Val Gln Ser Ala Glu Glu His
            425                 430                 435

cag ctt ggt gcg aaa cgt gaa cgc tgg att aca caa gaa ggc gta gct   1459
Gln Leu Gly Ala Lys Arg Glu Arg Trp Ile Thr Gln Glu Gly Val Ala
        440                 445                 450

gcc aag ttc acc gaa gaa gat gaa atc gta ttc ctc gat cag ata tct   1507
Ala Lys Phe Thr Glu Glu Asp Glu Ile Val Phe Leu Asp Gln Ile Ser
    455                 460                 465

gaa agc gaa ata acc agg tgg aaa aca cca gaa gga tac ttc act gag   1555
Glu Ser Glu Ile Thr Arg Trp Lys Thr Pro Glu Gly Tyr Phe Thr Glu
470                 475                 480                 485

gtc aga att ctg tca cca aac cac ttc aac ata ctg gtt act ccg cct   1603
Val Arg Ile Leu Ser Pro Asn His Phe Asn Ile Leu Val Thr Pro Pro
                490                 495                 500

act ggt tct gac tat ctc aaa cca gta cct tcc tct gtc tca gtg ttt   1651
Thr Gly Ser Asp Tyr Leu Lys Pro Val Pro Ser Ser Val Ser Val Phe
            505                 510                 515

aga gac ggt caa tgg agc aac att aaa ttc gag gac gtc tct gta gaa   1699
Arg Asp Gly Gln Trp Ser Asn Ile Lys Phe Glu Asp Val Ser Val Glu
        520                 525                 530

atc tagggctttc gacgcttgag ccc                                    1725
Ile
```

US-09-900-704-2

<210> 1362
<211> 534
<212> PRT
<213> Corynebacterium glutamicum

<400> 1362

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Met Asn Leu His Ser Leu Glu Ile Arg Gln Ile Ser Ser Gly Thr Ile
  1               5                  10                  15

Ser Glu Arg Lys Thr Trp Ile Phe Pro Thr Ala Ala Arg Ser Phe Asn
             20                  25                  30

Gln Asn Leu Val His Pro Gln Ser Ile Glu Ile Asp Ala Gln Thr Gly
         35                  40                  45

Val Ile Leu Ala Met Glu Asn Arg Leu Gln Arg Thr Glu Val Glu Ser
     50                  55                  60

Val Glu Tyr Pro Thr Asp Leu Pro Asn Pro Ala Trp Thr Gly Pro Ala
 65                  70                  75                  80
```

```
Ile Ser Trp Pro Leu Lys Asp Pro Ser Ile Asp Phe Pro Asp Pro Leu
                  85                  90                  95

Pro His Ser Ile Ser Glu Leu Pro Pro Gln Ser Asp Asn Pro Arg His
             100                 105                 110

Leu Arg Val Ser Ile Ser Leu Asp Ala Val Glu Gly Ala Phe Pro Arg
         115                 120                 125

Tyr Arg Ile Gly Asp Ser Ile Arg Ile Pro Leu Val Phe Ala Arg Asp
     130                 135                 140

Thr Pro Phe Met Ser Gly Leu Glu Thr Thr Arg Arg Ala Trp Ile Glu
145                 150                 155                 160

Ala Ala Thr Glu Met Asp Ile His Asn Thr Trp Pro Ile Ile Leu Thr
                  165                 170                 175

Gly Asp Gly Trp Thr Ala Leu Ser His Ser Asp Lys Pro Ile Arg His
             180                 185                 190

Glu Ala Glu Leu Lys Gly Trp Phe Phe His Ser Leu Phe Gly Ser Glu
         195                 200                 205

Met Pro Leu Thr Asp Leu Lys Ile Glu Arg Ile Tyr Gly Gly Leu Gly
     210                 215                 220

Thr Phe Asp Ser Gly Ala Thr Arg Trp Gln Glu Leu Thr Asp Thr Asp
225                 230                 235                 240

Asp Ala Tyr Thr Glu Asn Gly Ser Trp Leu Leu Glu Val Ile Val Asp
                  245                 250                 255

Ala Thr Leu Asp Gly Ala Ile Pro Pro Pro Leu Gln Pro Gln Gln Phe
             260                 265                 270

Glu Ala Ser Ile Thr His Ile Val Asp Glu Gln Leu Trp Val Leu Gly
         275                 280                 285

Gln Met Leu Pro Val Leu Arg Cys Trp Asp Leu Glu Thr Gly Lys Tyr
     290                 295                 300

Leu Gly Gln Thr Tyr Val Pro Ile Ser Val Ser His Ser Ser Arg Leu
305                 310                 315                 320

Gln Phe Ser Glu Gly Leu Ile His Asp Tyr Glu Asn Ala Trp Ser Leu
                  325                 330                 335

Asn Pro Gly Val Arg Met Leu Ala Glu Pro Gln Pro Trp Ile Glu Pro
             340                 345                 350

Val Ile Glu Leu Asp Val Pro Ala Pro Trp Glu Leu Gln Glu Ser Phe
         355                 360                 365

Pro Asp Gly Leu Tyr Ser Leu Thr Asp Gly Glu Gln Thr Ala Leu Gly
     370                 375                 380

Arg Ser Thr Pro Ala Gly Gln Leu Glu Ile Cys Val Ile Ser Asn Asp
385                 390                 395                 400
```

```
Gly Ser Arg Ile Leu Asn Ala Gly Arg Val Glu Asp Leu Tyr Phe Val
                405                 410                 415

Gln Phe Trp Gly Met Thr Val Phe Leu Asn Ser Asn Phe Gln Val Gln
            420                 425                 430

Ser Ala Glu Glu His Gln Leu Gly Ala Lys Arg Glu Arg Trp Ile Thr
        435                 440                 445

Gln Glu Gly Val Ala Ala Lys Phe Thr Glu Glu Asp Glu Ile Val Phe
    450                 455                 460

Leu Asp Gln Ile Ser Glu Ser Glu Ile Thr Arg Trp Lys Thr Pro Glu
465                 470                 475                 480

Gly Tyr Phe Thr Glu Val Arg Ile Leu Ser Pro Asn His Phe Asn Ile
                485                 490                 495

Leu Val Thr Pro Pro Thr Gly Ser Asp Tyr Leu Lys Pro Val Pro Ser
            500                 505                 510

Ser Val Ser Val Phe Arg Asp Gly Gln Trp Ser Asn Ile Lys Phe Glu
        515                 520                 525

Asp Val Ser Val Glu Ile
    530
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<210> 1363
<211> 1243
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1243)
<223> FRXA01383

<400> 1363

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cttcgaagaa gacgatatcc cctacgaagt cgacgtggat gacttattta tcctcggtgg 60

cttagacaac ttcataaatc cccttggagt gattgagata atg aat ctc cac tcc   115
                                            Met Asn Leu His Ser
                                              1               5

tta gag att cgc caa att tca tcc ggc aca att tca gaa cga aaa act   163
Leu Glu Ile Arg Gln Ile Ser Ser Gly Thr Ile Ser Glu Arg Lys Thr
                  10                  15                  20

tgg atc ttt ccc act gct gct cgc tca ttc aat caa aat cta gta cac   211
Trp Ile Phe Pro Thr Ala Ala Arg Ser Phe Asn Gln Asn Leu Val His
              25                  30                  35

ccg caa agc att gaa atc gat gca caa acc ggc gtt att ttg gct atg   259
Pro Gln Ser Ile Glu Ile Asp Ala Gln Thr Gly Val Ile Leu Ala Met
          40                  45                  50

gaa aac cga cta caa cgt acc gaa gtt gaa tca gta gag tac cca acg   307
Glu Asn Arg Leu Gln Arg Thr Glu Val Glu Ser Val Glu Tyr Pro Thr
      55                  60                  65
```

```
gat ctt cct aat cct gca tgg aca ggt cca gcc att tct tgg cca cta   355
Asp Leu Pro Asn Pro Ala Trp Thr Gly Pro Ala Ile Ser Trp Pro Leu
 70                  75                  80                  85

aaa gac cca tca atc gat ttc cct gac ccg ctc ccc cac agc att tcc   403
Lys Asp Pro Ser Ile Asp Phe Pro Asp Pro Leu Pro His Ser Ile Ser
                90                  95                 100

gaa tta cca cct caa tcc gat aat cct cgg cat ttg cga gta tcc atc   451
Glu Leu Pro Pro Gln Ser Asp Asn Pro Arg His Leu Arg Val Ser Ile
            105                 110                 115

agc tta gat gca gtg gaa ggt gct ttt ccg cgc tac cgg atc gga gat   499
Ser Leu Asp Ala Val Glu Gly Ala Phe Pro Arg Tyr Arg Ile Gly Asp
        120                 125                 130

tca ata cgt att ccg ctt gtc ttt gcc cgg gac acg ccc ttc atg tcc   547
Ser Ile Arg Ile Pro Leu Val Phe Ala Arg Asp Thr Pro Phe Met Ser
    135                 140                 145

ggc tta gaa aca aca cgt cgc gcc tgg att gag gcg gcc acg gaa atg   595
Gly Leu Glu Thr Thr Arg Arg Ala Trp Ile Glu Ala Ala Thr Glu Met
150                 155                 160                 165

gac atc cat aac aca tgg ccc ata atc ctc acc ggt gac ggc tgg act   643
Asp Ile His Asn Thr Trp Pro Ile Ile Leu Thr Gly Asp Gly Trp Thr
                170                 175                 180

gca ctc tct cat tca gac aaa cca ata cgc cac gaa gcc gag tta aag   691
Ala Leu Ser His Ser Asp Lys Pro Ile Arg His Glu Ala Glu Leu Lys
            185                 190                 195

gga tgg ttt ttc cac agt ttg ttc ggc agt gaa atg ccc ttg act gat   739
Gly Trp Phe Phe His Ser Leu Phe Gly Ser Glu Met Pro Leu Thr Asp
        200                 205                 210

ctg aag att gaa cga atc tac gga ggc ctg ggt act ttc gac agc gga   787
Leu Lys Ile Glu Arg Ile Tyr Gly Gly Leu Gly Thr Phe Asp Ser Gly
    215                 220                 225

gcc acc cgg tgg caa gaa ctc aca gac aca gat gat gcc tac aca gaa   835
Ala Thr Arg Trp Gln Glu Leu Thr Asp Thr Asp Asp Ala Tyr Thr Glu
230                 235                 240                 245

aat ggc agc tgg ctg ttg gaa gtt atc gtc gat gcc acc ctt gac ggt   883
Asn Gly Ser Trp Leu Leu Glu Val Ile Val Asp Ala Thr Leu Asp Gly
                250                 255                 260

gca att cca cca cca ctt cag cca caa cag ttt gaa gca tcc atc act   931
Ala Ile Pro Pro Pro Leu Gln Pro Gln Gln Phe Glu Ala Ser Ile Thr
            265                 270                 275

cac atc gtc gat gag caa cta tgg gtc ctt ggg cag atg ctt cca gtt   979
His Ile Val Asp Glu Gln Leu Trp Val Leu Gly Gln Met Leu Pro Val
        280                 285                 290

cta cga tgc tgg gat ctt gaa acc gga aaa tac ctg ggg caa acc tat   1027
Leu Arg Cys Trp Asp Leu Glu Thr Gly Lys Tyr Leu Gly Gln Thr Tyr
    295                 300                 305

gta cct att tcg gtt tct cat agt tct cgg ctt cag ttt tcg gaa ggg   1075
```

```
Val Pro Ile Ser Val Ser His Ser Ser Arg Leu Gln Phe Ser Glu Gly
310                 315                 320                 325

ttg att cac gat tat gaa aat gcc tgg tcg ctg aat cct ggg gtg cgc   1123
Leu Ile His Asp Tyr Glu Asn Ala Trp Ser Leu Asn Pro Gly Val Arg
                330                 335                 340

atg ctt gcg gag cca cag ccg tgg ata gag cct gtc att gaa ctc gac   1171
Met Leu Ala Glu Pro Gln Pro Trp Ile Glu Pro Val Ile Glu Leu Asp
            345                 350                 355

gtt cca gcg cca tgg gaa tta caa gaa agc ttc ccc gat ggg ctt tac   1219
Val Pro Ala Pro Trp Glu Leu Gln Glu Ser Phe Pro Asp Gly Leu Tyr
        360                 365                 370

ttc cta act gat ggc aag caa aca                                  1243
Phe Leu Thr Asp Gly Lys Gln Thr
    375                 380


<210> 1364
<211> 381
<212> PRT
<213> Corynebacterium glutamicum

<400> 1364
Met Asn Leu His Ser Leu Glu Ile Arg Gln Ile Ser Ser Gly Thr Ile
  1               5                  10                  15

Ser Glu Arg Lys Thr Trp Ile Phe Pro Thr Ala Ala Arg Ser Phe Asn
             20                  25                  30

Gln Asn Leu Val His Pro Gln Ser Ile Glu Ile Asp Ala Gln Thr Gly
         35                  40                  45

Val Ile Leu Ala Met Glu Asn Arg Leu Gln Arg Thr Glu Val Glu Ser
     50                  55                  60

Val Glu Tyr Pro Thr Asp Leu Pro Asn Pro Ala Trp Thr Gly Pro Ala
 65                  70                  75                  80

Ile Ser Trp Pro Leu Lys Asp Pro Ser Ile Asp Phe Pro Asp Pro Leu
                 85                  90                  95

Pro His Ser Ile Ser Glu Leu Pro Pro Gln Ser Asp Asn Pro Arg His
            100                 105                 110

Leu Arg Val Ser Ile Ser Leu Asp Ala Val Glu Gly Ala Phe Pro Arg
        115                 120                 125

Tyr Arg Ile Gly Asp Ser Ile Arg Ile Pro Leu Val Phe Ala Arg Asp
    130                 135                 140

Thr Pro Phe Met Ser Gly Leu Glu Thr Thr Arg Arg Ala Trp Ile Glu
145                 150                 155                 160

Ala Ala Thr Glu Met Asp Ile His Asn Thr Trp Pro Ile Ile Leu Thr
                165                 170                 175

Gly Asp Gly Trp Thr Ala Leu Ser His Ser Asp Lys Pro Ile Arg His
            180                 185                 190
```

```
Glu Ala Glu Leu Lys Gly Trp Phe Phe His Ser Leu Phe Gly Ser Glu
        195                 200                 205

Met Pro Leu Thr Asp Leu Lys Ile Glu Arg Ile Tyr Gly Gly Leu Gly
    210                 215                 220

Thr Phe Asp Ser Gly Ala Thr Arg Trp Gln Glu Leu Thr Asp Thr Asp
225                 230                 235                 240

Asp Ala Tyr Thr Glu Asn Gly Ser Trp Leu Leu Glu Val Ile Val Asp
                245                 250                 255

Ala Thr Leu Asp Gly Ala Ile Pro Pro Pro Leu Gln Pro Gln Gln Phe
            260                 265                 270

Glu Ala Ser Ile Thr His Ile Val Asp Glu Gln Leu Trp Val Leu Gly
        275                 280                 285

Gln Met Leu Pro Val Leu Arg Cys Trp Asp Leu Glu Thr Gly Lys Tyr
    290                 295                 300

Leu Gly Gln Thr Tyr Val Pro Ile Ser Val Ser His Ser Ser Arg Leu
305                 310                 315                 320

Gln Phe Ser Glu Gly Leu Ile His Asp Tyr Glu Asn Ala Trp Ser Leu
                325                 330                 335

Asn Pro Gly Val Arg Met Leu Ala Glu Pro Gln Pro Trp Ile Glu Pro
            340                 345                 350

Val Ile Glu Leu Asp Val Pro Ala Pro Trp Glu Leu Gln Glu Ser Phe
        355                 360                 365

Pro Asp Gly Leu Tyr Phe Leu Thr Asp Gly Lys Gln Thr
    370                 375                 380
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20050208000

<210> 1365
<211> 447
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(424)
<223> RXN02950

<400> 1365

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tccgccctat ttcagcaatg tttaataccg gtggaatcgt ttttattagg atgggtggat 60

acctatcttt agtgagccgt actagcgaga aagctgcccc atg act gtt ttc aat   115
                                            Met Thr Val Phe Asn
                                              1               5

gtt ctc cat gac gca ccc gca cca cag ccg gat aaa aac cgc ccc ggt   163
Val Leu His Asp Ala Pro Ala Pro Gln Pro Asp Lys Asn Arg Pro Gly
                 10                  15                  20

gtc aaa cgt ctc ctc caa ggt gat ggc gca aac ctc atc gcc ttc act   211
Val Lys Arg Leu Leu Gln Gly Asp Gly Ala Asn Leu Ile Ala Phe Thr
```

```
            25                  30                  35

ttc agc cct gga cag tca ctt ccc gac cac cgc gcc gca cat ccc atc   259
Phe Ser Pro Gly Gln Ser Leu Pro Asp His Arg Ala Ala His Pro Ile
         40                  45                  50

acc gtg acc gca ttt tct ggc cag ctc acc ttc agc tat ggc gag gaa   307
Thr Val Thr Ala Phe Ser Gly Gln Leu Thr Phe Ser Tyr Gly Glu Glu
     55                  60                  65

acc ttt gag ctc tcc ccc ggt gtg aca gtg cac ttg gaa gca gga gtt   355
Thr Phe Glu Leu Ser Pro Gly Val Thr Val His Leu Glu Ala Gly Val
 70                  75                  80                  85

acc cac cgc gtg gac tgc ccg cca gaa gca cca ggc gat gca agt aat   403
Thr His Arg Val Asp Cys Pro Pro Glu Ala Pro Gly Asp Ala Ser Asn
                90                  95                 100

gct gtt aac tat gct cac tgg tgaaaaacac tcagtcaacc agg             447
Ala Val Asn Tyr Ala His Trp
            105
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<210> 1366
<211> 108
<212> PRT
<213> Corynebacterium glutamicum

<400> 1366

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Met Thr Val Phe Asn Val Leu His Asp Ala Pro Ala Pro Gln Pro Asp
  1               5                  10                  15

Lys Asn Arg Pro Gly Val Lys Arg Leu Leu Gln Gly Asp Gly Ala Asn
            20                  25                  30

Leu Ile Ala Phe Thr Phe Ser Pro Gly Gln Ser Leu Pro Asp His Arg
        35                  40                  45

Ala Ala His Pro Ile Thr Val Thr Ala Phe Ser Gly Gln Leu Thr Phe
    50                  55                  60

Ser Tyr Gly Glu Glu Thr Phe Glu Leu Ser Pro Gly Val Thr Val His
65                  70                  75                  80

Leu Glu Ala Gly Val Thr His Arg Val Asp Cys Pro Pro Glu Ala Pro
                85                  90                  95

Gly Asp Ala Ser Asn Ala Val Asn Tyr Ala His Trp
            100                 105
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<210> 1367
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> RXN02951

<400> 1367
gataatgagt cagaaaatga aggtagcact acttgctgga ttaattttca aggttttctt 60

tcagaaatta atccatagcc gatatttaag gtgagaacac atg agc tcc acg ctc 115
Met Ser Ser Thr Leu
1 5

gca cga aaa gct tca ggc gac ggt tcc gaa aag aag aag cct ggc ttg 163
Ala Arg Lys Ala Ser Gly Asp Gly Ser Glu Lys Lys Lys Pro Gly Leu
10 15 20

ttt aga cgt gcg ctt cgt ttc ctc acc cac cca cct cac aaa cag gta 211
Phe Arg Arg Ala Leu Arg Phe Leu Thr His Pro Pro His Lys Gln Val
25 30 35

gac aac agc ctt gcg gat atc cgt gaa gga tta ggc ctc ggg gtg gac 259
Asp Asn Ser Leu Ala Asp Ile Arg Glu Gly Leu Gly Leu Gly Val Asp
40 45 50

gat tcc cac gaa gga tcc aaa ccc agc aac gat cat tct ttg ctg cat 307
Asp Ser His Glu Gly Ser Lys Pro Ser Asn Asp His Ser Leu Leu His
55 60 65

gaa aag cct gaa att tcc gtc atg ccg acc gaa tca atg gca cgg ctg 355
Glu Lys Pro Glu Ile Ser Val Met Pro Thr Glu Ser Met Ala Arg Leu
70 75 80 85

atc ttt tat gcg cct gat atg gat ggg caa aca gac ccc ggt gaa gta 403
Ile Phe Tyr Ala Pro Asp Met Asp Gly Gln Thr Asp Pro Gly Glu Val
90 95 100

gtg tgg att tgg gca cca gcc gat ggc ccc cag caa cca ccc cgt aaa 451
Val Trp Ile Trp Ala Pro Ala Asp Gly Pro Gln Gln Pro Pro Arg Lys
105 110 115

cgt gcc atc gtt gtt gtt gga aga aac cga aac gcc att tta ggt ctg 499
Arg Ala Ile Val Val Val Gly Arg Asn Arg Asn Ala Ile Leu Gly Leu
120 125 130

ctc att tcc tgc aac ccc gag cac cgc act gat gaa gac tgg atc gac 547
Leu Ile Ser Cys Asn Pro Glu His Arg Thr Asp Glu Asp Trp Ile Asp
135 140 145

att gga tct ggc agc tgg gac cct cga ggt cgc caa agt tgg gta cga 595
Ile Gly Ser Gly Ser Trp Asp Pro Arg Gly Arg Gln Ser Trp Val Arg
150 155 160 165

ctc gac cgc gtt ctg gag gta ccc gaa ttg ggt atc cgg cgc caa gga 643
Leu Asp Arg Val Leu Glu Val Pro Glu Leu Gly Ile Arg Arg Gln Gly
170 175 180

aca gtc gtc ccc ccg ggg cgc ttt gag cgt atc gcc aac cgc ctc cgc 691
Thr Val Val Pro Pro Gly Arg Phe Glu Arg Ile Ala Asn Arg Leu Arg
185 190 195

aac gat ttc aac tgg gtc taacatttat ttggtaattg ggc 732
Asn Asp Phe Asn Trp Val
200

<210> 1368

<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 1368
Met Ser Ser Thr Leu Ala Arg Lys Ala Ser Gly Asp Gly Ser Glu Lys
1 5 10 15

Lys Lys Pro Gly Leu Phe Arg Arg Ala Leu Arg Phe Leu Thr His Pro
20 25 30

Pro His Lys Gln Val Asp Asn Ser Leu Ala Asp Ile Arg Glu Gly Leu
35 40 45

Gly Leu Gly Val Asp Asp Ser His Glu Gly Ser Lys Pro Ser Asn Asp
50 55 60

His Ser Leu Leu His Glu Lys Pro Glu Ile Ser Val Met Pro Thr Glu
65 70 75 80

Ser Met Ala Arg Leu Ile Phe Tyr Ala Pro Asp Met Asp Gly Gln Thr
85 90 95

Asp Pro Gly Glu Val Val Trp Ile Trp Ala Pro Ala Asp Gly Pro Gln
100 105 110

Gln Pro Pro Arg Lys Arg Ala Ile Val Val Val Gly Arg Asn Arg Asn
115 120 125

Ala Ile Leu Gly Leu Leu Ile Ser Cys Asn Pro Glu His Arg Thr Asp
130 135 140

Glu Asp Trp Ile Asp Ile Gly Ser Gly Ser Trp Asp Pro Arg Gly Arg
145 150 155 160

Gln Ser Trp Val Arg Leu Asp Arg Val Leu Glu Val Pro Glu Leu Gly
165 170 175

Ile Arg Arg Gln Gly Thr Val Val Pro Pro Gly Arg Phe Glu Arg Ile
180 185 190

Ala Asn Arg Leu Arg Asn Asp Phe Asn Trp Val
195 200

<210> 1369
<211> 414
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(391)
<223> RXN02957

<400> 1369
gcatgctatt gcgctccggg tgggagattc tgtcgtccat gccgcggttg tggtggcgca 60

atgactgcgc cccgggcacg gaatggctcc gggtcaccaa atg caa act gcc caa 115
Met Gln Thr Ala Gln
1 5

```
gga gga agg gtc tac acc tca ctg atg gac gag aag tcc ctt tcc ccg   163
Gly Gly Arg Val Tyr Thr Ser Leu Met Asp Glu Lys Ser Leu Ser Pro
                 10                  15                  20

ttg atc ggt ctg ccg ggt cgg gag aac atc ggc ctg ggc cga cac tgg   211
Leu Ile Gly Leu Pro Gly Arg Glu Asn Ile Gly Leu Gly Arg His Trp
             25                  30                  35

cac ggt ctg tcg acg atg ttg cgg gtg ctc aac ggc atc gtc tac gtc   259
His Gly Leu Ser Thr Met Leu Arg Val Leu Asn Gly Ile Val Tyr Val
         40                  45                  50

gtt ctg ctg ttc gcc acc ggg ctg tgg caa ggc att atc ccc acc tcc   307
Val Leu Leu Phe Ala Thr Gly Leu Trp Gln Gly Ile Ile Pro Thr Ser
     55                  60                  65

tgg gac gtc ttc ccc gag gcg tgg gag aca ttg aag gtt tac ctg ggc   355
Trp Asp Val Phe Pro Glu Ala Trp Glu Thr Leu Lys Val Tyr Leu Gly
 70                  75                  80                  85

ttt cgt gcc cca ggc atc gag cac ttc acc ccc cta tgacgccttg        401
Phe Arg Ala Pro Gly Ile Glu His Phe Thr Pro Leu
                 90                  95

caaatgctgg gct                                                   414
```

<210> 1370
<211> 97
<212> PRT
<213> Corynebacterium glutamicum

<400> 1370

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Met Gln Thr Ala Gln Gly Gly Arg Val Tyr Thr Ser Leu Met Asp Glu
  1               5                  10                  15

Lys Ser Leu Ser Pro Leu Ile Gly Leu Pro Gly Arg Glu Asn Ile Gly
             20                  25                  30

Leu Gly Arg His Trp His Gly Leu Ser Thr Met Leu Arg Val Leu Asn
         35                  40                  45

Gly Ile Val Tyr Val Val Leu Leu Phe Ala Thr Gly Leu Trp Gln Gly
     50                  55                  60

Ile Ile Pro Thr Ser Trp Asp Val Phe Pro Glu Ala Trp Glu Thr Leu
 65                  70                  75                  80

Lys Val Tyr Leu Gly Phe Arg Ala Pro Gly Ile Glu His Phe Thr Pro
                 85                  90                  95

Leu
```

<210> 1371
<211> 441
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(418)
<223> RXN02967

<400> 1371
gggaatctag tcggccttca ccggtgatca acaagtcagt ttctggcagc gcatcctcga 60

ttccgttgga gcgggcaatc agtggcgcgc cggggaggat atg gat ctg ttg gtc 115
Met Asp Leu Leu Val
1 5

gtt gcc gtg cat gag ggt gga cag cca cgt cag tcc gat tgc aat gcc 163
Val Ala Val His Glu Gly Gly Gln Pro Arg Gln Ser Asp Cys Asn Ala
10 15 20

ccc ggc tgc gcc cat acc tgg ctt tgt gcc atc aac ttc cag ttg ggc 211
Pro Gly Cys Ala His Thr Trp Leu Cys Ala Ile Asn Phe Gln Leu Gly
25 30 35

gca ggc gtg gtg gag ggc ggc gtc gag aag cga aat gtc ttt ttc ggt 259
Ala Gly Val Val Glu Gly Gly Val Glu Lys Arg Asn Val Phe Phe Gly
40 45 50

ggc acc ttt ttg ggg ccc gaa tac ggt ggc cgc gcc ctg cgg gcc ggt 307
Gly Thr Phe Leu Gly Pro Glu Tyr Gly Gly Arg Ala Leu Arg Ala Gly
55 60 65

ggc ggg ggc gtc gac atc ggt gag cag gat cca ttc gac ggc ggc tgc 355
Gly Gly Gly Val Asp Ile Gly Glu Gln Asp Pro Phe Asp Gly Gly Cys
70 75 80 85

ggg gat gtt gag ttc ggc ggt atc gat gta atc gag gtt gat gag gtc 403
Gly Asp Val Glu Phe Gly Gly Ile Asp Val Ile Glu Val Asp Glu Val
90 95 100

ggc gcc acc ggt tcg tagtgcgtag ccctctttgt tgc 441
Gly Ala Thr Gly Ser
105

<210> 1372
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 1372
Met Asp Leu Leu Val Val Ala Val His Glu Gly Gly Gln Pro Arg Gln
1 5 10 15

Ser Asp Cys Asn Ala Pro Gly Cys Ala His Thr Trp Leu Cys Ala Ile
20 25 30

Asn Phe Gln Leu Gly Ala Gly Val Val Glu Gly Gly Val Glu Lys Arg
35 40 45

Asn Val Phe Phe Gly Gly Thr Phe Leu Gly Pro Glu Tyr Gly Gly Arg
50 55 60

Ala Leu Arg Ala Gly Gly Gly Gly Val Asp Ile Gly Glu Gln Asp Pro
65 70 75 80

```
Phe Asp Gly Gly Cys Gly Asp Val Glu Phe Gly Gly Ile Asp Val Ile
                  85                  90                  95

Glu Val Asp Glu Val Gly Ala Thr Gly Ser
            100                 105


<210> 1373
<211> 435
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(412)
<223> RXN02971

<400> 1373
ttctggtccg gattttcggg gaatacagcg agggagaaac gtggcacgcc attcaagtgg 60

gaattcaaac ttaaggttat ctaaatcgct aaccattgcg ttg att gcc atc gtc   115
                                        Leu Ile Ala Ile Val
                                          1               5

gct ctc atc gtg gca ctt gtg gtg tgg ctt ttt aac cgt tca gat gat   163
Ala Leu Ile Val Ala Leu Val Val Trp Leu Phe Asn Arg Ser Asp Asp
                  10                  15                  20

tct ggc tcc acc acg acc acc tca caa gag tgc atc tcc gga aac ttg   211
Ser Gly Ser Thr Thr Thr Thr Ser Gln Glu Cys Ile Ser Gly Asn Leu
              25                  30                  35

agt ctg ccc gtt ggt ggc gat tcc acc gca gcc gaa gaa tta gtg aac   259
Ser Leu Pro Val Gly Gly Asp Ser Thr Ala Ala Glu Glu Leu Val Asn
          40                  45                  50

aaa ttt aat gac tca tca cct gtc agc cgt gat ttc tgt gtt gag gcg   307
Lys Phe Asn Asp Ser Ser Pro Val Ser Arg Asp Phe Cys Val Glu Ala
      55                  60                  65

gaa gct gtg gac ggt aac gtc ccc gct gcc acg tac ctg ttc gct ggt   355
Glu Ala Val Asp Gly Asn Val Pro Ala Ala Thr Tyr Leu Phe Ala Gly
  70                  75                  80                  85

tct cgt tct gat gct gcc acc gca ctt gct gaa acc ggt gcc gta gca   403
Ser Arg Ser Asp Ala Ala Thr Ala Leu Ala Glu Thr Gly Ala Val Ala
                  90                  95                 100

agc agc tct taaagctctt ggccctaggt tgg                            435
Ser Ser Ser


<210> 1374
<211> 104
<212> PRT
<213> Corynebacterium glutamicum

<400> 1374
Leu Ile Ala Ile Val Ala Leu Ile Val Ala Leu Val Val Trp Leu Phe
```

```
  1               5                  10                  15

Asn Arg Ser Asp Asp Ser Gly Ser Thr Thr Thr Thr Ser Gln Glu Cys
            20                  25                  30

Ile Ser Gly Asn Leu Ser Leu Pro Val Gly Gly Asp Ser Thr Ala Ala
        35                  40                  45

Glu Glu Leu Val Asn Lys Phe Asn Asp Ser Ser Pro Val Ser Arg Asp
    50                  55                  60

Phe Cys Val Glu Ala Glu Ala Val Asp Gly Asn Val Pro Ala Ala Thr
65                  70                  75                  80

Tyr Leu Phe Ala Gly Ser Arg Ser Asp Ala Ala Thr Ala Leu Ala Glu
                85                  90                  95

Thr Gly Ala Val Ala Ser Ser Ser
            100
```

<210> 1375
<211> 1632
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1609)
<223> RXN02978

<400> 1375

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gcctcttaaa atcagacaat ttcagtgttg gaatagctac aagggtctac tgtaaacgaa 60

gaacgctcga tagggctgtg tacctcaacg gaggtaaaac gtg att gat cga cct   115
                                        Val Ile Asp Arg Pro
                                          1               5

gta tgg ttg ttt gaa ctt tat aac acc gcg aaa gaa gta gta tat tcg   163
Val Trp Leu Phe Glu Leu Tyr Asn Thr Ala Lys Glu Val Val Tyr Ser
                10                  15                  20

cta ctc att gat caa gta act ggg gaa aat aca ata ctc aag aag gat   211
Leu Leu Ile Asp Gln Val Thr Gly Glu Asn Thr Ile Leu Lys Lys Asp
            25                  30                  35

gat ggt tgg cga gat caa ttc atg att gag tct ttc ttt gct tat gat   259
Asp Gly Trp Arg Asp Gln Phe Met Ile Glu Ser Phe Phe Ala Tyr Asp
        40                  45                  50

tca gaa gct gac gcg acc tcg tgg agc ggt aag aac atg aat agc tac   307
Ser Glu Ala Asp Ala Thr Ser Trp Ser Gly Lys Asn Met Asn Ser Tyr
    55                  60                  65

tgg ttc gtt agc gat cta atc agc aat ata tcc ttc gct gag cga tcc   355
Trp Phe Val Ser Asp Leu Ile Ser Asn Ile Ser Phe Ala Glu Arg Ser
70                  75                  80                  85

ttg gaa agc ttt tct tgg gct ctt cga gat ctt gag gat ctt tct tct   403
Leu Glu Ser Phe Ser Trp Ala Leu Arg Asp Leu Glu Asp Leu Ser Ser
                90                  95                  100
```

```
agt gaa act gaa ttt gaa ggg ctt gaa gag ctg aat cta aag ttt agt   451
Ser Glu Thr Glu Phe Glu Gly Leu Glu Glu Leu Asn Leu Lys Phe Ser
            105                 110                 115

gag ctc caa gaa tgg tat acg aac ctg gaa ctt cct ttt cag ccg tcg   499
Glu Leu Gln Glu Trp Tyr Thr Asn Leu Glu Leu Pro Phe Gln Pro Ser
        120                 125                 130

gct gct gat gtt gat gag gtg gag cag tat ctg caa gct gaa gtg aca   547
Ala Ala Asp Val Asp Glu Val Glu Gln Tyr Leu Gln Ala Glu Val Thr
    135                 140                 145

agg caa cgg ggt gac tat caa tgg tct cct gag ttt tgg ata cca aag   595
Arg Gln Arg Gly Asp Tyr Gln Trp Ser Pro Glu Phe Trp Ile Pro Lys
150                 155                 160                 165

ccg gat tca tac tat atc gac cat gca cta gcg gtt gtc aca gat gtt   643
Pro Asp Ser Tyr Tyr Ile Asp His Ala Leu Ala Val Val Thr Asp Val
                170                 175                 180

ttg gga gct att gaa caa ggg gag ctg cgt gaa gaa gta gag gtg cag   691
Leu Gly Ala Ile Glu Gln Gly Glu Leu Arg Glu Glu Val Glu Val Gln
            185                 190                 195

cag gct tta gac gag gta tct gaa aat tgg aat cct ttg gaa gat tct   739
Gln Ala Leu Asp Glu Val Ser Glu Asn Trp Asn Pro Leu Glu Asp Ser
        200                 205                 210

gat tac tac tta cag gat cac cgt ggg cgc cct gta caa gat ctt tcc   787
Asp Tyr Tyr Leu Gln Asp His Arg Gly Arg Pro Val Gln Asp Leu Ser
    215                 220                 225

cgg gaa atg gag gag ttg gtc aga tgt cta atg ctt gac caa gag tgg   835
Arg Glu Met Glu Glu Leu Val Arg Cys Leu Met Leu Asp Gln Glu Trp
230                 235                 240                 245

tgg ggt gca gag gca agg att aga aag ctt gtt gaa tca gtt gag tgg   883
Trp Gly Ala Glu Ala Arg Ile Arg Lys Leu Val Glu Ser Val Glu Trp
                250                 255                 260

gag gat act cag gcg atc agc tct tta att gaa cac gag caa tat tgg   931
Glu Asp Thr Gln Ala Ile Ser Ser Leu Ile Glu His Glu Gln Tyr Trp
            265                 270                 275

gag gat ggt cgt ttt cgc cca cct cta cat aag ttt tcg gaa gga cta   979
Glu Asp Gly Arg Phe Arg Pro Pro Leu His Lys Phe Ser Glu Gly Leu
        280                 285                 290

gac gag cca gag ccc ttg ccg atg acg aga aaa atg ata ctt gcg acg   1027
Asp Glu Pro Glu Pro Leu Pro Met Thr Arg Lys Met Ile Leu Ala Thr
    295                 300                 305

aat cac cct gat gtt tta cgc gta aac att gct gat tat tat cag cag   1075
Asn His Pro Asp Val Leu Arg Val Asn Ile Ala Asp Tyr Tyr Gln Gln
310                 315                 320                 325

cat agg cgc att gct act cag aag gtg gaa tgt tat aag gaa gtt ttg   1123
His Arg Arg Ile Ala Thr Gln Lys Val Glu Cys Tyr Lys Glu Val Leu
                330                 335                 340
```

```
gca ttg tat cca gag att ctt aag aaa ttt gat gat tca tct ttc gtc   1171
Ala Leu Tyr Pro Glu Ile Leu Lys Lys Phe Asp Asp Ser Ser Phe Val
            345                 350                 355

aat cga cat tgg atc tat agg gcg ttt gat cgc gaa ggt cag ctt ttg   1219
Asn Arg His Trp Ile Tyr Arg Ala Phe Asp Arg Glu Gly Gln Leu Leu
        360                 365                 370

tat atc ggg gag aca ata aac cct ctt gta cgg ttg agg gag cat gcc   1267
Tyr Ile Gly Glu Thr Ile Asn Pro Leu Val Arg Leu Arg Glu His Ala
    375                 380                 385

ggc tta ggg tct att aac cac gca cat cat agg cta gta tcg ccg tgg   1315
Gly Leu Gly Ser Ile Asn His Ala His His Arg Leu Val Ser Pro Trp
390                 395                 400                 405

ttt tct acg atg gct aca ttt cat ctt gaa tct tgc ttt acc cag gct   1363
Phe Ser Thr Met Ala Thr Phe His Leu Glu Ser Cys Phe Thr Gln Ala
                410                 415                 420

gag gca aaa gag aag gag gct tta tat att aag ctg gaa cag cca aga   1411
Glu Ala Lys Glu Lys Glu Ala Leu Tyr Ile Lys Leu Glu Gln Pro Arg
            425                 430                 435

tat aat aag acg cat aat tct gct aga ttg gcg gtt tct gaa gaa ggg   1459
Tyr Asn Lys Thr His Asn Ser Ala Arg Leu Ala Val Ser Glu Glu Gly
        440                 445                 450

gtg ccg gtg aac gag gtg ccg tca aga aat gat ccg agg aat gtc ggt   1507
Val Pro Val Asn Glu Val Pro Ser Arg Asn Asp Pro Arg Asn Val Gly
    455                 460                 465

tgg aag ggt cat agg cac gtg cca cca atg ttg ccg att gtt gca cgt   1555
Trp Lys Gly His Arg His Val Pro Pro Met Leu Pro Ile Val Ala Arg
470                 475                 480                 485

gtt gtc gat gaa tcg aca aca cgt gag gga tat gcg ttt tac gag gac   1603
Val Val Asp Glu Ser Thr Thr Arg Glu Gly Tyr Ala Phe Tyr Glu Asp
                490                 495                 500

aac cgg tagcgttgcg atctctcgtg gaa                                1632
Asn Arg
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<210> 1376
<211> 503
<212> PRT
<213> Corynebacterium glutamicum

<400> 1376

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Val Ile Asp Arg Pro Val Trp Leu Phe Glu Leu Tyr Asn Thr Ala Lys
  1               5                  10                  15

Glu Val Val Tyr Ser Leu Leu Ile Asp Gln Val Thr Gly Glu Asn Thr
             20                  25                  30

Ile Leu Lys Lys Asp Asp Gly Trp Arg Asp Gln Phe Met Ile Glu Ser
         35                  40                  45

Phe Phe Ala Tyr Asp Ser Glu Ala Asp Ala Thr Ser Trp Ser Gly Lys
```

```
     50                  55                  60

Asn Met Asn Ser Tyr Trp Phe Val Ser Asp Leu Ile Ser Asn Ile Ser
 65                  70                  75                  80

Phe Ala Glu Arg Ser Leu Glu Ser Phe Ser Trp Ala Leu Arg Asp Leu
                 85                  90                  95

Glu Asp Leu Ser Ser Ser Glu Thr Glu Phe Glu Gly Leu Glu Glu Leu
            100                 105                 110

Asn Leu Lys Phe Ser Glu Leu Gln Glu Trp Tyr Thr Asn Leu Glu Leu
        115                 120                 125

Pro Phe Gln Pro Ser Ala Ala Asp Val Asp Glu Val Glu Gln Tyr Leu
    130                 135                 140

Gln Ala Glu Val Thr Arg Gln Arg Gly Asp Tyr Gln Trp Ser Pro Glu
145                 150                 155                 160

Phe Trp Ile Pro Lys Pro Asp Ser Tyr Tyr Ile Asp His Ala Leu Ala
                165                 170                 175

Val Val Thr Asp Val Leu Gly Ala Ile Glu Gln Gly Glu Leu Arg Glu
            180                 185                 190

Glu Val Glu Val Gln Gln Ala Leu Asp Glu Val Ser Glu Asn Trp Asn
        195                 200                 205

Pro Leu Glu Asp Ser Asp Tyr Tyr Leu Gln Asp His Arg Gly Arg Pro
    210                 215                 220

Val Gln Asp Leu Ser Arg Glu Met Glu Glu Leu Val Arg Cys Leu Met
225                 230                 235                 240

Leu Asp Gln Glu Trp Trp Gly Ala Glu Ala Arg Ile Arg Lys Leu Val
                245                 250                 255

Glu Ser Val Glu Trp Glu Asp Thr Gln Ala Ile Ser Ser Leu Ile Glu
            260                 265                 270

His Glu Gln Tyr Trp Glu Asp Gly Arg Phe Arg Pro Pro Leu His Lys
        275                 280                 285

Phe Ser Glu Gly Leu Asp Glu Pro Glu Pro Leu Pro Met Thr Arg Lys
    290                 295                 300

Met Ile Leu Ala Thr Asn His Pro Asp Val Leu Arg Val Asn Ile Ala
305                 310                 315                 320

Asp Tyr Tyr Gln Gln His Arg Arg Ile Ala Thr Gln Lys Val Glu Cys
                325                 330                 335

Tyr Lys Glu Val Leu Ala Leu Tyr Pro Glu Ile Leu Lys Lys Phe Asp
            340                 345                 350

Asp Ser Ser Phe Val Asn Arg His Trp Ile Tyr Arg Ala Phe Asp Arg
        355                 360                 365

Glu Gly Gln Leu Leu Tyr Ile Gly Glu Thr Ile Asn Pro Leu Val Arg
    370                 375                 380
```

```
Leu Arg Glu His Ala Gly Leu Gly Ser Ile Asn His Ala His His Arg
385                 390                 395                 400

Leu Val Ser Pro Trp Phe Ser Thr Met Ala Thr Phe His Leu Glu Ser
                405                 410                 415

Cys Phe Thr Gln Ala Glu Ala Lys Glu Lys Glu Ala Leu Tyr Ile Lys
            420                 425                 430

Leu Glu Gln Pro Arg Tyr Asn Lys Thr His Asn Ser Ala Arg Leu Ala
        435                 440                 445

Val Ser Glu Glu Gly Val Pro Val Asn Glu Val Pro Ser Arg Asn Asp
    450                 455                 460

Pro Arg Asn Val Gly Trp Lys Gly His Arg His Val Pro Pro Met Leu
465                 470                 475                 480

Pro Ile Val Ala Arg Val Val Asp Glu Ser Thr Thr Arg Glu Gly Tyr
                485                 490                 495

Ala Phe Tyr Glu Asp Asn Arg
            500


<210> 1377
<211> 1689
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1666)
<223> RXN02995

<400> 1377
aaggcaaggt cggagacgag ccttgttagt tcagagtcct aaataggcgt ttatgtcagc 60

tcgcgcaaca gggatacaat gagcaaccgt gacgcagcaa ttg aac cac gca aag   115
                                        Leu Asn His Ala Lys
                                          1               5

gta aat caa cat ccc ggt caa gcc acc ctc cca gaa acc gca gag ggg   163
Val Asn Gln His Pro Gly Gln Ala Thr Leu Pro Glu Thr Ala Glu Gly
                 10                  15                  20

cag gtt cgc acc tac gag gta aaa acc tac ggc tgt cag atg aat gtg   211
Gln Val Arg Thr Tyr Glu Val Lys Thr Tyr Gly Cys Gln Met Asn Val
             25                  30                  35

cac gat tct gag cgc ctt tcg ggc ctg ctc gag gag gct gga tac gtt   259
His Asp Ser Glu Arg Leu Ser Gly Leu Leu Glu Glu Ala Gly Tyr Val
         40                  45                  50

gct gct ccg gag gac acc act ccg gat ctt gtc gta ttt aat acg tgc   307
Ala Ala Pro Glu Asp Thr Thr Pro Asp Leu Val Val Phe Asn Thr Cys
     55                  60                  65

gcc gtg cgt gaa aac gcc gat atg cgc ctc tat ggc act ttg ggc aac   355
Ala Val Arg Glu Asn Ala Asp Met Arg Leu Tyr Gly Thr Leu Gly Asn
```

```
 70                  75                  80                  85

ctg cgc agc gtg aaa gaa aag aac cca ggc atg caa atc gct gtc ggt   403
Leu Arg Ser Val Lys Glu Lys Asn Pro Gly Met Gln Ile Ala Val Gly
                 90                  95                 100

ggt tgt ttg gct caa aaa gac aaa gat acc gtg gtg aaa aaa gca ccg   451
Gly Cys Leu Ala Gln Lys Asp Lys Asp Thr Val Val Lys Lys Ala Pro
            105                 110                 115

tgg gtg gac gtg gtg ttt ggt acc cac aac att ggt tcc ttg cca acc   499
Trp Val Asp Val Val Phe Gly Thr His Asn Ile Gly Ser Leu Pro Thr
        120                 125                 130

ttg ctt cag cgc gcg gag cac aat gcc caa gcg gaa gtc gaa att gtc   547
Leu Leu Gln Arg Ala Glu His Asn Ala Gln Ala Glu Val Glu Ile Val
    135                 140                 145

gat tcc ctc gag cag ttc ccg tca gta ctt cct gca aag cgc gag tct   595
Asp Ser Leu Glu Gln Phe Pro Ser Val Leu Pro Ala Lys Arg Glu Ser
150                 155                 160                 165

gct tac gct ggt tgg gtg tcc gta tca gtc gga tgt aac aac acc tgt   643
Ala Tyr Ala Gly Trp Val Ser Val Ser Val Gly Cys Asn Asn Thr Cys
                170                 175                 180

act ttc tgc atc gtt ccg tcg ctg cgc ggt aaa gag cag gac cgt cga   691
Thr Phe Cys Ile Val Pro Ser Leu Arg Gly Lys Glu Gln Asp Arg Arg
            185                 190                 195

cca gga gac atc ctc gca gag gta caa gca ctg gtg gat cag gga gtt   739
Pro Gly Asp Ile Leu Ala Glu Val Gln Ala Leu Val Asp Gln Gly Val
        200                 205                 210

acc gag gta act cta ctt ggc caa aac gta aat gct tac ggc gtg aac   787
Thr Glu Val Thr Leu Leu Gly Gln Asn Val Asn Ala Tyr Gly Val Asn
    215                 220                 225

ttt gtt gat cct gag cta gag cgc gat cgc agt gca ttt tcc aag ctg   835
Phe Val Asp Pro Glu Leu Glu Arg Asp Arg Ser Ala Phe Ser Lys Leu
230                 235                 240                 245

ctt cgt gcc tgt ggt gag atc gaa ggc ctc gag cgg gtt cgc ttc acc   883
Leu Arg Ala Cys Gly Glu Ile Glu Gly Leu Glu Arg Val Arg Phe Thr
                250                 255                 260

agc cct cac cct gca gaa ttc acc tct gat gtc att gac gcc atg gca   931
Ser Pro His Pro Ala Glu Phe Thr Ser Asp Val Ile Asp Ala Met Ala
            265                 270                 275

gag acc cca aac atc tgc ccg cag ctg cac atg cca ctg cag tcc gga   979
Glu Thr Pro Asn Ile Cys Pro Gln Leu His Met Pro Leu Gln Ser Gly
        280                 285                 290

tct gac aag gtg ctc aaa gag atg cgc cgt tcc tac cga tcc aag aag   1027
Ser Asp Lys Val Leu Lys Glu Met Arg Arg Ser Tyr Arg Ser Lys Lys
    295                 300                 305

ttc ctc tcc atc ttg gat gag gtc cgt gcg aag atc cct cac gcc tct   1075
Phe Leu Ser Ile Leu Asp Glu Val Arg Ala Lys Ile Pro His Ala Ser
310                 315                 320                 325
```

```
atc acc acc gat att att gtc gga ttc cct ggc gaa aca gag gag gat   1123
Ile Thr Thr Asp Ile Ile Val Gly Phe Pro Gly Glu Thr Glu Glu Asp
                330                 335                 340

ttc caa gca acc ctc gac gtt gtc aag aag gca cgc ttt act tct gct   1171
Phe Gln Ala Thr Leu Asp Val Val Lys Lys Ala Arg Phe Thr Ser Ala
            345                 350                 355

tac acc ttc caa tac agc cca cgc cct ggc acc cct gca gcg gaa tat   1219
Tyr Thr Phe Gln Tyr Ser Pro Arg Pro Gly Thr Pro Ala Ala Glu Tyr
        360                 365                 370

gaa aac cag ctt cca aaa gaa gtt gtg cag gaa cgc tac gag cgc ctc   1267
Glu Asn Gln Leu Pro Lys Glu Val Val Gln Glu Arg Tyr Glu Arg Leu
    375                 380                 385

atg gtc gtt cag gaa caa gtc tgc gaa gaa gaa aac caa aag ctc atc   1315
Met Val Val Gln Glu Gln Val Cys Glu Glu Glu Asn Gln Lys Leu Ile
390                 395                 400                 405

ggc acc acc gtc gaa ttg ctg gtc cag gct ggc gga ggc cgc aag aac   1363
Gly Thr Thr Val Glu Leu Leu Val Gln Ala Gly Gly Gly Arg Lys Asn
                410                 415                 420

gat gcc acc aag cgc atg agt ggt cgc gca cgc gat gga cgc ctc gtg   1411
Asp Ala Thr Lys Arg Met Ser Gly Arg Ala Arg Asp Gly Arg Leu Val
            425                 430                 435

cac ttt gcg cca gag ggc gac att gat ggt gag atc cgc ccc ggc gat   1459
His Phe Ala Pro Glu Gly Asp Ile Asp Gly Glu Ile Arg Pro Gly Asp
        440                 445                 450

ttt gtc act gtc acg gtg act gag gcc aag cct ttc ttc ctc atc gca   1507
Phe Val Thr Val Thr Val Thr Glu Ala Lys Pro Phe Phe Leu Ile Ala
    455                 460                 465

gac tcc ggt gtg cag acc cac cgc cgc acc aaa gct ggt gac aac tct   1555
Asp Ser Gly Val Gln Thr His Arg Arg Thr Lys Ala Gly Asp Asn Ser
470                 475                 480                 485

gca gtt ggt caa gtt cca acc aca gca ccg atc ggt gtg ggc ttg gga   1603
Ala Val Gly Gln Val Pro Thr Thr Ala Pro Ile Gly Val Gly Leu Gly
                490                 495                 500

ctg cca caa atc ggc gca cca aag gtg gct cct gcc aca gaa tct gcc   1651
Leu Pro Gln Ile Gly Ala Pro Lys Val Ala Pro Ala Thr Glu Ser Ala
            505                 510                 515

tgc tgc tcc att aac taaaaattgc aggctagaat aga                    1689
Cys Cys Ser Ile Asn
        520
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<210> 1378
<211> 522
<212> PRT
<213> Corynebacterium glutamicum

<400> 1378
Leu Asn His Ala Lys Val Asn Gln His Pro Gly Gln Ala Thr Leu Pro

```
  1               5                  10                  15

Glu Thr Ala Glu Gly Gln Val Arg Thr Tyr Glu Val Lys Thr Tyr Gly
            20                  25                  30

Cys Gln Met Asn Val His Asp Ser Glu Arg Leu Ser Gly Leu Leu Glu
        35                  40                  45

Glu Ala Gly Tyr Val Ala Ala Pro Glu Asp Thr Thr Pro Asp Leu Val
    50                  55                  60

Val Phe Asn Thr Cys Ala Val Arg Glu Asn Ala Asp Met Arg Leu Tyr
65                  70                  75                  80

Gly Thr Leu Gly Asn Leu Arg Ser Val Lys Glu Lys Asn Pro Gly Met
                85                  90                  95

Gln Ile Ala Val Gly Gly Cys Leu Ala Gln Lys Asp Lys Asp Thr Val
            100                 105                 110

Val Lys Lys Ala Pro Trp Val Asp Val Val Phe Gly Thr His Asn Ile
        115                 120                 125

Gly Ser Leu Pro Thr Leu Leu Gln Arg Ala Glu His Asn Ala Gln Ala
    130                 135                 140

Glu Val Glu Ile Val Asp Ser Leu Glu Gln Phe Pro Ser Val Leu Pro
145                 150                 155                 160

Ala Lys Arg Glu Ser Ala Tyr Ala Gly Trp Val Ser Val Ser Val Gly
                165                 170                 175

Cys Asn Asn Thr Cys Thr Phe Cys Ile Val Pro Ser Leu Arg Gly Lys
            180                 185                 190

Glu Gln Asp Arg Arg Pro Gly Asp Ile Leu Ala Glu Val Gln Ala Leu
        195                 200                 205

Val Asp Gln Gly Val Thr Glu Val Thr Leu Leu Gly Gln Asn Val Asn
    210                 215                 220

Ala Tyr Gly Val Asn Phe Val Asp Pro Glu Leu Glu Arg Asp Arg Ser
225                 230                 235                 240

Ala Phe Ser Lys Leu Leu Arg Ala Cys Gly Glu Ile Glu Gly Leu Glu
                245                 250                 255

Arg Val Arg Phe Thr Ser Pro His Pro Ala Glu Phe Thr Ser Asp Val
            260                 265                 270

Ile Asp Ala Met Ala Glu Thr Pro Asn Ile Cys Pro Gln Leu His Met
        275                 280                 285

Pro Leu Gln Ser Gly Ser Asp Lys Val Leu Lys Glu Met Arg Arg Ser
    290                 295                 300

Tyr Arg Ser Lys Lys Phe Leu Ser Ile Leu Asp Glu Val Arg Ala Lys
305                 310                 315                 320

Ile Pro His Ala Ser Ile Thr Thr Asp Ile Ile Val Gly Phe Pro Gly
                325                 330                 335
```

```
Glu Thr Glu Glu Asp Phe Gln Ala Thr Leu Asp Val Val Lys Lys Ala
            340                 345                 350

Arg Phe Thr Ser Ala Tyr Thr Phe Gln Tyr Ser Pro Arg Pro Gly Thr
        355                 360                 365

Pro Ala Ala Glu Tyr Glu Asn Gln Leu Pro Lys Glu Val Val Gln Glu
    370                 375                 380

Arg Tyr Glu Arg Leu Met Val Val Gln Glu Gln Val Cys Glu Glu Glu
385                 390                 395                 400

Asn Gln Lys Leu Ile Gly Thr Thr Val Glu Leu Leu Val Gln Ala Gly
                405                 410                 415

Gly Gly Arg Lys Asn Asp Ala Thr Lys Arg Met Ser Gly Arg Ala Arg
            420                 425                 430

Asp Gly Arg Leu Val His Phe Ala Pro Glu Gly Asp Ile Asp Gly Glu
        435                 440                 445

Ile Arg Pro Gly Asp Phe Val Thr Val Thr Val Thr Glu Ala Lys Pro
    450                 455                 460

Phe Phe Leu Ile Ala Asp Ser Gly Val Gln Thr His Arg Arg Thr Lys
465                 470                 475                 480

Ala Gly Asp Asn Ser Ala Val Gly Gln Val Pro Thr Thr Ala Pro Ile
                485                 490                 495

Gly Val Gly Leu Gly Leu Pro Gln Ile Gly Ala Pro Lys Val Ala Pro
            500                 505                 510

Ala Thr Glu Ser Ala Cys Cys Ser Ile Asn
        515                 520


<210> 1379
<211> 752
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(729)
<223> RXN02997

<400> 1379
ccc cta ccg ggc cag ccc ttt gag ggc gag gct tta acg ctt ata aac   48
Pro Leu Pro Gly Gln Pro Phe Glu Gly Glu Ala Leu Thr Leu Ile Asn
  1               5                  10                  15

gcc ctc ctc cac cac gcc gaa aac gtc gca gcc tcc aac ccc tgg aag   96
Ala Leu Leu His His Ala Glu Asn Val Ala Ala Ser Asn Pro Trp Lys
            20                  25                  30

cgc acc acc ttc cac acc gct cac atg cac cct cca ggg agt aat gcg   144
Arg Thr Thr Phe His Thr Ala His Met His Pro Pro Gly Ser Asn Ala
        35                  40                  45
```

```
gat tgt gac tac tgc ctg gtg ctg caa cgc cgc gga tac gtt aaa gcc   192
Asp Cys Asp Tyr Cys Leu Val Leu Gln Arg Arg Gly Tyr Val Lys Ala
     50                  55                  60

cac gaa gaa atc caa caa acc atc ccg ctt cct tca ggt gac tgg tcc   240
His Glu Glu Ile Gln Gln Thr Ile Pro Leu Pro Ser Gly Asp Trp Ser
 65                  70                  75                  80

gct gga gaa ttc acc gtg gtg gac gtt gaa ggc acc gcc ttc cca agc   288
Ala Gly Glu Phe Thr Val Val Asp Val Glu Gly Thr Ala Phe Pro Ser
                 85                  90                  95

gcg ctg atc ccc agc atc gtg gaa ctc caa cac cgc gca gcc ctc gat   336
Ala Leu Ile Pro Ser Ile Val Glu Leu Gln His Arg Ala Ala Leu Asp
            100                 105                 110

gtg ccc cac gga aac tta agt gtt gcg cct gca cag tgg gat gaa cac   384
Val Pro His Gly Asn Leu Ser Val Ala Pro Ala Gln Trp Asp Glu His
        115                 120                 125

cgc ttg gcg cag caa tct gaa aga atc ctt aaa aca gga acg aaa ctg   432
Arg Leu Ala Gln Gln Ser Glu Arg Ile Leu Lys Thr Gly Thr Lys Leu
    130                 135                 140

ttc acc gta ctg ttt gcc gaa gga tcc aca gtc gct gcc atg tcc tcc   480
Phe Thr Val Leu Phe Ala Glu Gly Ser Thr Val Ala Ala Met Ser Ser
145                 150                 155                 160

atc gcg att ccc cca ggc tcc aac cct gac atc gcc gaa cag gga ctg   528
Ile Ala Ile Pro Pro Gly Ser Asn Pro Asp Ile Ala Glu Gln Gly Leu
                165                 170                 175

acc atc gtg cac cca gat ttc aga ggc cgt ggt ctt gga acc gct gtg   576
Thr Ile Val His Pro Asp Phe Arg Gly Arg Gly Leu Gly Thr Ala Val
            180                 185                 190

aaa tta gcg gga ctg tca cta ctt tcg agg tgc cac cca gaa att caa   624
Lys Leu Ala Gly Leu Ser Leu Leu Ser Arg Cys His Pro Glu Ile Gln
        195                 200                 205

cgc gta gcc acc tca aat gca gta gac aac cat gcg atg ctg gcg att   672
Arg Val Ala Thr Ser Asn Ala Val Asp Asn His Ala Met Leu Ala Ile
    210                 215                 220

aac cgc tcc ata ggg gca aca gag atc gcc cga acc acc ctg tgg gag   720
Asn Arg Ser Ile Gly Ala Thr Glu Ile Ala Arg Thr Thr Leu Trp Glu
225                 230                 235                 240

aag aaa ctc taggtgatgg aattcgagac caa                            752
Lys Lys Leu
```

<210> 1380
<211> 243
<212> PRT
<213> Corynebacterium glutamicum

<400> 1380

```
Pro Leu Pro Gly Gln Pro Phe Glu Gly Glu Ala Leu Thr Leu Ile Asn
  1               5                  10                  15
```

```
Ala Leu Leu His His Ala Glu Asn Val Ala Ala Ser Asn Pro Trp Lys
            20                  25                  30

Arg Thr Thr Phe His Thr Ala His Met His Pro Pro Gly Ser Asn Ala
        35                  40                  45

Asp Cys Asp Tyr Cys Leu Val Leu Gln Arg Arg Gly Tyr Val Lys Ala
    50                  55                  60

His Glu Glu Ile Gln Gln Thr Ile Pro Leu Pro Ser Gly Asp Trp Ser
65                  70                  75                  80

Ala Gly Glu Phe Thr Val Val Asp Val Glu Gly Thr Ala Phe Pro Ser
                85                  90                  95

Ala Leu Ile Pro Ser Ile Val Glu Leu Gln His Arg Ala Ala Leu Asp
            100                 105                 110

Val Pro His Gly Asn Leu Ser Val Ala Pro Ala Gln Trp Asp Glu His
        115                 120                 125

Arg Leu Ala Gln Gln Ser Glu Arg Ile Leu Lys Thr Gly Thr Lys Leu
    130                 135                 140

Phe Thr Val Leu Phe Ala Glu Gly Ser Thr Val Ala Ala Met Ser Ser
145                 150                 155                 160

Ile Ala Ile Pro Pro Gly Ser Asn Pro Asp Ile Ala Glu Gln Gly Leu
                165                 170                 175

Thr Ile Val His Pro Asp Phe Arg Gly Arg Gly Leu Gly Thr Ala Val
            180                 185                 190

Lys Leu Ala Gly Leu Ser Leu Leu Ser Arg Cys His Pro Glu Ile Gln
        195                 200                 205

Arg Val Ala Thr Ser Asn Ala Val Asp Asn His Ala Met Leu Ala Ile
    210                 215                 220

Asn Arg Ser Ile Gly Ala Thr Glu Ile Ala Arg Thr Thr Leu Trp Glu
225                 230                 235                 240

Lys Lys Leu
```

<210> 1381
<211> 553
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(553)
<223> RXN03001

<400> 1381
cccggttcac gtgatcaatg acttcacgag caccgatgaa atcgatgctg cgcttcgtga 60

acgctacgac atctaactac tttaaaagga cgaaaatatt atg gac tgg tta acc 115

```
                                                    Met Asp Trp Leu Thr
                                                      1               5

att cct ctt ttc ctc gtt aat gaa atc ctt gcg gtt ccg gct ttc ctc   163
Ile Pro Leu Phe Leu Val Asn Glu Ile Leu Ala Val Pro Ala Phe Leu
                 10                  15                  20

atc ggt atc atc acc gcc gtg gga ttg ggt gcc atg ggg cgt tcc gtc   211
Ile Gly Ile Ile Thr Ala Val Gly Leu Gly Ala Met Gly Arg Ser Val
             25                  30                  35

ggt cag gtt atc ggt gga gca atc aaa gca acg ttg ggc ttt ttg ctc   259
Gly Gln Val Ile Gly Gly Ala Ile Lys Ala Thr Leu Gly Phe Leu Leu
         40                  45                  50

att ggt gcg ggt gcc acg ttg gtc act gcc tcc ctg gag cca ctg ggt   307
Ile Gly Ala Gly Ala Thr Leu Val Thr Ala Ser Leu Glu Pro Leu Gly
     55                  60                  65

gcg atg atc atg ggt gcc aca ggc atg cgt ggt gtt gtc cca acg aat   355
Ala Met Ile Met Gly Ala Thr Gly Met Arg Gly Val Val Pro Thr Asn
 70                  75                  80                  85

gaa gcc atc gcc gga atc gca cag gct gaa tac ggc gcg cag gtg gcg   403
Glu Ala Ile Ala Gly Ile Ala Gln Ala Glu Tyr Gly Ala Gln Val Ala
                 90                  95                 100

tgg ctg atg att ctg ggc ttc gcc atc tct ttg gtg ttg gct cgt ttc   451
Trp Leu Met Ile Leu Gly Phe Ala Ile Ser Leu Val Leu Ala Arg Phe
            105                 110                 115

acc aac ctg cgt tat gtc ttg ctc aac gga cac cac gtg ctg ttg atg   499
Thr Asn Leu Arg Tyr Val Leu Leu Asn Gly His His Val Leu Leu Met
        120                 125                 130

tgc acc atg ctc acc atg gtc ttg gcc acc gga aga gtt gat gcg tgg   547
Cys Thr Met Leu Thr Met Val Leu Ala Thr Gly Arg Val Asp Ala Trp
    135                 140                 145

atc ttc                                                           553
Ile Phe
150
```

<210> 1382
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 1382

```
Met Asp Trp Leu Thr Ile Pro Leu Phe Leu Val Asn Glu Ile Leu Ala
  1               5                  10                  15

Val Pro Ala Phe Leu Ile Gly Ile Ile Thr Ala Val Gly Leu Gly Ala
             20                  25                  30

Met Gly Arg Ser Val Gly Gln Val Ile Gly Gly Ala Ile Lys Ala Thr
         35                  40                  45

Leu Gly Phe Leu Leu Ile Gly Ala Gly Ala Thr Leu Val Thr Ala Ser
     50                  55                  60
```

```
Leu Glu Pro Leu Gly Ala Met Ile Met Gly Ala Thr Gly Met Arg Gly
 65                  70                  75                  80

Val Val Pro Thr Asn Glu Ala Ile Ala Gly Ile Ala Gln Ala Glu Tyr
                 85                  90                  95

Gly Ala Gln Val Ala Trp Leu Met Ile Leu Gly Phe Ala Ile Ser Leu
            100                 105                 110

Val Leu Ala Arg Phe Thr Asn Leu Arg Tyr Val Leu Leu Asn Gly His
        115                 120                 125

His Val Leu Leu Met Cys Thr Met Leu Thr Met Val Leu Ala Thr Gly
    130                 135                 140

Arg Val Asp Ala Trp Ile Phe
145                 150
```

<210> 1383
<211> 891
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(868)
<223> RXN03005

<400> 1383

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taggtaaacc ttaaacagtc gccattgaag aattttaaaa acaaacaacc ttcaacgcgc 60

taacaagcat cttcccactc tcgttaccgg agtttctcac atg tct cac aag ttt   115
                                              Met Ser His Lys Phe
                                                1               5

tcc cgc cgt gct ttc gca gta ctg acc gct gcc gca att tcc act tcc   163
Ser Arg Arg Ala Phe Ala Val Leu Thr Ala Ala Ala Ile Ser Thr Ser
                10                  15                  20

gct ttc gca acc act gct ccg tct gcg att gca gag cca gtt cta atg   211
Ala Phe Ala Thr Thr Ala Pro Ser Ala Ile Ala Glu Pro Val Leu Met
            25                  30                  35

tcg cac tgc aga cga ttc cag cgt cgc aac ttc aga aaa ctc cct cga   259
Ser His Cys Arg Arg Phe Gln Arg Arg Asn Phe Arg Lys Leu Pro Arg
        40                  45                  50

ctg ggg ctt caa ggc ttc ctg gcg cac cta tgt cac cgg acc ttg gac   307
Leu Gly Leu Gln Gly Phe Leu Ala His Leu Cys His Arg Thr Leu Asp
    55                  60                  65

tgg tgg aac cgt gac gca act ggc ggt gca act gtc aac gaa gat gga   355
Trp Trp Asn Arg Asp Ala Thr Gly Gly Ala Thr Val Asn Glu Asp Gly
70                  75                  80                  85

acc tac aac ttc acc ctc gga act ggc tcc aat tac gac gtc gac acc   403
Thr Tyr Asn Phe Thr Leu Gly Thr Gly Ser Asn Tyr Asp Val Asp Thr
                90                  95                  100
```

```
gag aag ggc cag ctg aac tac gaa gga act gtt gcc ttc gcc agt gac   451
Glu Lys Gly Gln Leu Asn Tyr Glu Gly Thr Val Ala Phe Ala Ser Asp
            105                 110                 115

gct cac ggc ttc aac atc acc ttg tcc aac ccg cag atc acc gtc gag   499
Ala His Gly Phe Asn Ile Thr Leu Ser Asn Pro Gln Ile Thr Val Glu
        120                 125                 130

ggc gac act gca act ttg agc gcc gag ctg tct gac aat gcc gct ccc   547
Gly Asp Thr Ala Thr Leu Ser Ala Glu Leu Ser Asp Asn Ala Ala Pro
    135                 140                 145

gaa gag acc tcc act act cgc gtt gat gtt gct gag ttc gaa ctg acc   595
Glu Glu Thr Ser Thr Thr Arg Val Asp Val Ala Glu Phe Glu Leu Thr
150                 155                 160                 165

gct cct gag gtt tca gaa acc gat gcg gac att acc tac acc tgg acc   643
Ala Pro Glu Val Ser Glu Thr Asp Ala Asp Ile Thr Tyr Thr Trp Thr
                170                 175                 180

gat gct tcc ggc act ttc ttg gag acc ctg cag cct gaa gaa ttg agc   691
Asp Ala Ser Gly Thr Phe Leu Glu Thr Leu Gln Pro Glu Glu Leu Ser
            185                 190                 195

cgt tac gca ggc cag gaa gcg gat gcg ctg agc ttc tcc atc acc gtg   739
Arg Tyr Ala Gly Gln Glu Ala Asp Ala Leu Ser Phe Ser Ile Thr Val
        200                 205                 210

gac aag gct tca gag aac cct tcc gat gat gtt gct acc gga tct tcc   787
Asp Lys Ala Ser Glu Asn Pro Ser Asp Asp Val Ala Thr Gly Ser Ser
    215                 220                 225

tcc agc ttc ctc tcc acc atc ttg aac ttc ctt cag cag ctg gcg agc   835
Ser Ser Phe Leu Ser Thr Ile Leu Asn Phe Leu Gln Gln Leu Ala Ser
230                 235                 240                 245

cca ctg ctc aag ctc ttc ggt tcg ctt tct tcc taaataatca gtaatgcccc 888
Pro Leu Leu Lys Leu Phe Gly Ser Leu Ser Ser
                250                 255

acc                                                               891
```

<210> 1384
<211> 256
<212> PRT
<213> Corynebacterium glutamicum

<400> 1384

```
Met Ser His Lys Phe Ser Arg Arg Ala Phe Ala Val Leu Thr Ala Ala
  1               5                  10                  15

Ala Ile Ser Thr Ser Ala Phe Ala Thr Thr Ala Pro Ser Ala Ile Ala
             20                  25                  30

Glu Pro Val Leu Met Ser His Cys Arg Arg Phe Gln Arg Arg Asn Phe
         35                  40                  45

Arg Lys Leu Pro Arg Leu Gly Leu Gln Gly Phe Leu Ala His Leu Cys
     50                  55                  60
```

```
His Arg Thr Leu Asp Trp Trp Asn Arg Asp Ala Thr Gly Gly Ala Thr
 65                  70                  75                  80

Val Asn Glu Asp Gly Thr Tyr Asn Phe Thr Leu Gly Thr Gly Ser Asn
                 85                  90                  95

Tyr Asp Val Asp Thr Glu Lys Gly Gln Leu Asn Tyr Glu Gly Thr Val
            100                 105                 110

Ala Phe Ala Ser Asp Ala His Gly Phe Asn Ile Thr Leu Ser Asn Pro
        115                 120                 125

Gln Ile Thr Val Glu Gly Asp Thr Ala Thr Leu Ser Ala Glu Leu Ser
    130                 135                 140

Asp Asn Ala Ala Pro Glu Glu Thr Ser Thr Thr Arg Val Asp Val Ala
145                 150                 155                 160

Glu Phe Glu Leu Thr Ala Pro Glu Val Ser Glu Thr Asp Ala Asp Ile
                165                 170                 175

Thr Tyr Thr Trp Thr Asp Ala Ser Gly Thr Phe Leu Glu Thr Leu Gln
            180                 185                 190

Pro Glu Glu Leu Ser Arg Tyr Ala Gly Gln Glu Ala Asp Ala Leu Ser
        195                 200                 205

Phe Ser Ile Thr Val Asp Lys Ala Ser Glu Asn Pro Ser Asp Asp Val
    210                 215                 220

Ala Thr Gly Ser Ser Ser Ser Phe Leu Ser Thr Ile Leu Asn Phe Leu
225                 230                 235                 240

Gln Gln Leu Ala Ser Pro Leu Leu Lys Leu Phe Gly Ser Leu Ser Ser
                245                 250                 255
```

09529350.030209

<210> 1385
<211> 448
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(448)
<223> RXN03009

<400> 1385
atgtgaacct gatgctggca cctgaagata gccacagccc aggcaccgca acagtgacct 60

accgtcatgg tttcagcgat caccgtttac cctgcactgc gtg gct aat atc gcc 115
                                            Val Ala Asn Ile Ala
                                              1   5

agc ttg tac gga ctg tgg gaa ggc agc aca tcc aca cca atc gaa cag 163
Ser Leu Tyr Gly Leu Trp Glu Gly Ser Thr Ser Thr Pro Ile Glu Gln
                10   15   20

```
ctc gta cct gcg aaa ggt tcc agc ttt cgt ttg gtg agg tct ttt tac   211
Leu Val Pro Ala Lys Gly Ser Ser Phe Arg Leu Val Arg Ser Phe Tyr
             25                  30                  35

agg cga att gac ggc caa gca gtt cag gct cgt ctc aag gag aag att   259
Arg Arg Ile Asp Gly Gln Ala Val Gln Ala Arg Leu Lys Glu Lys Ile
         40                  45                  50

ctc aac acc gcg gaa aac ccg ctt cct cgc ttg gac att cca ggt aag   307
Leu Asn Thr Ala Glu Asn Pro Leu Pro Arg Leu Asp Ile Pro Gly Lys
     55                  60                  65

gag cgc act gcg cag tac cca gaa aat ccg gat acc ttc gcc caa aaa   355
Glu Arg Thr Ala Gln Tyr Pro Glu Asn Pro Asp Thr Phe Ala Gln Lys
 70                  75                  80                  85

gca gct caa gaa att ctt gat gag ttc aga act cca ctg atc ggt gaa   403
Ala Ala Gln Glu Ile Leu Asp Glu Phe Arg Thr Pro Leu Ile Gly Glu
                 90                  95                 100

gaa gct gca gct cat gtt gag aaa acg aag acg att ttc tgg aag       448
Glu Ala Ala Ala His Val Glu Lys Thr Lys Thr Ile Phe Trp Lys
            105                 110                 115
```

Sequence Listing

<210> 1386
<211> 116
<212> PRT
<213> Corynebacterium glutamicum

<400> 1386

```
Val Ala Asn Ile Ala Ser Leu Tyr Gly Leu Trp Glu Gly Ser Thr Ser
  1               5                  10                  15

Thr Pro Ile Glu Gln Leu Val Pro Ala Lys Gly Ser Ser Phe Arg Leu
             20                  25                  30

Val Arg Ser Phe Tyr Arg Arg Ile Asp Gly Gln Ala Val Gln Ala Arg
         35                  40                  45

Leu Lys Glu Lys Ile Leu Asn Thr Ala Glu Asn Pro Leu Pro Arg Leu
     50                  55                  60

Asp Ile Pro Gly Lys Glu Arg Thr Ala Gln Tyr Pro Glu Asn Pro Asp
 65                  70                  75                  80

Thr Phe Ala Gln Lys Ala Ala Gln Glu Ile Leu Asp Glu Phe Arg Thr
                 85                  90                  95

Pro Leu Ile Gly Glu Glu Ala Ala Ala His Val Glu Lys Thr Lys Thr
            100                 105                 110

Ile Phe Trp Lys
        115
```

<210> 1387
<211> 360
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(337)
<223> RXN03010

<400> 1387
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cagcctggga ctcaatgcgt ggattacctt cggtgcgcca gtg ccc acc gat aat 115
Val Pro Thr Asp Asn
1 5

ctt ttt ctc atc gtt gct gga att gcg tgg gtg ttg gca gga att ttg 163
Leu Phe Leu Ile Val Ala Gly Ile Ala Trp Val Leu Ala Gly Ile Leu
10 15 20

agc gtg ctg tcc atc ggc aag tac atg tca gca gta aat gag cga aag 211
Ser Val Leu Ser Ile Gly Lys Tyr Met Ser Ala Val Asn Glu Arg Lys
25 30 35

tcg aca ggc ttt tat aca gaa gtg ccg tgg aag aaa gcg ctc ttt act 259
Ser Thr Gly Phe Tyr Thr Glu Val Pro Trp Lys Lys Ala Leu Phe Thr
40 45 50

gcg aca gcc gtc cta ttg gtg ttt gct gtt gtg tgg tcg gcc ttg gat 307
Ala Thr Ala Val Leu Leu Val Phe Ala Val Val Trp Ser Ala Leu Asp
55 60 65

att gcc ctg tgg gta gga aag cag tca tgg tgaacacgtt gaactctaaa 357
Ile Ala Leu Trp Val Gly Lys Gln Ser Trp
70 75

acc 360

<210> 1388
<211> 79
<212> PRT
<213> Corynebacterium glutamicum

<400> 1388
Val Pro Thr Asp Asn Leu Phe Leu Ile Val Ala Gly Ile Ala Trp Val
1 5 10 15

Leu Ala Gly Ile Leu Ser Val Leu Ser Ile Gly Lys Tyr Met Ser Ala
20 25 30

Val Asn Glu Arg Lys Ser Thr Gly Phe Tyr Thr Glu Val Pro Trp Lys
35 40 45

Lys Ala Leu Phe Thr Ala Thr Ala Val Leu Leu Val Phe Ala Val Val
50 55 60

Trp Ser Ala Leu Asp Ile Ala Leu Trp Val Gly Lys Gln Ser Trp
65 70 75

<210> 1389
<211> 324
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(301)
<223> RXN03011

<400> 1389
ccgacgtacc agtttttgtc gttccacccc tggactaaaa ccgagacgag aaccaagaag 60

atgaaaccaa ggggtaaaaa ctggtagtct cttccacgtc atg gca tac gaa act 115
Met Ala Tyr Glu Thr
1 5

gat tcc ctc aac cga cgc acc ctc ggg ccc gcg att gca agc gca gtc 163
Asp Ser Leu Asn Arg Arg Thr Leu Gly Pro Ala Ile Ala Ser Ala Val
10 15 20

gtg gga atc gcc gtc ggc gca gtc gca gta gtt ggg gtt tca atg atc 211
Val Gly Ile Ala Val Gly Ala Val Ala Val Val Gly Val Ser Met Ile
25 30 35

tca ggg cag gac act gtt ccc act ggt aac gcc gta act gca gac gat 259
Ser Gly Gln Asp Thr Val Pro Thr Gly Asn Ala Val Thr Ala Asp Asp
40 45 50

gcc ctg ctc ggt ggc cct gag tat ggt tca cgc gaa gca gac 301
Ala Leu Leu Gly Gly Pro Glu Tyr Gly Ser Arg Glu Ala Asp
55 60 65

taagaagcca cttccccgtt ttc 324

<210> 1390
<211> 67
<212> PRT
<213> Corynebacterium glutamicum

<400> 1390
Met Ala Tyr Glu Thr Asp Ser Leu Asn Arg Arg Thr Leu Gly Pro Ala
1 5 10 15

Ile Ala Ser Ala Val Val Gly Ile Ala Val Gly Ala Val Ala Val Val
20 25 30

Gly Val Ser Met Ile Ser Gly Gln Asp Thr Val Pro Thr Gly Asn Ala
35 40 45

Val Thr Ala Asp Asp Ala Leu Leu Gly Gly Pro Glu Tyr Gly Ser Arg
50 55 60

Glu Ala Asp
65

<210> 1391
<211> 593
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (1)..(570)
<223> RXN03012

<400> 1391

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acc act atc aac atc atc atc acc aat ggc gct gca cca cac cca act   48
Thr Thr Ile Asn Ile Ile Ile Thr Asn Gly Ala Ala Pro His Pro Thr
  1               5                  10                  15

aat ctc aat cgc gca gaa att cat gat cac cta ccc ctc act gcc tct   96
Asn Leu Asn Arg Ala Glu Ile His Asp His Leu Pro Leu Thr Ala Ser
             20                  25                  30

gat tcg gag cta acc cgc ccc tcc cag gaa tca gtt ctc tat gac cat  144
Asp Ser Glu Leu Thr Arg Pro Ser Gln Glu Ser Val Leu Tyr Asp His
         35                  40                  45

gaa tcc gaa act gtc ttg cgc acc atg gtc atc cct gca gac ctg cac  192
Glu Ser Glu Thr Val Leu Arg Thr Met Val Ile Pro Ala Asp Leu His
     50                  55                  60

gtc gct atg aag cat cta gct aaa aaa cac aac ctc acg gtc aca gag  240
Val Ala Met Lys His Leu Ala Lys Lys His Asn Leu Thr Val Thr Glu
 65                  70                  75                  80

atc tcg cgc atc ctt ctg cag cgc tac atc gac cgc aat att aac cat  288
Ile Ser Arg Ile Leu Leu Gln Arg Tyr Ile Asp Arg Asn Ile Asn His
                 85                  90                  95

gta gag caa aac cag gct gaa tcc gac atg gtg gaa gtc ttt gcc agc  336
Val Glu Gln Asn Gln Ala Glu Ser Asp Met Val Glu Val Phe Ala Ser
            100                 105                 110

caa cca acc aat gca acc gca atg atc cct gta cct gga acc agc ttc  384
Gln Pro Thr Asn Ala Thr Ala Met Ile Pro Val Pro Gly Thr Ser Phe
        115                 120                 125

agg caa ata ttt atc aag cac agc act ggt ttc tgg aaa aac att gat  432
Arg Gln Ile Phe Ile Lys His Ser Thr Gly Phe Trp Lys Asn Ile Asp
    130                 135                 140

cat gat ctt gtc gat ctc gac gcc tct aag acc ccg cgt gta cgc gac  480
His Asp Leu Val Asp Leu Asp Ala Ser Lys Thr Pro Arg Val Arg Asp
145                 150                 155                 160

cgc agt gtc tta cca caa cct caa ctc cac aga gcg ttg tta tca gat  528
Arg Ser Val Leu Pro Gln Pro Gln Leu His Arg Ala Leu Leu Ser Asp
                165                 170                 175

gct gat atg gct cgc ctt gca gca caa ctg acc gac aaa cac          570
Ala Asp Met Ala Arg Leu Ala Ala Gln Leu Thr Asp Lys His
            180                 185                 190

taaaacctcc acaacaagga cat                                       593
```

<210> 1392
<211> 190
<212> PRT
<213> Corynebacterium glutamicum

<400> 1392

```
Thr Thr Ile Asn Ile Ile Ile Thr Asn Gly Ala Ala Pro His Pro Thr
  1               5                  10                  15

Asn Leu Asn Arg Ala Glu Ile His Asp His Leu Pro Leu Thr Ala Ser
             20                  25                  30

Asp Ser Glu Leu Thr Arg Pro Ser Gln Glu Ser Val Leu Tyr Asp His
         35                  40                  45

Glu Ser Glu Thr Val Leu Arg Thr Met Val Ile Pro Ala Asp Leu His
     50                  55                  60

Val Ala Met Lys His Leu Ala Lys Lys His Asn Leu Thr Val Thr Glu
 65                  70                  75                  80

Ile Ser Arg Ile Leu Leu Gln Arg Tyr Ile Asp Arg Asn Ile Asn His
                 85                  90                  95

Val Glu Gln Asn Gln Ala Glu Ser Asp Met Val Glu Val Phe Ala Ser
            100                 105                 110

Gln Pro Thr Asn Ala Thr Ala Met Ile Pro Val Pro Gly Thr Ser Phe
        115                 120                 125

Arg Gln Ile Phe Ile Lys His Ser Thr Gly Phe Trp Lys Asn Ile Asp
    130                 135                 140

His Asp Leu Val Asp Leu Asp Ala Ser Lys Thr Pro Arg Val Arg Asp
145                 150                 155                 160

Arg Ser Val Leu Pro Gln Pro Gln Leu His Arg Ala Leu Leu Ser Asp
                165                 170                 175

Ala Asp Met Ala Arg Leu Ala Ala Gln Leu Thr Asp Lys His
            180                 185                 190
```

<210> 1393
<211> 1662
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1639)
<223> RXN03017

<400> 1393

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aactcaatat taaagtcgcg taattagtgt tatattaatt acgcgacttt aatagttttc 60

gaatacgtag attctcgaaa tacagcagaa agcaggggtt atg ctc gat tca ttg   115
                                                Met Leu Asp Ser Leu
                                                  1               5

aaa aat cgc ttc acc aaa gcg aaa ggt tct cat gga gtg ggg gag ggg   163
Lys Asn Arg Phe Thr Lys Ala Lys Gly Ser His Gly Val Gly Glu Gly
                  10                  15                  20

gct gtt tct ggc gat gca gca gta aag cca ctg cgc aaa gaa gaa cga   211
Ala Val Ser Gly Asp Ala Ala Val Lys Pro Leu Arg Lys Glu Glu Arg
             25                  30                  35
```

```
ctc gcc tca gtc att cag gaa acc gaa cca ggt gct gca gtc gag gtc   259
Leu Ala Ser Val Ile Gln Glu Thr Glu Pro Gly Ala Ala Val Glu Val
         40                  45                  50

atg cgt cgc aat gac gca ttc gct ttg cca ggt gag acc ggt tgg gta   307
Met Arg Arg Asn Asp Ala Phe Ala Leu Pro Gly Glu Thr Gly Trp Val
     55                  60                  65

gtc atg ctg ttg cca act cac gat tca caa ttc ggt ggg ctc aac gct   355
Val Met Leu Leu Pro Thr His Asp Ser Gln Phe Gly Gly Leu Asn Ala
 70                  75                  80                  85

aag gaa aag aac cgc gag gat aaa ggc acg atc atc aac ctg gtg gtc   403
Lys Glu Lys Asn Arg Glu Asp Lys Gly Thr Ile Ile Asn Leu Val Val
                 90                  95                 100

aac gat gat att cat tcc gtt gtc act cca gaa ctt ctt gac agc gat   451
Asn Asp Asp Ile His Ser Val Val Thr Pro Glu Leu Leu Asp Ser Asp
            105                 110                 115

gtg ctt ggt gtc att cct gat gca gat tct ttc gat cgc atg gat gag   499
Val Leu Gly Val Ile Pro Asp Ala Asp Ser Phe Asp Arg Met Asp Glu
        120                 125                 130

ttt gat tta ctg cgt aac aaa gca cgc tgg cac tac gga gtg gct gca   547
Phe Asp Leu Leu Arg Asn Lys Ala Arg Trp His Tyr Gly Val Ala Ala
    135                 140                 145

att gaa cct gac acg ggt gag ctg gtg gtg ttt aag gtg ccc gcg aaa   595
Ile Glu Pro Asp Thr Gly Glu Leu Val Val Phe Lys Val Pro Ala Lys
150                 155                 160                 165

aat agc gct tcg gca cgc ggt gac att ttt tcc gag gtc ggc gat gtg   643
Asn Ser Ala Ser Ala Arg Gly Asp Ile Phe Ser Glu Val Gly Asp Val
                170                 175                 180

ctt agc ggt gct gct gac ctc gaa gac gtg gtt gat ttt gag gtc att   691
Leu Ser Gly Ala Ala Asp Leu Glu Asp Val Val Asp Phe Glu Val Ile
            185                 190                 195

gcc acc ttc cta gag gtg ctg aat gag acc tct gag gtg gat att gat   739
Ala Thr Phe Leu Glu Val Leu Asn Glu Thr Ser Glu Val Asp Ile Asp
        200                 205                 210

gac gaa gat ggc gac gtg cct tat ggt ctt gag ggt gtc aat gca gcg   787
Asp Glu Asp Gly Asp Val Pro Tyr Gly Leu Glu Gly Val Asn Ala Ala
    215                 220                 225

gga gtt atc acg gat gac ctc att cgc gag aag ctt gat gtg gat tcc   835
Gly Val Ile Thr Asp Asp Leu Ile Arg Glu Lys Leu Asp Val Asp Ser
230                 235                 240                 245

tat ccg agc agt gca gag atc att gac aat att gtg cat gtg ttc acc   883
Tyr Pro Ser Ser Ala Glu Ile Ile Asp Asn Ile Val His Val Phe Thr
                250                 255                 260

aag ttg cag ggc aag cat cat gtg gca cca cag ccg gtg ctt cac agc   931
Lys Leu Gln Gly Lys His His Val Ala Pro Gln Pro Val Leu His Ser
            265                 270                 275
```

```
gca gac gta gtg gat gtt gat gca cag gag tcc cat gac aca gtg gtt   979
Ala Asp Val Val Asp Val Asp Ala Gln Glu Ser His Asp Thr Val Val
        280                 285                 290

att gag agc cct gat gat gtc gca cta gca gaa cag gtg gat gta ccg   1027
Ile Glu Ser Pro Asp Asp Val Ala Leu Ala Glu Gln Val Asp Val Pro
    295                 300                 305

gat ttc agt gat gga ttt ggt att gac gat gcc gag gtt act gag cca   1075
Asp Phe Ser Asp Gly Phe Gly Ile Asp Asp Ala Glu Val Thr Glu Pro
310                 315                 320                 325

gag gat gag gag gtt gtc gaa gca aca gct gat gca gat cct ttt ggt   1123
Glu Asp Glu Glu Val Val Glu Ala Thr Ala Asp Ala Asp Pro Phe Gly
                330                 335                 340

gat gta gca gaa gac gat cct ttc ggc agt gat gat gaa cca gat ttt   1171
Asp Val Ala Glu Asp Asp Pro Phe Gly Ser Asp Asp Glu Pro Asp Phe
            345                 350                 355

ggt gca tcc gat gtt gtt gct gca ccg gca cct gta gcc ggc atg tcc   1219
Gly Ala Ser Asp Val Val Ala Ala Pro Ala Pro Val Ala Gly Met Ser
        360                 365                 370

gat gag cag atc cag gcg ctg att cgt ggt gtg tct gag tcc gtg caa   1267
Asp Glu Gln Ile Gln Ala Leu Ile Arg Gly Val Ser Glu Ser Val Gln
    375                 380                 385

gca aag act ggt tca gaa ctt aat gct ttg cga gaa gaa ctt gca caa   1315
Ala Lys Thr Gly Ser Glu Leu Asn Ala Leu Arg Glu Glu Leu Ala Gln
390                 395                 400                 405

gca ctg gct tac aat ccg gtt cag gat tca cag gca gca ttg gca cag   1363
Ala Leu Ala Tyr Asn Pro Val Gln Asp Ser Gln Ala Ala Leu Ala Gln
                410                 415                 420

gtg cac gca gct gat gcc cgc agc ttt gat gcc gat caa gtg ggt gat   1411
Val His Ala Ala Asp Ala Arg Ser Phe Asp Ala Asp Gln Val Gly Asp
            425                 430                 435

gct gtc acc aaa cgt tat gtt aat gac gac ttg ggg ctg tat gtc gat   1459
Ala Val Thr Lys Arg Tyr Val Asn Asp Asp Leu Gly Leu Tyr Val Asp
        440                 445                 450

gag gca aac ttc aat aat gct ttg acc agg gca ccg ttc cag gtg gcg   1507
Glu Ala Asn Phe Asn Asn Ala Leu Thr Arg Ala Pro Phe Gln Val Ala
    455                 460                 465

atg ccg caa ttc cag gag act aca ccg tgg tta ggt gat cag ctt cgt   1555
Met Pro Gln Phe Gln Glu Thr Thr Pro Trp Leu Gly Asp Gln Leu Arg
470                 475                 480                 485

aca ttg gtg gct gtg ttt aat ggt cag ctg ctt gat cag cat cag cgt   1603
Thr Leu Val Ala Val Phe Asn Gly Gln Leu Leu Asp Gln His Gln Arg
                490                 495                 500

gac tac cga aga agt gcg cgc gat gta cat tgc gct taatgatcgc       1649
Asp Tyr Arg Arg Ser Ala Arg Asp Val His Cys Ala
            505                 510

tctaatcttg aga                                                  1662
```

<210> 1394
<211> 513
<212> PRT
<213> Corynebacterium glutamicum

<400> 1394

```
Met Leu Asp Ser Leu Lys Asn Arg Phe Thr Lys Ala Lys Gly Ser His
  1               5                  10                  15

Gly Val Gly Glu Gly Ala Val Ser Gly Asp Ala Ala Val Lys Pro Leu
             20                  25                  30

Arg Lys Glu Glu Arg Leu Ala Ser Val Ile Gln Glu Thr Glu Pro Gly
         35                  40                  45

Ala Ala Val Glu Val Met Arg Arg Asn Asp Ala Phe Ala Leu Pro Gly
     50                  55                  60

Glu Thr Gly Trp Val Val Met Leu Leu Pro Thr His Asp Ser Gln Phe
 65                  70                  75                  80

Gly Gly Leu Asn Ala Lys Glu Lys Asn Arg Glu Asp Lys Gly Thr Ile
                 85                  90                  95

Ile Asn Leu Val Val Asn Asp Asp Ile His Ser Val Val Thr Pro Glu
            100                 105                 110

Leu Leu Asp Ser Asp Val Leu Gly Val Ile Pro Asp Ala Asp Ser Phe
        115                 120                 125

Asp Arg Met Asp Glu Phe Asp Leu Leu Arg Asn Lys Ala Arg Trp His
    130                 135                 140

Tyr Gly Val Ala Ala Ile Glu Pro Asp Thr Gly Glu Leu Val Val Phe
145                 150                 155                 160

Lys Val Pro Ala Lys Asn Ser Ala Ser Ala Arg Gly Asp Ile Phe Ser
                165                 170                 175

Glu Val Gly Asp Val Leu Ser Gly Ala Ala Asp Leu Glu Asp Val Val
            180                 185                 190

Asp Phe Glu Val Ile Ala Thr Phe Leu Glu Val Leu Asn Glu Thr Ser
        195                 200                 205

Glu Val Asp Ile Asp Asp Glu Asp Gly Asp Val Pro Tyr Gly Leu Glu
    210                 215                 220

Gly Val Asn Ala Ala Gly Val Ile Thr Asp Asp Leu Ile Arg Glu Lys
225                 230                 235                 240

Leu Asp Val Asp Ser Tyr Pro Ser Ser Ala Glu Ile Ile Asp Asn Ile
                245                 250                 255

Val His Val Phe Thr Lys Leu Gln Gly Lys His His Val Ala Pro Gln
            260                 265                 270

Pro Val Leu His Ser Ala Asp Val Val Asp Val Asp Ala Gln Glu Ser
        275                 280                 285
```

```
His Asp Thr Val Val Ile Glu Ser Pro Asp Asp Val Ala Leu Ala Glu
    290                 295                 300

Gln Val Asp Val Pro Asp Phe Ser Asp Gly Phe Gly Ile Asp Asp Ala
305                 310                 315                 320

Glu Val Thr Glu Pro Glu Asp Glu Glu Val Val Glu Ala Thr Ala Asp
                325                 330                 335

Ala Asp Pro Phe Gly Asp Val Ala Glu Asp Asp Pro Phe Gly Ser Asp
            340                 345                 350

Asp Glu Pro Asp Phe Gly Ala Ser Asp Val Val Ala Ala Pro Ala Pro
        355                 360                 365

Val Ala Gly Met Ser Asp Glu Gln Ile Gln Ala Leu Ile Arg Gly Val
    370                 375                 380

Ser Glu Ser Val Gln Ala Lys Thr Gly Ser Glu Leu Asn Ala Leu Arg
385                 390                 395                 400

Glu Glu Leu Ala Gln Ala Leu Ala Tyr Asn Pro Val Gln Asp Ser Gln
                405                 410                 415

Ala Ala Leu Ala Gln Val His Ala Ala Asp Ala Arg Ser Phe Asp Ala
            420                 425                 430

Asp Gln Val Gly Asp Ala Val Thr Lys Arg Tyr Val Asn Asp Asp Leu
        435                 440                 445

Gly Leu Tyr Val Asp Glu Ala Asn Phe Asn Asn Ala Leu Thr Arg Ala
    450                 455                 460

Pro Phe Gln Val Ala Met Pro Gln Phe Gln Glu Thr Thr Pro Trp Leu
465                 470                 475                 480

Gly Asp Gln Leu Arg Thr Leu Val Ala Val Phe Asn Gly Gln Leu Leu
                485                 490                 495

Asp Gln His Gln Arg Asp Tyr Arg Arg Ser Ala Arg Asp Val His Cys
            500                 505                 510

Ala
```

<210> 1395
<211> 2616
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2593)
<223> FRXA02753

<400> 1395
aactcaatat taaagtcgcg taattagtgt tatattaatt acgcgacttt aatagttttc 60

gaatacgtag attctcgaaa tacagcagaa agcaggggtt atg ctc gat tca ttg 115

```
                                                    Met Leu Asp Ser Leu
                                                      1               5

aaa aat cgc ttc acc aaa gcg aaa ggt tct cat gga gtg ggg gag ggg   163
Lys Asn Arg Phe Thr Lys Ala Lys Gly Ser His Gly Val Gly Glu Gly
                 10                  15                  20

gct gtt tct ggc gat gca gca gta aag cca ctg cgc aaa gaa gaa cga   211
Ala Val Ser Gly Asp Ala Ala Val Lys Pro Leu Arg Lys Glu Glu Arg
             25                  30                  35

ctc gcc tca gtc att cag gaa acc gaa cca ggt gct gca gtc gag gtc   259
Leu Ala Ser Val Ile Gln Glu Thr Glu Pro Gly Ala Ala Val Glu Val
         40                  45                  50

atg cgt cgc aat gac gca ttc gct ttg cca ggt gag acc ggt tgg gta   307
Met Arg Arg Asn Asp Ala Phe Ala Leu Pro Gly Glu Thr Gly Trp Val
     55                  60                  65

gtc atg ctg ttg cca act cac gat tca caa ttc ggt ggg ctc aac gct   355
Val Met Leu Leu Pro Thr His Asp Ser Gln Phe Gly Gly Leu Asn Ala
 70                  75                  80                  85

aag gaa aag aac cgc gag gat aaa ggc acg atc atc aac ctg gtg gtc   403
Lys Glu Lys Asn Arg Glu Asp Lys Gly Thr Ile Ile Asn Leu Val Val
                 90                  95                 100

aac gat gat att cat tcc gtt gtc act cca gaa ctt ctt gac agc gat   451
Asn Asp Asp Ile His Ser Val Val Thr Pro Glu Leu Leu Asp Ser Asp
             105                 110                 115

gtg ctt ggt gtc att cct gat gca gat tct ttc gat cgc atg gat gag   499
Val Leu Gly Val Ile Pro Asp Ala Asp Ser Phe Asp Arg Met Asp Glu
         120                 125                 130

ttt gat tta ctg cgt aac aaa gca cgc tgg cac tac gga gtg gct gca   547
Phe Asp Leu Leu Arg Asn Lys Ala Arg Trp His Tyr Gly Val Ala Ala
     135                 140                 145

att gaa cct gac acg ggt gag ctg gtg gtg ttt aag gtg ccc gcg aaa   595
Ile Glu Pro Asp Thr Gly Glu Leu Val Val Phe Lys Val Pro Ala Lys
150                 155                 160                 165

aat agc gct tcg gca cgc ggt gac att ttt tcc gag gtc ggc gat gtg   643
Asn Ser Ala Ser Ala Arg Gly Asp Ile Phe Ser Glu Val Gly Asp Val
                 170                 175                 180

ctt agc ggt gct gct gac ctc gaa gac gtg gtt gat ttt gag gtc att   691
Leu Ser Gly Ala Ala Asp Leu Glu Asp Val Val Asp Phe Glu Val Ile
             185                 190                 195

gcc acc ttc cta gag gtg ctg aat gag acc tct gag gtg gat att gat   739
Ala Thr Phe Leu Glu Val Leu Asn Glu Thr Ser Glu Val Asp Ile Asp
         200                 205                 210

gac gaa gat ggc gac gtg cct tat ggt ctt gag ggt gtc aat gca gcg   787
Asp Glu Asp Gly Asp Val Pro Tyr Gly Leu Glu Gly Val Asn Ala Ala
     215                 220                 225

gga gtt atc acg gat gac ctc att cgc gag aag ctt gat gtg gat tcc   835
Gly Val Ile Thr Asp Asp Leu Ile Arg Glu Lys Leu Asp Val Asp Ser
```

```
230                 235                 240                 245

tat ccg agc agt gca gag atc att gac aat att gtg cat gtg ttc acc   883
Tyr Pro Ser Ser Ala Glu Ile Ile Asp Asn Ile Val His Val Phe Thr
                250                 255                 260

aag ttg cag ggc aag cat cat gtg gca cca cag ccg gtg ctt cac agc   931
Lys Leu Gln Gly Lys His His Val Ala Pro Gln Pro Val Leu His Ser
            265                 270                 275

gca gac gta gtg gat gtt gat gca cag gag tcc cat gac aca gtg gtt   979
Ala Asp Val Val Asp Val Asp Ala Gln Glu Ser His Asp Thr Val Val
        280                 285                 290

att gag agc cct gat gat gtc gca cta gca gaa cag gtg gat gta ccg   1027
Ile Glu Ser Pro Asp Asp Val Ala Leu Ala Glu Gln Val Asp Val Pro
    295                 300                 305

gat ttc agt gat gga ttt ggt att gac gat gcc gag gtt act gag cca   1075
Asp Phe Ser Asp Gly Phe Gly Ile Asp Asp Ala Glu Val Thr Glu Pro
310                 315                 320                 325

gag gat gag gag gtt gtc gaa gca aca gct gat gca gat cct ttt ggt   1123
Glu Asp Glu Glu Val Val Glu Ala Thr Ala Asp Ala Asp Pro Phe Gly
                330                 335                 340

gat gta gca gaa gac gat cct ttc ggc agt gat gat gaa cca gat ttt   1171
Asp Val Ala Glu Asp Asp Pro Phe Gly Ser Asp Asp Glu Pro Asp Phe
            345                 350                 355

ggt gca tcc gat gtt gtt gct gca ccg gca cct gta gcc ggc atg tcc   1219
Gly Ala Ser Asp Val Val Ala Ala Pro Ala Pro Val Ala Gly Met Ser
        360                 365                 370

gat gag cag atc cag gcg ctg att cgt ggt gtg tct gag tcc gtg caa   1267
Asp Glu Gln Ile Gln Ala Leu Ile Arg Gly Val Ser Glu Ser Val Gln
    375                 380                 385

gca aag act ggt tca gaa ctt aat gct ttg cga gaa gaa ctt gca caa   1315
Ala Lys Thr Gly Ser Glu Leu Asn Ala Leu Arg Glu Glu Leu Ala Gln
390                 395                 400                 405

gca ctg gct tac aat ccg gtt cag gat tca cag gca gca ttg gca cag   1363
Ala Leu Ala Tyr Asn Pro Val Gln Asp Ser Gln Ala Ala Leu Ala Gln
                410                 415                 420

gtg cac gca gct gat gcc cgc agc ttt gat gcc gat caa gtg ggt gat   1411
Val His Ala Ala Asp Ala Arg Ser Phe Asp Ala Asp Gln Val Gly Asp
            425                 430                 435

gct gtc acc aaa cgt tat gtt aat gac gac ttg ggg ctg tat gtc gat   1459
Ala Val Thr Lys Arg Tyr Val Asn Asp Asp Leu Gly Leu Tyr Val Asp
        440                 445                 450

gag gca aac ttc aat aat gct ttg acc agg gca ccg ttc cag gtg gcg   1507
Glu Ala Asn Phe Asn Asn Ala Leu Thr Arg Ala Pro Phe Gln Val Ala
    455                 460                 465

atg ccg caa ttc cag gag act aca ccg tgg tta ggt gat cag ctt cgt   1555
Met Pro Gln Phe Gln Glu Thr Thr Pro Trp Leu Gly Asp Gln Leu Arg
470                 475                 480                 485
```

```
aca ttg gtg gct gtg ttt aat ggt cag ctg ctt gat cag cat cag cgt   1603
Thr Leu Val Ala Val Phe Asn Gly Gln Leu Leu Asp Gln His Gln Arg
                490                 495                 500

gac tac gaa gaa gtg cgc gcg atg tac att gcg ctt aat gat cgc tct   1651
Asp Tyr Glu Glu Val Arg Ala Met Tyr Ile Ala Leu Asn Asp Arg Ser
            505                 510                 515

aat ctt gag atc gct cgt gat ctt gga ctg gat aat aag gat tcc gaa   1699
Asn Leu Glu Ile Ala Arg Asp Leu Gly Leu Asp Asn Lys Asp Ser Glu
        520                 525                 530

ttc tac gag gtt tac cgt gcc att gag cgt gac cgc gat gtt atg gct   1747
Phe Tyr Glu Val Tyr Arg Ala Ile Glu Arg Asp Arg Asp Val Met Ala
    535                 540                 545

ggt gat caa cag cgt gtg gag tca gag cgt cgt cag caa ttg cag cag   1795
Gly Asp Gln Gln Arg Val Glu Ser Glu Arg Arg Gln Gln Leu Gln Gln
550                 555                 560                 565

gag tat gag gcg aac cgt gaa gaa tat gtc atg gca aag atc gcg gag   1843
Glu Tyr Glu Ala Asn Arg Glu Glu Tyr Val Met Ala Lys Ile Ala Glu
                570                 575                 580

cag cgc gtg gag tat gat cgc cgt cat atg cct cgc cat acc gca tca   1891
Gln Arg Val Glu Tyr Asp Arg Arg His Met Pro Arg His Thr Ala Ser
            585                 590                 595

cta gaa gcg gta ggt cga gag ctg acg agc ctg cgg gat cgc acc att   1939
Leu Glu Ala Val Gly Arg Glu Leu Thr Ser Leu Arg Asp Arg Thr Ile
        600                 605                 610

gag gat tac acc gca cgc atg aac acg ctg cgt cgt gca cgt gct ggt   1987
Glu Asp Tyr Thr Ala Arg Met Asn Thr Leu Arg Arg Ala Arg Ala Gly
    615                 620                 625

gaa cgg gct aac gct gca gaa tct cgc att att gac gaa ttg cgc ccg   2035
Glu Arg Ala Asn Ala Ala Glu Ser Arg Ile Ile Asp Glu Leu Arg Pro
630                 635                 640                 645

att gtg gag cgc cag gca gaa ctg caa cga gca gct ttc gat ggt ttc   2083
Ile Val Glu Arg Gln Ala Glu Leu Gln Arg Ala Ala Phe Asp Gly Phe
                650                 655                 660

att gtt gat ctt gac aag ttt att gct gat cac cgc gaa gat gac ctg   2131
Ile Val Asp Leu Asp Lys Phe Ile Ala Asp His Arg Glu Asp Asp Leu
            665                 670                 675

cgt ttg gca tcg gtg aat gag cag aag ctt gct gca gat aat cgt gtg   2179
Arg Leu Ala Ser Val Asn Glu Gln Lys Leu Ala Ala Asp Asn Arg Val
        680                 685                 690

gca cag ttg acc aag gaa gcc gaa gag cgc atc gag ggt atc cgc gtc   2227
Ala Gln Leu Thr Lys Glu Ala Glu Glu Arg Ile Glu Gly Ile Arg Val
    695                 700                 705

gag acc gat aag atg atc gcc tcc cag cgc aag gca ctt gag cgt cag   2275
Glu Thr Asp Lys Met Ile Ala Ser Gln Arg Lys Ala Leu Glu Arg Gln
710                 715                 720                 725
```

```
gaa gcg gaa ttc gca gca gag ctt aag cgt cgc gac act att gtc gct   2323
Glu Ala Glu Phe Ala Ala Glu Leu Lys Arg Arg Asp Thr Ile Val Ala
                730                 735                 740

gca tcg gag gaa cgt gct gag cgg gaa att acc aca gca cgt ctt gat   2371
Ala Ser Glu Glu Arg Ala Glu Arg Glu Ile Thr Thr Ala Arg Leu Asp
            745                 750                 755

gct gag gcg gcg ctc aag cgc atg gaa gag caa att cgt gta aat aat   2419
Ala Glu Ala Ala Leu Lys Arg Met Glu Glu Gln Ile Arg Val Asn Asn
        760                 765                 770

gag gcg cat gag gcg gag att gtt att gag cgc gat cga gcc acc caa   2467
Glu Ala His Glu Ala Glu Ile Val Ile Glu Arg Asp Arg Ala Thr Gln
    775                 780                 785

gca gag gcg aac tcc atg acg ttt gtt gag tca gtc aag cag cag gat   2515
Ala Glu Ala Asn Ser Met Thr Phe Val Glu Ser Val Lys Gln Gln Asp
790                 795                 800                 805

cgc agc aac aac atc att ttg att gcc gtc ctc att gtg ggg ctg att   2563
Arg Ser Asn Asn Ile Ile Leu Ile Ala Val Leu Ile Val Gly Leu Ile
                810                 815                 820

gcc ggc atg gtc gct ggc gca gcc ttc ttc taaaagatcg ttgcgcgggc     2613
Ala Gly Met Val Ala Gly Ala Ala Phe Phe
            825                 830

tgt                                                               2616


<210> 1396
<211> 831
<212> PRT
<213> Corynebacterium glutamicum

<400> 1396
Met Leu Asp Ser Leu Lys Asn Arg Phe Thr Lys Ala Lys Gly Ser His
  1               5                  10                  15

Gly Val Gly Glu Gly Ala Val Ser Gly Asp Ala Ala Val Lys Pro Leu
             20                  25                  30

Arg Lys Glu Glu Arg Leu Ala Ser Val Ile Gln Glu Thr Glu Pro Gly
         35                  40                  45

Ala Ala Val Glu Val Met Arg Arg Asn Asp Ala Phe Ala Leu Pro Gly
     50                  55                  60

Glu Thr Gly Trp Val Val Met Leu Leu Pro Thr His Asp Ser Gln Phe
 65                  70                  75                  80

Gly Gly Leu Asn Ala Lys Glu Lys Asn Arg Glu Asp Lys Gly Thr Ile
                 85                  90                  95

Ile Asn Leu Val Val Asn Asp Asp Ile His Ser Val Val Thr Pro Glu
            100                 105                 110

Leu Leu Asp Ser Asp Val Leu Gly Val Ile Pro Asp Ala Asp Ser Phe
        115                 120                 125
```

```
Asp Arg Met Asp Glu Phe Asp Leu Leu Arg Asn Lys Ala Arg Trp His
    130                 135                 140

Tyr Gly Val Ala Ala Ile Glu Pro Asp Thr Gly Glu Leu Val Val Phe
145                 150                 155                 160

Lys Val Pro Ala Lys Asn Ser Ala Ser Ala Arg Gly Asp Ile Phe Ser
                165                 170                 175

Glu Val Gly Asp Val Leu Ser Gly Ala Ala Asp Leu Glu Asp Val Val
            180                 185                 190

Asp Phe Glu Val Ile Ala Thr Phe Leu Glu Val Leu Asn Glu Thr Ser
        195                 200                 205

Glu Val Asp Ile Asp Asp Glu Asp Gly Asp Val Pro Tyr Gly Leu Glu
    210                 215                 220

Gly Val Asn Ala Ala Gly Val Ile Thr Asp Asp Leu Ile Arg Glu Lys
225                 230                 235                 240

Leu Asp Val Asp Ser Tyr Pro Ser Ser Ala Glu Ile Ile Asp Asn Ile
                245                 250                 255

Val His Val Phe Thr Lys Leu Gln Gly Lys His His Val Ala Pro Gln
            260                 265                 270

Pro Val Leu His Ser Ala Asp Val Val Asp Val Asp Ala Gln Glu Ser
        275                 280                 285

His Asp Thr Val Val Ile Glu Ser Pro Asp Asp Val Ala Leu Ala Glu
    290                 295                 300

Gln Val Asp Val Pro Asp Phe Ser Asp Gly Phe Gly Ile Asp Asp Ala
305                 310                 315                 320

Glu Val Thr Glu Pro Glu Asp Glu Glu Val Val Glu Ala Thr Ala Asp
                325                 330                 335

Ala Asp Pro Phe Gly Asp Val Ala Glu Asp Asp Pro Phe Gly Ser Asp
            340                 345                 350

Asp Glu Pro Asp Phe Gly Ala Ser Asp Val Val Ala Ala Pro Ala Pro
        355                 360                 365

Val Ala Gly Met Ser Asp Glu Gln Ile Gln Ala Leu Ile Arg Gly Val
    370                 375                 380

Ser Glu Ser Val Gln Ala Lys Thr Gly Ser Glu Leu Asn Ala Leu Arg
385                 390                 395                 400

Glu Glu Leu Ala Gln Ala Leu Ala Tyr Asn Pro Val Gln Asp Ser Gln
                405                 410                 415

Ala Ala Leu Ala Gln Val His Ala Ala Asp Ala Arg Ser Phe Asp Ala
            420                 425                 430

Asp Gln Val Gly Asp Ala Val Thr Lys Arg Tyr Val Asn Asp Asp Leu
        435                 440                 445

Gly Leu Tyr Val Asp Glu Ala Asn Phe Asn Asn Ala Leu Thr Arg Ala
```

```
    450                 455                 460

Pro Phe Gln Val Ala Met Pro Gln Phe Gln Glu Thr Thr Pro Trp Leu
465                 470                 475                 480

Gly Asp Gln Leu Arg Thr Leu Val Ala Val Phe Asn Gly Gln Leu Leu
                485                 490                 495

Asp Gln His Gln Arg Asp Tyr Glu Glu Val Arg Ala Met Tyr Ile Ala
            500                 505                 510

Leu Asn Asp Arg Ser Asn Leu Glu Ile Ala Arg Asp Leu Gly Leu Asp
        515                 520                 525

Asn Lys Asp Ser Glu Phe Tyr Glu Val Tyr Arg Ala Ile Glu Arg Asp
    530                 535                 540

Arg Asp Val Met Ala Gly Asp Gln Gln Arg Val Glu Ser Glu Arg Arg
545                 550                 555                 560

Gln Gln Leu Gln Gln Glu Tyr Glu Ala Asn Arg Glu Glu Tyr Val Met
                565                 570                 575

Ala Lys Ile Ala Glu Gln Arg Val Glu Tyr Asp Arg Arg His Met Pro
            580                 585                 590

Arg His Thr Ala Ser Leu Glu Ala Val Gly Arg Glu Leu Thr Ser Leu
        595                 600                 605

Arg Asp Arg Thr Ile Glu Asp Tyr Thr Ala Arg Met Asn Thr Leu Arg
    610                 615                 620

Arg Ala Arg Ala Gly Glu Arg Ala Asn Ala Ala Glu Ser Arg Ile Ile
625                 630                 635                 640

Asp Glu Leu Arg Pro Ile Val Glu Arg Gln Ala Glu Leu Gln Arg Ala
                645                 650                 655

Ala Phe Asp Gly Phe Ile Val Asp Leu Asp Lys Phe Ile Ala Asp His
            660                 665                 670

Arg Glu Asp Asp Leu Arg Leu Ala Ser Val Asn Glu Gln Lys Leu Ala
        675                 680                 685

Ala Asp Asn Arg Val Ala Gln Leu Thr Lys Glu Ala Glu Glu Arg Ile
    690                 695                 700

Glu Gly Ile Arg Val Glu Thr Asp Lys Met Ile Ala Ser Gln Arg Lys
705                 710                 715                 720

Ala Leu Glu Arg Gln Glu Ala Glu Phe Ala Ala Glu Leu Lys Arg Arg
                725                 730                 735

Asp Thr Ile Val Ala Ala Ser Glu Glu Arg Ala Glu Arg Glu Ile Thr
            740                 745                 750

Thr Ala Arg Leu Asp Ala Glu Ala Ala Leu Lys Arg Met Glu Glu Gln
        755                 760                 765

Ile Arg Val Asn Asn Glu Ala His Glu Ala Glu Ile Val Ile Glu Arg
    770                 775                 780
```

```
Asp Arg Ala Thr Gln Ala Glu Ala Asn Ser Met Thr Phe Val Glu Ser
785                 790                 795                 800

Val Lys Gln Gln Asp Arg Ser Asn Asn Ile Ile Leu Ile Ala Val Leu
                805                 810                 815

Ile Val Gly Leu Ile Ala Gly Met Val Ala Gly Ala Ala Phe Phe
            820                 825                 830


<210> 1397
<211> 1116
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1093)
<223> RXN03018

<400> 1397
gtggcgatgc cgcaattcca ggagactaca ccgtggttag gtgatcagct tcgtacattg 60

gtggctgtgt ttaatggtca gctgcttgat cagcatcagc gtg act acc gaa gaa   115
                                        Val Thr Thr Glu Glu
                                          1               5

gtg cgc gcg atg tac att gcg ctt aat gat cgc tct aat ctt gag atc   163
Val Arg Ala Met Tyr Ile Ala Leu Asn Asp Arg Ser Asn Leu Glu Ile
                  10                  15                  20

gct cgt gat ctt gga ctg gat aat aag gat tcc gaa ttc tac gag gtt   211
Ala Arg Asp Leu Gly Leu Asp Asn Lys Asp Ser Glu Phe Tyr Glu Val
              25                  30                  35

tac cgt gcc att gag cgt gac cgc gat gtt atg gct ggt gat caa cag   259
Tyr Arg Ala Ile Glu Arg Asp Arg Asp Val Met Ala Gly Asp Gln Gln
          40                  45                  50

cgt gtg gag tca gag cgt cgt cag caa ttg cag cag gag tat gag gcg   307
Arg Val Glu Ser Glu Arg Arg Gln Gln Leu Gln Gln Glu Tyr Glu Ala
      55                  60                  65

aac cgt gaa gaa tat gtc atg gca aag atc gcg gag cag cgc gtg gag   355
Asn Arg Glu Glu Tyr Val Met Ala Lys Ile Ala Glu Gln Arg Val Glu
  70                  75                  80                  85

tat gat cgc cgt cat atg cct cgc cat acc gca tca cta gaa gcg gta   403
Tyr Asp Arg Arg His Met Pro Arg His Thr Ala Ser Leu Glu Ala Val
                  90                  95                 100

ggt cga gag ctg acg agc ctg cgg gat cgc acc att gag gat tac acc   451
Gly Arg Glu Leu Thr Ser Leu Arg Asp Arg Thr Ile Glu Asp Tyr Thr
            105                 110                 115

gca cgc atg aac acg ctg cgt cgt gca cgt gct ggt gaa cgg gct aac   499
Ala Arg Met Asn Thr Leu Arg Arg Ala Arg Ala Gly Glu Arg Ala Asn
        120                 125                 130

gct gca gaa tct cgc att att gac gaa ttg cgc ccg att gtg gag cgc   547
```

```
Ala Ala Glu Ser Arg Ile Ile Asp Glu Leu Arg Pro Ile Val Glu Arg
    135                 140                 145

cag gca gaa ctg caa cga gca gct ttc gat ggt ttc att gtt gat ctt   595
Gln Ala Glu Leu Gln Arg Ala Ala Phe Asp Gly Phe Ile Val Asp Leu
150                 155                 160                 165

gac aag ttt att gct gat cac cgc gaa gat gac ctg cgt ttg gca tcg   643
Asp Lys Phe Ile Ala Asp His Arg Glu Asp Asp Leu Arg Leu Ala Ser
                170                 175                 180

gtg aat gag cag aag ctt gct gca gat aat cgt gtg gca cag ttg acc   691
Val Asn Glu Gln Lys Leu Ala Ala Asp Asn Arg Val Ala Gln Leu Thr
            185                 190                 195

aag gaa gcc gaa gag cgc atc gag ggt atc cgc gtc gag acc gat aag   739
Lys Glu Ala Glu Glu Arg Ile Glu Gly Ile Arg Val Glu Thr Asp Lys
        200                 205                 210

atg atc gcc tcc cag cgc aag gca ctt gag cgt cag gaa gcg gaa ttc   787
Met Ile Ala Ser Gln Arg Lys Ala Leu Glu Arg Gln Glu Ala Glu Phe
    215                 220                 225

gca gca gag ctt aag cgt cgc gac act att gtc gct gca tcg gag gaa   835
Ala Ala Glu Leu Lys Arg Arg Asp Thr Ile Val Ala Ala Ser Glu Glu
230                 235                 240                 245

cgt gct gag cgg gaa att acc aca gca cgt ctt gat gct gag gcg gcg   883
Arg Ala Glu Arg Glu Ile Thr Thr Ala Arg Leu Asp Ala Glu Ala Ala
                250                 255                 260

ctc aag cgc atg gaa gag caa att cgt gta aat aat gag gcg cat gag   931
Leu Lys Arg Met Glu Glu Gln Ile Arg Val Asn Asn Glu Ala His Glu
            265                 270                 275

gcg gag att gtt att gag cgc gat cga gcc acc caa gca gag gcg aac   979
Ala Glu Ile Val Ile Glu Arg Asp Arg Ala Thr Gln Ala Glu Ala Asn
        280                 285                 290

tcc atg acg ttt gtt gag tca gtc aag cag cag gat cgc agc aac aac   1027
Ser Met Thr Phe Val Glu Ser Val Lys Gln Gln Asp Arg Ser Asn Asn
    295                 300                 305

atc att ttg att gcc gtc ctc att gtg ggg ctg att gcc ggc atg gtc   1075
Ile Ile Leu Ile Ala Val Leu Ile Val Gly Leu Ile Ala Gly Met Val
310                 315                 320                 325

gct ggc gca gcc ttc ttc taaaagatcg ttgcgcgggc tgt                 1116
Ala Gly Ala Ala Phe Phe
                330
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<210> 1398
<211> 331
<212> PRT
<213> Corynebacterium glutamicum

<400> 1398

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Val Thr Thr Glu Glu Val Arg Ala Met Tyr Ile Ala Leu Asn Asp Arg
  1               5                  10                  15
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Ser Asn Leu Glu Ile Ala Arg Asp Leu Gly Leu Asp Asn Lys Asp Ser
            20                  25                  30

Glu Phe Tyr Glu Val Tyr Arg Ala Ile Glu Arg Asp Arg Asp Val Met
        35                  40                  45

Ala Gly Asp Gln Gln Arg Val Glu Ser Glu Arg Arg Gln Gln Leu Gln
    50                  55                  60

Gln Glu Tyr Glu Ala Asn Arg Glu Glu Tyr Val Met Ala Lys Ile Ala
65                  70                  75                  80

Glu Gln Arg Val Glu Tyr Asp Arg Arg His Met Pro Arg His Thr Ala
                85                  90                  95

Ser Leu Glu Ala Val Gly Arg Glu Leu Thr Ser Leu Arg Asp Arg Thr
            100                 105                 110

Ile Glu Asp Tyr Thr Ala Arg Met Asn Thr Leu Arg Arg Ala Arg Ala
        115                 120                 125

Gly Glu Arg Ala Asn Ala Ala Glu Ser Arg Ile Ile Asp Glu Leu Arg
    130                 135                 140

Pro Ile Val Glu Arg Gln Ala Glu Leu Gln Arg Ala Ala Phe Asp Gly
145                 150                 155                 160

Phe Ile Val Asp Leu Asp Lys Phe Ile Ala Asp His Arg Glu Asp Asp
                165                 170                 175

Leu Arg Leu Ala Ser Val Asn Glu Gln Lys Leu Ala Ala Asp Asn Arg
            180                 185                 190

Val Ala Gln Leu Thr Lys Glu Ala Glu Glu Arg Ile Glu Gly Ile Arg
        195                 200                 205

Val Glu Thr Asp Lys Met Ile Ala Ser Gln Arg Lys Ala Leu Glu Arg
    210                 215                 220

Gln Glu Ala Glu Phe Ala Ala Glu Leu Lys Arg Arg Asp Thr Ile Val
225                 230                 235                 240

Ala Ala Ser Glu Glu Arg Ala Glu Arg Glu Ile Thr Thr Ala Arg Leu
                245                 250                 255

Asp Ala Glu Ala Ala Leu Lys Arg Met Glu Glu Gln Ile Arg Val Asn
            260                 265                 270

Asn Glu Ala His Glu Ala Glu Ile Val Ile Glu Arg Asp Arg Ala Thr
        275                 280                 285

Gln Ala Glu Ala Asn Ser Met Thr Phe Val Glu Ser Val Lys Gln Gln
    290                 295                 300

Asp Arg Ser Asn Asn Ile Ile Leu Ile Ala Val Leu Ile Val Gly Leu
305                 310                 315                 320

Ile Ala Gly Met Val Ala Gly Ala Ala Phe Phe
                325                 330
```

<210> 1399
<211> 1539
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1516)
<223> RXN03024

<400> 1399
ctctacccac ttaaaatgga cgcatattcg caagataagg catgcttgga tgaatagatt 60

ttaactcaac gtttactaaa cagaatcgga attaggagcc atg ctt gaa cgc aca 115
Met Leu Glu Arg Thr
1 5

cag gta ttc gtg gat acg tcc tac ctg ctc gca agc ttt tac aac tct 163
Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala Ser Phe Tyr Asn Ser
10 15 20

tgg gag aca ggg gca cgt gcc caa tta gaa atc gac ctc ccc gaa gta 211
Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile Asp Leu Pro Glu Val
25 30 35

gtc ggg gta tta gga agg atg att gaa caa caa ctt aaa cag cca gta 259
Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln Leu Lys Gln Pro Val
40 45 50

caa cgc caa atg tgg tac gac gga atc ccc gat tcc ggc ccc cac cgc 307
Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp Ser Gly Pro His Arg
55 60 65

tat caa cga gca cta cgc acc tgc gat ggt gtg caa ctt cgt gct ggc 355
Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val Gln Leu Arg Ala Gly
70 75 80 85

caa tta att gaa tgg ggc gaa cgc cgc aca caa aag gca gta gat acc 403
Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln Lys Ala Val Asp Thr
90 95 100

cgc ctt gtt gca gac ctc gtt ctc gca ggt gtt cgc gga caa tgc tcc 451
Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val Arg Gly Gln Cys Ser
105 110 115

gat atc gtg ctc gtc agt ggc gac gcc gac atg atc ccc ggt gtt caa 499
Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met Ile Pro Gly Val Gln
120 125 130

gaa gct gcc aat gca ggc ctt cgc gtt cac ctc tac ggc ttc ggc tgg 547
Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu Tyr Gly Phe Gly Trp
135 140 145

gat tcc atg tcc tcc caa ctg cgc cac tgc tgt gac acc acc acc att 595
Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys Asp Thr Thr Thr Ile
150 155 160 165

ttg gat cct cga gaa gat ttt gct gaa tgc atg cag ctg cag gtt ctc 643
Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met Gln Leu Gln Val Leu
170 175 180

```
gaa ggt cca cta ccc cct gtc gtt cgg gta aag ccc atc aac gat gca   691
Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys Pro Ile Asn Asp Ala
            185                 190                 195

gaa ccc atc gag gat ttg gat ttc act cca gtt cca ggc gtc gcc tca   739
Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val Pro Gly Val Ala Ser
        200                 205                 210

cca ttt gaa gag gtc agc gcg aaa gat gag aaa ttc tct cca cgc cca   787
Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys Phe Ser Pro Arg Pro
    215                 220                 225

agt gaa cct gcc gaa gct ttg tcg gaa cag gtc tgt gaa gcg cag tat   835
Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val Cys Glu Ala Gln Tyr
230                 235                 240                 245

gag atc tcc aaa cac gaa ggt caa acc gct gat tca gga gaa atc acc   883
Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp Ser Gly Glu Ile Thr
                250                 255                 260

gag tct ttc gag gcc gct gaa atc aag gta act gag ttt ttt gga gaa   931
Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr Glu Phe Phe Gly Glu
            265                 270                 275

cca gct gct cca gta gcg gaa tca ggc gta gaa gct ccc act ccg gaa   979
Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu Ala Pro Thr Pro Glu
        280                 285                 290

gct ccc acg gtt cct gaa gca gct aag ccc act ccg gcg aaa cct aag   1027
Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr Pro Ala Lys Pro Lys
    295                 300                 305

act cca aag gca gag ccc caa aag caa gaa tcc ccc aag ccg gga act   1075
Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser Pro Lys Pro Gly Thr
310                 315                 320                 325

cca aaa cca aaa gct cca agc cct gcg gat att cca ccg aaa gcc cca   1123
Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile Pro Pro Lys Ala Pro
                330                 335                 340

gct gac act gag gaa cat tcg gaa gtc gaa gct gaa atc gag gac tca   1171
Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala Glu Ile Glu Asp Ser
            345                 350                 355

cgt cca aag atc ccc agc cct tcg atg atg gct ccc cgc cgc aag ctt   1219
Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala Pro Arg Arg Lys Leu
        360                 365                 370

cgt tcc cgc tac gtt ccg ctt ccc aac gaa gtg tgg gca aca gca gga   1267
Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val Trp Ala Thr Ala Gly
    375                 380                 385

ttc caa act cct tac gat gtc ggg caa cag tac gca tcg tgg tgg ttt   1315
Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr Ala Ser Trp Trp Phe
390                 395                 400                 405

gaa aac gca gct acc agc act caa aga gat cag gct cat cta ttg tct   1363
Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln Ala His Leu Leu Ser
                410                 415                 420

ggt ggc gga ctt cca cca gag atc gat cgc ccg ctt ctg cag ttt gct   1411
```

```
Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro Leu Leu Gln Phe Ala
            425                 430                 435

tgt gaa act ctc cac gaa tac acc ctg act gaa gcg cag cgc gta gct   1459
Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu Ala Gln Arg Val Ala
        440                 445                 450

tta cgc gat ggc ttt cac tcc gga atc cgt ggt gta ttg ctc aac cag   1507
Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly Val Leu Leu Asn Gln
    455                 460                 465

cga gat agc tagaatcaca aaaaactggg gct                             1539
Arg Asp Ser
470
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<210> 1400
<211> 472
<212> PRT
<213> Corynebacterium glutamicum

<400> 1400

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Met Leu Glu Arg Thr Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala
  1               5                  10                  15

Ser Phe Tyr Asn Ser Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile
            20                  25                  30

Asp Leu Pro Glu Val Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln
        35                  40                  45

Leu Lys Gln Pro Val Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp
    50                  55                  60

Ser Gly Pro His Arg Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val
65                  70                  75                  80

Gln Leu Arg Ala Gly Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln
                85                  90                  95

Lys Ala Val Asp Thr Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val
            100                 105                 110

Arg Gly Gln Cys Ser Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met
        115                 120                 125

Ile Pro Gly Val Gln Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu
    130                 135                 140

Tyr Gly Phe Gly Trp Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys
145                 150                 155                 160

Asp Thr Thr Thr Ile Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met
                165                 170                 175

Gln Leu Gln Val Leu Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys
            180                 185                 190

Pro Ile Asn Asp Ala Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val
        195                 200                 205
```

```
Pro Gly Val Ala Ser Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys
    210                 215                 220

Phe Ser Pro Arg Pro Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val
225                 230                 235                 240

Cys Glu Ala Gln Tyr Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp
                245                 250                 255

Ser Gly Glu Ile Thr Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr
            260                 265                 270

Glu Phe Phe Gly Glu Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu
        275                 280                 285

Ala Pro Thr Pro Glu Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr
    290                 295                 300

Pro Ala Lys Pro Lys Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser
305                 310                 315                 320

Pro Lys Pro Gly Thr Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile
                325                 330                 335

Pro Pro Lys Ala Pro Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala
            340                 345                 350

Glu Ile Glu Asp Ser Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala
        355                 360                 365

Pro Arg Arg Lys Leu Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val
    370                 375                 380

Trp Ala Thr Ala Gly Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr
385                 390                 395                 400

Ala Ser Trp Trp Phe Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln
                405                 410                 415

Ala His Leu Leu Ser Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro
            420                 425                 430

Leu Leu Gln Phe Ala Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu
        435                 440                 445

Ala Gln Arg Val Ala Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly
    450                 455                 460

Val Leu Leu Asn Gln Arg Asp Ser
465                 470
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<210> 1401
<211> 996
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(973)
<223> RXN03025

<400> 1401
agcgaatcgg attcagtgat ttgcttgcgg gcgcagaaat gatttttcaa ttagacacac 60

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ttagacacac gtaactaaaa cctcagggaa gtgactgata atg gct aat ccg ctc   115
                                              Met Ala Asn Pro Leu
                                                1               5

agc aag ggc tgg aag tat ctc atg gca tcg ttc gac aac aag atc gat   163
Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe Asp Asn Lys Ile Asp
                10                  15                  20

gag aat gca gat cca aag atc caa att cag caa gct aca gaa gct gcc   211
Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln Ala Thr Glu Ala Ala
            25                  30                  35

cag aag cag cac cag cag att atg cag cac gct tct cag att atc ggt   259
Gln Lys Gln His Gln Gln Ile Met Gln His Ala Ser Gln Ile Ile Gly
        40                  45                  50

cag cag aag cag ctt gag atg aaa ttg aac cgc ttg gtt act gac cgc   307
Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg Leu Val Thr Asp Arg
    55                  60                  65

gat aag ttg cag gaa cag gct cgt cag gca att cag ttg gca gat aag   355
Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile Gln Leu Ala Asp Lys
70                  75                  80                  85

tcc gca aac gaa ggc gac agt gtt aag gct cag gag ttc aac aac act   403
Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln Glu Phe Asn Asn Thr
                90                  95                  100

gct gag gtt ttt gct tcc cag ttg gta gct gtg gaa cag cag ttg gag   451
Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val Glu Gln Gln Leu Glu
            105                 110                 115

cag act act gcg ctt cat cag cag gct gag gtt gcg gcg aag gat gct   499
Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val Ala Ala Lys Asp Ala
        120                 125                 130

gtt gcg aag tct aaa gag tct gag atg cgc ctg aaa gag cag atg tct   547
Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu Lys Glu Gln Met Ser
    135                 140                 145

cag att gat gct cta cgt gcg cag gct gat cag gcg aag atg cag gaa   595
Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln Ala Lys Met Gln Glu
150                 155                 160                 165

agt gtc act aag tct atg gat tct ttg aat cag ttt ggc act cag gat   643
Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln Phe Gly Thr Gln Asp
                170                 175                 180

tct tct gtt cct acc ctt gat gcg gtg cgt gag aag atc gag cgt cga   691
Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu Lys Ile Glu Arg Arg
            185                 190                 195

tac gca gat gct ttg ggc gcg cag gaa ctt acc cag aac act gtt agt   739
Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr Gln Asn Thr Val Ser
        200                 205                 210

gat cgc atg gct gag att gcg cag tcc ggc acc gat atg cgg gcg tca   787
```

```
Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr Asp Met Arg Ala Ser
    215                 220                 225

gct cgt ttg gct gaa ctt cgc gcg gag gcg ctg ggc acg tcc gca acg   835
Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu Gly Thr Ser Ala Thr
230                 235                 240                 245

cct aag ggc cag cta gag gca ggt gtc gag gat gcg gaa gaa ctt atc   883
Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp Ala Glu Glu Leu Ile
                250                 255                 260

gac gaa acc tcc acc cct tca gct acc cca gaa acc gca agc cca gaa   931
Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu Thr Ala Ser Pro Glu
            265                 270                 275

gct gat gct cca gaa gca tcc gca gac gag tcc gag aag aaa           973
Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser Glu Lys Lys
        280                 285                 290

taacctaaac acaaaaaact ggg                                        996
```

US-09-893-543-1402

<210> 1402
<211> 291
<212> PRT
<213> Corynebacterium glutamicum

<400> 1402

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Met Ala Asn Pro Leu Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe
  1               5                  10                  15

Asp Asn Lys Ile Asp Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln
             20                  25                  30

Ala Thr Glu Ala Ala Gln Lys Gln His Gln Gln Ile Met Gln His Ala
         35                  40                  45

Ser Gln Ile Ile Gly Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg
     50                  55                  60

Leu Val Thr Asp Arg Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile
 65                  70                  75                  80

Gln Leu Ala Asp Lys Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln
                 85                  90                  95

Glu Phe Asn Asn Thr Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val
            100                 105                 110

Glu Gln Gln Leu Glu Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val
        115                 120                 125

Ala Ala Lys Asp Ala Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu
    130                 135                 140

Lys Glu Gln Met Ser Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln
145                 150                 155                 160

Ala Lys Met Gln Glu Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln
                165                 170                 175
```

```
Phe Gly Thr Gln Asp Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu
            180                 185                 190

Lys Ile Glu Arg Arg Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr
        195                 200                 205

Gln Asn Thr Val Ser Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr
    210                 215                 220

Asp Met Arg Ala Ser Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu
225                 230                 235                 240

Gly Thr Ser Ala Thr Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp
                245                 250                 255

Ala Glu Glu Leu Ile Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu
            260                 265                 270

Thr Ala Ser Pro Glu Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser
        275                 280                 285

Glu Lys Lys
    290
```

09360760.090705

<210> 1403
<211> 174
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (17)..(151)
<223> RXN03027

<400> 1403

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aataggagaa tttaaaatg gaa aac gtt tac gag ttc ctt gga aac ctt gat  52
                  Met Glu Asn Val Tyr Glu Phe Leu Gly Asn Leu Asp
                    1               5                  10

gtc ctt tcc ggc tcc ggc ctc atc ggc tac gtc ttc gac ttc ctc ggc  100
Val Leu Ser Gly Ser Gly Leu Ile Gly Tyr Val Phe Asp Phe Leu Gly
         15                  20                  25

gct tcc agc aag tgg gct ggc gca gtt gct gac ctc atc ggt ctg ctt  148
Ala Ser Ser Lys Trp Ala Gly Ala Val Ala Asp Leu Ile Gly Leu Leu
     30                  35                  40

ggc taattaactt cgcccacggg caa                                   174
Gly
 45
```

<210> 1404
<211> 45
<212> PRT
<213> Corynebacterium glutamicum

<400> 1404

```
Met Glu Asn Val Tyr Glu Phe Leu Gly Asn Leu Asp Val Leu Ser Gly
  1               5                  10                  15
```

```
Ser Gly Leu Ile Gly Tyr Val Phe Asp Phe Leu Gly Ala Ser Ser Lys
             20                  25                  30

Trp Ala Gly Ala Val Ala Asp Leu Ile Gly Leu Leu Gly
         35                  40                  45


<210> 1405
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (95)..(607)
<223> RXN03029

<400> 1405
ggtgtggctt cctattcgct gcatcctgaa tatgccatca aaatcttcac tctgaggccg 60

aaaaatccgg ttatgacatt aagtacctag gacaatg ttt gga gtg ggc tat tat  115
                                    Met Phe Gly Val Gly Tyr Tyr
                                      1               5

aca acc gcc cac cga ttg tcc acc ctg cag cgc ccc aac ttg cgc ggc   163
Thr Thr Ala His Arg Leu Ser Thr Leu Gln Arg Pro Asn Leu Arg Gly
         10                  15                  20

atc ccc tta acc ttc gtg agc gtc gac cga gcc ggc aac atg tcc aaa   211
Ile Pro Leu Thr Phe Val Ser Val Asp Arg Ala Gly Asn Met Ser Lys
     25                  30                  35

cgc caa tcc gcc acg ggc ttc cac ttc acc cat tac ggc ggc acc tgc   259
Arg Gln Ser Ala Thr Gly Phe His Phe Thr His Tyr Gly Gly Thr Cys
 40                  45                  50                  55

ccc ctg tgg aac gtg ttt gaa acc ttc acc aac ccc ggc caa gtg ctc   307
Pro Leu Trp Asn Val Phe Glu Thr Phe Thr Asn Pro Gly Gln Val Leu
                 60                  65                  70

cgc caa ttc gcg caa atg ccc gac gga cgc aac tac ctg tgg atc tca   355
Arg Gln Phe Ala Gln Met Pro Asp Gly Arg Asn Tyr Leu Trp Ile Ser
             75                  80                  85

cgc acc gtg cga cac cac gaa gcc cgg ttc ggc gaa gta gac aaa atg   403
Arg Thr Val Arg His His Glu Ala Arg Phe Gly Glu Val Asp Lys Met
         90                  95                  100

ttc gcc atc ggc ttg ggc tgc gaa gcg cgc cac gcc gac cgc act gtg   451
Phe Ala Ile Gly Leu Gly Cys Glu Ala Arg His Ala Asp Arg Thr Val
    105                 110                 115

tac tcc cgc ggt ttc aac ctc cag gac ctc tcc acc gcc acc ccc atc   499
Tyr Ser Arg Gly Phe Asn Leu Gln Asp Leu Ser Thr Ala Thr Pro Ile
120                 125                 130                 135

ggg tcc ggc tgc cga gtg tgc acc cgc gag aac tgc gcg cag cgc gca   547
Gly Ser Gly Cys Arg Val Cys Thr Arg Glu Asn Cys Ala Gln Arg Ala
                140                 145                 150
```

```
ttc cca tcc gtc cac ggc cgc atc aac atc gac gcg cac gaa tcc act   595
Phe Pro Ser Val His Gly Arg Ile Asn Ile Asp Ala His Glu Ser Thr
            155                 160                 165

atc gcg ccg tac taagaaaagg agcttgcttt acg                        630
Ile Ala Pro Tyr
        170


<210> 1406
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 1406
Met Phe Gly Val Gly Tyr Tyr Thr Thr Ala His Arg Leu Ser Thr Leu
  1               5                  10                  15

Gln Arg Pro Asn Leu Arg Gly Ile Pro Leu Thr Phe Val Ser Val Asp
             20                  25                  30

Arg Ala Gly Asn Met Ser Lys Arg Gln Ser Ala Thr Gly Phe His Phe
         35                  40                  45

Thr His Tyr Gly Gly Thr Cys Pro Leu Trp Asn Val Phe Glu Thr Phe
     50                  55                  60

Thr Asn Pro Gly Gln Val Leu Arg Gln Phe Ala Gln Met Pro Asp Gly
 65                  70                  75                  80

Arg Asn Tyr Leu Trp Ile Ser Arg Thr Val Arg His His Glu Ala Arg
                 85                  90                  95

Phe Gly Glu Val Asp Lys Met Phe Ala Ile Gly Leu Gly Cys Glu Ala
            100                 105                 110

Arg His Ala Asp Arg Thr Val Tyr Ser Arg Gly Phe Asn Leu Gln Asp
        115                 120                 125

Leu Ser Thr Ala Thr Pro Ile Gly Ser Gly Cys Arg Val Cys Thr Arg
    130                 135                 140

Glu Asn Cys Ala Gln Arg Ala Phe Pro Ser Val His Gly Arg Ile Asn
145                 150                 155                 160

Ile Asp Ala His Glu Ser Thr Ile Ala Pro Tyr
                165                 170


<210> 1407
<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(789)
<223> RXN03031

<400> 1407
aac aac ggc ctt aac gcc atg gcc gcg atg acc aac ctc cca cac ctg   48
```

```
Asn Asn Gly Leu Asn Ala Met Ala Ala Met Thr Asn Leu Pro His Leu
  1               5                  10                  15

cgc gcc atc caa gaa cgc tac tac ttc ctg agc atc cgc tac ctc gcc   96
Arg Ala Ile Gln Glu Arg Tyr Tyr Phe Leu Ser Ile Arg Tyr Leu Ala
            20                  25                  30

tcc atc atg atc gcc gtg gcc aaa gca gac ccc acc ctg tgg gaa gaa   144
Ser Ile Met Ile Ala Val Ala Lys Ala Asp Pro Thr Leu Trp Glu Glu
        35                  40                  45

ctc gac ctg cgc atc acc gac gcc tta aca cca gtc acc gca ggg gaa   192
Leu Asp Leu Arg Ile Thr Asp Ala Leu Thr Pro Val Thr Ala Gly Glu
    50                  55                  60

gtg atg atc caa tcc tcc acc ctg tcc aaa cgc atc gcc gcc tgg atc   240
Val Met Ile Gln Ser Ser Thr Leu Ser Lys Arg Ile Ala Ala Trp Ile
65                  70                  75                  80

aaa gaa ctc gac ccc gaa ccc aca cca gag ccc ata ccg aaa gag gac   288
Lys Glu Leu Asp Pro Glu Pro Thr Pro Glu Pro Ile Pro Lys Glu Asp
                85                  90                  95

tat gtt cac gtc cac acc act gat gag gcg acc tat gtc cgc atc aaa   336
Tyr Val His Val His Thr Thr Asp Glu Ala Thr Tyr Val Arg Ile Lys
            100                 105                 110

atc agc ggc ccc aac cgc ctg atc ctc aat gac atc atc acc caa ctc   384
Ile Ser Gly Pro Asn Arg Leu Ile Leu Asn Asp Ile Ile Thr Gln Leu
        115                 120                 125

aaa gac aca gac acc gag gac agc ctg cct gaa gcg ctc atg gcg ttc   432
Lys Asp Thr Asp Thr Glu Asp Ser Leu Pro Glu Ala Leu Met Ala Phe
    130                 135                 140

ctg atg gag aaa atc cag tta aag atc acc aag tac ctt ttc acc cca   480
Leu Met Glu Lys Ile Gln Leu Lys Ile Thr Lys Tyr Leu Phe Thr Pro
145                 150                 155                 160

cat aag cac cct gag cag gtg tgg tca ccg gac tac ggt gac att ggt   528
His Lys His Pro Glu Gln Val Trp Ser Pro Asp Tyr Gly Asp Ile Gly
                165                 170                 175

ccc gaa gcc tat gcc aat gcc acc ctc gtg tgc gcc aag gac tta gat   576
Pro Glu Ala Tyr Ala Asn Ala Thr Leu Val Cys Ala Lys Asp Leu Asp
            180                 185                 190

gag gtc gct gga gcc acg gag aag agc tac acc ccg agt gag aag atg   624
Glu Val Ala Gly Ala Thr Glu Lys Ser Tyr Thr Pro Ser Glu Lys Met
        195                 200                 205

aaa gcc ctg atc aga gct cgg gat ggg cat tgc cgc ttc cca ggg tgt   672
Lys Ala Leu Ile Arg Ala Arg Asp Gly His Cys Arg Phe Pro Gly Cys
    210                 215                 220

tgc gtc ccg gcg agt aaa tgc cag gtc gat cac att atc ccg tgg gcg   720
Cys Val Pro Ala Ser Lys Cys Gln Val Asp His Ile Ile Pro Trp Ala
225                 230                 235                 240

gag ggc ggc ccg aca gcg gcg tgg aac ctg cag ttg ttg tgc cag cgg   768
Glu Gly Gly Pro Thr Ala Ala Trp Asn Leu Gln Leu Leu Cys Gln Arg
```

```
                245                 250                 255

cat cac aat atg aaa acc gat                                     789
His His Asn Met Lys Thr Asp
            260


<210> 1408
<211> 263
<212> PRT
<213> Corynebacterium glutamicum

<400> 1408
Asn Asn Gly Leu Asn Ala Met Ala Ala Met Thr Asn Leu Pro His Leu
  1               5                  10                  15

Arg Ala Ile Gln Glu Arg Tyr Tyr Phe Leu Ser Ile Arg Tyr Leu Ala
            20                  25                  30

Ser Ile Met Ile Ala Val Ala Lys Ala Asp Pro Thr Leu Trp Glu Glu
        35                  40                  45

Leu Asp Leu Arg Ile Thr Asp Ala Leu Thr Pro Val Thr Ala Gly Glu
    50                  55                  60

Val Met Ile Gln Ser Ser Thr Leu Ser Lys Arg Ile Ala Ala Trp Ile
65                  70                  75                  80

Lys Glu Leu Asp Pro Glu Pro Thr Pro Glu Pro Ile Pro Lys Glu Asp
                85                  90                  95

Tyr Val His Val His Thr Thr Asp Glu Ala Thr Tyr Val Arg Ile Lys
            100                 105                 110

Ile Ser Gly Pro Asn Arg Leu Ile Leu Asn Asp Ile Ile Thr Gln Leu
        115                 120                 125

Lys Asp Thr Asp Thr Glu Asp Ser Leu Pro Glu Ala Leu Met Ala Phe
    130                 135                 140

Leu Met Glu Lys Ile Gln Leu Lys Ile Thr Lys Tyr Leu Phe Thr Pro
145                 150                 155                 160

His Lys His Pro Glu Gln Val Trp Ser Pro Asp Tyr Gly Asp Ile Gly
                165                 170                 175

Pro Glu Ala Tyr Ala Asn Ala Thr Leu Val Cys Ala Lys Asp Leu Asp
            180                 185                 190

Glu Val Ala Gly Ala Thr Glu Lys Ser Tyr Thr Pro Ser Glu Lys Met
        195                 200                 205

Lys Ala Leu Ile Arg Ala Arg Asp Gly His Cys Arg Phe Pro Gly Cys
    210                 215                 220

Cys Val Pro Ala Ser Lys Cys Gln Val Asp His Ile Ile Pro Trp Ala
225                 230                 235                 240

Glu Gly Gly Pro Thr Ala Ala Trp Asn Leu Gln Leu Leu Cys Gln Arg
                245                 250                 255
```

```
His His Asn Met Lys Thr Asp
            260


<210> 1409
<211> 408
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> RXN03032

<400> 1409
cctggtcata ggatacttag ctcaaccaca cggtcagggc cagcaattcc tcacgtttta 60

ccaactccgt aagcacacca tcatggcctg gtgcgccgct atg acc gac ggg gac   115
                                          Met Thr Asp Gly Asp
                                            1               5

tta gac gct gat atc tca ccc cgc cag atc ggg ttg atg acc acc cga   163
Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly Leu Met Thr Thr Arg
                  10                  15                  20

acc gtg gtc gaa atc gtt cga cta cgc cac atg att gcc caa caa cta   211
Thr Val Val Glu Ile Val Arg Leu Arg His Met Ile Ala Gln Gln Leu
              25                  30                  35

gaa aga gcc acg atc atg gaa aac gag tac ctc aaa gaa atc gca gcg   259
Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu Lys Glu Ile Ala Ala
          40                  45                  50

ctg aag aaa gaa ctc gcg cac tac aag caa aaa gac cat cag aat caa   307
Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys Asp His Gln Asn Gln
      55                  60                  65

atg gtg atc gat atc ttg gga aaa gct att ggg acc agg ccc aat cct   355
Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly Thr Arg Pro Asn Pro
 70                  75                  80                  85

ggc gag ggc tta gac gag gag gac gcc acc taaacgtgga tgagcaacgc     405
Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
                  90                  95

gcc                                                              408


<210> 1410
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 1410
Met Thr Asp Gly Asp Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly
  1               5                  10                  15

Leu Met Thr Thr Arg Thr Val Val Glu Ile Val Arg Leu Arg His Met
              20                  25                  30

Ile Ala Gln Gln Leu Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu
```

```
         35                  40                  45

Lys Glu Ile Ala Ala Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys
     50                  55                  60

Asp His Gln Asn Gln Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly
 65                  70                  75                  80

Thr Arg Pro Asn Pro Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
                 85                  90                  95


<210> 1411
<211> 683
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(660)
<223> RXN03034

<400> 1411
ttc cca cca gat cga atc tcc gcc aac ggg cga cgc tat tac gag cca   48
Phe Pro Pro Asp Arg Ile Ser Ala Asn Gly Arg Arg Tyr Tyr Glu Pro
  1               5                  10                  15

caa aca cga ctc gag ttc atg cgg atc tac acc acc ctg ccg cac ggc   96
Gln Thr Arg Leu Glu Phe Met Arg Ile Tyr Thr Thr Leu Pro His Gly
             20                  25                  30

tac cgc cag ccc ttc ctt aaa gcc aac aac atc ggc cac tgc acc gtt   144
Tyr Arg Gln Pro Phe Leu Lys Ala Asn Asn Ile Gly His Cys Thr Val
         35                  40                  45

cga acc tgg cta gca gca ata agc acc ttc agc cga ctt ccc cat gct   192
Arg Thr Trp Leu Ala Ala Ile Ser Thr Phe Ser Arg Leu Pro His Ala
     50                  55                  60

ttt gat gat gcc cac cgc ttc ggg atc gaa cgc acc acc cca gtc gac   240
Phe Asp Asp Ala His Arg Phe Gly Ile Glu Arg Thr Thr Pro Val Asp
 65                  70                  75                  80

gat gtc acc aca cta acg gct gat gac aaa cgt gac ctg gtc ata gga   288
Asp Val Thr Thr Leu Thr Ala Asp Asp Lys Arg Asp Leu Val Ile Gly
                 85                  90                  95

tac tta gct caa cca cac ggt cag ggc cag caa ttc ctc acg ttt tac   336
Tyr Leu Ala Gln Pro His Gly Gln Gly Gln Gln Phe Leu Thr Phe Tyr
            100                 105                 110

caa ctc cgt aag cac acc atc atg gcc tgg tgc gcc gct atg acc gac   384
Gln Leu Arg Lys His Thr Ile Met Ala Trp Cys Ala Ala Met Thr Asp
        115                 120                 125

ggg gac tta gac gct gat atc tca ccc cgc cag atc ggg ttg atg acc   432
Gly Asp Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly Leu Met Thr
    130                 135                 140

acc cga acc gtg gtc gaa atc gtt cga cta cgc cac atg att gcc caa   480
Thr Arg Thr Val Val Glu Ile Val Arg Leu Arg His Met Ile Ala Gln
```

```
145                 150                 155                 160

caa cta gaa aga gcc acg atc atg gaa aac gag tac ctc aaa gaa atc   528
Gln Leu Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu Lys Glu Ile
                165                 170                 175

gca gcg ctg aag aaa gaa ctc gcg cac tac aag caa aaa gac cat cag   576
Ala Ala Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys Asp His Gln
            180                 185                 190

aat caa atg gtg atc gat atc ttg gga aaa gct att ggg acc agg ccc   624
Asn Gln Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly Thr Arg Pro
        195                 200                 205

aat cct ggc gag ggc tta gac gag gag gac gcc acc taaacgtgga        670
Asn Pro Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
    210                 215                 220

tgagcaacgc gcc                                                   683


<210> 1412
<211> 220
<212> PRT
<213> Corynebacterium glutamicum

<400> 1412
Phe Pro Pro Asp Arg Ile Ser Ala Asn Gly Arg Arg Tyr Tyr Glu Pro
  1               5                  10                  15

Gln Thr Arg Leu Glu Phe Met Arg Ile Tyr Thr Thr Leu Pro His Gly
             20                  25                  30

Tyr Arg Gln Pro Phe Leu Lys Ala Asn Asn Ile Gly His Cys Thr Val
         35                  40                  45

Arg Thr Trp Leu Ala Ala Ile Ser Thr Phe Ser Arg Leu Pro His Ala
     50                  55                  60

Phe Asp Asp Ala His Arg Phe Gly Ile Glu Arg Thr Thr Pro Val Asp
 65                  70                  75                  80

Asp Val Thr Thr Leu Thr Ala Asp Asp Lys Arg Asp Leu Val Ile Gly
                 85                  90                  95

Tyr Leu Ala Gln Pro His Gly Gln Gly Gln Gln Phe Leu Thr Phe Tyr
            100                 105                 110

Gln Leu Arg Lys His Thr Ile Met Ala Trp Cys Ala Ala Met Thr Asp
        115                 120                 125

Gly Asp Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly Leu Met Thr
    130                 135                 140

Thr Arg Thr Val Val Glu Ile Val Arg Leu Arg His Met Ile Ala Gln
145                 150                 155                 160

Gln Leu Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu Lys Glu Ile
                165                 170                 175

Ala Ala Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys Asp His Gln
```

```
            180                 185                 190

Asn Gln Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly Thr Arg Pro
        195                 200                 205

Asn Pro Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
    210                 215                 220


<210> 1413
<211> 408
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> FRXA00063

<400> 1413
cctggtcata ggatacttag ctcaaccaca cggtcagggc cagcaattcc tcacgtttta 60

ccaactccgt aagcacacca tcatggcctg gtgcgccgct atg acc gac ggg gac   115
                                              Met Thr Asp Gly Asp
                                                1               5

tta gac gct gat atc tca ccc cgc cag atc ggg ttg atg acc acc cga   163
Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly Leu Met Thr Thr Arg
                  10                  15                  20

acc gtg gtc gaa atc gtt cga cta cgc cac atg att gcc caa caa cta   211
Thr Val Val Glu Ile Val Arg Leu Arg His Met Ile Ala Gln Gln Leu
              25                  30                  35

gaa aga gcc acg atc atg gaa aac gag tac ctc aaa gaa atc gca gcg   259
Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu Lys Glu Ile Ala Ala
          40                  45                  50

ctg aag aaa gaa ctc gcg cac tac aag caa aaa gac cat cag aat caa   307
Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys Asp His Gln Asn Gln
      55                  60                  65

atg gtg atc gat atc ttg gga aaa gct att ggg acc agg ccc aat cct   355
Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly Thr Arg Pro Asn Pro
  70                  75                  80                  85

ggc gag ggc tta gac gag gag gac gcc acc taaacgtgga tgagcaacgc     405
Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
                  90                  95

gcc                                                              408


<210> 1414
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 1414
Met Thr Asp Gly Asp Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly
  1               5                  10                  15
```

```
Leu Met Thr Thr Arg Thr Val Val Glu Ile Val Arg Leu Arg His Met
             20                  25                  30

Ile Ala Gln Gln Leu Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu
         35                  40                  45

Lys Glu Ile Ala Ala Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys
     50                  55                  60

Asp His Gln Asn Gln Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly
 65                  70                  75                  80

Thr Arg Pro Asn Pro Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
                 85                  90                  95
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<210> 1415
<211> 309
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(286)
<223> RXN03037

<400> 1415
cgctaaaaga caaatgacag cgaagctgca ttcggataca cacctgaaga acactcttca 60

ccactagcat tccaccaacg cctcggaaag ggctatctcc atg tct gtt gac gat 115
Met Ser Val Asp Asp
1 5

ctt tac gct gtt gct ctc gat act cac acc ggt aag cct atc ccc tgc 163
Leu Tyr Ala Val Ala Leu Asp Thr His Thr Gly Lys Pro Ile Pro Cys
10 15 20

gta ctc tgt gaa aat gct cca cag att gtt atc tac gat ggt tgc tgc 211
Val Leu Cys Glu Asn Ala Pro Gln Ile Val Ile Tyr Asp Gly Cys Cys
25 30 35

tcg ctt gca tat acc caa gca ctt ggc gat ctc gcc gaa gcg gaa tac 259
Ser Leu Ala Tyr Thr Gln Ala Leu Gly Asp Leu Ala Glu Ala Glu Tyr
40 45 50

tac ggc gcc gat ctt gct gca gct gcc taaacaaact tcatagaacg 306
Tyr Gly Ala Asp Leu Ala Ala Ala Ala
55 60

aca 309

<210> 1416
<211> 62
<212> PRT
<213> Corynebacterium glutamicum

<400> 1416
```
Met Ser Val Asp Asp Leu Tyr Ala Val Ala Leu Asp Thr His Thr Gly
  1               5                  10                  15
```

```
Lys Pro Ile Pro Cys Val Leu Cys Glu Asn Ala Pro Gln Ile Val Ile
            20                  25                  30

Tyr Asp Gly Cys Cys Ser Leu Ala Tyr Thr Gln Ala Leu Gly Asp Leu
        35                  40                  45

Ala Glu Ala Glu Tyr Tyr Gly Ala Asp Leu Ala Ala Ala Ala
    50                  55                  60


<210> 1417
<211> 621
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(598)
<223> RXN03041

<400> 1417
accgaggaac tgaaggaaaa tgtaggtgtc ggggcttaga gaaacaaaaa aggctgctac 60

gcggacagca ttgtcacgtg ctgctgcgga tcgccttg atg gaa ggc cct gag   115
                                          Met Glu Gly Pro Glu
                                            1               5

gcg ttc acg gtt gcg gcc att gca gct gca gcc ggg gtc tcc ccc agg   163
Ala Phe Thr Val Ala Ala Ile Ala Ala Ala Ala Gly Val Ser Pro Arg
                10                  15                  20

act ttt cat aac tac ttc cct tct cgg gaa gac gca ttg gtg caa ttt   211
Thr Phe His Asn Tyr Phe Pro Ser Arg Glu Asp Ala Leu Val Gln Phe
            25                  30                  35

gtg gtc att cgc gtt cag gaa ctc acg gat cag cta tac gag ttt cct   259
Val Val Ile Arg Val Gln Glu Leu Thr Asp Gln Leu Tyr Glu Phe Pro
        40                  45                  50

aca agc gtg ccc cca cga gat gcc att gaa caa ttg gtg ata aac caa   307
Thr Ser Val Pro Pro Arg Asp Ala Ile Glu Gln Leu Val Ile Asn Gln
    55                  60                  65

ttg cgg gat ggc gat gac gct atg gat tct ttc agc gca atg ttt cga   355
Leu Arg Asp Gly Asp Asp Ala Met Asp Ser Phe Ser Ala Met Phe Arg
70                  75                  80                  85

atc ggt gag atc ctt gaa aat ctt gac ccc atc aag tgt gtt atc gat   403
Ile Gly Glu Ile Leu Glu Asn Leu Asp Pro Ile Lys Cys Val Ile Asp
                90                  95                  100

aag gag cga ctc att gct ccg ttg ctt gag ttc atg gtt gaa cgt gac   451
Lys Glu Arg Leu Ile Ala Pro Leu Leu Glu Phe Met Val Glu Arg Asp
            105                 110                 115

aaa gac ctt gac aag ttc gat ngc ggc aac tct gat cca ttt gca tgc   499
Lys Asp Leu Asp Lys Phe Asp Xaa Gly Asn Ser Asp Pro Phe Ala Cys
        120                 125                 130

agc ggc aat tgc aac ctc gct gca tac gtt tta cca agc ttc cga gcc   547
```

```
Ser Gly Asn Cys Asn Leu Ala Ala Tyr Val Leu Pro Ser Phe Arg Ala
    135                 140                 145

ccg gga cat aga aga tgg agt cgc att gat ccg tcg ggc atg cgc ctg   595
Pro Gly His Arg Arg Trp Ser Arg Ile Asp Pro Ser Gly Met Arg Leu
150                 155                 160                 165

gat taagaaanta aaaatctstg aca                                     621
Asp
```

<210> 1418
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

<400> 1418

```
Met Glu Gly Pro Glu Ala Phe Thr Val Ala Ala Ile Ala Ala Ala Ala
  1               5                  10                  15

Gly Val Ser Pro Arg Thr Phe His Asn Tyr Phe Pro Ser Arg Glu Asp
             20                  25                  30

Ala Leu Val Gln Phe Val Val Ile Arg Val Gln Glu Leu Thr Asp Gln
         35                  40                  45

Leu Tyr Glu Phe Pro Thr Ser Val Pro Pro Arg Asp Ala Ile Glu Gln
     50                  55                  60

Leu Val Ile Asn Gln Leu Arg Asp Gly Asp Asp Ala Met Asp Ser Phe
 65                  70                  75                  80

Ser Ala Met Phe Arg Ile Gly Glu Ile Leu Glu Asn Leu Asp Pro Ile
                 85                  90                  95

Lys Cys Val Ile Asp Lys Glu Arg Leu Ile Ala Pro Leu Leu Glu Phe
            100                 105                 110

Met Val Glu Arg Asp Lys Asp Leu Asp Lys Phe Asp Xaa Gly Asn Ser
        115                 120                 125

Asp Pro Phe Ala Cys Ser Gly Asn Cys Asn Leu Ala Ala Tyr Val Leu
    130                 135                 140

Pro Ser Phe Arg Ala Pro Gly His Arg Arg Trp Ser Arg Ile Asp Pro
145                 150                 155                 160

Ser Gly Met Arg Leu Asp
                165
```

<210> 1419
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> FRXA02892

<400> 1419
accgaggaac tgaaggaaaa tgtaggtgtc ggggcttaga gaaacaaaaa aggctgctac 60

gcggacagca ttgtcacgtg ctgctgcgga gatcgccttg atg gaa ggc cct gag 115
Met Glu Gly Pro Glu
1 5

gcg ttc acg gtt gcg gcc att gca gct gca gcc ggg gtc tcc ccc agg 163
Ala Phe Thr Val Ala Ala Ile Ala Ala Ala Ala Gly Val Ser Pro Arg
10 15 20

act ttt cat aac tac ttc cct tct cgg gaa gac gca ttg gtg caa ttt 211
Thr Phe His Asn Tyr Phe Pro Ser Arg Glu Asp Ala Leu Val Gln Phe
25 30 35

gtg gtc att cgc gtt cag gaa ctc acg gat cag cta tac gag ttt cct 259
Val Val Ile Arg Val Gln Glu Leu Thr Asp Gln Leu Tyr Glu Phe Pro
40 45 50

aca agc gtg ccc cca cga gat gcc att gaa caa ttg gtg ata aac caa 307
Thr Ser Val Pro Pro Arg Asp Ala Ile Glu Gln Leu Val Ile Asn Gln
55 60 65

ttg cgg gat ggc gat gac gct atg gat tct ttc agc gca atg ttt cga 355
Leu Arg Asp Gly Asp Asp Ala Met Asp Ser Phe Ser Ala Met Phe Arg
70 75 80 85

atc ggt gag atc ctt gaa aat ctt gac ccc atc aag tgt gtt atc gat 403
Ile Gly Glu Ile Leu Glu Asn Leu Asp Pro Ile Lys Cys Val Ile Asp
90 95 100

aag gag cga ctc att gct ccg ttg ctt gag ttc atg gtt gaa cgt gac 451
Lys Glu Arg Leu Ile Ala Pro Leu Leu Glu Phe Met Val Glu Arg Asp
105 110 115

aaa gac ctt gac aag ttc gat gcg gca act ctg atc cat ttg cat gca 499
Lys Asp Leu Asp Lys Phe Asp Ala Ala Thr Leu Ile His Leu His Ala
120 125 130

gcg gca att gca acc tcg ctg cat acg ttt tac caa gct tcc gag ccc 547
Ala Ala Ile Ala Thr Ser Leu His Thr Phe Tyr Gln Ala Ser Glu Pro
135 140 145

cgg gac ata gaa gat gga gtc gca ttg atc cgt cgg gca tgc gcc tgg 595
Arg Asp Ile Glu Asp Gly Val Ala Leu Ile Arg Arg Ala Cys Ala Trp
150 155 160 165

att aag aaa taaaaattgt ggcgtgtgaa cct 627
Ile Lys Lys

<210> 1420
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 1420
Met Glu Gly Pro Glu Ala Phe Thr Val Ala Ala Ile Ala Ala Ala Ala
1 5 10 15

```
Gly Val Ser Pro Arg Thr Phe His Asn Tyr Phe Pro Ser Arg Glu Asp
             20                  25                  30

Ala Leu Val Gln Phe Val Val Ile Arg Val Gln Glu Leu Thr Asp Gln
         35                  40                  45

Leu Tyr Glu Phe Pro Thr Ser Val Pro Pro Arg Asp Ala Ile Glu Gln
     50                  55                  60

Leu Val Ile Asn Gln Leu Arg Asp Gly Asp Asp Ala Met Asp Ser Phe
 65                  70                  75                  80

Ser Ala Met Phe Arg Ile Gly Glu Ile Leu Glu Asn Leu Asp Pro Ile
                 85                  90                  95

Lys Cys Val Ile Asp Lys Glu Arg Leu Ile Ala Pro Leu Leu Glu Phe
            100                 105                 110

Met Val Glu Arg Asp Lys Asp Leu Asp Lys Phe Asp Ala Ala Thr Leu
        115                 120                 125

Ile His Leu His Ala Ala Ala Ile Ala Thr Ser Leu His Thr Phe Tyr
    130                 135                 140

Gln Ala Ser Glu Pro Arg Asp Ile Glu Asp Gly Val Ala Leu Ile Arg
145                 150                 155                 160

Arg Ala Cys Ala Trp Ile Lys Lys
                165
```

<210> 1421
<211> 1096
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1096)
<223> RXN03045

<400> 1421
agcttttcta tttcgaaaaa tagccttgta ttcgaaaatt tgatcgggta tggtggttgg 60

tattagcaca gggaactaaa cgggaaaggg ggaagacacc atg agc atc acc aca 115
                                        Met Ser Ile Thr Thr
                                          1   5

cac gtc caa gca ctc acc aca gca ctc aac gcc atc gac aac cat ttg 163
His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala Ile Asp Asn His Leu
                10   15   20

gcc agc atg ctt gac cat ggt gtc acc cca gac caa tac aag gcc atc 211
Ala Ser Met Leu Asp His Gly Val Thr Pro Asp Gln Tyr Lys Ala Ile
            25   30   35

gag ccc gac ctc atc gcc cta gaa cac acc atc aac cac cac gcc acc 259
Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile Asn His His Ala Thr
        40   45   50
```
```

```
atc gcc gcc caa acc acc gcc ctc gcc gaa cgc acc aat gct gcg cag   307
Ile Ala Ala Gln Thr Thr Ala Leu Ala Glu Arg Thr Asn Ala Ala Gln
     55                  60                  65

tcg att ggc tcc acc cac ctc atc gac tac ctc acc acc acc ttc ggc   355
Ser Ile Gly Ser Thr His Leu Ile Asp Tyr Leu Thr Thr Thr Phe Gly
 70                  75                  80                  85

cta tct aaa gca cgc gcc cac cac cgc atc aat ctc gcc cac tcc ctc   403
Leu Ser Lys Ala Arg Ala His His Arg Ile Asn Leu Ala His Ser Leu
                 90                  95                 100

tac ccc ata ccg aag cca aac tct gga tct ggc aac ggc ggt aat ggt   451
Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly Asn Gly Gly Asn Gly
            105                 110                 115

ggc aat ccc gac ggt ggt cct gat ggt ggc gac tcg ggt gat gac gac   499
Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly Asp Asp Asp
        120                 125                 130

tcc ggc gat gat gac ccc gac ccc gaa ccg gac aag cct gaa gac ggc   547
Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Pro Glu Asp Gly
    135                 140                 145

aaa cct gat agt gat aag ccc cgt agg cca cgg atc agc gcg gaa aaa   595
Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg Ile Ser Ala Glu Lys
150                 155                 160                 165

cac gcc atc atc acc gac gaa ctc gcc cgc ctc aac ccg aat acc aca   643
His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro Asn Thr Thr
                170                 175                 180

ccc agc gcc gag gaa ctg cgc aac caa gcc ctg agt cag gcg atc tgg   691
Pro Ser Ala Glu Glu Leu Arg Asn Gln Ala Leu Ser Gln Ala Ile Trp
            185                 190                 195

cgc acc cca gaa gac ctc cgc acg tgg cta cgc cac cag gtc acc acc   739
Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His Gln Val Thr Thr
        200                 205                 210

gcg aac aaa aac aac ccc aac ccc atc acc gcc atg aaa agg cgc tac   787
Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys Arg Arg Tyr
    215                 220                 225

ctc tca gta ggt aaa ccc gat gcc gac aac atg gtc cgc atc agc ggc   835
Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg Ile Ser Gly
230                 235                 240                 245

ctc gtg ccc gca gcc acc gca gca ctg atc acc gcg aac acc gca ccg   883
Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn Thr Ala Pro
                250                 255                 260

tta acc aaa cgc ggc aac ctc gtg gat cta cca gca gca gaa gat atg   931
Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala Glu Asp Met
            265                 270                 275

cgc acc cgc ggg caa cgc cat gcg gac gcg ttg cat cac atc atg gag   979
Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His Ile Met Glu
        280                 285                 290

atc tac aac cac ggt att gtc acc cca gct cgt ggt gga aca gcc agc   1027
```

```
Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly Thr Ala Ser
    295                 300                 305

atc atc atc tcc atg acc acc gat gat ctt gac gag atc aac cac gcc   1075
Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile Asn His Ala
310                 315                 320                 325

aac agc agt ggt gaa agt ctg                                       1096
Asn Ser Ser Gly Glu Ser Leu
                330
```

<210> 1422
<211> 332
<212> PRT
<213> Corynebacterium glutamicum

<400> 1422

```
Met Ser Ile Thr Thr His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala
  1               5                  10                  15

Ile Asp Asn His Leu Ala Ser Met Leu Asp His Gly Val Thr Pro Asp
             20                  25                  30

Gln Tyr Lys Ala Ile Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile
         35                  40                  45

Asn His His Ala Thr Ile Ala Ala Gln Thr Thr Ala Leu Ala Glu Arg
     50                  55                  60

Thr Asn Ala Ala Gln Ser Ile Gly Ser Thr His Leu Ile Asp Tyr Leu
 65                  70                  75                  80

Thr Thr Thr Phe Gly Leu Ser Lys Ala Arg Ala His His Arg Ile Asn
                85                  90                  95

Leu Ala His Ser Leu Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly
            100                 105                 110

Asn Gly Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp
        115                 120                 125

Ser Gly Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp
    130                 135                 140

Lys Pro Glu Asp Gly Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg
145                 150                 155                 160

Ile Ser Ala Glu Lys His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu
                165                 170                 175

Asn Pro Asn Thr Thr Pro Ser Ala Glu Glu Leu Arg Asn Gln Ala Leu
            180                 185                 190

Ser Gln Ala Ile Trp Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg
        195                 200                 205

His Gln Val Thr Thr Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala
    210                 215                 220

Met Lys Arg Arg Tyr Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met
```

```
225                 230                 235                 240

Val Arg Ile Ser Gly Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr
                245                 250                 255

Ala Asn Thr Ala Pro Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro
            260                 265                 270

Ala Ala Glu Asp Met Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu
        275                 280                 285

His His Ile Met Glu Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg
    290                 295                 300

Gly Gly Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp
305                 310                 315                 320

Glu Ile Asn His Ala Asn Ser Ser Gly Glu Ser Leu
                325                 330
```

<210> 1423
<211> 359
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(336)
<223> RXN03046

<400> 1423

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gcc tca att gct aat tcc acc ctg aat att cca gtg gga ttg ggc ggc   48
Ala Ser Ile Ala Asn Ser Thr Leu Asn Ile Pro Val Gly Leu Gly Gly
  1               5                  10                  15

tcc aat ttg ctg ctc aag gcg caa acc gcg acc cca tct gag cct gcg   96
Ser Asn Leu Leu Leu Lys Ala Gln Thr Ala Thr Pro Ser Glu Pro Ala
             20                  25                  30

aat gct cag gac aaa ctg tac cgt ttc tgc atc gcc aat ggt aag agg   144
Asn Ala Gln Asp Lys Leu Tyr Arg Phe Cys Ile Ala Asn Gly Lys Arg
         35                  40                  45

gca ttt tcc gat gcg cag cga ttc ttg ctc aac gcc gac gag ctc gcg   192
Ala Phe Ser Asp Ala Gln Arg Phe Leu Leu Asn Ala Asp Glu Leu Ala
     50                  55                  60

gag ctt tct gat tat gag cgt ctg gct tat gcc atc acc ttg ctt gat   240
Glu Leu Ser Asp Tyr Glu Arg Leu Ala Tyr Ala Ile Thr Leu Leu Asp
 65                  70                  75                  80

cag cct gga aaa gaa gca gaa gga cgc gaa ctt ttt cct ttc gga gct   288
Gln Pro Gly Lys Glu Ala Glu Gly Arg Glu Leu Phe Pro Phe Gly Ala
                 85                  90                  95

tcg ccg cca ggg cta ccg cgc tgt cga ttt ctt gga atc cca gac tgt   336
Ser Pro Pro Gly Leu Pro Arg Cys Arg Phe Leu Gly Ile Pro Asp Cys
            100                 105                 110

tgaccagctg aataaccccg atg                                        359
```

<210> 1424
<211> 112
<212> PRT
<213> Corynebacterium glutamicum

<400> 1424
Ala Ser Ile Ala Asn Ser Thr Leu Asn Ile Pro Val Gly Leu Gly Gly
1 5 10 15

Ser Asn Leu Leu Leu Lys Ala Gln Thr Ala Thr Pro Ser Glu Pro Ala
20 25 30

Asn Ala Gln Asp Lys Leu Tyr Arg Phe Cys Ile Ala Asn Gly Lys Arg
35 40 45

Ala Phe Ser Asp Ala Gln Arg Phe Leu Leu Asn Ala Asp Glu Leu Ala
50 55 60

Glu Leu Ser Asp Tyr Glu Arg Leu Ala Tyr Ala Ile Thr Leu Leu Asp
65 70 75 80

Gln Pro Gly Lys Glu Ala Glu Gly Arg Glu Leu Phe Pro Phe Gly Ala
85 90 95

Ser Pro Pro Gly Leu Pro Arg Cys Arg Phe Leu Gly Ile Pro Asp Cys
100 105 110

<210> 1425
<211> 1539
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1516)
<223> RXN03047

<400> 1425
ctctacccac ttaaaatgga cgcatattcg caagataagg catgcttgga tgaatagatt 60

ttaactcaac gtttactaaa cagaatcgga attaggagcc atg ctt gaa cgc aca 115
Met Leu Glu Arg Thr
1 5

cag gta ttc gtg gat acg tcc tac ctg ctc gca agc ttt tac aac tct 163
Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala Ser Phe Tyr Asn Ser
10 15 20

tgg gag aca ggg gca cgt gcc caa tta gaa atc gac ctc ccc gaa gta 211
Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile Asp Leu Pro Glu Val
25 30 35

gtc ggg gta tta gga agg atg att gaa caa caa ctt aaa cag cca gta 259
Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln Leu Lys Gln Pro Val
40 45 50

```
caa cgc caa atg tgg tac gac gga atc ccc gat tcc ggc ccc cac cgc   307
Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp Ser Gly Pro His Arg
     55                  60                  65

tat caa cga gca cta cgc acc tgc gat ggt gtg caa ctt cgt gct ggc   355
Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val Gln Leu Arg Ala Gly
 70                  75                  80                  85

caa tta att gaa tgg ggc gaa cgc cgc aca caa aag gca gta gat acc   403
Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln Lys Ala Val Asp Thr
                 90                  95                 100

cgc ctt gtt gca gac ctc gtt ctc gca ggt gtt cgc gga caa tgc tcc   451
Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val Arg Gly Gln Cys Ser
            105                 110                 115

gat atc gtg ctc gtc agt ggc gac gcc gac atg atc ccc ggt gtt caa   499
Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met Ile Pro Gly Val Gln
        120                 125                 130

gaa gct gcc aat gca ggc ctt cgc gtt cac ctc tac ggc ttc ggc tgg   547
Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu Tyr Gly Phe Gly Trp
    135                 140                 145

gat tcc atg tcc tcc caa ctg cgc cac tgc tgt gac acc acc acc att   595
Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys Asp Thr Thr Thr Ile
150                 155                 160                 165

ttg gat cct cga gaa gat ttt gct gaa tgc atg cag ctg cag gtt ctc   643
Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met Gln Leu Gln Val Leu
                170                 175                 180

gaa ggt cca cta ccc cct gtc gtt cgg gta aag ccc atc aac gat gca   691
Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys Pro Ile Asn Asp Ala
            185                 190                 195

gaa ccc atc gag gat ttg gat ttc act cca gtt cca ggc gtc gcc tca   739
Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val Pro Gly Val Ala Ser
        200                 205                 210

cca ttt gaa gag gtc agc gcg aaa gat gag aaa ttc tct cca cgc cca   787
Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys Phe Ser Pro Arg Pro
    215                 220                 225

agt gaa cct gcc gaa gct ttg tcg gaa cag gtc tgt gaa gcg cag tat   835
Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val Cys Glu Ala Gln Tyr
230                 235                 240                 245

gag atc tcc aaa cac gaa ggt caa acc gct gat tca gga gaa atc acc   883
Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp Ser Gly Glu Ile Thr
                250                 255                 260

gag tct ttc gag gcc gct gaa atc aag gta act gag ttt ttt gga gaa   931
Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr Glu Phe Phe Gly Glu
            265                 270                 275

cca gct gct cca gta gcg gaa tca ggc gta gaa gct ccc act ccg gaa   979
Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu Ala Pro Thr Pro Glu
        280                 285                 290
```

```
gct ccc acg gtt cct gaa gca gct aag ccc act ccg gcg aaa cct aag   1027
Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr Pro Ala Lys Pro Lys
    295                 300                 305

act cca aag gca gag ccc caa aag caa gaa tcc ccc aag ccg gga act   1075
Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser Pro Lys Pro Gly Thr
310                 315                 320                 325

cca aaa cca aaa gct cca agc cct gcg gat att cca ccg aaa gcc cca   1123
Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile Pro Pro Lys Ala Pro
                330                 335                 340

gct gac act gag gaa cat tcg gaa gtc gaa gct gaa atc gag gac tca   1171
Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala Glu Ile Glu Asp Ser
            345                 350                 355

cgt cca aag atc ccc agc cct tcg atg atg gct ccc cgc cgc aag ctt   1219
Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala Pro Arg Arg Lys Leu
        360                 365                 370

cgt tcc cgc tac gtt ccg ctt ccc aac gaa gtg tgg gca aca gca gga   1267
Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val Trp Ala Thr Ala Gly
    375                 380                 385

ttc caa act cct tac gat gtc ggg caa cag tac gca tcg tgg tgg ttt   1315
Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr Ala Ser Trp Trp Phe
390                 395                 400                 405

gaa aac gca gct acc agc act caa aga gat cag gct cat cta ttg tct   1363
Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln Ala His Leu Leu Ser
                410                 415                 420

ggt ggc gga ctt cca cca gag atc gat cgc ccg ctt ctg cag ttt gct   1411
Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro Leu Leu Gln Phe Ala
            425                 430                 435

tgt gaa act ctc cac gaa tac acc ctg act gaa gcg cag cgc gta gct   1459
Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu Ala Gln Arg Val Ala
        440                 445                 450

tta cgc gat ggc ttt cac tcc gga atc cgt ggt gta ttg ctc aac cag   1507
Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly Val Leu Leu Asn Gln
    455                 460                 465

cga gat agc tagaatcaca aaaaactggg gct                            1539
Arg Asp Ser
470
```

<210> 1426
<211> 472
<212> PRT
<213> Corynebacterium glutamicum

<400> 1426

```
Met Leu Glu Arg Thr Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala
  1               5                  10                  15

Ser Phe Tyr Asn Ser Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile
             20                  25                  30
```

```
Asp Leu Pro Glu Val Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln
          35                  40                  45

Leu Lys Gln Pro Val Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp
      50                  55                  60

Ser Gly Pro His Arg Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val
 65                  70                  75                  80

Gln Leu Arg Ala Gly Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln
                 85                  90                  95

Lys Ala Val Asp Thr Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val
            100                 105                 110

Arg Gly Gln Cys Ser Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met
        115                 120                 125

Ile Pro Gly Val Gln Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu
    130                 135                 140

Tyr Gly Phe Gly Trp Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys
145                 150                 155                 160

Asp Thr Thr Thr Ile Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met
                165                 170                 175

Gln Leu Gln Val Leu Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys
            180                 185                 190

Pro Ile Asn Asp Ala Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val
        195                 200                 205

Pro Gly Val Ala Ser Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys
    210                 215                 220

Phe Ser Pro Arg Pro Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val
225                 230                 235                 240

Cys Glu Ala Gln Tyr Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp
                245                 250                 255

Ser Gly Glu Ile Thr Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr
            260                 265                 270

Glu Phe Phe Gly Glu Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu
        275                 280                 285

Ala Pro Thr Pro Glu Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr
    290                 295                 300

Pro Ala Lys Pro Lys Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser
305                 310                 315                 320

Pro Lys Pro Gly Thr Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile
                325                 330                 335

Pro Pro Lys Ala Pro Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala
            340                 345                 350

Glu Ile Glu Asp Ser Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala
```

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        355                 360                 365

Pro Arg Arg Lys Leu Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val
    370                 375                 380

Trp Ala Thr Ala Gly Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr
385                 390                 395                 400

Ala Ser Trp Trp Phe Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln
                405                 410                 415

Ala His Leu Leu Ser Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro
            420                 425                 430

Leu Leu Gln Phe Ala Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu
        435                 440                 445

Ala Gln Arg Val Ala Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly
    450                 455                 460

Val Leu Leu Asn Gln Arg Asp Ser
465                 470
```

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<210> 1427
<211> 1539
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1516)
<223> FRXA00036

<400> 1427

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ctctacccac ttaaaatgga cgcatattcg caagataagg catgcttgga tgaatagatt 60

ttaactcaac gtttactaaa cagaatcgga attaggagcc atg ctt gaa cgc aca   115
                                            Met Leu Glu Arg Thr
                                              1               5

cag gta ttc gtg gat acg tcc tac ctg ctc gca agc ttt tac aac tct   163
Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala Ser Phe Tyr Asn Ser
                 10                  15                  20

tgg gag aca ggg gca cgt gcc caa tta gaa atc gac ctc ccc gaa gta   211
Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile Asp Leu Pro Glu Val
             25                  30                  35

gtc ggg gta tta gga agg atg att gaa caa caa ctt aaa cag cca gta   259
Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln Leu Lys Gln Pro Val
         40                  45                  50

caa cgc caa atg tgg tac gac gga atc ccc gat tcc ggc ccc cac cgc   307
Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp Ser Gly Pro His Arg
     55                  60                  65

tat caa cga gca cta cgc acc tgc gat ggt gtg caa ctt cgt gct ggc   355
Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val Gln Leu Arg Ala Gly
 70                  75                  80                  85
```

```
caa tta att gaa tgg ggc gaa cgc cgc aca caa aag gca gta gat acc   403
Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln Lys Ala Val Asp Thr
                 90                  95                 100

cgc ctt gtt gca gac ctc gtt ctc gca ggt gtt cgc gga caa tgc tcc   451
Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val Arg Gly Gln Cys Ser
            105                 110                 115

gat atc gtg ctc gtc agt ggc gac gcc gac atg atc ccc ggt gtt caa   499
Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met Ile Pro Gly Val Gln
        120                 125                 130

gaa gct gcc aat gca ggc ctt cgc gtt cac ctc tac ggc ttc ggc tgg   547
Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu Tyr Gly Phe Gly Trp
    135                 140                 145

gat tcc atg tcc tcc caa ctg cgc cac tgc tgt gac acc acc acc att   595
Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys Asp Thr Thr Thr Ile
150                 155                 160                 165

ttg gat cct cga gaa gat ttt gct gaa tgc atg cag ctg cag gtt ctc   643
Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met Gln Leu Gln Val Leu
                170                 175                 180

gaa ggt cca cta ccc cct gtc gtt cgg gta aag ccc atc aac gat gca   691
Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys Pro Ile Asn Asp Ala
            185                 190                 195

gaa ccc atc gag gat ttg gat ttc act cca gtt cca ggc gtc gcc tca   739
Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val Pro Gly Val Ala Ser
        200                 205                 210

cca ttt gaa gag gtc agc gcg aaa gat gag aaa ttc tct cca cgc cca   787
Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys Phe Ser Pro Arg Pro
    215                 220                 225

agt gaa cct gcc gaa gct ttg tcg gaa cag gtc tgt gaa gcg cag tat   835
Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val Cys Glu Ala Gln Tyr
230                 235                 240                 245

gag atc tcc aaa cac gaa ggt caa acc gct gat tca gga gaa atc acc   883
Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp Ser Gly Glu Ile Thr
                250                 255                 260

gag tct ttc gag gcc gct gaa atc aag gta act gag ttt ttt gga gaa   931
Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr Glu Phe Phe Gly Glu
            265                 270                 275

cca gct gct cca gta gcg gaa tca ggc gta gaa gct ccc act ccg gaa   979
Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu Ala Pro Thr Pro Glu
        280                 285                 290

gct ccc acg gtt cct gaa gca gct aag ccc act ccg gcg aaa cct aag   1027
Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr Pro Ala Lys Pro Lys
    295                 300                 305

act cca aag gca gag ccc caa aag caa gaa tcc ccc aag ccg gga act   1075
Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser Pro Lys Pro Gly Thr
310                 315                 320                 325

cca aaa cca aaa gct cca agc cct gcg gat att cca ccg aaa gcc cca   1123
```

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Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile Pro Pro Lys Ala Pro
                330                 335                 340

gct gac act gag gaa cat tcg gaa gtc gaa gct gaa atc gag gac tca   1171
Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala Glu Ile Glu Asp Ser
            345                 350                 355

cgt cca aag atc ccc agc cct tcg atg atg gct ccc cgc cgc aag ctt   1219
Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala Pro Arg Arg Lys Leu
        360                 365                 370

cgt tcc cgc tac gtt ccg ctt ccc aac gaa gtg tgg gca aca gca gga   1267
Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val Trp Ala Thr Ala Gly
    375                 380                 385

ttc caa act cct tac gat gtc ggg caa cag tac gca tcg tgg tgg ttt   1315
Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr Ala Ser Trp Trp Phe
390                 395                 400                 405

gaa aac gca gct acc agc act caa aga gat cag gct cat cta ttg tct   1363
Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln Ala His Leu Leu Ser
                410                 415                 420

ggt ggc gga ctt cca cca gag atc gat cgc ccg ctt ctg cag ttt gct   1411
Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro Leu Leu Gln Phe Ala
            425                 430                 435

tgt gaa act ctc cac gaa tac acc ctg act gaa gcg cag cgc gta gct   1459
Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu Ala Gln Arg Val Ala
        440                 445                 450

tta cgc gat ggc ttt cac tcc gga atc cgt ggt gta ttg ctc aac cag   1507
Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly Val Leu Leu Asn Gln
    455                 460                 465

cga gat agc tagaatcaca aaaaactggg gct                            1539
Arg Asp Ser
470
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<210> 1428
<211> 472
<212> PRT
<213> Corynebacterium glutamicum

<400> 1428

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Met Leu Glu Arg Thr Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala
  1               5                  10                  15

Ser Phe Tyr Asn Ser Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile
             20                  25                  30

Asp Leu Pro Glu Val Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln
         35                  40                  45

Leu Lys Gln Pro Val Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp
     50                  55                  60

Ser Gly Pro His Arg Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val
 65                  70                  75                  80
```

```
Gln Leu Arg Ala Gly Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln
                  85                  90                  95

Lys Ala Val Asp Thr Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val
            100                 105                 110

Arg Gly Gln Cys Ser Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met
        115                 120                 125

Ile Pro Gly Val Gln Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu
    130                 135                 140

Tyr Gly Phe Gly Trp Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys
145                 150                 155                 160

Asp Thr Thr Thr Ile Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met
                165                 170                 175

Gln Leu Gln Val Leu Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys
            180                 185                 190

Pro Ile Asn Asp Ala Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val
        195                 200                 205

Pro Gly Val Ala Ser Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys
    210                 215                 220

Phe Ser Pro Arg Pro Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val
225                 230                 235                 240

Cys Glu Ala Gln Tyr Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp
                245                 250                 255

Ser Gly Glu Ile Thr Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr
            260                 265                 270

Glu Phe Phe Gly Glu Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu
        275                 280                 285

Ala Pro Thr Pro Glu Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr
    290                 295                 300

Pro Ala Lys Pro Lys Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser
305                 310                 315                 320

Pro Lys Pro Gly Thr Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile
                325                 330                 335

Pro Pro Lys Ala Pro Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala
            340                 345                 350

Glu Ile Glu Asp Ser Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala
        355                 360                 365

Pro Arg Arg Lys Leu Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val
    370                 375                 380

Trp Ala Thr Ala Gly Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr
385                 390                 395                 400

Ala Ser Trp Trp Phe Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln
```

```
                405                 410                 415

Ala His Leu Leu Ser Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro
            420                 425                 430

Leu Leu Gln Phe Ala Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu
        435                 440                 445

Ala Gln Arg Val Ala Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly
    450                 455                 460

Val Leu Leu Asn Gln Arg Asp Ser
465                 470


<210> 1429
<211> 996
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(973)
<223> RXN03048

<400> 1429
agcgaatcgg attcagtgat ttgcttgcgg gcgcagaaat gatttttcaa ttagacacac 60

ttagacacac gtaactaaaa cctcagggaa gtgactgata atg gct aat ccg ctc   115
                                            Met Ala Asn Pro Leu
                                              1               5

agc aag ggc tgg aag tat ctc atg gca tcg ttc gac aac aag atc gat   163
Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe Asp Asn Lys Ile Asp
                  10                  15                  20

gag aat gca gat cca aag atc caa att cag caa gct aca gaa gct gcc   211
Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln Ala Thr Glu Ala Ala
              25                  30                  35

cag aag cag cac cag cag att atg cag cac gct tct cag att atc ggt   259
Gln Lys Gln His Gln Gln Ile Met Gln His Ala Ser Gln Ile Ile Gly
          40                  45                  50

cag cag aag cag ctt gag atg aaa ttg aac cgc ttg gtt act gac cgc   307
Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg Leu Val Thr Asp Arg
      55                  60                  65

gat aag ttg cag gaa cag gct cgt cag gca att cag ttg gca gat aag   355
Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile Gln Leu Ala Asp Lys
  70                  75                  80                  85

tcc gca aac gaa ggc gac agt gtt aag gct cag gag ttc aac aac act   403
Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln Glu Phe Asn Asn Thr
                  90                  95                 100

gct gag gtt ttt gct tcc cag ttg gta gct gtg gaa cag cag ttg gag   451
Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val Glu Gln Gln Leu Glu
              105                 110                 115

cag act act gcg ctt cat cag cag gct gag gtt gcg gcg aag gat gct   499
```

```
Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val Ala Ala Lys Asp Ala
        120                 125                 130

gtt gcg aag tct aaa gag tct gag atg cgc ctg aaa gag cag atg tct   547
Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu Lys Glu Gln Met Ser
    135                 140                 145

cag att gat gct cta cgt gcg cag gct gat cag gcg aag atg cag gaa   595
Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln Ala Lys Met Gln Glu
150                 155                 160                 165

agt gtc act aag tct atg gat tct ttg aat cag ttt ggc act cag gat   643
Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln Phe Gly Thr Gln Asp
                170                 175                 180

tct tct gtt cct acc ctt gat gcg gtg cgt gag aag atc gag cgt cga   691
Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu Lys Ile Glu Arg Arg
            185                 190                 195

tac gca gat gct ttg ggc gcg cag gaa ctt acc cag aac act gtt agt   739
Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr Gln Asn Thr Val Ser
        200                 205                 210

gat cgc atg gct gag att gcg cag tcc ggc acc gat atg cgg gcg tca   787
Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr Asp Met Arg Ala Ser
    215                 220                 225

gct cgt ttg gct gaa ctt cgc gcg gag gcg ctg ggc acg tcc gca acg   835
Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu Gly Thr Ser Ala Thr
230                 235                 240                 245

cct aag ggc cag cta gag gca ggt gtc gag gat gcg gaa gaa ctt atc   883
Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp Ala Glu Glu Leu Ile
                250                 255                 260

gac gaa acc tcc acc cct tca gct acc cca gaa acc gca agc cca gaa   931
Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu Thr Ala Ser Pro Glu
            265                 270                 275

gct gat gct cca gaa gca tcc gca gac gag tcc gag aag aaa           973
Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser Glu Lys Lys
        280                 285                 290

taacctaaac acaaaaaact ggg                                        996


<210> 1430
<211> 291
<212> PRT
<213> Corynebacterium glutamicum

<400> 1430
Met Ala Asn Pro Leu Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe
  1               5                  10                  15

Asp Asn Lys Ile Asp Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln
             20                  25                  30

Ala Thr Glu Ala Ala Gln Lys Gln His Gln Gln Ile Met Gln His Ala
         35                  40                  45
```

```
Ser Gln Ile Ile Gly Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg
     50                  55                  60

Leu Val Thr Asp Arg Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile
 65                  70                  75                  80

Gln Leu Ala Asp Lys Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln
                 85                  90                  95

Glu Phe Asn Asn Thr Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val
            100                 105                 110

Glu Gln Gln Leu Glu Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val
        115                 120                 125

Ala Ala Lys Asp Ala Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu
    130                 135                 140

Lys Glu Gln Met Ser Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln
145                 150                 155                 160

Ala Lys Met Gln Glu Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln
                165                 170                 175

Phe Gly Thr Gln Asp Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu
            180                 185                 190

Lys Ile Glu Arg Arg Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr
        195                 200                 205

Gln Asn Thr Val Ser Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr
    210                 215                 220

Asp Met Arg Ala Ser Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu
225                 230                 235                 240

Gly Thr Ser Ala Thr Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp
                245                 250                 255

Ala Glu Glu Leu Ile Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu
            260                 265                 270

Thr Ala Ser Pro Glu Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser
        275                 280                 285

Glu Lys Lys
    290
```

<210> 1431
<211> 996
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(973)
<223> FRXA00037

<400> 1431
agcgaatcgg attcagtgat ttgcttgcgg gcgcagaaat gatttttcaa ttagacacac 60

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ttagacacac gtaactaaaa cctcagggaa gtgactgata atg gct aat ccg ctc   115
                                              Met Ala Asn Pro Leu
                                                1               5

agc aag ggc tgg aag tat ctc atg gca tcg ttc gac aac aag atc gat   163
Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe Asp Asn Lys Ile Asp
                  10                  15                  20

gag aat gca gat cca aag atc caa att cag caa gct aca gaa gct gcc   211
Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln Ala Thr Glu Ala Ala
             25                  30                  35

cag aag cag cac cag cag att atg cag cac gct tct cag att atc ggt   259
Gln Lys Gln His Gln Gln Ile Met Gln His Ala Ser Gln Ile Ile Gly
         40                  45                  50

cag cag aag cag ctt gag atg aaa ttg aac cgc ttg gtt act gac cgc   307
Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg Leu Val Thr Asp Arg
     55                  60                  65

gat aag ttg cag gaa cag gct cgt cag gca att cag ttg gca gat aag   355
Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile Gln Leu Ala Asp Lys
 70                  75                  80                  85

tcc gca aac gaa ggc gac agt gtt aag gct cag gag ttc aac aac act   403
Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln Glu Phe Asn Asn Thr
                 90                  95                 100

gct gag gtt ttt gct tcc cag ttg gta gct gtg gaa cag cag ttg gag   451
Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val Glu Gln Gln Leu Glu
            105                 110                 115

cag act act gcg ctt cat cag cag gct gag gtt gcg gcg aag gat gct   499
Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val Ala Ala Lys Asp Ala
        120                 125                 130

gtt gcg aag tct aaa gag tct gag atg cgc ctg aaa gag cag atg tct   547
Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu Lys Glu Gln Met Ser
    135                 140                 145

cag att gat gct cta cgt gcg cag gct gat cag gcg aag atg cag gaa   595
Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln Ala Lys Met Gln Glu
150                 155                 160                 165

agt gtc act aag tct atg gat tct ttg aat cag ttt ggc act cag gat   643
Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln Phe Gly Thr Gln Asp
                170                 175                 180

tct tct gtt cct acc ctt gat gcg gtg cgt gag aag atc gag cgt cga   691
Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu Lys Ile Glu Arg Arg
            185                 190                 195

tac gca gat gct ttg ggc gcg cag gaa ctt acc cag aac act gtt agt   739
Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr Gln Asn Thr Val Ser
        200                 205                 210

gat cgc atg gct gag att gcg cag tcc ggc acc gat atg cgg gcg tca   787
Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr Asp Met Arg Ala Ser
    215                 220                 225
```

```
gct cgt ttg gct gaa ctt cgc gcg gag gcg ctg ggc acg tcc gca acg   835
Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu Gly Thr Ser Ala Thr
230                 235                 240                 245

cct aag ggc cag cta gag gca ggt gtc gag gat gcg gaa gaa ctt atc   883
Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp Ala Glu Glu Leu Ile
                250                 255                 260

gac gaa acc tcc acc cct tca gct acc cca gaa acc gca agc cca gaa   931
Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu Thr Ala Ser Pro Glu
            265                 270                 275

gct gat gct cca gaa gca tcc gca gac gag tcc gag aag aaa           973
Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser Glu Lys Lys
        280                 285                 290

taacctaaac acaaaaaact ggg                                        996


<210> 1432
<211> 291
<212> PRT
<213> Corynebacterium glutamicum

<400> 1432
Met Ala Asn Pro Leu Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe
  1               5                  10                  15

Asp Asn Lys Ile Asp Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln
             20                  25                  30

Ala Thr Glu Ala Ala Gln Lys Gln His Gln Gln Ile Met Gln His Ala
         35                  40                  45

Ser Gln Ile Ile Gly Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg
     50                  55                  60

Leu Val Thr Asp Arg Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile
 65                  70                  75                  80

Gln Leu Ala Asp Lys Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln
                 85                  90                  95

Glu Phe Asn Asn Thr Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val
            100                 105                 110

Glu Gln Gln Leu Glu Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val
        115                 120                 125

Ala Ala Lys Asp Ala Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu
    130                 135                 140

Lys Glu Gln Met Ser Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln
145                 150                 155                 160

Ala Lys Met Gln Glu Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln
                165                 170                 175

Phe Gly Thr Gln Asp Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu
            180                 185                 190
```

```
Lys Ile Glu Arg Arg Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr
        195                 200                 205

Gln Asn Thr Val Ser Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr
    210                 215                 220

Asp Met Arg Ala Ser Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu
225                 230                 235                 240

Gly Thr Ser Ala Thr Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp
                245                 250                 255

Ala Glu Glu Leu Ile Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu
            260                 265                 270

Thr Ala Ser Pro Glu Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser
        275                 280                 285

Glu Lys Lys
    290
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<210> 1433
<211> 1066
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1066)
<223> RXN03050

<400> 1433

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gttaagccta taggaaaaag tgtttgcata tcacccttgt attcgaacac gtgagcgggt 60

agagtgggtg gtaacaacac ggggaaaggg ggaagacacc atg agc atc acc aca   115
                                          Met Ser Ile Thr Thr
                                            1               5

cac gtc caa gca ctc acc aca gca ctc aac gcc atc gac aac cat ttg   163
His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala Ile Asp Asn His Leu
                10                  15                  20

gcc agc atg ctc gac cat ggt gtc acc cca gac caa tac aag gcc atc   211
Ala Ser Met Leu Asp His Gly Val Thr Pro Asp Gln Tyr Lys Ala Ile
            25                  30                  35

gag ccc gac ctc atc gcc cta gaa cac acc atc aac cac cac gcc acc   259
Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile Asn His His Ala Thr
        40                  45                  50

atc gcc gcc caa acc aca gcc ctc gcc gaa cgc acc aac gcc gcc cac   307
Ile Ala Ala Gln Thr Thr Ala Leu Ala Glu Arg Thr Asn Ala Ala His
    55                  60                  65

acc att ggc tcc acc cac ctc atc gac tac ctc acc acc acc ttc gga   355
Thr Ile Gly Ser Thr His Leu Ile Asp Tyr Leu Thr Thr Thr Phe Gly
70                  75                  80                  85

cta tcc aaa gca cgc gcc cac cac cgc atc aat ctc gcc cac tcc ctc   403
Leu Ser Lys Ala Arg Ala His His Arg Ile Asn Leu Ala His Ser Leu
```

```
                    90                  95                 100

tac ccc ata ccg aag cca aac cct gga tct ggc aac ggc ggt aat ggt   451
Tyr Pro Ile Pro Lys Pro Asn Pro Gly Ser Gly Asn Gly Gly Asn Gly
            105                 110                 115

ggc aat ccc gac ggc ggt cct gat ggt ggc gac tcg ggt gat gac gac   499
Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly Asp Asp Asp
        120                 125                 130

tcc ggc gac gat gac ccc gac ccc gaa ccg gac aag cct gaa gac ggc   547
Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Pro Glu Asp Gly
    135                 140                 145

aaa cct gat ggt gat aag cct cgt ggg cca cgg atc agc gcg gaa aaa   595
Lys Pro Asp Gly Asp Lys Pro Arg Gly Pro Arg Ile Ser Ala Glu Lys
150                 155                 160                 165

cac gcc atc atc acc gac gaa ctc gcc cgc ctc aac ccg aat acc aca   643
His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro Asn Thr Thr
                170                 175                 180

ccc agc gcc gag gag cta cgc acc caa gcc ctg agt caa gcg atc tgg   691
Pro Ser Ala Glu Glu Leu Arg Thr Gln Ala Leu Ser Gln Ala Ile Trp
            185                 190                 195

cgc acc cca gaa gac ctc cgc acg tgg cta cgc cac cac gtc acc acc   739
Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His His Val Thr Thr
        200                 205                 210

gcc aat aaa aac aac ccc aac ccc atc acc gcc atg aaa agg cgc tac   787
Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys Arg Arg Tyr
    215                 220                 225

ctc gct gta ggt aaa ccc gat gcc gac aac atg gtc cgc atc agc ggc   835
Leu Ala Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg Ile Ser Gly
230                 235                 240                 245

ctc gtg ccc gca gcc acc gca gca ctg atc acc gcg aac acc gca ccg   883
Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn Thr Ala Pro
                250                 255                 260

tta acc aaa cgc ggc aac ctc gtg gat cta ccc gca gca gaa gat atg   931
Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala Glu Asp Met
            265                 270                 275

cgc acc cgc ggg caa cgc cat gcg gac gcg ttg cat cac atc atg gag   979
Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His Ile Met Glu
        280                 285                 290

atc tac aac cac ggt att gtc acc cca gct cgt ggt gga aca gcc agc   1027
Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly Thr Ala Ser
    295                 300                 305

atc atc atc tcc atg acc acc gat gat ctt gat gag atc               1066
Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile
310                 315                 320
```

<210> 1434
<211> 322

<212> PRT
<213> Corynebacterium glutamicum

<400> 1434

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Met Ser Ile Thr Thr His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala
  1               5                  10                  15

Ile Asp Asn His Leu Ala Ser Met Leu Asp His Gly Val Thr Pro Asp
             20                  25                  30

Gln Tyr Lys Ala Ile Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile
         35                  40                  45

Asn His His Ala Thr Ile Ala Ala Gln Thr Thr Ala Leu Ala Glu Arg
     50                  55                  60

Thr Asn Ala Ala His Thr Ile Gly Ser Thr His Leu Ile Asp Tyr Leu
 65                  70                  75                  80

Thr Thr Thr Phe Gly Leu Ser Lys Ala Arg Ala His His Arg Ile Asn
                 85                  90                  95

Leu Ala His Ser Leu Tyr Pro Ile Pro Lys Pro Asn Pro Gly Ser Gly
            100                 105                 110

Asn Gly Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp
        115                 120                 125

Ser Gly Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp
    130                 135                 140

Lys Pro Glu Asp Gly Lys Pro Asp Gly Asp Lys Pro Arg Gly Pro Arg
145                 150                 155                 160

Ile Ser Ala Glu Lys His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu
                165                 170                 175

Asn Pro Asn Thr Thr Pro Ser Ala Glu Glu Leu Arg Thr Gln Ala Leu
            180                 185                 190

Ser Gln Ala Ile Trp Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg
        195                 200                 205

His His Val Thr Thr Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala
    210                 215                 220

Met Lys Arg Arg Tyr Leu Ala Val Gly Lys Pro Asp Ala Asp Asn Met
225                 230                 235                 240

Val Arg Ile Ser Gly Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr
                245                 250                 255

Ala Asn Thr Ala Pro Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro
            260                 265                 270

Ala Ala Glu Asp Met Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu
        275                 280                 285

His His Ile Met Glu Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg
    290                 295                 300
```

```
Gly Gly Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp
305                 310                 315                 320

Glu Ile
```

<210> 1435
<211> 1558
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (12)..(1535)
<223> RXN03053

<400> 1435

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gaggtaaagg attc cac ttc acc tcg act gag ttt gcc ggt tct tat tct   50
            Phe His Phe Thr Ser Thr Glu Phe Ala Gly Ser Tyr Ser
              1               5                  10

ttg gtc acc aat ggt ctt aac gat gtt gct ggc gaa tac gtc ggt gtc   98
Leu Val Thr Asn Gly Leu Asn Asp Val Ala Gly Glu Tyr Val Gly Val
     15                  20                  25

atg cgt ggc gat gtc aac aac tcc gct gtg ctt ttt gat gtg gat cgc   146
Met Arg Gly Asp Val Asn Asn Ser Ala Val Leu Phe Asp Val Asp Arg
 30                  35                  40                  45

tgg tcg gga cat gtc gta tgc gca gat agc tcg att aat aca tca cca   194
Trp Ser Gly His Val Val Cys Ala Asp Ser Ser Ile Asn Thr Ser Pro
                 50                  55                  60

cta ctt aag cgt ccc cgt gtc gtt gac atg tgg ggg tcg aag att tct   242
Leu Leu Lys Arg Pro Arg Val Val Asp Met Trp Gly Ser Lys Ile Ser
             65                  70                  75

cag gca gcg cta ctg aat aac cgt cgc gta gtg cac ctg gtg ctc aat   290
Gln Ala Ala Leu Leu Asn Asn Arg Arg Val Val His Leu Val Leu Asn
         80                  85                  90

ggt gcc aag ctc gat gaa atg gga cca aag cta gaa tcc atg acc gct   338
Gly Ala Lys Leu Asp Glu Met Gly Pro Lys Leu Glu Ser Met Thr Ala
     95                  100                 105

cat gtg gat atg act agc gga gat ctc aac atg ttc gag ctg ttt ggt   386
His Val Asp Met Thr Ser Gly Asp Leu Asn Met Phe Glu Leu Phe Gly
110                 115                 120                 125

aag caa gaa gat gag ctg tcg ctg tat tcc aca cac atg gac aaa atc   434
Lys Gln Glu Asp Glu Leu Ser Leu Tyr Ser Thr His Met Asp Lys Ile
                130                 135                 140

gtg ttt atg acc gag cag gca ttg ggc gat aag acc tct gag ctg gcg   482
Val Phe Met Thr Glu Gln Ala Leu Gly Asp Lys Thr Ser Glu Leu Ala
            145                 150                 155

cta ttg cgc gga aag ctc aaa gaa att att aca gcc ttt tat gtg gat   530
Leu Leu Arg Gly Lys Leu Lys Glu Ile Ile Thr Ala Phe Tyr Val Asp
        160                 165                 170
```

```
atg aaa atg tgg gct ctt aat gcc ggt gaa aac cgt gac aag ctg cgt   578
Met Lys Met Trp Ala Leu Asn Ala Gly Glu Asn Arg Asp Lys Leu Arg
    175                 180                 185

ctt gtt ggt gtg cct cat gag cag atc ccg ttg ctc tct gtc ttc gtg   626
Leu Val Gly Val Pro His Glu Gln Ile Pro Leu Leu Ser Val Phe Val
190                 195                 200                 205

tcc tat ttg gat caa gaa tat gag cgc cag aaa tat gag gga acc aaa   674
Ser Tyr Leu Asp Gln Glu Tyr Glu Arg Gln Lys Tyr Glu Gly Thr Lys
                210                 215                 220

gac cct gaa atg ttt cgt gcc att tct gtg ctg cga ctg acc tat aag   722
Asp Pro Glu Met Phe Arg Ala Ile Ser Val Leu Arg Leu Thr Tyr Lys
            225                 230                 235

gat ttg ctc gat act cat ggc gat ctg ttt aat cag cac acg gca gat   770
Asp Leu Leu Asp Thr His Gly Asp Leu Phe Asn Gln His Thr Ala Asp
        240                 245                 250

ggc att gat tct gtg aac tct gca cgc cgc gtg atc tat gat ttt tct   818
Gly Ile Asp Ser Val Asn Ser Ala Arg Arg Val Ile Tyr Asp Phe Ser
    255                 260                 265

gga gtg ctg cga cgt ggc gca ggt gtc gcg atg gca cag ctg gtt aac   866
Gly Val Leu Arg Arg Gly Ala Gly Val Ala Met Ala Gln Leu Val Asn
270                 275                 280                 285

gtg att ggt ttt gct gtg gag acg ctt ggt caa ggc gat gtg gtc atc   914
Val Ile Gly Phe Ala Val Glu Thr Leu Gly Gln Gly Asp Val Val Ile
                290                 295                 300

att cac ggt gct gat ggc att gtc gat gtt gat gtt cag gat tat ttg   962
Ile His Gly Ala Asp Gly Ile Val Asp Val Asp Val Gln Asp Tyr Leu
            305                 310                 315

gct aat cag ttc gca tat atg gct gag cgt ggt ggg cga gtg gcg tat  1010
Ala Asn Gln Phe Ala Tyr Met Ala Glu Arg Gly Gly Arg Val Ala Tyr
        320                 325                 330

ctc tac agc tcg atg gac gcg atg ctt ggc act gtt ggc ttc aat caa  1058
Leu Tyr Ser Ser Met Asp Ala Met Leu Gly Thr Val Gly Phe Asn Gln
    335                 340                 345

ttc caa cgt gct gcg tac acc att ttg ggc ccg atg aac gtt gac tcg  1106
Phe Gln Arg Ala Ala Tyr Thr Ile Leu Gly Pro Met Asn Val Asp Ser
350                 355                 360                 365

gtg gat act tat caa tct ctg att aat agt cag atc ccg atg gac ttg  1154
Val Asp Thr Tyr Gln Ser Leu Ile Asn Ser Gln Ile Pro Met Asp Leu
                370                 375                 380

gca cgg ttg gtg aca acg cag aat tct ggt gcg agc tat ttg cgc cga  1202
Ala Arg Leu Val Thr Thr Gln Asn Ser Gly Ala Ser Tyr Leu Arg Arg
            385                 390                 395

gga tct acc aat gtg gtg ttt gaa acc aac ctt gcg ttg ggc gtt aat  1250
Gly Ser Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val Asn
        400                 405                 410
```

```
cct tat atg gag cag cgt cgc aag att gaa gca cag cga ggt cag cga   1298
Pro Tyr Met Glu Gln Arg Arg Lys Ile Glu Ala Gln Arg Gly Gln Arg
    415                 420                 425

cga tcc aag cga gac aag cac tac ggt ggt ggc acg acg atg gtg ggc   1346
Arg Ser Lys Arg Asp Lys His Tyr Gly Gly Gly Thr Thr Met Val Gly
430                 435                 440                 445

aca gcg gat ctt gat gtt gtc gca att cag gcg aag gcc gag cac cgc   1394
Thr Ala Asp Leu Asp Val Val Ala Ile Gln Ala Lys Ala Glu His Arg
                450                 455                 460

gaa gag cgc ttt gat gag aaa tct gcg cgc aag atg aag gag ctt gat   1442
Glu Glu Arg Phe Asp Glu Lys Ser Ala Arg Lys Met Lys Glu Leu Asp
            465                 470                 475

gat gta gaa gcg aaa gaa cta gct ttg aaa act ggg ccg aag aat ctt   1490
Asp Val Glu Ala Lys Glu Leu Ala Leu Lys Thr Gly Pro Lys Asn Leu
        480                 485                 490

gat gat gcg ctt gca cag gtg gag aag aag cgc ctg gcg aag cgg       1535
Asp Asp Ala Leu Ala Gln Val Glu Lys Lys Arg Leu Ala Lys Arg
    495                 500                 505

tagttgttgg ctgtggtgaa taa                                        1558
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<210> 1436
<211> 508
<212> PRT
<213> Corynebacterium glutamicum

<400> 1436

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Phe His Phe Thr Ser Thr Glu Phe Ala Gly Ser Tyr Ser Leu Val Thr
  1               5                  10                  15

Asn Gly Leu Asn Asp Val Ala Gly Glu Tyr Val Gly Val Met Arg Gly
             20                  25                  30

Asp Val Asn Asn Ser Ala Val Leu Phe Asp Val Asp Arg Trp Ser Gly
         35                  40                  45

His Val Val Cys Ala Asp Ser Ser Ile Asn Thr Ser Pro Leu Leu Lys
     50                  55                  60

Arg Pro Arg Val Val Asp Met Trp Gly Ser Lys Ile Ser Gln Ala Ala
 65                  70                  75                  80

Leu Leu Asn Asn Arg Arg Val Val His Leu Val Leu Asn Gly Ala Lys
                 85                  90                  95

Leu Asp Glu Met Gly Pro Lys Leu Glu Ser Met Thr Ala His Val Asp
            100                 105                 110

Met Thr Ser Gly Asp Leu Asn Met Phe Glu Leu Phe Gly Lys Gln Glu
        115                 120                 125

Asp Glu Leu Ser Leu Tyr Ser Thr His Met Asp Lys Ile Val Phe Met
    130                 135                 140

Thr Glu Gln Ala Leu Gly Asp Lys Thr Ser Glu Leu Ala Leu Leu Arg
```

```
145                 150                 155                 160

Gly Lys Leu Lys Glu Ile Ile Thr Ala Phe Tyr Val Asp Met Lys Met
                165                 170                 175

Trp Ala Leu Asn Ala Gly Glu Asn Arg Asp Lys Leu Arg Leu Val Gly
            180                 185                 190

Val Pro His Glu Gln Ile Pro Leu Leu Ser Val Phe Val Ser Tyr Leu
        195                 200                 205

Asp Gln Glu Tyr Glu Arg Gln Lys Tyr Glu Gly Thr Lys Asp Pro Glu
    210                 215                 220

Met Phe Arg Ala Ile Ser Val Leu Arg Leu Thr Tyr Lys Asp Leu Leu
225                 230                 235                 240

Asp Thr His Gly Asp Leu Phe Asn Gln His Thr Ala Asp Gly Ile Asp
                245                 250                 255

Ser Val Asn Ser Ala Arg Arg Val Ile Tyr Asp Phe Ser Gly Val Leu
            260                 265                 270

Arg Arg Gly Ala Gly Val Ala Met Ala Gln Leu Val Asn Val Ile Gly
        275                 280                 285

Phe Ala Val Glu Thr Leu Gly Gln Gly Asp Val Val Ile Ile His Gly
    290                 295                 300

Ala Asp Gly Ile Val Asp Val Asp Val Gln Asp Tyr Leu Ala Asn Gln
305                 310                 315                 320

Phe Ala Tyr Met Ala Glu Arg Gly Gly Arg Val Ala Tyr Leu Tyr Ser
                325                 330                 335

Ser Met Asp Ala Met Leu Gly Thr Val Gly Phe Asn Gln Phe Gln Arg
            340                 345                 350

Ala Ala Tyr Thr Ile Leu Gly Pro Met Asn Val Asp Ser Val Asp Thr
        355                 360                 365

Tyr Gln Ser Leu Ile Asn Ser Gln Ile Pro Met Asp Leu Ala Arg Leu
    370                 375                 380

Val Thr Thr Gln Asn Ser Gly Ala Ser Tyr Leu Arg Arg Gly Ser Thr
385                 390                 395                 400

Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val Asn Pro Tyr Met
                405                 410                 415

Glu Gln Arg Arg Lys Ile Glu Ala Gln Arg Gly Gln Arg Arg Ser Lys
            420                 425                 430

Arg Asp Lys His Tyr Gly Gly Gly Thr Thr Met Val Gly Thr Ala Asp
        435                 440                 445

Leu Asp Val Val Ala Ile Gln Ala Lys Ala Glu His Arg Glu Glu Arg
    450                 455                 460

Phe Asp Glu Lys Ser Ala Arg Lys Met Lys Glu Leu Asp Asp Val Glu
465                 470                 475                 480
```

```
Ala Lys Glu Leu Ala Leu Lys Thr Gly Pro Lys Asn Leu Asp Asp Ala
                485                 490                 495

Leu Ala Gln Val Glu Lys Lys Arg Leu Ala Lys Arg
            500                 505
```

<210> 1437
<211> 1559
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1536)
<223> FRXA02885

<400> 1437

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cga ggt aaa gga ttc cac ttc acc tcg act gag ttt gcc ggt tct tat   48
Arg Gly Lys Gly Phe His Phe Thr Ser Thr Glu Phe Ala Gly Ser Tyr
  1               5                  10                  15

tct ttg gtc acc aat ggt ctt aac gat gtt gct ggc gaa tac gtc ggt   96
Ser Leu Val Thr Asn Gly Leu Asn Asp Val Ala Gly Glu Tyr Val Gly
             20                  25                  30

gtc atg cgt ggc gat gtc aac aac tcc gct gtg ctt ttt gat gtg gat   144
Val Met Arg Gly Asp Val Asn Asn Ser Ala Val Leu Phe Asp Val Asp
         35                  40                  45

cgc tgg tcg gga cat gtc gta tgc gca gat agc tcg att aat aca tca   192
Arg Trp Ser Gly His Val Val Cys Ala Asp Ser Ser Ile Asn Thr Ser
     50                  55                  60

cca cta ctt aag cgt ccc cgt gtc gtt gac atg tgg ggg tcg aag att   240
Pro Leu Leu Lys Arg Pro Arg Val Val Asp Met Trp Gly Ser Lys Ile
 65                  70                  75                  80

tct cag gca gcg cta ctg aat aac cgt cgc gta gtg cac ctg gtg ctc   288
Ser Gln Ala Ala Leu Leu Asn Asn Arg Arg Val Val His Leu Val Leu
                 85                  90                  95

aat ggt gcc aag ctc gat gaa atg gga cca aag cta gaa tcc atg acc   336
Asn Gly Ala Lys Leu Asp Glu Met Gly Pro Lys Leu Glu Ser Met Thr
            100                 105                 110

gct cat gtg gat atg act agc gga gat ctc aac atg ttc gag ctg ttt   384
Ala His Val Asp Met Thr Ser Gly Asp Leu Asn Met Phe Glu Leu Phe
        115                 120                 125

ggt aag caa gaa gat gag ctg tcg ctg tat tcc aca cac atg gac aaa   432
Gly Lys Gln Glu Asp Glu Leu Ser Leu Tyr Ser Thr His Met Asp Lys
    130                 135                 140

atc gtg ttt atg acc gag cag gca ttg ggc gat aag acc tct gag ctg   480
Ile Val Phe Met Thr Glu Gln Ala Leu Gly Asp Lys Thr Ser Glu Leu
145                 150                 155                 160

gcg cta ttg cgc gga aag ctc aaa gaa att att aca gcc ttt tat gtg   528
Ala Leu Leu Arg Gly Lys Leu Lys Glu Ile Ile Thr Ala Phe Tyr Val
```

```
                    165                 170                 175

gat atg aaa atg tgg gct ctt aat gcc ggt gaa aac cgt gac aag ctg   576
Asp Met Lys Met Trp Ala Leu Asn Ala Gly Glu Asn Arg Asp Lys Leu
            180                 185                 190

cgt ctt gtt ggt gtg cct cat gag cag atc ccg ttg ctc tct gtc ttc   624
Arg Leu Val Gly Val Pro His Glu Gln Ile Pro Leu Leu Ser Val Phe
        195                 200                 205

gtg tcc tat ttg gat caa gaa tat gag cgc cag aaa tat gag gga acc   672
Val Ser Tyr Leu Asp Gln Glu Tyr Glu Arg Gln Lys Tyr Glu Gly Thr
    210                 215                 220

aaa gac cct gaa atg ttt cgt gcc att tct gtg ctg cga ctg acc tat   720
Lys Asp Pro Glu Met Phe Arg Ala Ile Ser Val Leu Arg Leu Thr Tyr
225                 230                 235                 240

aag gat ttg ctc gat act cat ggc gat ctg ttt aat cag cac acg gca   768
Lys Asp Leu Leu Asp Thr His Gly Asp Leu Phe Asn Gln His Thr Ala
                245                 250                 255

gat ggc att gat tct gtg aac tct gca cgc cgc gtg atc tat gat ttt   816
Asp Gly Ile Asp Ser Val Asn Ser Ala Arg Arg Val Ile Tyr Asp Phe
            260                 265                 270

tct gga gtg ctg cga cgt ggc gca ggt gtc gcg atg gca cag ctg gtt   864
Ser Gly Val Leu Arg Arg Gly Ala Gly Val Ala Met Ala Gln Leu Val
        275                 280                 285

aac gtg att ggt ttt gct gtg gag acg ctt ggt caa ggc gat gtg gtc   912
Asn Val Ile Gly Phe Ala Val Glu Thr Leu Gly Gln Gly Asp Val Val
    290                 295                 300

atc att cac ggt gct gat ggc att gtc gat gtt gat gtt cag gat tat   960
Ile Ile His Gly Ala Asp Gly Ile Val Asp Val Asp Val Gln Asp Tyr
305                 310                 315                 320

ttg gct aat cag ttc gca tat atg gct gag cgt ggt ggg cga gtg gcg   1008
Leu Ala Asn Gln Phe Ala Tyr Met Ala Glu Arg Gly Gly Arg Val Ala
                325                 330                 335

tat ctc tac agc tcg atg gac gcg atg ctt ggc act gtt ggc ttc aat   1056
Tyr Leu Tyr Ser Ser Met Asp Ala Met Leu Gly Thr Val Gly Phe Asn
            340                 345                 350

caa ttc caa cgt gct gcg tac acc att ttg ggc ccg atg aac gtt gac   1104
Gln Phe Gln Arg Ala Ala Tyr Thr Ile Leu Gly Pro Met Asn Val Asp
        355                 360                 365

tcg gtg gat act tat caa tct ctg att aat agt cag atc ccg atg gac   1152
Ser Val Asp Thr Tyr Gln Ser Leu Ile Asn Ser Gln Ile Pro Met Asp
    370                 375                 380

ttg gca cgg ttg gtg aca acg cag aat tct ggt gcg agc tat ttg cgc   1200
Leu Ala Arg Leu Val Thr Thr Gln Asn Ser Gly Ala Ser Tyr Leu Arg
385                 390                 395                 400

cga gga tct acc aat gtg gtg ttt gaa acc aac ctt gcg ttg ggc gtt   1248
Arg Gly Ser Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val
                405                 410                 415
```

```
aat cct tat atg gag cag cgt cgc aag att gaa gca cag cga ggt cag   1296
Asn Pro Tyr Met Glu Gln Arg Arg Lys Ile Glu Ala Gln Arg Gly Gln
            420                 425                 430

cga cga tcc aag cga gac aag cac tac ggt ggt ggc acg acg atg gtg   1344
Arg Arg Ser Lys Arg Asp Lys His Tyr Gly Gly Gly Thr Thr Met Val
        435                 440                 445

ggc aca gcg gat ctt gat gtt gtc gca att cag gcg aag gcc gag cac   1392
Gly Thr Ala Asp Leu Asp Val Val Ala Ile Gln Ala Lys Ala Glu His
    450                 455                 460

cgc gaa gag cgc ttt gat gag aaa tct gcg cgc aag atg aag gag ctt   1440
Arg Glu Glu Arg Phe Asp Glu Lys Ser Ala Arg Lys Met Lys Glu Leu
465                 470                 475                 480

gat gat gta gaa gcg aaa gaa cta gct ttg aaa act ggg ccg aag aat   1488
Asp Asp Val Glu Ala Lys Glu Leu Ala Leu Lys Thr Gly Pro Lys Asn
                485                 490                 495

ctt gat gat gcg ctt gca cag gtg gag aag aag cgc ctg gcg aag cgg   1536
Leu Asp Asp Ala Leu Ala Gln Val Glu Lys Lys Arg Leu Ala Lys Arg
            500                 505                 510

tagttgttgg ctgtggtgaa taa                                       1559


<210> 1438
<211> 512
<212> PRT
<213> Corynebacterium glutamicum

<400> 1438
Arg Gly Lys Gly Phe His Phe Thr Ser Thr Glu Phe Ala Gly Ser Tyr
  1               5                  10                  15

Ser Leu Val Thr Asn Gly Leu Asn Asp Val Ala Gly Glu Tyr Val Gly
             20                  25                  30

Val Met Arg Gly Asp Val Asn Asn Ser Ala Val Leu Phe Asp Val Asp
         35                  40                  45

Arg Trp Ser Gly His Val Val Cys Ala Asp Ser Ser Ile Asn Thr Ser
     50                  55                  60

Pro Leu Leu Lys Arg Pro Arg Val Val Asp Met Trp Gly Ser Lys Ile
 65                  70                  75                  80

Ser Gln Ala Ala Leu Leu Asn Asn Arg Arg Val Val His Leu Val Leu
                 85                  90                  95

Asn Gly Ala Lys Leu Asp Glu Met Gly Pro Lys Leu Glu Ser Met Thr
            100                 105                 110

Ala His Val Asp Met Thr Ser Gly Asp Leu Asn Met Phe Glu Leu Phe
        115                 120                 125

Gly Lys Gln Glu Asp Glu Leu Ser Leu Tyr Ser Thr His Met Asp Lys
    130                 135                 140
```

```
Ile Val Phe Met Thr Glu Gln Ala Leu Gly Asp Lys Thr Ser Glu Leu
145                 150                 155                 160

Ala Leu Leu Arg Gly Lys Leu Lys Glu Ile Ile Thr Ala Phe Tyr Val
                165                 170                 175

Asp Met Lys Met Trp Ala Leu Asn Ala Gly Glu Asn Arg Asp Lys Leu
            180                 185                 190

Arg Leu Val Gly Val Pro His Glu Gln Ile Pro Leu Leu Ser Val Phe
        195                 200                 205

Val Ser Tyr Leu Asp Gln Glu Tyr Glu Arg Gln Lys Tyr Glu Gly Thr
    210                 215                 220

Lys Asp Pro Glu Met Phe Arg Ala Ile Ser Val Leu Arg Leu Thr Tyr
225                 230                 235                 240

Lys Asp Leu Leu Asp Thr His Gly Asp Leu Phe Asn Gln His Thr Ala
                245                 250                 255

Asp Gly Ile Asp Ser Val Asn Ser Ala Arg Arg Val Ile Tyr Asp Phe
            260                 265                 270

Ser Gly Val Leu Arg Arg Gly Ala Gly Val Ala Met Ala Gln Leu Val
        275                 280                 285

Asn Val Ile Gly Phe Ala Val Glu Thr Leu Gly Gln Gly Asp Val Val
    290                 295                 300

Ile Ile His Gly Ala Asp Gly Ile Val Asp Val Asp Val Gln Asp Tyr
305                 310                 315                 320

Leu Ala Asn Gln Phe Ala Tyr Met Ala Glu Arg Gly Gly Arg Val Ala
                325                 330                 335

Tyr Leu Tyr Ser Ser Met Asp Ala Met Leu Gly Thr Val Gly Phe Asn
            340                 345                 350

Gln Phe Gln Arg Ala Ala Tyr Thr Ile Leu Gly Pro Met Asn Val Asp
        355                 360                 365

Ser Val Asp Thr Tyr Gln Ser Leu Ile Asn Ser Gln Ile Pro Met Asp
    370                 375                 380

Leu Ala Arg Leu Val Thr Thr Gln Asn Ser Gly Ala Ser Tyr Leu Arg
385                 390                 395                 400

Arg Gly Ser Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val
                405                 410                 415

Asn Pro Tyr Met Glu Gln Arg Arg Lys Ile Glu Ala Gln Arg Gly Gln
            420                 425                 430

Arg Arg Ser Lys Arg Asp Lys His Tyr Gly Gly Gly Thr Thr Met Val
        435                 440                 445

Gly Thr Ala Asp Leu Asp Val Val Ala Ile Gln Ala Lys Ala Glu His
    450                 455                 460

Arg Glu Glu Arg Phe Asp Glu Lys Ser Ala Arg Lys Met Lys Glu Leu
```

```
465                 470                 475                 480

Asp Asp Val Glu Ala Lys Glu Leu Ala Leu Lys Thr Gly Pro Lys Asn
                485                 490                 495

Leu Asp Asp Ala Leu Ala Gln Val Glu Lys Lys Arg Leu Ala Lys Arg
            500                 505                 510
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<210> 1439
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> RXN03055

Sequence Listing

<400> 1439

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aaggtcagcc gtatttcggt cagtcagcaa ctaattacgc ttatcttccg tgtacgatag 60

accgtagtta acataaggaa tggaatagga gaattgcggc atg tat tcc gac aag   115
                                            Met Tyr Ser Asp Lys
                                              1               5

ctg att ctc ttg ttc ctt tct gag cag gat tca agc tat gaa tgc tgc   163
Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser Ser Tyr Glu Cys Cys
                10                  15                  20

gta ggt tta tta gat ggc tca gat gga cgt gat tat att gaa aag ctt   211
Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp Tyr Ile Glu Lys Leu
            25                  30                  35

ctg aag ggt agg aag ctg aag aac cat ttt ctt gaa tgg gaa gat att   259
Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu Glu Trp Glu Asp Ile
        40                  45                  50

aac aag gct gat gtt gct cgt gaa gaa ata tat aaa ggg caa ttg gtg   307
Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr Lys Gly Gln Leu Val
    55                  60                  65

cat ctg gtg ttt gtg acg gct ctt tcc acg cct ggt gaa att tct ttt   355
His Leu Val Phe Val Thr Ala Leu Ser Thr Pro Gly Glu Ile Ser Phe
70                  75                  80                  85

gtt ttt cca ggt caa tct ctt atg agt gca aca ctc gaa gaa gac ttt   403
Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr Leu Glu Glu Asp Phe
                90                  95                  100

gct gcg ctt gtg ctc gaa gag gag cgc aca tca ttt aga cct gaa ctg   451
Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser Phe Arg Pro Glu Leu
            105                 110                 115

tct cac ctg tgg tca ctc ccc gta ggg tgg gta gct ccg ggg ctt gag   499
Ser His Leu Trp Ser Leu Pro Val Gly Trp Val Ala Pro Gly Leu Glu
        120                 125                 130
```

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ggt ttc gtg gag cgt aat tcc gag gca gct tgaaccaccg ctttctgagc     549
Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
    135                 140

cgg                                                               552


<210> 1440
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 1440
Met Tyr Ser Asp Lys Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser
  1               5                  10                  15

Ser Tyr Glu Cys Cys Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp
             20                  25                  30

Tyr Ile Glu Lys Leu Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu
         35                  40                  45

Glu Trp Glu Asp Ile Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr
     50                  55                  60

Lys Gly Gln Leu Val His Leu Val Phe Val Thr Ala Leu Ser Thr Pro
 65                  70                  75                  80

Gly Glu Ile Ser Phe Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr
                 85                  90                  95

Leu Glu Glu Asp Phe Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser
            100                 105                 110

Phe Arg Pro Glu Leu Ser His Leu Trp Ser Leu Pro Val Gly Trp Val
        115                 120                 125

Ala Pro Gly Leu Glu Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
    130                 135                 140


<210> 1441
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> FRXA00261

<400> 1441
aaggtcagcc gtatttcggt cagtcagcaa ctaattacgc ttatcttccg tgtacgatag 60

accgtagtta acataaggaa tggaatagga gaattgcggc atg tat tcc gac aag   115
                                            Met Tyr Ser Asp Lys
                                              1               5

ctg att ctc ttg ttc ctt tct gag cag gat tca agc tat gaa tgc tgc   163
Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser Ser Tyr Glu Cys Cys
                10                  15                  20
```

```
gta ggt tta tta gat ggc tca gat gga cgt gat tat att gaa aag ctt   211
Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp Tyr Ile Glu Lys Leu
             25                  30                  35

ctg aag ggt agg aag ctg aag aac cat ttt ctt gaa tgg gaa gat att   259
Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu Glu Trp Glu Asp Ile
         40                  45                  50

aac aag gct gat gtt gct cgt gaa gaa ata tat aaa ggg caa ttg gtg   307
Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr Lys Gly Gln Leu Val
     55                  60                  65

cat ctg gtg ttt gtg acg gct ctt tcc acg cct ggt gaa att tct ttt   355
His Leu Val Phe Val Thr Ala Leu Ser Thr Pro Gly Glu Ile Ser Phe
 70                  75                  80                  85

gtt ttt cca ggt caa tct ctc atg agt gca aca ctc gaa gaa gac ttt   403
Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr Leu Glu Glu Asp Phe
             90                  95                 100

gct gca ctt gtg ctc gaa gag gag cgc aca tca ttt aga cct gat ctg   451
Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser Phe Arg Pro Asp Leu
            105                 110                 115

tct cac ttg tgg tca ctc ccc gta ggg tgg gta gct ccg ggg ctt gag   499
Ser His Leu Trp Ser Leu Pro Val Gly Trp Val Ala Pro Gly Leu Glu
        120                 125                 130

ggt ttc gtg gag cgt aat tca gag gca gct tgaaccaccg ctctttgagc     549
Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
    135                 140

cgg                                                               552


<210> 1442
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 1442
Met Tyr Ser Asp Lys Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser
  1               5                  10                  15

Ser Tyr Glu Cys Cys Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp
             20                  25                  30

Tyr Ile Glu Lys Leu Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu
         35                  40                  45

Glu Trp Glu Asp Ile Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr
     50                  55                  60

Lys Gly Gln Leu Val His Leu Val Phe Val Thr Ala Leu Ser Thr Pro
 65                  70                  75                  80

Gly Glu Ile Ser Phe Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr
                 85                  90                  95

Leu Glu Glu Asp Phe Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser
```

```
            100                 105                 110

Phe Arg Pro Asp Leu Ser His Leu Trp Ser Leu Pro Val Gly Trp Val
        115                 120                 125

Ala Pro Gly Leu Glu Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
    130                 135                 140


<210> 1443
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> FRXA02888

<400> 1443
aaggtcagcc gtatttcggt cagtcagcaa ctaattacgc ttatcttccg tgtacgatag 60

accgtagtta acataaggaa tggaatagga gaattgcggc atg tat tcc gac aag   115
                                            Met Tyr Ser Asp Lys
                                              1               5

ctg att ctc ttg ttc ctt tct gag cag gat tca agc tat gaa tgc tgc   163
Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser Ser Tyr Glu Cys Cys
                10                  15                  20

gta ggt tta tta gat ggc tca gat gga cgt gat tat att gaa aag ctt   211
Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp Tyr Ile Glu Lys Leu
            25                  30                  35

ctg aag ggt agg aag ctg aag aac cat ttt ctt gaa tgg gaa gat att   259
Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu Glu Trp Glu Asp Ile
        40                  45                  50

aac aag gct gat gtt gct cgt gaa gaa ata tat aaa ggg caa ttg gtg   307
Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr Lys Gly Gln Leu Val
    55                  60                  65

cat ctg gtg ttt gtg acg gct ctt tcc acg cct ggt gaa att tct ttt   355
His Leu Val Phe Val Thr Ala Leu Ser Thr Pro Gly Glu Ile Ser Phe
70                  75                  80                  85

gtt ttt cca ggt caa tct ctt atg agt gca aca ctc gaa gaa gac ttt   403
Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr Leu Glu Glu Asp Phe
                90                  95                  100

gct gcg ctt gtg ctc gaa gag gag cgc aca tca ttt aga cct gaa ctg   451
Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser Phe Arg Pro Glu Leu
            105                 110                 115

tct cac ctg tgg tca ctc ccc gta ggg tgg gta gct ccg ggg ctt gag   499
Ser His Leu Trp Ser Leu Pro Val Gly Trp Val Ala Pro Gly Leu Glu
        120                 125                 130

ggt ttc gtg gag cgt aat tcc gag gca gct tgaaccaccg ctttctgagc     549
Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
    135                 140
```

cgg 552

<210> 1444
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 1444
Met Tyr Ser Asp Lys Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser
1 5 10 15

Ser Tyr Glu Cys Cys Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp
20 25 30

Tyr Ile Glu Lys Leu Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu
35 40 45

Glu Trp Glu Asp Ile Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr
50 55 60

Lys Gly Gln Leu Val His Leu Val Phe Val Thr Ala Leu Ser Thr Pro
65 70 75 80

Gly Glu Ile Ser Phe Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr
85 90 95

Leu Glu Glu Asp Phe Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser
100 105 110

Phe Arg Pro Glu Leu Ser His Leu Trp Ser Leu Pro Val Gly Trp Val
115 120 125

Ala Pro Gly Leu Glu Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
130 135 140

<210> 1445
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> RXN03059

<400> 1445
gtgtcatttt cttggcggac ggtcgtatcg tgaaccagtt gtttgatccc accatcgagg 60

aaatcttggc cacgatgaac ggaattgagg atattgccta atg aat tcc ggt tcc 115
Met Asn Ser Gly Ser
1 5

aca atg cgc aga atc agt ctg cgc aat att ggc gcg cac aag gtc agg 163
Thr Met Arg Arg Ile Ser Leu Arg Asn Ile Gly Ala His Lys Val Arg
10 15 20

ctg ttt ttg aca gtt ctg gca gtg gtg ctc ggc acg tct ttt gtt tcc 211
Leu Phe Leu Thr Val Leu Ala Val Val Leu Gly Thr Ser Phe Val Ser

```
            25                  30                  35

ggc gcg atg atg ttt acc aac gcg ctg tcc tcc act ttt gat gag gct   259
Gly Ala Met Met Phe Thr Asn Ala Leu Ser Ser Thr Phe Asp Glu Ala
         40                  45                  50

att gcc agc agc ttt gac ggc gtg gat gtg gtg gtt tca cca aac ggt   307
Ile Ala Ser Ser Phe Asp Gly Val Asp Val Val Val Ser Pro Asn Gly
     55                  60                  65

gca tca gag gtg cag ggt gtt cct gtt gag acg gtt gaa tct ttg cgt   355
Ala Ser Glu Val Gln Gly Val Pro Val Glu Thr Val Glu Ser Leu Arg
 70                  75                  80                  85

gag gat tcc cgc atc aac cat ctc aac atc aac ggt tcc cag act gtc   403
Glu Asp Ser Arg Ile Asn His Leu Asn Ile Asn Gly Ser Gln Thr Val
                 90                  95                 100

gtt ctg gcg gat gct gat tcc aag gca att caa acg act ggg gga tcg   451
Val Leu Ala Asp Ala Asp Ser Lys Ala Ile Gln Thr Thr Gly Gly Ser
            105                 110                 115

tcg tta agc att tat tac agc gcg gac gac gcg gtt gcc cag gca cct   499
Ser Leu Ser Ile Tyr Tyr Ser Ala Asp Asp Ala Val Ala Gln Ala Pro
        120                 125                 130

gaa ttg gct gag gga gag gca ccg act ggc acc gaa gag gtg ctt gcc   547
Glu Leu Ala Glu Gly Glu Ala Pro Thr Gly Thr Glu Glu Val Leu Ala
    135                 140                 145

tcg aag gcg ggc gct gag gcg aat ggc ctg gag taggggacca gatcttggtc 600
Ser Lys Ala Gly Ala Glu Ala Asn Gly Leu Glu
150                 155                 160

gtg                                                               603


<210> 1446
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 1446
Met Asn Ser Gly Ser Thr Met Arg Arg Ile Ser Leu Arg Asn Ile Gly
  1               5                  10                  15

Ala His Lys Val Arg Leu Phe Leu Thr Val Leu Ala Val Val Leu Gly
             20                  25                  30

Thr Ser Phe Val Ser Gly Ala Met Met Phe Thr Asn Ala Leu Ser Ser
         35                  40                  45

Thr Phe Asp Glu Ala Ile Ala Ser Ser Phe Asp Gly Val Asp Val Val
     50                  55                  60

Val Ser Pro Asn Gly Ala Ser Glu Val Gln Gly Val Pro Val Glu Thr
 65                  70                  75                  80

Val Glu Ser Leu Arg Glu Asp Ser Arg Ile Asn His Leu Asn Ile Asn
                 85                  90                  95
```

```
Gly Ser Gln Thr Val Val Leu Ala Asp Ala Asp Ser Lys Ala Ile Gln
            100                 105                 110

Thr Thr Gly Gly Ser Ser Leu Ser Ile Tyr Tyr Ser Ala Asp Asp Ala
        115                 120                 125

Val Ala Gln Ala Pro Glu Leu Ala Glu Gly Glu Ala Pro Thr Gly Thr
    130                 135                 140

Glu Glu Val Leu Ala Ser Lys Ala Gly Ala Glu Ala Asn Gly Leu Glu
145                 150                 155                 160
```

<210> 1447
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> FRXA02899

<400> 1447

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gtgtcatttt cttggcggac ggtcgtatcg tgaaccagtt gtttgatccc accatcgagg 60

aaatcttggc cacgatgaac ggaattgagg atattgccta atg aat tcc ggt tcc   115
                                              Met Asn Ser Gly Ser
                                                1               5

aca atg cgc aga atc agt ctg cgc aat att ggc gcg cac aag gtc agg   163
Thr Met Arg Arg Ile Ser Leu Arg Asn Ile Gly Ala His Lys Val Arg
                10                  15                  20

ctg ttt ttg aca gtt ctg gca gtg gtg ctc ggc acg tct ttt gtt tcc   211
Leu Phe Leu Thr Val Leu Ala Val Val Leu Gly Thr Ser Phe Val Ser
            25                  30                  35

ggc gcg atg atg ttt acc aac gcg ctg tcc tcc act ttt gat gag gct   259
Gly Ala Met Met Phe Thr Asn Ala Leu Ser Ser Thr Phe Asp Glu Ala
        40                  45                  50

att gcc agc agc ttt gac ggc gtg gat gtg gtg gtt tca cca aac ggt   307
Ile Ala Ser Ser Phe Asp Gly Val Asp Val Val Val Ser Pro Asn Gly
    55                  60                  65

gca tca gag gtg cag ggt gtt cct gtt gag acg gtt gaa tct ttg cgt   355
Ala Ser Glu Val Gln Gly Val Pro Val Glu Thr Val Glu Ser Leu Arg
70                  75                  80                  85

gag gat tcc cgc atc aac cat ctc aac atc aac ggt tcc cag act gtc   403
Glu Asp Ser Arg Ile Asn His Leu Asn Ile Asn Gly Ser Gln Thr Val
                90                  95                  100

gtt ctg gcg gat gct gat tcc aag gca att caa acg act ggg gga tcg   451
Val Leu Ala Asp Ala Asp Ser Lys Ala Ile Gln Thr Thr Gly Gly Ser
            105                 110                 115
```

```
tcg tta agc att tat tac agc gcg gac gac gcg gtt gcc cag gca cct   499
Ser Leu Ser Ile Tyr Tyr Ser Ala Asp Asp Ala Val Ala Gln Ala Pro
        120                 125                 130

gaa ttg gct gag gga gag gca ccg act ggc acc gaa gag gtg ctt gcc   547
Glu Leu Ala Glu Gly Glu Ala Pro Thr Gly Thr Glu Glu Val Leu Ala
    135                 140                 145

tcg aag gcg ggc gct gag gcg aat ggc ctg gag taggggacca gatcttggtc 600
Ser Lys Ala Gly Ala Glu Ala Asn Gly Leu Glu
150                 155                 160

gtg                                                               603
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<210> 1448
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 1448

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Met Asn Ser Gly Ser Thr Met Arg Arg Ile Ser Leu Arg Asn Ile Gly
  1               5                  10                  15

Ala His Lys Val Arg Leu Phe Leu Thr Val Leu Ala Val Val Leu Gly
             20                  25                  30

Thr Ser Phe Val Ser Gly Ala Met Met Phe Thr Asn Ala Leu Ser Ser
         35                  40                  45

Thr Phe Asp Glu Ala Ile Ala Ser Ser Phe Asp Gly Val Asp Val Val
     50                  55                  60

Val Ser Pro Asn Gly Ala Ser Glu Val Gln Gly Val Pro Val Glu Thr
 65                  70                  75                  80

Val Glu Ser Leu Arg Glu Asp Ser Arg Ile Asn His Leu Asn Ile Asn
                 85                  90                  95

Gly Ser Gln Thr Val Val Leu Ala Asp Ala Asp Ser Lys Ala Ile Gln
            100                 105                 110

Thr Thr Gly Gly Ser Ser Leu Ser Ile Tyr Tyr Ser Ala Asp Asp Ala
        115                 120                 125

Val Ala Gln Ala Pro Glu Leu Ala Glu Gly Glu Ala Pro Thr Gly Thr
    130                 135                 140

Glu Glu Val Leu Ala Ser Lys Ala Gly Ala Glu Ala Asn Gly Leu Glu
145                 150                 155                 160
```

<210> 1449
<211> 622
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(622)
<223> RXN03062

<400> 1449
gatgagtatt ctctccgagg caacgaagtt aatatgtcca tgagggcgaa gttgtagaca 60

atatttggcc catatggata attgacagga gtttaacgcc atg gaa acc cca acc 115
Met Glu Thr Pro Thr
1 5

caa gac atg gat gtc cgc tgg tta tac acc caa agc cag ctc aaa ctc 163
Gln Asp Met Asp Val Arg Trp Leu Tyr Thr Gln Ser Gln Leu Lys Leu
10 15 20

cgc gaa att ctc ccc aca aac aaa acc ttc gat gtc atc caa atc agc 211
Arg Glu Ile Leu Pro Thr Asn Lys Thr Phe Asp Val Ile Gln Ile Ser
25 30 35

gaa ctc gtt gac ccc acc gac ttc atc agg ccc aac agc gtg gtc tta 259
Glu Leu Val Asp Pro Thr Asp Phe Ile Arg Pro Asn Ser Val Val Leu
40 45 50

tcc gtt ggc atc gcc ttc gca gaa acg ccc gac ggg ctt cgc gat tgg 307
Ser Val Gly Ile Ala Phe Ala Glu Thr Pro Asp Gly Leu Arg Asp Trp
55 60 65

gca cac cga ctc gcc gac gca ggg gtc atc gcg atc ggg ttc ggc tcc 355
Ala His Arg Leu Ala Asp Ala Gly Val Ile Ala Ile Gly Phe Gly Ser
70 75 80 85

ggc ctc acc ttc cca cag gtt ccg cag gcg ctt atc gac gcc tcc ctc 403
Gly Leu Thr Phe Pro Gln Val Pro Gln Ala Leu Ile Asp Ala Ser Leu
90 95 100

cac ctt ggc ctc ggc ctc ttt gaa gtc ccc cgt gaa att cca ttt atc 451
His Leu Gly Leu Gly Leu Phe Glu Val Pro Arg Glu Ile Pro Phe Ile
105 110 115

tcg atc acc tcc agc gtg cgt gat gag caa acc cgc cgt gcc ggc cgc 499
Ser Ile Thr Ser Ser Val Arg Asp Glu Gln Thr Arg Arg Ala Gly Arg
120 125 130

ctg caa caa gaa ctc ctc ctg gaa cag gaa cgg ctt aac tcc atc gcc 547
Leu Gln Gln Glu Leu Leu Leu Glu Gln Glu Arg Leu Asn Ser Ile Ala
135 140 145

atc tcc ggt ggc atc gaa gcc ctg tgc cgt gct gcc gcc gac tat ttg 595
Ile Ser Gly Gly Ile Glu Ala Leu Cys Arg Ala Ala Ala Asp Tyr Leu
150 155 160 165

ggt ggt gca gta acc atc gtg gac agc 622
Gly Gly Ala Val Thr Ile Val Asp Ser
170

<210> 1450
<211> 174
<212> PRT
<213> Corynebacterium glutamicum

<400> 1450
Met Glu Thr Pro Thr Gln Asp Met Asp Val Arg Trp Leu Tyr Thr Gln
1 5 10 15

Ser Gln Leu Lys Leu Arg Glu Ile Leu Pro Thr Asn Lys Thr Phe Asp
20 25 30

Val Ile Gln Ile Ser Glu Leu Val Asp Pro Thr Asp Phe Ile Arg Pro
35 40 45

Asn Ser Val Val Leu Ser Val Gly Ile Ala Phe Ala Glu Thr Pro Asp
50 55 60

Gly Leu Arg Asp Trp Ala His Arg Leu Ala Asp Ala Gly Val Ile Ala
65 70 75 80

Ile Gly Phe Gly Ser Gly Leu Thr Phe Pro Gln Val Pro Gln Ala Leu
85 90 95

Ile Asp Ala Ser Leu His Leu Gly Leu Gly Leu Phe Glu Val Pro Arg
100 105 110

Glu Ile Pro Phe Ile Ser Ile Thr Ser Ser Val Arg Asp Glu Gln Thr
115 120 125

Arg Arg Ala Gly Arg Leu Gln Gln Glu Leu Leu Leu Glu Gln Glu Arg
130 135 140

Leu Asn Ser Ile Ala Ile Ser Gly Gly Ile Glu Ala Leu Cys Arg Ala
145 150 155 160

Ala Ala Asp Tyr Leu Gly Gly Ala Val Thr Ile Val Asp Ser
165 170

<210> 1451
<211> 786
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(763)
<223> RXN03066

<400> 1451
aactgttggc atggcgaagt acaatgttcg tgcaactggt cacgtggagc gcatcgtccg 60

cgaaatcacc gcggcgtaat agcaccagct taaaaacctt atg aca tca gac aaa 115
Met Thr Ser Asp Lys
1 5

gac act gaa caa ttg gaa gcg gca ggc act gaa att tta atg cct cgc 163
Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu Ile Leu Met Pro Arg
10 15 20

cgc cgt ccg gca cag cag cgc agt cgt gaa cga ttc aat cga atc ctc 211
Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg Phe Asn Arg Ile Leu
25 30 35

acc gct gcg cgt tca gtg ctt gtc gat cta ggt ttt gaa tcg ttc acg 259

```
Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly Phe Glu Ser Phe Thr
         40                  45                  50

ttt gat gaa gtc gct aag cgt gca gag gta ccg atc ggc acg ctg tac   307
Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro Ile Gly Thr Leu Tyr
     55                  60                  65

caa ttc ttt gcc aat aag tat gta ttg atc tgc gaa ttg gat cgt gtg   355
Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys Glu Leu Asp Arg Val
 70                  75                  80                  85

gat acc gca gaa gct gtc gcg gag ttg aag aaa ttc tcc gat cag gtt   403
Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys Phe Ser Asp Gln Val
                 90                  95                 100

cct gcg ttg cag tgg ccg gat atc ctt gat gaa ttc att gag cac ttg   451
Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu Phe Ile Glu His Leu
            105                 110                 115

gct agg ctc tgg cgc gat gat ccg tct cgg cgg gcc gtg tgg cat gcc   499
Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg Ala Val Trp His Ala
        120                 125                 130

atc cag tcc acg ccg gca act cgt gcg aca gct gcg gcg acg gaa aaa   547
Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala Ala Ala Thr Glu Lys
    135                 140                 145

gag atg ctg gaa atc atc gcg gaa gtt atg cgc ccg ctt gcc cgc ggt   595
Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg Pro Leu Ala Arg Gly
150                 155                 160                 165

gcc ggc tac gag gag cgc atg tca ctg gcg gga ttg ctg gtg cac acg   643
Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly Leu Leu Val His Thr
                170                 175                 180

gta agt tcc ctg ctt aac tat gcc gtg cgt gat gtc aat agt tcc gaa   691
Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp Val Asn Ser Ser Glu
            185                 190                 195

gag gat ttc gac agc atc gtg gaa gaa ata aaa cga atg ctg att tct   739
Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys Arg Met Leu Ile Ser
        200                 205                 210

tac ctc ttc tcc gtg gct act gga tagtcaacac gcacgttcca ccg         786
Tyr Leu Phe Ser Val Ala Thr Gly
    215                 220
```

CONFIDENTIAL

<210> 1452
<211> 221
<212> PRT
<213> Corynebacterium glutamicum

<400> 1452

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Met Thr Ser Asp Lys Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu
  1               5                  10                  15

Ile Leu Met Pro Arg Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg
             20                  25                  30

Phe Asn Arg Ile Leu Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly
```

```
         35                  40                  45

Phe Glu Ser Phe Thr Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro
     50                  55                  60

Ile Gly Thr Leu Tyr Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys
 65                  70                  75                  80

Glu Leu Asp Arg Val Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys
                 85                  90                  95

Phe Ser Asp Gln Val Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu
            100                 105                 110

Phe Ile Glu His Leu Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg
        115                 120                 125

Ala Val Trp His Ala Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala
    130                 135                 140

Ala Ala Thr Glu Lys Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg
145                 150                 155                 160

Pro Leu Ala Arg Gly Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly
                165                 170                 175

Leu Leu Val His Thr Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp
            180                 185                 190

Val Asn Ser Ser Glu Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys
        195                 200                 205

Arg Met Leu Ile Ser Tyr Leu Phe Ser Val Ala Thr Gly
    210                 215                 220


<210> 1453
<211> 786
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(763)
<223> FRXA02876

<400> 1453
aactgttggc atggcgaagt acaatgttcg tgcaactggt cacgtggagc gcatcgtccg 60

cgaaatcacc gcggcgtaat agcaccagct taaaaacctt atg aca tca gac aaa   115
                                              Met Thr Ser Asp Lys
                                                1               5

gac act gaa caa ttg gaa gcg gca ggc act gaa att tta atg cct cgc   163
Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu Ile Leu Met Pro Arg
                10                  15                  20

cgc cgt ccg gca cag cag cgc agt cgt gaa cga ttc aat cga atc ctc   211
Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg Phe Asn Arg Ile Leu
            25                  30                  35
```

```
acc gct gcg cgt tca gtg ctt gtc gat cta ggt ttt gaa tcg ttc acg   259
Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly Phe Glu Ser Phe Thr
        40                  45                  50

ttt gat gaa gtc gct aag cgt gca gag gta ccg atc ggc acg ctg tac   307
Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro Ile Gly Thr Leu Tyr
     55                  60                  65

caa ttc ttt gcc aat aag tat gta ttg atc tgc gaa ttg gat cgt gtg   355
Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys Glu Leu Asp Arg Val
 70                  75                  80                  85

gat acc gca gaa gct gtc gcg gag ttg aag aaa ttc tcc gat cag gtt   403
Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys Phe Ser Asp Gln Val
                 90                  95                 100

cct gcg ttg cag tgg ccg gat atc ctt gat gaa ttc att gag cac ttg   451
Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu Phe Ile Glu His Leu
            105                 110                 115

gct agg ctc tgg cgc gat gat ccg tct cgg cgg gcc gtg tgg cat gcc   499
Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg Ala Val Trp His Ala
        120                 125                 130

atc cag tcc acg ccg gca act cgt gcg aca gct gcg gcg acg gaa aaa   547
Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala Ala Ala Thr Glu Lys
    135                 140                 145

gag atg ctg gaa atc atc gcg gaa gtt atg cgc ccg ctt gcc cgc ggt   595
Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg Pro Leu Ala Arg Gly
150                 155                 160                 165

gcc ggc tac gag gag cgc atg tca ctg gcg gga ttg ctg gtg cac acg   643
Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly Leu Leu Val His Thr
                170                 175                 180

gta agt tcc ctg ctt aac tat gcc gtg cgt gat gtc aat agt tcc gaa   691
Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp Val Asn Ser Ser Glu
            185                 190                 195

gag gat ttc gac agc atc gtg gaa gaa atc aaa cga atg ctg att tct   739
Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys Arg Met Leu Ile Ser
        200                 205                 210

tac ctc ttc tcc gtg gct act gga tagtcaacac gcacgtcgcc acc         786
Tyr Leu Phe Ser Val Ala Thr Gly
    215                 220
```

<210> 1454
<211> 221
<212> PRT
<213> Corynebacterium glutamicum

<400> 1454

```
Met Thr Ser Asp Lys Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu
  1               5                  10                  15

Ile Leu Met Pro Arg Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg
             20                  25                  30
```

```
Phe Asn Arg Ile Leu Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly
          35                  40                  45

Phe Glu Ser Phe Thr Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro
      50                  55                  60

Ile Gly Thr Leu Tyr Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys
 65                  70                  75                  80

Glu Leu Asp Arg Val Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys
                 85                  90                  95

Phe Ser Asp Gln Val Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu
            100                 105                 110

Phe Ile Glu His Leu Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg
        115                 120                 125

Ala Val Trp His Ala Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala
    130                 135                 140

Ala Ala Thr Glu Lys Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg
145                 150                 155                 160

Pro Leu Ala Arg Gly Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly
                165                 170                 175

Leu Leu Val His Thr Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp
            180                 185                 190

Val Asn Ser Ser Glu Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys
        195                 200                 205

Arg Met Leu Ile Ser Tyr Leu Phe Ser Val Ala Thr Gly
    210                 215                 220


<210> 1455
<211> 294
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(271)
<223> RXN03067

<400> 1455
ttgctgttgt tggcatttcc ccggatccgg tggacaagct ggtaagttcc gtgaggacca 60

tgagctgaac ttccctcttc tttccgatga ggacaagtct gtg atg act gcg tgg   115
                                              Val Met Thr Ala Trp
                                                1               5

ggt gcg ttt ggt gag aag aag aat tac ggc aag att gtt cag ggt gta   163
Gly Ala Phe Gly Glu Lys Lys Asn Tyr Gly Lys Ile Val Gln Gly Val
                10                  15                  20

att cgt tcc aca ttc ctc atc aat gct gac gga act gtt ggc atg gcg   211
Ile Arg Ser Thr Phe Leu Ile Asn Ala Asp Gly Thr Val Gly Met Ala
            25                  30                  35
```

```
aag tac aat gtt cgt gca act ggt cac gtg gag cgc atc gtc cgc gaa   259
Lys Tyr Asn Val Arg Ala Thr Gly His Val Glu Arg Ile Val Arg Glu
         40                  45                  50

atc acc gcg gcg taatagcacc agcttaaaaa cct                        294
Ile Thr Ala Ala
     55


<210> 1456
<211> 57
<212> PRT
<213> Corynebacterium glutamicum

<400> 1456
Val Met Thr Ala Trp Gly Ala Phe Gly Glu Lys Lys Asn Tyr Gly Lys
  1               5                  10                  15

Ile Val Gln Gly Val Ile Arg Ser Thr Phe Leu Ile Asn Ala Asp Gly
             20                  25                  30

Thr Val Gly Met Ala Lys Tyr Asn Val Arg Ala Thr Gly His Val Glu
         35                  40                  45

Arg Ile Val Arg Glu Ile Thr Ala Ala
     50                  55


<210> 1457
<211> 143
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(120)
<223> RXN03068

<400> 1457
acc aag gaa gca tgc gat ttc cgt gat tct ttg agc aac ctc aac gat   48
Thr Lys Glu Ala Cys Asp Phe Arg Asp Ser Leu Ser Asn Leu Asn Asp
  1               5                  10                  15

ctc gac att gct gtt gtt ggc att tcc ccg gat ccg gtg gac aag ctg   96
Leu Asp Ile Ala Val Val Gly Ile Ser Pro Asp Pro Val Asp Lys Leu
             20                  25                  30

gta agt tcc gtg agg acc atg agc tgaacttccc tcttctttcc gat        143
Val Ser Ser Val Arg Thr Met Ser
         35                  40


<210> 1458
<211> 40
<212> PRT
<213> Corynebacterium glutamicum

<400> 1458
Thr Lys Glu Ala Cys Asp Phe Arg Asp Ser Leu Ser Asn Leu Asn Asp
  1               5                  10                  15
```

```
Leu Asp Ile Ala Val Val Gly Ile Ser Pro Asp Pro Val Asp Lys Leu
             20                  25                  30

Val Ser Ser Val Arg Thr Met Ser
         35                  40


<210> 1459
<211> 753
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(730)
<223> RXN03073

<400> 1459
cgaaacatct aggcaacccg acttttatgt ccctgcttga gttgaaaact gctgtcgatc 60

aaaggtgccc caattgtttc atgccgtgag ttttgcatta atg gac tcc gta aat   115
                                        Met Asp Ser Val Asn
                                          1               5

gtc ctg ctc att ggc ata atc gtc gcg att gct gct ttg ctg cct cgc   163
Val Leu Leu Ile Gly Ile Ile Val Ala Ile Ala Ala Leu Leu Pro Arg
                 10                  15                  20

aag ggt aaa tat ggg cca atc gcc acg cta ctg gtt gcc ggc gat tgg   211
Lys Gly Lys Tyr Gly Pro Ile Ala Thr Leu Leu Val Ala Gly Asp Trp
             25                  30                  35

ctt ggc gtt ttc ctc ctc agt att ttg gtg atg ctc gtt ttt gat gga   259
Leu Gly Val Phe Leu Leu Ser Ile Leu Val Met Leu Val Phe Asp Gly
         40                  45                  50

cta gag gat tta gtt cag ggc ttt ttg gat tca atc tgg ttc gga gtc   307
Leu Glu Asp Leu Val Gln Gly Phe Leu Asp Ser Ile Trp Phe Gly Val
     55                  60                  65

atc ctt ctt gta act ggc atc gtt tcc ttc gtt gcg aca ctg gtt tct   355
Ile Leu Leu Val Thr Gly Ile Val Ser Phe Val Ala Thr Leu Val Ser
 70                  75                  80                  85

aaa acc gac agc act aga aag ctt gat gga ttc cta gcg cca gta aaa   403
Lys Thr Asp Ser Thr Arg Lys Leu Asp Gly Phe Leu Ala Pro Val Lys
                 90                  95                 100

act cct agt tgg aaa act gtt gga gcc gga ttg atc ctt gga atc gtt   451
Thr Pro Ser Trp Lys Thr Val Gly Ala Gly Leu Ile Leu Gly Ile Val
            105                 110                 115

cag tca gcg aca tct gta cct ttt tat gca ggg ctt gga tat ttg agc   499
Gln Ser Ala Thr Ser Val Pro Phe Tyr Ala Gly Leu Gly Tyr Leu Ser
        120                 125                 130

gtt ggc aat ttc agt cca gaa att agg tat ggc gga ctt gtg gtc tat   547
Val Gly Asn Phe Ser Pro Glu Ile Arg Tyr Gly Gly Leu Val Val Tyr
    135                 140                 145
```

```
gcg acc ttg gct ctg agt ctg ccg att atc gtg gca att ctc gtt gga   595
Ala Thr Leu Ala Leu Ser Leu Pro Ile Ile Val Ala Ile Leu Val Gly
150                 155                 160                 165

atg gtt cgc aaa tac cct gaa agt cct gtt ggt agg ttg ttt gaa ctg   643
Met Val Arg Lys Tyr Pro Glu Ser Pro Val Gly Arg Leu Phe Glu Leu
                170                 175                 180

att ggt caa aat aaa gag aga gtc acc aaa tgg tcg ggc tat ctc gtg   691
Ile Gly Gln Asn Lys Glu Arg Val Thr Lys Trp Ser Gly Tyr Leu Val
            185                 190                 195

tca ctg gtt ctg tgc ata atg ggc att act tcg atc ctg taactagcgc   740
Ser Leu Val Leu Cys Ile Met Gly Ile Thr Ser Ile Leu
        200                 205                 210

atgtactcat gag                                                  753
```

<210> 1460
<211> 210
<212> PRT
<213> Corynebacterium glutamicum

<400> 1460

```
Met Asp Ser Val Asn Val Leu Leu Ile Gly Ile Ile Val Ala Ile Ala
  1               5                  10                  15

Ala Leu Leu Pro Arg Lys Gly Lys Tyr Gly Pro Ile Ala Thr Leu Leu
             20                  25                  30

Val Ala Gly Asp Trp Leu Gly Val Phe Leu Leu Ser Ile Leu Val Met
         35                  40                  45

Leu Val Phe Asp Gly Leu Glu Asp Leu Val Gln Gly Phe Leu Asp Ser
     50                  55                  60

Ile Trp Phe Gly Val Ile Leu Leu Val Thr Gly Ile Val Ser Phe Val
 65                  70                  75                  80

Ala Thr Leu Val Ser Lys Thr Asp Ser Thr Arg Lys Leu Asp Gly Phe
                 85                  90                  95

Leu Ala Pro Val Lys Thr Pro Ser Trp Lys Thr Val Gly Ala Gly Leu
            100                 105                 110

Ile Leu Gly Ile Val Gln Ser Ala Thr Ser Val Pro Phe Tyr Ala Gly
        115                 120                 125

Leu Gly Tyr Leu Ser Val Gly Asn Phe Ser Pro Glu Ile Arg Tyr Gly
    130                 135                 140

Gly Leu Val Val Tyr Ala Thr Leu Ala Leu Ser Leu Pro Ile Ile Val
145                 150                 155                 160

Ala Ile Leu Val Gly Met Val Arg Lys Tyr Pro Glu Ser Pro Val Gly
                165                 170                 175

Arg Leu Phe Glu Leu Ile Gly Gln Asn Lys Glu Arg Val Thr Lys Trp
            180                 185                 190
```

```
Ser Gly Tyr Leu Val Ser Leu Val Leu Cys Ile Met Gly Ile Thr Ser
        195                 200                 205

Ile Leu
    210


<210> 1461
<211> 574
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> FRXA02905

<400> 1461
cgaaacatct aggcaacccg acttttatgt ccctgcttga gttgaaaact gctgtcgatc 60

aaaggtgccc caattgtttc atgccgtgag ttttgcatta atg gac tcc gta aat   115
                                            Met Asp Ser Val Asn
                                              1               5

gtc ctg ctc att ggc ata atc gtc gcg att gct gct ttg ctg cct cgc   163
Val Leu Leu Ile Gly Ile Ile Val Ala Ile Ala Ala Leu Leu Pro Arg
                 10                  15                  20

aag ggt aaa tat ggg cca atc gcc acg cta ctg gtt gcc ggc gat tgg   211
Lys Gly Lys Tyr Gly Pro Ile Ala Thr Leu Leu Val Ala Gly Asp Trp
             25                  30                  35

ctt ggc gtt ttc ctc ctc agt att ttg gtg atg ctc gtt ttt gat gga   259
Leu Gly Val Phe Leu Leu Ser Ile Leu Val Met Leu Val Phe Asp Gly
         40                  45                  50

cta gag gat tta gtt cag ggc ttt ttg gat tca atc tgg ttc gga gtc   307
Leu Glu Asp Leu Val Gln Gly Phe Leu Asp Ser Ile Trp Phe Gly Val
     55                  60                  65

atc ctt ctt gta act ggc atc gtt tcc ttc gtt gcg aca ctg gtt tct   355
Ile Leu Leu Val Thr Gly Ile Val Ser Phe Val Ala Thr Leu Val Ser
 70                  75                  80                  85

aaa acc gac agc act aga aag ctt gat gga ttc cta gcg cca gta aaa   403
Lys Thr Asp Ser Thr Arg Lys Leu Asp Gly Phe Leu Ala Pro Val Lys
                 90                  95                 100

act cct agt tgg aaa act gtt gga gcc gga ttg atc ctt gga atc gtt   451
Thr Pro Ser Trp Lys Thr Val Gly Ala Gly Leu Ile Leu Gly Ile Val
            105                 110                 115

cag tca gcg aca tct gta cct ttt tat gca ggg ctt gga tat ttg agc   499
Gln Ser Ala Thr Ser Val Pro Phe Tyr Ala Gly Leu Gly Tyr Leu Ser
        120                 125                 130

gtt ggc aat ttc agt cca gaa att agg tat ggc gga ctt gtg gtc tat   547
Val Gly Asn Phe Ser Pro Glu Ile Arg Tyr Gly Gly Leu Val Val Tyr
    135                 140                 145

gcg acc ttg gct ctg agt ctg ccg att                              574
```

Ala Thr Leu Ala Leu Ser Leu Pro Ile
150 155

<210> 1462
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 1462
Met Asp Ser Val Asn Val Leu Leu Ile Gly Ile Ile Val Ala Ile Ala
1 5 10 15

Ala Leu Leu Pro Arg Lys Gly Lys Tyr Gly Pro Ile Ala Thr Leu Leu
20 25 30

Val Ala Gly Asp Trp Leu Gly Val Phe Leu Leu Ser Ile Leu Val Met
35 40 45

Leu Val Phe Asp Gly Leu Glu Asp Leu Val Gln Gly Phe Leu Asp Ser
50 55 60

Ile Trp Phe Gly Val Ile Leu Leu Val Thr Gly Ile Val Ser Phe Val
65 70 75 80

Ala Thr Leu Val Ser Lys Thr Asp Ser Thr Arg Lys Leu Asp Gly Phe
85 90 95

Leu Ala Pro Val Lys Thr Pro Ser Trp Lys Thr Val Gly Ala Gly Leu
100 105 110

Ile Leu Gly Ile Val Gln Ser Ala Thr Ser Val Pro Phe Tyr Ala Gly
115 120 125

Leu Gly Tyr Leu Ser Val Gly Asn Phe Ser Pro Glu Ile Arg Tyr Gly
130 135 140

Gly Leu Val Val Tyr Ala Thr Leu Ala Leu Ser Leu Pro Ile
145 150 155

<210> 1463
<211> 474
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(451)
<223> RXN03085

<400> 1463
taagcaggat tacgacaagc gccaagatat caagcgtcgc accgaagaac gcgaagtcac 60

ccgtgagctc ggccgtcgca ttaagggaat caacgcgtaa atg agt att cac atc 115
Met Ser Ile His Ile
1 5

gca aaa gtc cac gac gtc ctc aaa ggt gaa aaa acc tac gga acc acc 163
Ala Lys Val His Asp Val Leu Lys Gly Glu Lys Thr Tyr Gly Thr Thr
10 15 20

```
att ttg gtg gat cgg ctc tgg cca cgc ggt gtg aaa aaa gac gac ctt   211
Ile Leu Val Asp Arg Leu Trp Pro Arg Gly Val Lys Lys Asp Asp Leu
             25                  30                  35

gag cca gac ctc tgg ctc aaa agc gtc gcc ccc aca acc gaa ctc cga   259
Glu Pro Asp Leu Trp Leu Lys Ser Val Ala Pro Thr Thr Glu Leu Arg
         40                  45                  50

aaa tgg ttc ggc cac gac cca gct aaa ttc tcc gaa ttc agc acc cgt   307
Lys Trp Phe Gly His Asp Pro Ala Lys Phe Ser Glu Phe Ser Thr Arg
     55                  60                  65

tac acc gaa gag ctc aac gcc agc aac gac aaa gac cta gag acg ctt   355
Tyr Thr Glu Glu Leu Asn Ala Ser Asn Asp Lys Asp Leu Glu Thr Leu
 70                  75                  80                  85

gtc gac gcc acc tcc cgc cac ccc gta acc ctc ctc tac ggt gct gcc   403
Val Asp Ala Thr Ser Arg His Pro Val Thr Leu Leu Tyr Gly Ala Ala
                 90                  95                 100

gac cgc gac cac aac cac gcc att gtt cta gcc aag tgg cta aag aaa   451
Asp Arg Asp His Asn His Ala Ile Val Leu Ala Lys Trp Leu Lys Lys
            105                 110                 115

taactccttg caaatagttg caa                                       474
```

CONFIDENTIAL

<210> 1464
<211> 117
<212> PRT
<213> Corynebacterium glutamicum

<400> 1464

```
Met Ser Ile His Ile Ala Lys Val His Asp Val Leu Lys Gly Glu Lys
  1               5                  10                  15

Thr Tyr Gly Thr Thr Ile Leu Val Asp Arg Leu Trp Pro Arg Gly Val
             20                  25                  30

Lys Lys Asp Asp Leu Glu Pro Asp Leu Trp Leu Lys Ser Val Ala Pro
         35                  40                  45

Thr Thr Glu Leu Arg Lys Trp Phe Gly His Asp Pro Ala Lys Phe Ser
     50                  55                  60

Glu Phe Ser Thr Arg Tyr Thr Glu Glu Leu Asn Ala Ser Asn Asp Lys
 65                  70                  75                  80

Asp Leu Glu Thr Leu Val Asp Ala Thr Ser Arg His Pro Val Thr Leu
                 85                  90                  95

Leu Tyr Gly Ala Ala Asp Arg Asp His Asn His Ala Ile Val Leu Ala
            100                 105                 110

Lys Trp Leu Lys Lys
        115
```

<210> 1465
<211> 1181

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1158)
<223> RXN03089

<400> 1465

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cac tcc ctc tac ccc ata ccg aag cca aac tct gga tct ggc aac ggc   48
His Ser Leu Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly Asn Gly
  1               5                  10                  15

ggt aat ggt ggc aat ccc gat ggc ggt cct gat ggt ggc gac tcg ggt   96
Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly
            20                  25                  30

gat gac gac tcc ggc gat gat gac ccc gac ccc gaa ccg gac aag cct   144
Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Pro
        35                  40                  45

gaa gac ggc aaa cct gat agt gat aag ccc cgt agg cca cgg atc agc   192
Glu Asp Gly Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg Ile Ser
    50                  55                  60

gcg gaa aaa cac gcc atc atc acc gac gaa ctc gcc cgc ctc aac ccg   240
Ala Glu Lys His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro
65                  70                  75                  80

aat acc aca ccc agc gcc gag gaa cta cgc acc caa gcc ctg agt caa   288
Asn Thr Thr Pro Ser Ala Glu Glu Leu Arg Thr Gln Ala Leu Ser Gln
                85                  90                  95

gcg atc tgg cgc acc cca gaa gac ctc cgc acg tgg cta cgc cac cag   336
Ala Ile Trp Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His Gln
            100                 105                 110

gtc acc acc gcg aac aaa aac aac ccc aac ccc atc acc gcc atg aaa   384
Val Thr Thr Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys
        115                 120                 125

agg cgc tac ctc tca gta ggt aaa ccc gat gcc gac aac atg gtc cgc   432
Arg Arg Tyr Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg
    130                 135                 140

atc agc ggc ctc gtg ccc gca gcc acc gca gca ctg atc acc gcg aac   480
Ile Ser Gly Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn
145                 150                 155                 160

acc gca ccg tta acc aaa cgt ggc aac ctc gtg gat cta cca gca gca   528
Thr Ala Pro Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala
                165                 170                 175

gaa gat atg cgc acc cgc ggg caa cgc cat gcg gat gcg ttg cat cac   576
Glu Asp Met Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His
            180                 185                 190

atc atg gag atc tac aac cac ggt att gtc acc cca gct cgt ggt gga   624
Ile Met Glu Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly
        195                 200                 205
```

```
aca gcc agc atc atc atc tcc atg acc acc gat gat ctt gac gag atc   672
Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile
    210                 215                 220

aac cac ggt gat cat ggc gat ggc agt cta ctt aac aac ctg tac ccc   720
Asn His Gly Asp His Gly Asp Gly Ser Leu Leu Asn Asn Leu Tyr Pro
225                 230                 235                 240

acg aac acg ggt tac tca ttg aac ttg gcg gag atc atg aac ctc atc   768
Thr Asn Thr Gly Tyr Ser Leu Asn Leu Ala Glu Ile Met Asn Leu Ile
                245                 250                 255

gct gcg aaa tac gac ttc gct gtg ctc ctc gat ggt gag acg ggg cag   816
Ala Ala Lys Tyr Asp Phe Ala Val Leu Leu Asp Gly Glu Thr Gly Gln
            260                 265                 270

ccg ttg aac gtc aat agg atg cag cgc tca gcg aac ctg act caa cgc   864
Pro Leu Asn Val Asn Arg Met Gln Arg Ser Ala Asn Leu Thr Gln Arg
        275                 280                 285

atc gcg ttg ttt gct tct gag ttg gtg tgc tcg gca ccc aat tgt gac   912
Ile Ala Leu Phe Ala Ser Glu Leu Val Cys Ser Ala Pro Asn Cys Asp
    290                 295                 300

agg ccg cag tta gag tgc gag gtt cat cat tta gat ccc tgg atg aga   960
Arg Pro Gln Leu Glu Cys Glu Val His His Leu Asp Pro Trp Met Arg
305                 310                 315                 320

ggt ggg ctg acc aac ctg gtc aat ctc acg cat cag tgc ttt aat cac  1008
Gly Gly Leu Thr Asn Leu Val Asn Leu Thr His Gln Cys Phe Asn His
                325                 330                 335

cac cca cgc aac gat gat tcc agg agt ggg gtc aat ggt aaa ggg ttt  1056
His Pro Arg Asn Asp Asp Ser Arg Ser Gly Val Asn Gly Lys Gly Phe
            340                 345                 350

atg gac cgc gat ccc gtc act ggc aga gta ggt cac tac tca gca agt  1104
Met Asp Arg Asp Pro Val Thr Gly Arg Val Gly His Tyr Ser Ala Ser
        355                 360                 365

ggt gag ggg ccg gtg ttt aac cgg tcg gct gct gct gat cgt tcc ggt  1152
Gly Glu Gly Pro Val Phe Asn Arg Ser Ala Ala Ala Asp Arg Ser Gly
    370                 375                 380

ggt gca tagtccagac gtaagcatta tgg                               1181
Gly Ala
385
```

<210> 1466
<211> 386
<212> PRT
<213> Corynebacterium glutamicum

<400> 1466

```
His Ser Leu Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly Asn Gly
  1               5                  10                  15

Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly
            20                  25                  30
```

```
Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Pro
         35                  40                  45

Glu Asp Gly Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg Ile Ser
     50                  55                  60

Ala Glu Lys His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro
 65                  70                  75                  80

Asn Thr Thr Pro Ser Ala Glu Glu Leu Arg Thr Gln Ala Leu Ser Gln
                 85                  90                  95

Ala Ile Trp Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His Gln
            100                 105                 110

Val Thr Thr Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys
        115                 120                 125

Arg Arg Tyr Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg
    130                 135                 140

Ile Ser Gly Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn
145                 150                 155                 160

Thr Ala Pro Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala
                165                 170                 175

Glu Asp Met Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His
            180                 185                 190

Ile Met Glu Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly
        195                 200                 205

Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile
    210                 215                 220

Asn His Gly Asp His Gly Asp Gly Ser Leu Leu Asn Asn Leu Tyr Pro
225                 230                 235                 240

Thr Asn Thr Gly Tyr Ser Leu Asn Leu Ala Glu Ile Met Asn Leu Ile
                245                 250                 255

Ala Ala Lys Tyr Asp Phe Ala Val Leu Leu Asp Gly Glu Thr Gly Gln
            260                 265                 270

Pro Leu Asn Val Asn Arg Met Gln Arg Ser Ala Asn Leu Thr Gln Arg
        275                 280                 285

Ile Ala Leu Phe Ala Ser Glu Leu Val Cys Ser Ala Pro Asn Cys Asp
    290                 295                 300

Arg Pro Gln Leu Glu Cys Glu Val His His Leu Asp Pro Trp Met Arg
305                 310                 315                 320

Gly Gly Leu Thr Asn Leu Val Asn Leu Thr His Gln Cys Phe Asn His
                325                 330                 335

His Pro Arg Asn Asp Asp Ser Arg Ser Gly Val Asn Gly Lys Gly Phe
            340                 345                 350

Met Asp Arg Asp Pro Val Thr Gly Arg Val Gly His Tyr Ser Ala Ser
```

```
        355                 360                 365

Gly Glu Gly Pro Val Phe Asn Arg Ser Ala Ala Ala Asp Arg Ser Gly
    370                 375                 380

Gly Ala
385


<210> 1467
<211> 1575
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1552)
<223> FRXA00071

<400> 1467
gcttttctat ttcgaaaaat agccttgtat tcgaaaattt gatcgggtat ggtggttggt 60

akwrksrswg gkaacwamac ggggaaaggg ggaagacacc atg agc atc acc aca   115
                                              Met Ser Ile Thr Thr
                                                1               5

cac gtc caa gca ctc acc aca gca ctc aac gcc atc gac aac cat ttg   163
His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala Ile Asp Asn His Leu
                10                  15                  20

gcc agc atg cty gac cat ggt gtc acc cca gac caa tac aag gcc atc   211
Ala Ser Met Xaa Asp His Gly Val Thr Pro Asp Gln Tyr Lys Ala Ile
            25                  30                  35

gag ccc gac ctc atc gcc cta gaa cac acc atc aac cac cac gcc acc   259
Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile Asn His His Ala Thr
        40                  45                  50

atc gcc gcc caa acc acm gcc ctc gcc gaa cgc acc aay gcy gcs cas   307
Ile Ala Ala Gln Thr Xaa Ala Leu Ala Glu Arg Thr Xaa Xaa Xaa Xaa
    55                  60                  65

wcs att ggc tcc acc cac ctc atc gac tac ctc acc acc acc ttc ggc   355
Xaa Ile Gly Ser Thr His Leu Ile Asp Tyr Leu Thr Thr Thr Phe Gly
70                  75                  80                  85

cta tct aaa gca cgc gcc cac cac cgc atc aat ctc gcc cac tcc ctc   403
Leu Ser Lys Ala Arg Ala His His Arg Ile Asn Leu Ala His Ser Leu
                90                  95                  100

tac ccc ata ccg aag cca aac tct gga tct ggc aac ggc ggt aat ggt   451
Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly Asn Gly Gly Asn Gly
            105                 110                 115

ggc aat ccc gac ggc ggt cct gat ggt ggc gac tcg ggt gat gac gac   499
Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly Asp Asp Asp
        120                 125                 130

tcc ggc gat gat gac ccc gac ccc gaa ccg gac aag cct gaa gac ggc   547
Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Pro Glu Asp Gly
    135                 140                 145
```

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aaa cct gat agt gat aag ccc cgt agg cca cgg atc agc gcg gaa aaa   595
Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg Ile Ser Ala Glu Lys
150                 155                 160                 165

cac gcc atc atc acc gac gaa ctc gcc cgc ctc aac ccg aat acc aca   643
His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro Asn Thr Thr
                170                 175                 180

ccc agc gcc gag gaa ctr cgc amc caa gcc ctg agt car gcg atc tgg   691
Pro Ser Ala Glu Glu Xaa Arg Xaa Gln Ala Leu Ser Xaa Ala Ile Trp
            185                 190                 195

cgc acc cca gaa gac ctc cgc acg tgg cta cgc cac cag gtc acc acc   739
Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His Gln Val Thr Thr
        200                 205                 210

gcg aac aaa aac aac ccc aac ccc atc acc gcc atg aaa agg cgc tac   787
Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys Arg Arg Tyr
    215                 220                 225

ctc tca gta ggt aaa ccc gat gcc gac aac atg gtc cgc atc agc ggc   835
Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg Ile Ser Gly
230                 235                 240                 245

ctc gtg ccc gca gcc acc gca gca ctg atc acc gcg aac acc gca ccg   883
Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn Thr Ala Pro
                250                 255                 260

tta acc aaa cgt ggc aac ctc gtg gat cta cca gca gca gaa gat atg   931
Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala Glu Asp Met
            265                 270                 275

cgc acc cgc ggg caa cgc cat gcg gat gcg ttg cat cac atc atg gag   979
Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His Ile Met Glu
        280                 285                 290

atc tac aac cac ggt att gtc acc cca gct cgt ggt gga aca gcc agc   1027
Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly Thr Ala Ser
    295                 300                 305

atc atc atc tcc atg acc acc gat gat ctt gac gag atc aac cac ggt   1075
Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile Asn His Gly
310                 315                 320                 325

gat cat ggc gat ggc agt cta ctt aac aac ctg tac ccc acg aac acg   1123
Asp His Gly Asp Gly Ser Leu Leu Asn Asn Leu Tyr Pro Thr Asn Thr
                330                 335                 340

ggt tac tca ttg aac ttg gcg gag atc atg aac ctc atc gct gcg aaa   1171
Gly Tyr Ser Leu Asn Leu Ala Glu Ile Met Asn Leu Ile Ala Ala Lys
            345                 350                 355

tac gac ttc gct gtg ctc ctc gat ggt gag acg ggg cag ccg ttg aac   1219
Tyr Asp Phe Ala Val Leu Leu Asp Gly Glu Thr Gly Gln Pro Leu Asn
        360                 365                 370

gtc aat agg atg cag cgc tca gcg aac ctg act caa cgc atc gcg ttg   1267
Val Asn Arg Met Gln Arg Ser Ala Asn Leu Thr Gln Arg Ile Ala Leu
    375                 380                 385
```

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ttt gct tct gag ttg gtg tgc tcg gca ccc aat tgt gac agg ccg cag   1315
Phe Ala Ser Glu Leu Val Cys Ser Ala Pro Asn Cys Asp Arg Pro Gln
390                 395                 400                 405

tta gag tgc gag gtt cat cat tta gat ccc tgg atg aga ggt ggg ctg   1363
Leu Glu Cys Glu Val His His Leu Asp Pro Trp Met Arg Gly Gly Leu
                410                 415                 420

acc aac ctg gtc aat ctc acg cat cag tgc ttt aat cac cac cca cgc   1411
Thr Asn Leu Val Asn Leu Thr His Gln Cys Phe Asn His His Pro Arg
            425                 430                 435

aac gat gat tcc agg agt ggg gtc aat ggt aaa ggg ttt atg gac cgc   1459
Asn Asp Asp Ser Arg Ser Gly Val Asn Gly Lys Gly Phe Met Asp Arg
        440                 445                 450

gat ccc gtc act ggc aga gta ggt cac tac tca gca agt ggt gag ggg   1507
Asp Pro Val Thr Gly Arg Val Gly His Tyr Ser Ala Ser Gly Glu Gly
    455                 460                 465

ccg gtg ttt aac cgg tcg gct gct gct gat cgt tcc ggt ggt gca       1552
Pro Val Phe Asn Arg Ser Ala Ala Ala Asp Arg Ser Gly Gly Ala
470                 475                 480

tagtccagac gtaagcatta tgg                                        1575


<210> 1468
<211> 484
<212> PRT
<213> Corynebacterium glutamicum

<400> 1468
Met Ser Ile Thr Thr His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala
  1               5                  10                  15

Ile Asp Asn His Leu Ala Ser Met Xaa Asp His Gly Val Thr Pro Asp
             20                  25                  30

Gln Tyr Lys Ala Ile Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile
         35                  40                  45

Asn His His Ala Thr Ile Ala Ala Gln Thr Xaa Ala Leu Ala Glu Arg
     50                  55                  60

Thr Xaa Xaa Xaa Xaa Xaa Ile Gly Ser Thr His Leu Ile Asp Tyr Leu
 65                  70                  75                  80

Thr Thr Thr Phe Gly Leu Ser Lys Ala Arg Ala His His Arg Ile Asn
                 85                  90                  95

Leu Ala His Ser Leu Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly
            100                 105                 110

Asn Gly Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp
        115                 120                 125

Ser Gly Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp
    130                 135                 140

Lys Pro Glu Asp Gly Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg
```

```
145                 150                 155                 160

Ile Ser Ala Glu Lys His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu
                165                 170                 175

Asn Pro Asn Thr Thr Pro Ser Ala Glu Glu Xaa Arg Xaa Gln Ala Leu
            180                 185                 190

Ser Xaa Ala Ile Trp Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg
        195                 200                 205

His Gln Val Thr Thr Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala
    210                 215                 220

Met Lys Arg Arg Tyr Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met
225                 230                 235                 240

Val Arg Ile Ser Gly Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr
                245                 250                 255

Ala Asn Thr Ala Pro Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro
            260                 265                 270

Ala Ala Glu Asp Met Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu
        275                 280                 285

His His Ile Met Glu Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg
    290                 295                 300

Gly Gly Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp
305                 310                 315                 320

Glu Ile Asn His Gly Asp His Gly Asp Gly Ser Leu Leu Asn Asn Leu
                325                 330                 335

Tyr Pro Thr Asn Thr Gly Tyr Ser Leu Asn Leu Ala Glu Ile Met Asn
            340                 345                 350

Leu Ile Ala Ala Lys Tyr Asp Phe Ala Val Leu Leu Asp Gly Glu Thr
        355                 360                 365

Gly Gln Pro Leu Asn Val Asn Arg Met Gln Arg Ser Ala Asn Leu Thr
    370                 375                 380

Gln Arg Ile Ala Leu Phe Ala Ser Glu Leu Val Cys Ser Ala Pro Asn
385                 390                 395                 400

Cys Asp Arg Pro Gln Leu Glu Cys Glu Val His His Leu Asp Pro Trp
                405                 410                 415

Met Arg Gly Gly Leu Thr Asn Leu Val Asn Leu Thr His Gln Cys Phe
            420                 425                 430

Asn His His Pro Arg Asn Asp Asp Ser Arg Ser Gly Val Asn Gly Lys
        435                 440                 445

Gly Phe Met Asp Arg Asp Pro Val Thr Gly Arg Val Gly His Tyr Ser
    450                 455                 460

Ala Ser Gly Glu Gly Pro Val Phe Asn Arg Ser Ala Ala Ala Asp Arg
465                 470                 475                 480
```

Ser Gly Gly Ala

<210> 1469
<211> 747
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(724)
<223> RXN03098

<400> 1469
gaccgttttg tcgatcgcac cgctgctggc tcgcaccatc aacgagatct tcgaaaacgg 60

ttccgtcacc accctcttcg agggcgaggc ctaaacaccc atg ccc acc acg gac 115
Met Pro Thr Thr Asp
1 5

gtc ttc aac cgc gtc cgg ttg gca ttg gaa cct cta gct gat ccc gca 163
Val Phe Asn Arg Val Arg Leu Ala Leu Glu Pro Leu Ala Asp Pro Ala
10 15 20

cgt gcc acc gga atg gca agc tac atg cgg gat cag ttt tct ttt ctc 211
Arg Ala Thr Gly Met Ala Ser Tyr Met Arg Asp Gln Phe Ser Phe Leu
25 30 35

ggc atc cca tcc acc ccc aga aaa gaa gcc tgc aaa ccc gtg ctg tcc 259
Gly Ile Pro Ser Thr Pro Arg Lys Glu Ala Cys Lys Pro Val Leu Ser
40 45 50

gcg cta aaa gag ttg gac act gac ttt gtc tca gac tgc ttt ggc gca 307
Ala Leu Lys Glu Leu Asp Thr Asp Phe Val Ser Asp Cys Phe Gly Ala
55 60 65

gct gaa cgg gaa tac cag tat gtc gcc tgc gat cac atc aat cgc gtc 355
Ala Glu Arg Glu Tyr Gln Tyr Val Ala Cys Asp His Ile Asn Arg Val
70 75 80 85

ggc atc acc gat tta ggt ttt gcc aaa gca tta gtg cag acc aaa tcc 403
Gly Ile Thr Asp Leu Gly Phe Ala Lys Ala Leu Val Gln Thr Lys Ser
90 95 100

tgg tgg gac acc gtc gat tcc cta gca aaa ccg atc ggc gcc aaa cac 451
Trp Trp Asp Thr Val Asp Ser Leu Ala Lys Pro Ile Gly Ala Lys His
105 110 115

gat gat gat ctg atg aaa acg tgg gcg ctt gat gag gac ttc tgg gtg 499
Asp Asp Asp Leu Met Lys Thr Trp Ala Leu Asp Glu Asp Phe Trp Val
120 125 130

cgc cgc atc gcg atc atc cac caa ctg ggc cgc aag aaa aac acc gac 547
Arg Arg Ile Ala Ile Ile His Gln Leu Gly Arg Lys Lys Asn Thr Asp
135 140 145

gct gcc ctg ctg gcc tgg atc atc gag cag aac ctc ggc tcc agc gag 595
Ala Ala Leu Leu Ala Trp Ile Ile Glu Gln Asn Leu Gly Ser Ser Glu
150 155 160 165

```
ttc ttc atc aac aaa gcg atc ggc tgg gca ctg cgg gat ttc gcc cgc   643
Phe Phe Ile Asn Lys Ala Ile Gly Trp Ala Leu Arg Asp Phe Ala Arg
                170                 175                 180

cac gac ccc agc tgg gtc cgg gct ttt gtc gac gcc acg gac ctt tcc   691
His Asp Pro Ser Trp Val Arg Ala Phe Val Asp Ala Thr Asp Leu Ser
            185                 190                 195

cca ctg agc cgg cga gaa gcc ctg aag aat att tagccctcag gcatcatctg 744
Pro Leu Ser Arg Arg Glu Ala Leu Lys Asn Ile
        200                 205

agc                                                               747
```

<210> 1470
<211> 208
<212> PRT
<213> Corynebacterium glutamicum

<400> 1470

```
Met Pro Thr Thr Asp Val Phe Asn Arg Val Arg Leu Ala Leu Glu Pro
  1               5                  10                  15

Leu Ala Asp Pro Ala Arg Ala Thr Gly Met Ala Ser Tyr Met Arg Asp
             20                  25                  30

Gln Phe Ser Phe Leu Gly Ile Pro Ser Thr Pro Arg Lys Glu Ala Cys
         35                  40                  45

Lys Pro Val Leu Ser Ala Leu Lys Glu Leu Asp Thr Asp Phe Val Ser
     50                  55                  60

Asp Cys Phe Gly Ala Ala Glu Arg Glu Tyr Gln Tyr Val Ala Cys Asp
 65                  70                  75                  80

His Ile Asn Arg Val Gly Ile Thr Asp Leu Gly Phe Ala Lys Ala Leu
                 85                  90                  95

Val Gln Thr Lys Ser Trp Trp Asp Thr Val Asp Ser Leu Ala Lys Pro
            100                 105                 110

Ile Gly Ala Lys His Asp Asp Asp Leu Met Lys Thr Trp Ala Leu Asp
        115                 120                 125

Glu Asp Phe Trp Val Arg Arg Ile Ala Ile Ile His Gln Leu Gly Arg
    130                 135                 140

Lys Lys Asn Thr Asp Ala Ala Leu Leu Ala Trp Ile Ile Glu Gln Asn
145                 150                 155                 160

Leu Gly Ser Ser Glu Phe Phe Ile Asn Lys Ala Ile Gly Trp Ala Leu
                165                 170                 175

Arg Asp Phe Ala Arg His Asp Pro Ser Trp Val Arg Ala Phe Val Asp
            180                 185                 190

Ala Thr Asp Leu Ser Pro Leu Ser Arg Arg Glu Ala Leu Lys Asn Ile
        195                 200                 205
```

<210> 1471
<211> 798
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> RXN03099

<400> 1471
ccacgccgta gcgatcattg atcaccttga gcactggggt aatggcattg gtggtgcatg 60

atgctgcgga aacgatctga tcatctgcgg tgatgtcggt gtg gtt gat gcc gta 115
Val Val Asp Ala Val
1 5

cac gat gtt ctt cag atc gcc ctt gcc cgg cgc ggt gag tac aac ctt 163
His Asp Val Leu Gln Ile Ala Leu Ala Arg Arg Gly Glu Tyr Asn Leu
10 15 20

ggc aac gcc ctt gga ctt gag gtg ctg gga cag gcc ttc gcg gtc acg 211
Gly Asn Ala Leu Gly Leu Glu Val Leu Gly Gln Ala Phe Ala Val Thr
25 30 35

cca gcg gcc ggt gtt gtc tac cac gac ggc gtc att gat gcc gta ttc 259
Pro Ala Ala Gly Val Val Tyr His Asp Gly Val Ile Asp Ala Val Phe
40 45 50

ggt gta atc aat ggt ggc tgg gtc att gga gta gat gac ctt gat tgg 307
Gly Val Ile Asn Gly Gly Trp Val Ile Gly Val Asp Asp Leu Asp Trp
55 60 65

ggt gcc gtt ggc cca gat gat gtt gtt gtc ata atc ggt ggt gat ggt 355
Gly Ala Val Gly Pro Asp Asp Val Val Val Ile Ile Gly Gly Asp Gly
70 75 80 85

gcc atc gaa tcc acc gtg gac aga atc acg acg cag caa gga tgc gcg 403
Ala Ile Glu Ser Thr Val Asp Arg Ile Thr Thr Gln Gln Gly Cys Ala
90 95 100

ctt gac cag gtc ttc ttc acc att ttt gcg gac cac gat ggc gcg cag 451
Leu Asp Gln Val Phe Phe Thr Ile Phe Ala Asp His Asp Gly Ala Gln
105 110 115

acg agc acc gtc ata cag tgc ctc gcg gga aac cag gat gcg ggc cag 499
Thr Ser Thr Val Ile Gln Cys Leu Ala Gly Asn Gln Asp Ala Gly Gln
120 125 130

cag gcg acc gat gcg gcc gaa acc gta cag cac gat atc agt tgg gtt 547
Gln Ala Thr Asp Ala Ala Glu Thr Val Gln His Asp Ile Ser Trp Val
135 140 145

gat gtc ggt ttc cgc acc aat gac cgg cgc gag agc gtc ctc cag gaa 595
Asp Val Gly Phe Arg Thr Asn Asp Arg Arg Glu Ser Val Leu Gln Glu
150 155 160 165

```
ggc acg cag gtc ggt gct ttc gga ttc ttc gaa gct gta ggc cag ctg   643
Gly Thr Gln Val Gly Ala Phe Gly Phe Phe Glu Ala Val Gly Gln Leu
                170                 175                 180

tcc cag gtc gat cga tgc ggt acc aag gtt cat atc tac cag ttc gcg   691
Ser Gln Val Asp Arg Cys Gly Thr Lys Val His Ile Tyr Gln Phe Ala
            185                 190                 195

caa aat atc caa gga gct ttc cag tgg aag ttc ctt gga tat gat gtg   739
Gln Asn Ile Gln Gly Ala Phe Gln Trp Lys Phe Leu Gly Tyr Asp Val
        200                 205                 210

gcg ggc gta gcg gtg aga ctt gat gat atc gat gtc tgagacattc        785
Ala Gly Val Ala Val Arg Leu Asp Asp Ile Asp Val
    215                 220                 225

acaaggagac gac                                                   798
```

<210> 1472
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 1472

```
Val Val Asp Ala Val His Asp Val Leu Gln Ile Ala Leu Ala Arg Arg
  1               5                  10                  15

Gly Glu Tyr Asn Leu Gly Asn Ala Leu Gly Leu Glu Val Leu Gly Gln
             20                  25                  30

Ala Phe Ala Val Thr Pro Ala Ala Gly Val Val Tyr His Asp Gly Val
         35                  40                  45

Ile Asp Ala Val Phe Gly Val Ile Asn Gly Gly Trp Val Ile Gly Val
     50                  55                  60

Asp Asp Leu Asp Trp Gly Ala Val Gly Pro Asp Asp Val Val Val Ile
 65                  70                  75                  80

Ile Gly Gly Asp Gly Ala Ile Glu Ser Thr Val Asp Arg Ile Thr Thr
                 85                  90                  95

Gln Gln Gly Cys Ala Leu Asp Gln Val Phe Phe Thr Ile Phe Ala Asp
            100                 105                 110

His Asp Gly Ala Gln Thr Ser Thr Val Ile Gln Cys Leu Ala Gly Asn
        115                 120                 125

Gln Asp Ala Gly Gln Gln Ala Thr Asp Ala Ala Glu Thr Val Gln His
    130                 135                 140

Asp Ile Ser Trp Val Asp Val Gly Phe Arg Thr Asn Asp Arg Arg Glu
145                 150                 155                 160

Ser Val Leu Gln Glu Gly Thr Gln Val Gly Ala Phe Gly Phe Phe Glu
                165                 170                 175

Ala Val Gly Gln Leu Ser Gln Val Asp Arg Cys Gly Thr Lys Val His
            180                 185                 190
```

```
Ile Tyr Gln Phe Ala Gln Asn Ile Gln Gly Ala Phe Gln Trp Lys Phe
        195                 200                 205

Leu Gly Tyr Asp Val Ala Gly Val Ala Val Arg Leu Asp Asp Ile Asp
    210                 215                 220

Val
225
```

<210> 1473
<211> 300
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(277)
<223> RXN03104

<400> 1473

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actgctggga gtagccgaag aggatggtgg cgtcagtggt cagggcgtca acgttgccct 60

gggacagtgc ctcaacacag gaagagtagg tgtcgtattc ttg gag ctg aac gcc   115
                                        Leu Glu Leu Asn Ala
                                          1               5

tgg gag gac atc ctt gac ctt ctg agc tgg agt gga tcc gga aac gga   163
Trp Glu Asp Ile Leu Asp Leu Leu Ser Trp Ser Gly Ser Gly Asn Gly
                10                  15                  20

gca cag gat caa acc gtt atc caa gtc ctc gag ggt ttc aat gcg atc   211
Ala Gln Asp Gln Thr Val Ile Gln Val Leu Glu Gly Phe Asn Ala Ile
            25                  30                  35

gtc atc ttg gcg aac aag cag agc ctg gtg ggt aag cag gta tgg gcc   259
Val Ile Leu Ala Asn Lys Gln Ser Leu Val Gly Lys Gln Val Trp Ala
        40                  45                  50

acc gaa gtt gac gga ctc tgaacggcca gcgttgatgg agt                 300
Thr Glu Val Asp Gly Leu
    55
```

<210> 1474
<211> 59
<212> PRT
<213> Corynebacterium glutamicum

<400> 1474

```
Leu Glu Leu Asn Ala Trp Glu Asp Ile Leu Asp Leu Leu Ser Trp Ser
  1               5                  10                  15

Gly Ser Gly Asn Gly Ala Gln Asp Gln Thr Val Ile Gln Val Leu Glu
            20                  25                  30

Gly Phe Asn Ala Ile Val Ile Leu Ala Asn Lys Gln Ser Leu Val Gly
        35                  40                  45

Lys Gln Val Trp Ala Thr Glu Val Asp Gly Leu
    50                  55
```

<210> 1475
<211> 292
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(292)
<223> RXN03106

<400> 1475
aaatgccctc ctgaactgga agaatcaagc ttgcttagag tcctgattca cctgccagaa 60

aggcacctca caggtgcaat tattacacaa ccccacagcg atg tcc gca tcc ttt 115
Met Ser Ala Ser Phe
1 5

gat gac ccc aac ctc atc tcg ctt gct gga ctg gtt cca acc atg cac 163
Asp Asp Pro Asn Leu Ile Ser Leu Ala Gly Leu Val Pro Thr Met His
10 15 20

tta gcc gat gct gcc agc ctg tcc acc ttg gcc cag gac cgg ttg agc 211
Leu Ala Asp Ala Ala Ser Leu Ser Thr Leu Ala Gln Asp Arg Leu Ser
25 30 35

atc acc ggt gat aaa ggt gcc aat gct ggt gcg aag atc gcc tcc cta 259
Ile Thr Gly Asp Lys Gly Ala Asn Ala Gly Ala Lys Ile Ala Ser Leu
40 45 50

gtc gcg ggc atg gtc gcc ggt gct gat tcc atc 292
Val Ala Gly Met Val Ala Gly Ala Asp Ser Ile
55 60

<210> 1476
<211> 64
<212> PRT
<213> Corynebacterium glutamicum

<400> 1476
Met Ser Ala Ser Phe Asp Asp Pro Asn Leu Ile Ser Leu Ala Gly Leu
1 5 10 15

Val Pro Thr Met His Leu Ala Asp Ala Ala Ser Leu Ser Thr Leu Ala
20 25 30

Gln Asp Arg Leu Ser Ile Thr Gly Asp Lys Gly Ala Asn Ala Gly Ala
35 40 45

Lys Ile Ala Ser Leu Val Ala Gly Met Val Ala Gly Ala Asp Ser Ile
50 55 60

<210> 1477
<211> 324
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(301)
<223> RXN03107

<400> 1477
ggatttatat caatttcagg gcgtggcgag cttttagtga ttcacgctcc tacggtgggt 60

atcacaaata cctcaactag aagtaggaga tgagcaccac atg agc gat ttt tcc 115
Met Ser Asp Phe Ser
1 5

aac aag gca gag gac ctc aca ggt aag gct aaa gaa gga ttc ggc gag 163
Asn Lys Ala Glu Asp Leu Thr Gly Lys Ala Lys Glu Gly Phe Gly Glu
10 15 20

gca act gat aac gag tcc ctc gct gat gag ggc cgt gcg gat cag gct 211
Ala Thr Asp Asn Glu Ser Leu Ala Asp Glu Gly Arg Ala Asp Gln Ala
25 30 35

aag gca gac atc aag gat gct gtc gaa aac gcc ggt gaa aag gta aag 259
Lys Ala Asp Ile Lys Asp Ala Val Glu Asn Ala Gly Glu Lys Val Lys
40 45 50

gac gca gct aac aag gtt ctg ggt gcg ttc aag aag gac gac 301
Asp Ala Ala Asn Lys Val Leu Gly Ala Phe Lys Lys Asp Asp
55 60 65

taatcccgta cttgttcagg att 324

<210> 1478
<211> 67
<212> PRT
<213> Corynebacterium glutamicum

<400> 1478
Met Ser Asp Phe Ser Asn Lys Ala Glu Asp Leu Thr Gly Lys Ala Lys
1 5 10 15

Glu Gly Phe Gly Glu Ala Thr Asp Asn Glu Ser Leu Ala Asp Glu Gly
20 25 30

Arg Ala Asp Gln Ala Lys Ala Asp Ile Lys Asp Ala Val Glu Asn Ala
35 40 45

Gly Glu Lys Val Lys Asp Ala Ala Asn Lys Val Leu Gly Ala Phe Lys
50 55 60

Lys Asp Asp
65

<210> 1479
<211> 1722
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(1699)
<223> RXN03113

<400> 1479
gttggatctt gcattgaaaa aatgaaaacc tcgtcgggaa tgcaacttgg gatcacgtct 60

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cgggcaagaa acgtccttaa aaaaagggga gtgattgtga gtg ctt gat ttc tta   115
                                            Val Leu Asp Phe Leu
                                              1               5

gct gcg aac ccg ctg att gcg ctg gtg gtt att ttg gcc gtt ggt tta   163
Ala Ala Asn Pro Leu Ile Ala Leu Val Val Ile Leu Ala Val Gly Leu
                 10                  15                  20

gca att ggt cag att agg gtc ttt ggc ctt tct tta ggt gcc gcc gcg   211
Ala Ile Gly Gln Ile Arg Val Phe Gly Leu Ser Leu Gly Ala Ala Ala
             25                  30                  35

gtg ctg ttt gtg gcc ctg gtg gtt tca act gca aat acc gac atc gtc   259
Val Leu Phe Val Ala Leu Val Val Ser Thr Ala Asn Thr Asp Ile Val
         40                  45                  50

atc ccc atg att gtt tat cag ctg ggc ttg gcg atg ttc gtt tat gtc   307
Ile Pro Met Ile Val Tyr Gln Leu Gly Leu Ala Met Phe Val Tyr Val
     55                  60                  65

atc ggt ttg tcc gcc gga cca gca ttt ttc agt gag ttc gct aaa aag   355
Ile Gly Leu Ser Ala Gly Pro Ala Phe Phe Ser Glu Phe Ala Lys Lys
 70                  75                  80                  85

ggc tgg aag ctc acc atc ttt atg ctc ctg ctg ctg gca aca ctg att   403
Gly Trp Lys Leu Thr Ile Phe Met Leu Leu Leu Leu Ala Thr Leu Ile
                 90                  95                 100

ggt ttg gcg tgg gtg ctt att aag tca ctg ggg ctt gat gca gcg atc   451
Gly Leu Ala Trp Val Leu Ile Lys Ser Leu Gly Leu Asp Ala Ala Ile
            105                 110                 115

ggt acc ggt atg ttc acc ggc gcg ctg acc tcg act ccc ggt atg gca   499
Gly Thr Gly Met Phe Thr Gly Ala Leu Thr Ser Thr Pro Gly Met Ala
        120                 125                 130

gcg gtc gtg gaa ttg att gaa gga atc gat cca agc ctt gcc agt gaa   547
Ala Val Val Glu Leu Ile Glu Gly Ile Asp Pro Ser Leu Ala Ser Glu
    135                 140                 145

cct gtt att ggt tat tcc ttg gca tat ccg gga gcc gtg ctg gga tcc   595
Pro Val Ile Gly Tyr Ser Leu Ala Tyr Pro Gly Ala Val Leu Gly Ser
150                 155                 160                 165

att gtg gtg gcc gcg gtt gga gcg aaa ctg ctc aaa gta aat cac cgg   643
Ile Val Val Ala Ala Val Gly Ala Lys Leu Leu Lys Val Asn His Arg
                170                 175                 180

gaa gat gct cga aaa gaa ggc atg atc acc gca ccg ctg gtg tgg aag   691
Glu Asp Ala Arg Lys Glu Gly Met Ile Thr Ala Pro Leu Val Trp Lys
            185                 190                 195

ggt gtg cag ctc aaa cct gga atc aca ggc agg gtg gga gat ctt cca   739
Gly Val Gln Leu Lys Pro Gly Ile Thr Gly Arg Val Gly Asp Leu Pro
```

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        200                 205                 210

cgc ctt gca ggt gaa agt atc atc gca acc cgc att gtg gat gat cca   787
Arg Leu Ala Gly Glu Ser Ile Ile Ala Thr Arg Ile Val Asp Asp Pro
    215                 220                 225

cat aca cac cgc ctc gcg gat cca gat ctg ccg att act gaa ggc atg   835
His Thr His Arg Leu Ala Asp Pro Asp Leu Pro Ile Thr Glu Gly Met
230                 235                 240                 245

gaa ctg ttg atc aac ggc act gaa gaa gcc gtg gat cgg gca att aag   883
Glu Leu Leu Ile Asn Gly Thr Glu Glu Ala Val Asp Arg Ala Ile Lys
                250                 255                 260

gcg ttg ggt gaa gaa cgc gaa acc aaa att gag gac aca gag ctg atc   931
Ala Leu Gly Glu Glu Arg Glu Thr Lys Ile Glu Asp Thr Glu Leu Ile
            265                 270                 275

tac acc cgc ctg acg gta tct agc cct gag gtt gca ggt aga acc gtt   979
Tyr Thr Arg Leu Thr Val Ser Ser Pro Glu Val Ala Gly Arg Thr Val
        280                 285                 290

gct gag ctt gat act gta gct cac gga ttc atg att gcc cgt atc cgc   1027
Ala Glu Leu Asp Thr Val Ala His Gly Phe Met Ile Ala Arg Ile Arg
    295                 300                 305

cag ggc gat tct gag gta gtg cct aaa cct gac acc gtg atc aac tac   1075
Gln Gly Asp Ser Glu Val Val Pro Lys Pro Asp Thr Val Ile Asn Tyr
310                 315                 320                 325

tct gac cgc atc cgc gtg gtg gtt gct cct ggt cgt gtg gct gaa gtg   1123
Ser Asp Arg Ile Arg Val Val Val Ala Pro Gly Arg Val Ala Glu Val
                330                 335                 340

cga cga ttc tta ggg gac tct gaa aag tcc ctt gct gat gtt aat ctg   1171
Arg Arg Phe Leu Gly Asp Ser Glu Lys Ser Leu Ala Asp Val Asn Leu
            345                 350                 355

ctg cct tta gcc atc gga tta tct ctt ggc ctg ttg ttg ggc gcg atc   1219
Leu Pro Leu Ala Ile Gly Leu Ser Leu Gly Leu Leu Leu Gly Ala Ile
        360                 365                 370

ccg att cct ctt cca ggc ggc acc acg atg tcc ctt ggc ttt ggt ggc   1267
Pro Ile Pro Leu Pro Gly Gly Thr Thr Met Ser Leu Gly Phe Gly Gly
    375                 380                 385

ggc ccg att att gcc ggc ctg att ttg gga gca ctc aag cac aca gga   1315
Gly Pro Ile Ile Ala Gly Leu Ile Leu Gly Ala Leu Lys His Thr Gly
390                 395                 400                 405

ccg ctg acg tgg cag atg ccg ttc cac gcc aac cgc acg atc tcc acc   1363
Pro Leu Thr Trp Gln Met Pro Phe His Ala Asn Arg Thr Ile Ser Thr
                410                 415                 420

ttg ggc ctg gcg ctg ttt ttg gct ggt gtg ggt acc tct gca ggt gca   1411
Leu Gly Leu Ala Leu Phe Leu Ala Gly Val Gly Thr Ser Ala Gly Ala
            425                 430                 435

gga ttt aga gct gcg ctt acc gat tcc tcc tcc ttg atc tac atg gcc   1459
Gly Phe Arg Ala Ala Leu Thr Asp Ser Ser Ser Leu Ile Tyr Met Ala
        440                 445                 450
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ggt ggc ttg gtg atc acc ttg gcc tct gcg ctg ctg tgt gct gtg atc   1507
Gly Gly Leu Val Ile Thr Leu Ala Ser Ala Leu Leu Cys Ala Val Ile
    455                 460                 465

ggc atg tgg gta ctc agg ttg agg tgg gat gaa gcc atg ggt gtt gcc   1555
Gly Met Trp Val Leu Arg Leu Arg Trp Asp Glu Ala Met Gly Val Ala
470                 475                 480                 485

gct ggc acc acc aca aat cct gca att att tcc tat ctg aat ggg caa   1603
Ala Gly Thr Thr Thr Asn Pro Ala Ile Ile Ser Tyr Leu Asn Gly Gln
                490                 495                 500

acc gga acg gat ctt gcc aac agg gga tat gcc act gtg tac ccc acg   1651
Thr Gly Thr Asp Leu Ala Asn Arg Gly Tyr Ala Thr Val Tyr Pro Thr
            505                 510                 515

gcg atg atc ggt aaa atc ctc ggc gcg cag ata ttg ttc ttg ctg ctc   1699
Ala Met Ile Gly Lys Ile Leu Gly Ala Gln Ile Leu Phe Leu Leu Leu
        520                 525                 530

taaggtgatt tttgggcagt ggt                                        1722
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5a5a5a

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                165                 170                 175

Lys Val Asn His Arg Glu Asp Ala Arg Lys Glu Gly Met Ile Thr Ala
            180                 185                 190

Pro Leu Val Trp Lys Gly Val Gln Leu Lys Pro Gly Ile Thr Gly Arg
        195                 200                 205

Val Gly Asp Leu Pro Arg Leu Ala Gly Glu Ser Ile Ile Ala Thr Arg
    210                 215                 220

Ile Val Asp Asp Pro His Thr His Arg Leu Ala Asp Pro Asp Leu Pro
225                 230                 235                 240

Ile Thr Glu Gly Met Glu Leu Leu Ile Asn Gly Thr Glu Glu Ala Val
                245                 250                 255

Asp Arg Ala Ile Lys Ala Leu Gly Glu Glu Arg Glu Thr Lys Ile Glu
            260                 265                 270

Asp Thr Glu Leu Ile Tyr Thr Arg Leu Thr Val Ser Ser Pro Glu Val
        275                 280                 285

Ala Gly Arg Thr Val Ala Glu Leu Asp Thr Val Ala His Gly Phe Met
    290                 295                 300

Ile Ala Arg Ile Arg Gln Gly Asp Ser Glu Val Val Pro Lys Pro Asp
305                 310                 315                 320

Thr Val Ile Asn Tyr Ser Asp Arg Ile Arg Val Val Val Ala Pro Gly
                325                 330                 335

Arg Val Ala Glu Val Arg Arg Phe Leu Gly Asp Ser Glu Lys Ser Leu
            340                 345                 350

Ala Asp Val Asn Leu Leu Pro Leu Ala Ile Gly Leu Ser Leu Gly Leu
        355                 360                 365

Leu Leu Gly Ala Ile Pro Ile Pro Leu Pro Gly Gly Thr Thr Met Ser
    370                 375                 380

Leu Gly Phe Gly Gly Gly Pro Ile Ile Ala Gly Leu Ile Leu Gly Ala
385                 390                 395                 400

Leu Lys His Thr Gly Pro Leu Thr Trp Gln Met Pro Phe His Ala Asn
                405                 410                 415

Arg Thr Ile Ser Thr Leu Gly Leu Ala Leu Phe Leu Ala Gly Val Gly
            420                 425                 430

Thr Ser Ala Gly Ala Gly Phe Arg Ala Ala Leu Thr Asp Ser Ser Ser
        435                 440                 445

Leu Ile Tyr Met Ala Gly Gly Leu Val Ile Thr Leu Ala Ser Ala Leu
    450                 455                 460

Leu Cys Ala Val Ile Gly Met Trp Val Leu Arg Leu Arg Trp Asp Glu
465                 470                 475                 480

Ala Met Gly Val Ala Ala Gly Thr Thr Thr Asn Pro Ala Ile Ile Ser
                485                 490                 495
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Tyr Leu Asn Gly Gln Thr Gly Thr Asp Leu Ala Asn Arg Gly Tyr Ala
            500                 505                 510

Thr Val Tyr Pro Thr Ala Met Ile Gly Lys Ile Leu Gly Ala Gln Ile
        515                 520                 525

Leu Phe Leu Leu Leu
    530


<210> 1481
<211> 1441
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1441)
<223> FRXA00506

<400> 1481
gttggatctt gcattgaaaa aatgaaaacc tcgtcgggaa tgcaacttgg gatcacgtct 60

cgggcaagaa acgtccttaa aaaaagggga gtgattgtga gtg ctt gat ttc tta   115
                                            Val Leu Asp Phe Leu
                                              1               5

gct gcg aac ccg ctg att gcg ctg gtg gtt att ttg gcc gtt ggt tta   163
Ala Ala Asn Pro Leu Ile Ala Leu Val Val Ile Leu Ala Val Gly Leu
                  10                  15                  20

gca att ggt cag att agg gtc ttt ggc ctt tct tta ggt gcc gcc gcg   211
Ala Ile Gly Gln Ile Arg Val Phe Gly Leu Ser Leu Gly Ala Ala Ala
              25                  30                  35

gtg ctg ttt gtg gcc ctg gtg gtt tca act gca aat acc gac atc gtc   259
Val Leu Phe Val Ala Leu Val Val Ser Thr Ala Asn Thr Asp Ile Val
          40                  45                  50

atc ccc atg att gtt tat cag ctg ggc ttg gcg atg ttc gtt tat gtc   307
Ile Pro Met Ile Val Tyr Gln Leu Gly Leu Ala Met Phe Val Tyr Val
      55                  60                  65

atc ggt ttg tcc gcc gga cca gca ttt ttc agt gag ttc gct aaa aag   355
Ile Gly Leu Ser Ala Gly Pro Ala Phe Phe Ser Glu Phe Ala Lys Lys
  70                  75                  80                  85

ggc tgg aag ctc acc atc ttt atg ctc ctg ctg ctg gca aca ctg att   403
Gly Trp Lys Leu Thr Ile Phe Met Leu Leu Leu Leu Ala Thr Leu Ile
                  90                  95                 100

ggt ttg gcg tgg gtg ctt att aag tca ctg ggg ctt gat gca gcg atc   451
Gly Leu Ala Trp Val Leu Ile Lys Ser Leu Gly Leu Asp Ala Ala Ile
              105                 110                 115

ggt acc ggt atg ttc acc ggc gcg ctg acc tcg act ccc ggt atg gca   499
Gly Thr Gly Met Phe Thr Gly Ala Leu Thr Ser Thr Pro Gly Met Ala
          120                 125                 130

gcg gtc gtg gaa ttg att gaa gga atc gat cca agc ctt gcc agt gaa   547
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Ala Val Val Glu Leu Ile Glu Gly Ile Asp Pro Ser Leu Ala Ser Glu
    135                 140                 145

cct gtt att ggt tat tcc ttg gca tat ccg gga gcc gtg ctg gga tcc   595
Pro Val Ile Gly Tyr Ser Leu Ala Tyr Pro Gly Ala Val Leu Gly Ser
150                 155                 160                 165

att gtg gtg gcc gcg gtt gga gcg aaa ctg ctc aaa gta aat cac cgg   643
Ile Val Val Ala Ala Val Gly Ala Lys Leu Leu Lys Val Asn His Arg
                170                 175                 180

gaa gat gct cga aaa gaa ggc atg atc acc gca ccg ctg gtg tgg aag   691
Glu Asp Ala Arg Lys Glu Gly Met Ile Thr Ala Pro Leu Val Trp Lys
            185                 190                 195

ggt gtg cag ctc aaa cct gga atc aca ggc agg gtg gga gat ctt cca   739
Gly Val Gln Leu Lys Pro Gly Ile Thr Gly Arg Val Gly Asp Leu Pro
        200                 205                 210

cgc ctt gca ggt gaa agt atc atc gca acc cgc att gtg gat gat cca   787
Arg Leu Ala Gly Glu Ser Ile Ile Ala Thr Arg Ile Val Asp Asp Pro
    215                 220                 225

cat aca cac cgc ctc gcg gat cca gat ctg ccg att act gaa ggc atg   835
His Thr His Arg Leu Ala Asp Pro Asp Leu Pro Ile Thr Glu Gly Met
230                 235                 240                 245

gaa ctg ttg atc aac ggc act gaa gaa gcc gtg gat cgg gca att aag   883
Glu Leu Leu Ile Asn Gly Thr Glu Glu Ala Val Asp Arg Ala Ile Lys
                250                 255                 260

gcg ttg ggt gaa gaa cgc gaa acc aaa att gag gac aca gag ctg atc   931
Ala Leu Gly Glu Glu Arg Glu Thr Lys Ile Glu Asp Thr Glu Leu Ile
            265                 270                 275

tac acc cgc ctg acg gta tct agc cct gag gtt gca ggt aga acc gtt   979
Tyr Thr Arg Leu Thr Val Ser Ser Pro Glu Val Ala Gly Arg Thr Val
        280                 285                 290

gct gag ctt gat act gta gct cac gga ttc atg att gcc cgt atc cgc   1027
Ala Glu Leu Asp Thr Val Ala His Gly Phe Met Ile Ala Arg Ile Arg
    295                 300                 305

cag ggc gat tct gag gta gtg cct aaa cct gac acc gtg atc aac tac   1075
Gln Gly Asp Ser Glu Val Val Pro Lys Pro Asp Thr Val Ile Asn Tyr
310                 315                 320                 325

tct gac cgc atc cgc gtg gtg gtt gct cct ggt cgt gtg gct gaa gtg   1123
Ser Asp Arg Ile Arg Val Val Val Ala Pro Gly Arg Val Ala Glu Val
                330                 335                 340

cga cga ttc tta ggg gac tct gaa aag tcc ctt gct gat gtt aat ctg   1171
Arg Arg Phe Leu Gly Asp Ser Glu Lys Ser Leu Ala Asp Val Asn Leu
            345                 350                 355

ctg cct tta gcc atc gga tta tct ctt ggc ctg ttg ttg ggc gcg atc   1219
Leu Pro Leu Ala Ile Gly Leu Ser Leu Gly Leu Leu Leu Gly Ala Ile
        360                 365                 370

ccg att cct ctt cca ggc ggc acc acg atg tcc ctt ggc ttt ggt ggc   1267
Pro Ile Pro Leu Pro Gly Gly Thr Thr Met Ser Leu Gly Phe Gly Gly
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09650704.090705

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    375                 380                 385

ggc ccg att att gcc ggc ctg att ttg gga gca ctc aag cac aca gga   1315
Gly Pro Ile Ile Ala Gly Leu Ile Leu Gly Ala Leu Lys His Thr Gly
390                 395                 400                 405

ccg ctg acg tgg cag atg ccg ttc cac gcc aac cgc acg atc tcc acc   1363
Pro Leu Thr Trp Gln Met Pro Phe His Ala Asn Arg Thr Ile Ser Thr
                410                 415                 420

ttg ggc ctg gcg ctg ttt ttg gct ggt gtg ggt acc tct gca ggt gca   1411
Leu Gly Leu Ala Leu Phe Leu Ala Gly Val Gly Thr Ser Ala Gly Ala
            425                 430                 435

gga ttt aga gct gcg ctt acc gat tcc tcc                           1441
Gly Phe Arg Ala Ala Leu Thr Asp Ser Ser
        440                 445


<210> 1482
<211> 447
<212> PRT
<213> Corynebacterium glutamicum

<400> 1482
Val Leu Asp Phe Leu Ala Ala Asn Pro Leu Ile Ala Leu Val Val Ile
  1               5                  10                  15

Leu Ala Val Gly Leu Ala Ile Gly Gln Ile Arg Val Phe Gly Leu Ser
             20                  25                  30

Leu Gly Ala Ala Ala Val Leu Phe Val Ala Leu Val Val Ser Thr Ala
         35                  40                  45

Asn Thr Asp Ile Val Ile Pro Met Ile Val Tyr Gln Leu Gly Leu Ala
     50                  55                  60

Met Phe Val Tyr Val Ile Gly Leu Ser Ala Gly Pro Ala Phe Phe Ser
 65                  70                  75                  80

Glu Phe Ala Lys Lys Gly Trp Lys Leu Thr Ile Phe Met Leu Leu Leu
                 85                  90                  95

Leu Ala Thr Leu Ile Gly Leu Ala Trp Val Leu Ile Lys Ser Leu Gly
            100                 105                 110

Leu Asp Ala Ala Ile Gly Thr Gly Met Phe Thr Gly Ala Leu Thr Ser
        115                 120                 125

Thr Pro Gly Met Ala Ala Val Val Glu Leu Ile Glu Gly Ile Asp Pro
    130                 135                 140

Ser Leu Ala Ser Glu Pro Val Ile Gly Tyr Ser Leu Ala Tyr Pro Gly
145                 150                 155                 160

Ala Val Leu Gly Ser Ile Val Val Ala Ala Val Gly Ala Lys Leu Leu
                165                 170                 175

Lys Val Asn His Arg Glu Asp Ala Arg Lys Glu Gly Met Ile Thr Ala
            180                 185                 190
```

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Pro Leu Val Trp Lys Gly Val Gln Leu Lys Pro Gly Ile Thr Gly Arg
        195                 200                 205

Val Gly Asp Leu Pro Arg Leu Ala Gly Glu Ser Ile Ile Ala Thr Arg
    210                 215                 220

Ile Val Asp Asp Pro His Thr His Arg Leu Ala Asp Pro Asp Leu Pro
225                 230                 235                 240

Ile Thr Glu Gly Met Glu Leu Leu Ile Asn Gly Thr Glu Glu Ala Val
                245                 250                 255

Asp Arg Ala Ile Lys Ala Leu Gly Glu Glu Arg Glu Thr Lys Ile Glu
            260                 265                 270

Asp Thr Glu Leu Ile Tyr Thr Arg Leu Thr Val Ser Ser Pro Glu Val
        275                 280                 285

Ala Gly Arg Thr Val Ala Glu Leu Asp Thr Val Ala His Gly Phe Met
    290                 295                 300

Ile Ala Arg Ile Arg Gln Gly Asp Ser Glu Val Val Pro Lys Pro Asp
305                 310                 315                 320

Thr Val Ile Asn Tyr Ser Asp Arg Ile Arg Val Val Val Ala Pro Gly
                325                 330                 335

Arg Val Ala Glu Val Arg Arg Phe Leu Gly Asp Ser Glu Lys Ser Leu
            340                 345                 350

Ala Asp Val Asn Leu Leu Pro Leu Ala Ile Gly Leu Ser Leu Gly Leu
        355                 360                 365

Leu Leu Gly Ala Ile Pro Ile Pro Leu Pro Gly Gly Thr Thr Met Ser
    370                 375                 380

Leu Gly Phe Gly Gly Gly Pro Ile Ile Ala Gly Leu Ile Leu Gly Ala
385                 390                 395                 400

Leu Lys His Thr Gly Pro Leu Thr Trp Gln Met Pro Phe His Ala Asn
                405                 410                 415

Arg Thr Ile Ser Thr Leu Gly Leu Ala Leu Phe Leu Ala Gly Val Gly
            420                 425                 430

Thr Ser Ala Gly Ala Gly Phe Arg Ala Ala Leu Thr Asp Ser Ser
        435                 440                 445
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<210> 1483
<211> 522
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(499)
<223> RXN03115

<400> 1483
ggaactgctg gcaggcaacg tccgtgatgg cgatggtgtg cttgtcaacg tcgccgacgg 60

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cggccagaag ctcgacgttt ccagggcggt ctaacggctc gtg ggc aag cag gaa   115
                                             Val Gly Lys Gln Glu
                                               1               5

aag ctg cgc att cct ctc gat gtt ccg gga gtg gaa tca gaa gag gta   163
Lys Leu Arg Ile Pro Leu Asp Val Pro Gly Val Glu Ser Glu Glu Val
                 10                  15                  20

ggt gta gaa ctg ctt gcc gaa ggc tac tac ctg gta gcc act ttg ccg   211
Gly Val Glu Leu Leu Ala Glu Gly Tyr Tyr Leu Val Ala Thr Leu Pro
             25                  30                  35

gct gtc gcc cag gac tgt gcc ctg ggt gac gtc gtg cgg gca cat cat   259
Ala Val Ala Gln Asp Cys Ala Leu Gly Asp Val Val Arg Ala His His
         40                  45                  50

gtt gat gag gtc ttg gaa ttt caa gaa gtg gca gtt gct ggc gga aac   307
Val Asp Glu Val Leu Glu Phe Gln Glu Val Ala Val Ala Gly Gly Asn
     55                  60                  65

aaa acc ctc cgg gtg ctc gtt gat gcc atc gct gct gac cac gtg cga   355
Lys Thr Leu Arg Val Leu Val Asp Ala Ile Ala Ala Asp His Val Arg
 70                  75                  80                  85

gcc caa cta gaa aca ctt ggg cta cac gtg gaa gct ccc atg tca gaa   403
Ala Gln Leu Glu Thr Leu Gly Leu His Val Glu Ala Pro Met Ser Glu
                 90                  95                 100

atg cta act gtc aat att gcc ccc gat tca ccg tcg cac ggt ttg gag   451
Met Leu Thr Val Asn Ile Ala Pro Asp Ser Pro Ser His Gly Leu Glu
            105                 110                 115

atc ctg ctc gat gat ctg cat gct cag ggg gta att ttc agg gcg tta   499
Ile Leu Leu Asp Asp Leu His Ala Gln Gly Val Ile Phe Arg Ala Leu
        120                 125                 130

tagagcgcct aattgtagag agc                                        522
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09d0d0d0

Ala Asp His Val Arg Ala Gln Leu Glu Thr Leu Gly Leu His Val Glu
85 90 95

Ala Pro Met Ser Glu Met Leu Thr Val Asn Ile Ala Pro Asp Ser Pro
100 105 110

Ser His Gly Leu Glu Ile Leu Leu Asp Asp Leu His Ala Gln Gly Val
115 120 125

Ile Phe Arg Ala Leu
130

<210> 1485
<211> 270
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(247)
<223> RXN03122

<400> 1485
atggaccatg gcgggatgag tggaatgatg agcgaggagg acatgacagc cctcgaggac 60

gcccagggca cccgaggctg cccggctcta ccttgagcag atg acc gcc cac cat 115
Met Thr Ala His His
1 5

gag ggc gcg gtc gat atg gcc cgc gat gag gtc act gat ggc cag aac 163
Glu Gly Ala Val Asp Met Ala Arg Asp Glu Val Thr Asp Gly Gln Asn
10 15 20

ccg cag gcc atc gct ctg gct gag cag gtc att gaa gat cag gag gcc 211
Pro Gln Ala Ile Ala Leu Ala Glu Gln Val Ile Glu Asp Gln Glu Ala
25 30 35

gag atc gcc gag atg gag cat atg ctc aac gag ctc tgaacaagga 257
Glu Ile Ala Glu Met Glu His Met Leu Asn Glu Leu
40 45

cattccccga cca 270

<210> 1486
<211> 49
<212> PRT
<213> Corynebacterium glutamicum

<400> 1486
Met Thr Ala His His Glu Gly Ala Val Asp Met Ala Arg Asp Glu Val
1 5 10 15

Thr Asp Gly Gln Asn Pro Gln Ala Ile Ala Leu Ala Glu Gln Val Ile
20 25 30

Glu Asp Gln Glu Ala Glu Ile Ala Glu Met Glu His Met Leu Asn Glu
35 40 45

Leu

<210> 1487
<211> 474
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(451)
<223> RXN03134

<400> 1487
atgctgtttc atcgctggcg ttggcttttt cgagccattc gagctcttct ccggggagat 60

ccagtttgct gatcagcggg tttgtttcgc gtggggcgtg gtg gct tgg cgc gtc 115
Val Ala Trp Arg Val
1 5

ggc cca ggt tcc cat gag cat gac ata gtt ggg tcc tcc ggc ttt gga 163
Gly Pro Gly Ser His Glu His Asp Ile Val Gly Ser Ser Gly Phe Gly
10 15 20

tcc gag gcc gac gga gga ttt ttt cca gcc tcc gaa gga ttg gcg ttg 211
Ser Glu Ala Asp Gly Gly Phe Phe Pro Ala Ser Glu Gly Leu Ala Leu
25 30 35

gac aat ggc gcc ggt gat gcc gcg gtt gac gta ggc gtt tcc gac atc 259
Asp Asn Gly Ala Gly Asp Ala Ala Val Asp Val Gly Val Ser Asp Ile
40 45 50

gac gtg gtc aag cca ggt gcg gac ttc gtc ggc gtc gag gga ttg gag 307
Asp Val Val Lys Pro Gly Ala Asp Phe Val Gly Val Glu Gly Leu Glu
55 60 65

tcc gcc ggt gag tcc gaa gtc gtt gcc gtt ttg gaa ttc gat ggc ttc 355
Ser Ala Gly Glu Ser Glu Val Val Ala Val Leu Glu Phe Asp Gly Phe
70 75 80 85

att gag gtc ggt ggc ttt cat cag gcc gag gac tgg tcc gaa tac ttc 403
Ile Glu Val Gly Gly Phe His Gln Ala Glu Asp Trp Ser Glu Tyr Phe
90 95 100

tgt gag gtg gaa gaa ggt tcc tgg ttt gac gcc ttc ttt gat gcc ggg 451
Cys Glu Val Glu Glu Gly Ser Trp Phe Asp Ala Phe Phe Asp Ala Gly
105 110 115

tgaccagagt cggccggtgt cgt 474

<210> 1488
<211> 117
<212> PRT
<213> Corynebacterium glutamicum

<400> 1488
Val Ala Trp Arg Val Gly Pro Gly Ser His Glu His Asp Ile Val Gly
1 5 10 15

Ser Ser Gly Phe Gly Ser Glu Ala Asp Gly Gly Phe Phe Pro Ala Ser

```
            20                  25                  30

Glu Gly Leu Ala Leu Asp Asn Gly Ala Gly Asp Ala Ala Val Asp Val
         35                  40                  45

Gly Val Ser Asp Ile Asp Val Val Lys Pro Gly Ala Asp Phe Val Gly
     50                  55                  60

Val Glu Gly Leu Glu Ser Ala Gly Glu Ser Glu Val Val Ala Val Leu
 65                  70                  75                  80

Glu Phe Asp Gly Phe Ile Glu Val Gly Gly Phe His Gln Ala Glu Asp
                 85                  90                  95

Trp Ser Glu Tyr Phe Cys Glu Val Glu Glu Gly Ser Trp Phe Asp Ala
            100                 105                 110

Phe Phe Asp Ala Gly
        115


<210> 1489
<211> 852
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(829)
<223> RXN03135

<400> 1489
ttagcttgtc gacgtccccc tcttccaaca cctccggctt tgtttgtttt tccaaccaac 60

cgggctctgc tgcggtggcg acggcttttg tggcccactg ttg gtt ttg gat gag   115
                                            Leu Val Leu Asp Glu
                                              1               5

cgc tgg gtt ggt gtc ggg ctc gtt gat aaa tgg gac gag ggg ggc gtc   163
Arg Trp Val Gly Val Gly Leu Val Asp Lys Trp Asp Glu Gly Gly Val
                 10                  15                  20

gag aag cgt ctc ttt gct gcg gtc ttg tgt gtg gtt ggg gcc ggg cgc   211
Glu Lys Arg Leu Phe Ala Ala Val Leu Cys Val Val Gly Ala Gly Arg
             25                  30                  35

ggg cac gtc gat gag cgt ggc gag gtc aga tat gga ggc gcg gaa gcg   259
Gly His Val Asp Glu Arg Gly Glu Val Arg Tyr Gly Gly Ala Glu Ala
         40                  45                  50

gct ctc ctc tcg ctt gaa gga cgg gtt gtc ggc gtc gag gtc gaa gat   307
Ala Leu Leu Ser Leu Glu Gly Arg Val Val Gly Val Glu Val Glu Asp
     55                  60                  65

ggc gga cat gaa gtt ttc gct cgc ggc gtt ttc ctc gag gcg gcg cac   355
Gly Gly His Glu Val Phe Ala Arg Gly Val Phe Leu Glu Ala Ala His
 70                  75                  80                  85

gag gta aga aat ggc cac gtc gaa ttc ttg tgg gcg cac ggc tgg tac   403
Glu Val Arg Asn Gly His Val Glu Phe Leu Trp Ala His Gly Trp Tyr
                 90                  95                 100
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gta aag cag cag ctc acc gac gtc aac gct gac ggc gcg cgc ctg atc   451
Val Lys Gln Gln Leu Thr Asp Val Asn Ala Asp Gly Ala Arg Leu Ile
            105                 110                 115

gga cgc cat gcc ctg cag cat ttc gaa ctc cac acg gtc cgc tac ccc   499
Gly Arg His Ala Leu Gln His Phe Glu Leu His Thr Val Arg Tyr Pro
        120                 125                 130

acg ctc cac aga gag caa atg tgc gaa tgc tat gtc gaa aag gtt gtg   547
Thr Leu His Arg Glu Gln Met Cys Glu Cys Tyr Val Glu Lys Val Val
    135                 140                 145

gcc ggc aac gcc cag gcg cag gcc ctc cat gtt ttc ttt gcg cat cgt   595
Ala Gly Asn Ala Gln Ala Gln Ala Leu His Val Phe Phe Ala His Arg
150                 155                 160                 165

cca ata gag gac gcg ctt gta att ggc atc ggt ggc ttg ttt gga agg   643
Pro Ile Glu Asp Ala Leu Val Ile Gly Ile Gly Gly Leu Phe Gly Arg
                170                 175                 180

ttc tgt ggc aac tgg cca gcc ggt gat ctg cgc gtg gac gtg ctc cat   691
Phe Cys Gly Asn Trp Pro Ala Gly Asp Leu Arg Val Asp Val Leu His
            185                 190                 195

agg caa att agc acc ctt gac cag gcg aac ctt aac gcc cgc ccc gcc   739
Arg Gln Ile Ser Thr Leu Asp Gln Ala Asn Leu Asn Ala Arg Pro Ala
        200                 205                 210

tgt gtt gac gcg ctc gcg gcc gaa ctg cgc caa gtc ctg gat tgc acc   787
Cys Val Asp Ala Leu Ala Ala Glu Leu Arg Gln Val Leu Asp Cys Thr
    215                 220                 225

gag ggc atc ggg aag gta cgc ctg caa cac aat tcc ggc ttc           829
Glu Gly Ile Gly Lys Val Arg Leu Gln His Asn Ser Gly Phe
230                 235                 240

tagttcatgc agctctggat tgg                                        852
```

<210> 1490
<211> 243
<212> PRT
<213> Corynebacterium glutamicum

<400> 1490

```
Leu Val Leu Asp Glu Arg Trp Val Gly Val Gly Leu Val Asp Lys Trp
  1               5                  10                  15

Asp Glu Gly Gly Val Glu Lys Arg Leu Phe Ala Ala Val Leu Cys Val
             20                  25                  30

Val Gly Ala Gly Arg Gly His Val Asp Glu Arg Gly Glu Val Arg Tyr
         35                  40                  45

Gly Gly Ala Glu Ala Ala Leu Leu Ser Leu Glu Gly Arg Val Val Gly
     50                  55                  60

Val Glu Val Glu Asp Gly Gly His Glu Val Phe Ala Arg Gly Val Phe
 65                  70                  75                  80
```

```
Leu Glu Ala Ala His Glu Val Arg Asn Gly His Val Glu Phe Leu Trp
                 85                  90                  95

Ala His Gly Trp Tyr Val Lys Gln Gln Leu Thr Asp Val Asn Ala Asp
            100                 105                 110

Gly Ala Arg Leu Ile Gly Arg His Ala Leu Gln His Phe Glu Leu His
        115                 120                 125

Thr Val Arg Tyr Pro Thr Leu His Arg Glu Gln Met Cys Glu Cys Tyr
    130                 135                 140

Val Glu Lys Val Val Ala Gly Asn Ala Gln Ala Gln Ala Leu His Val
145                 150                 155                 160

Phe Phe Ala His Arg Pro Ile Glu Asp Ala Leu Val Ile Gly Ile Gly
                165                 170                 175

Gly Leu Phe Gly Arg Phe Cys Gly Asn Trp Pro Ala Gly Asp Leu Arg
            180                 185                 190

Val Asp Val Leu His Arg Gln Ile Ser Thr Leu Asp Gln Ala Asn Leu
        195                 200                 205

Asn Ala Arg Pro Ala Cys Val Asp Ala Leu Ala Ala Glu Leu Arg Gln
    210                 215                 220

Val Leu Asp Cys Thr Glu Gly Ile Gly Lys Val Arg Leu Gln His Asn
225                 230                 235                 240

Ser Gly Phe
```

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<210> 1491
<211> 852
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(829)
<223> FRXA02285

<400> 1491

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ttagcttgtc gacgtccccc tcttccaaca cctccggctt tgtttgtttt tccaaccaac 60

cgggctctgc tgcggtggcg acggcttttg tggcccactg ttg gtt ttg gat gag   115
                                              Leu Val Leu Asp Glu
                                                1               5

cgc tgg gtt ggt gtc ggg ctc gtt gat aaa tgg gac gag ggg ggc gtc   163
Arg Trp Val Gly Val Gly Leu Val Asp Lys Trp Asp Glu Gly Gly Val
                10                  15                  20

gag aag cgt ctc ttt gct gcg gtc ttg tgt gtg gtt ggg gcc ggg cgc   211
Glu Lys Arg Leu Phe Ala Ala Val Leu Cys Val Val Gly Ala Gly Arg
            25                  30                  35

ggg cac gtc gat gag cgt ggc gag gtc aga tat gga ggc gcg gaa gcg   259
Gly His Val Asp Glu Arg Gly Glu Val Arg Tyr Gly Gly Ala Glu Ala
```

```
         40                  45                  50

gct ctc ctc tcg ctt gaa gga cgg gtt gtc ggc gtc gag gtc gaa gat   307
Ala Leu Leu Ser Leu Glu Gly Arg Val Val Gly Val Glu Val Glu Asp
     55                  60                  65

ggc gga cat gaa gtt ttc gct cgc ggc gtt ttc ctc gag gcg gcg cac   355
Gly Gly His Glu Val Phe Ala Arg Gly Val Phe Leu Glu Ala Ala His
 70                  75                  80                  85

gag gta aga aat ggc cac gtc gaa ttc ttg tgg gcg cac ggc tgg tac   403
Glu Val Arg Asn Gly His Val Glu Phe Leu Trp Ala His Gly Trp Tyr
                 90                  95                 100

gta aag cag cag ctc acc gac gtc aac gct gac ggc gcg cgc ctg atc   451
Val Lys Gln Gln Leu Thr Asp Val Asn Ala Asp Gly Ala Arg Leu Ile
            105                 110                 115

gga cgc cat gcc ctg cag cat ttc gaa ctc cac acg gtc cgc tac ccc   499
Gly Arg His Ala Leu Gln His Phe Glu Leu His Thr Val Arg Tyr Pro
        120                 125                 130

acg ctc cac aga gag caa atg tgc gaa tgc tat gtc gaa aag gtt gtg   547
Thr Leu His Arg Glu Gln Met Cys Glu Cys Tyr Val Glu Lys Val Val
    135                 140                 145

gcc ggc aac gcc cag gcg cag gcc ctc cat gtt ttc ttt gcg cat cgt   595
Ala Gly Asn Ala Gln Ala Gln Ala Leu His Val Phe Phe Ala His Arg
150                 155                 160                 165

cca ata gag gac gcg ctt gta att ggc atc ggt ggc ttg ttt gga agg   643
Pro Ile Glu Asp Ala Leu Val Ile Gly Ile Gly Gly Leu Phe Gly Arg
                170                 175                 180

ttc tgt ggc aac tgg cca gcc ggt gat ctg cgc gtg gac gtg ctc cat   691
Phe Cys Gly Asn Trp Pro Ala Gly Asp Leu Arg Val Asp Val Leu His
            185                 190                 195

agg caa att agc acc ctt gac cag gcg aac ctt aac gcc cgc ccc gcc   739
Arg Gln Ile Ser Thr Leu Asp Gln Ala Asn Leu Asn Ala Arg Pro Ala
        200                 205                 210

tgt gtt gac gcg ctc gcg gcc gaa ctg cgc caa gtc ctg gat tgc acc   787
Cys Val Asp Ala Leu Ala Ala Glu Leu Arg Gln Val Leu Asp Cys Thr
    215                 220                 225

gag ggc atc ggg aag gta cgc ctg caa cac aat tcc ggc ttc           829
Glu Gly Ile Gly Lys Val Arg Leu Gln His Asn Ser Gly Phe
230                 235                 240

tagttcatgc agctctggat tgg                                        852
```

5d4d5d5d5

```
Asp Glu Gly Gly Val Glu Lys Arg Leu Phe Ala Ala Val Leu Cys Val
             20                  25                  30

Val Gly Ala Gly Arg Gly His Val Asp Glu Arg Gly Glu Val Arg Tyr
         35                  40                  45

Gly Gly Ala Glu Ala Ala Leu Leu Ser Leu Glu Gly Arg Val Val Gly
     50                  55                  60

Val Glu Val Glu Asp Gly Gly His Glu Val Phe Ala Arg Gly Val Phe
 65                  70                  75                  80

Leu Glu Ala Ala His Glu Val Arg Asn Gly His Val Glu Phe Leu Trp
                 85                  90                  95

Ala His Gly Trp Tyr Val Lys Gln Gln Leu Thr Asp Val Asn Ala Asp
            100                 105                 110

Gly Ala Arg Leu Ile Gly Arg His Ala Leu Gln His Phe Glu Leu His
        115                 120                 125

Thr Val Arg Tyr Pro Thr Leu His Arg Glu Gln Met Cys Glu Cys Tyr
    130                 135                 140

Val Glu Lys Val Val Ala Gly Asn Ala Gln Ala Gln Ala Leu His Val
145                 150                 155                 160

Phe Phe Ala His Arg Pro Ile Glu Asp Ala Leu Val Ile Gly Ile Gly
                165                 170                 175

Gly Leu Phe Gly Arg Phe Cys Gly Asn Trp Pro Ala Gly Asp Leu Arg
            180                 185                 190

Val Asp Val Leu His Arg Gln Ile Ser Thr Leu Asp Gln Ala Asn Leu
        195                 200                 205

Asn Ala Arg Pro Ala Cys Val Asp Ala Leu Ala Ala Glu Leu Arg Gln
    210                 215                 220

Val Leu Asp Cys Thr Glu Gly Ile Gly Lys Val Arg Leu Gln His Asn
225                 230                 235                 240

Ser Gly Phe
```

<210> 1493
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXN03138

<400> 1493
agaatgttcc agtcttggca tccaaccagc cgattccgct ggcccacact ggggcgttgg 60

cgaggtcttt ggcggtgtac aagttgagga ctaccttgac ttg gat att gtt ccg 115

```
                                                    Leu Asp Ile Val Pro
                                                      1               5

aag gat gtc gct gaa agc ttc gcc gta ggt gag gtc gtt ttt ctt cgc   163
Lys Asp Val Ala Glu Ser Phe Ala Val Gly Glu Val Val Phe Leu Arg
                 10                  15                  20

gtg ttg ggt gac ggc gtc gtt gat gat gtg ccc gtc cac agc atc gac   211
Val Leu Gly Asp Gly Val Val Asp Asp Val Pro Val His Ser Ile Asp
             25                  30                  35

gga ggc tcc gat ttc ggc ggt tcc gtc tgg gga gaa ggt cac tcc gaa   259
Gly Gly Ser Asp Phe Gly Gly Ser Val Trp Gly Glu Gly His Ser Glu
         40                  45                  50

aga gct gtc gtc ttg ggt acc gcg cga acc ggt ggc tct tgc gtc gtc   307
Arg Ala Val Val Leu Gly Thr Ala Arg Thr Gly Gly Ser Cys Val Val
     55                  60                  65

aag caa atc tct tat ttc ttt tat ctt gcg tcc tat gga cgc cgg gct   355
Lys Gln Ile Ser Tyr Phe Phe Tyr Leu Ala Ser Tyr Gly Arg Arg Ala
 70                  75                  80                  85

tgg cag aat ctg gtt ggg gct ggt ggc ggt gag gta ttc ggt gag gat   403
Trp Gln Asn Leu Val Gly Ala Gly Gly Gly Glu Val Phe Gly Glu Asp
                 90                  95                 100

tgc gtc ggc gcc ggc gag gtt gtc ggg gtt gat gcc ggc gag ttc gtt   451
Cys Val Gly Ala Gly Glu Val Val Gly Val Asp Ala Gly Glu Phe Val
             105                 110                 115

gct aat ggt gat cag tcg gga gag gtc gag gtg gta cag ctt ttg ttg   499
Ala Asn Gly Asp Gln Ser Gly Glu Val Glu Val Val Gln Leu Leu Leu
         120                 125                 130

cag ggc ttt gag ttc ggg caa gtc ggc gag cgt ggc aaa cgc gat gga   547
Gln Gly Phe Glu Phe Gly Gln Val Gly Glu Arg Gly Lys Arg Asp Gly
     135                 140                 145

tat gcg gga gac ctg cgc ttt tgt tagacctgtg acgatggcga ggc         594
Tyr Ala Gly Asp Leu Arg Phe Cys
150                 155
```

<210> 1494
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 1494

```
Leu Asp Ile Val Pro Lys Asp Val Ala Glu Ser Phe Ala Val Gly Glu
  1               5                  10                  15

Val Val Phe Leu Arg Val Leu Gly Asp Gly Val Val Asp Asp Val Pro
             20                  25                  30

Val His Ser Ile Asp Gly Gly Ser Asp Phe Gly Gly Ser Val Trp Gly
         35                  40                  45

Glu Gly His Ser Glu Arg Ala Val Val Leu Gly Thr Ala Arg Thr Gly
     50                  55                  60
```

```
Gly Ser Cys Val Val Lys Gln Ile Ser Tyr Phe Phe Tyr Leu Ala Ser
 65                  70                  75                  80

Tyr Gly Arg Arg Ala Trp Gln Asn Leu Val Gly Ala Gly Gly Gly Glu
                 85                  90                  95

Val Phe Gly Glu Asp Cys Val Gly Ala Gly Glu Val Val Gly Val Asp
            100                 105                 110

Ala Gly Glu Phe Val Ala Asn Gly Asp Gln Ser Gly Glu Val Glu Val
        115                 120                 125

Val Gln Leu Leu Leu Gln Gly Phe Glu Phe Gly Gln Val Gly Glu Arg
    130                 135                 140

Gly Lys Arg Asp Gly Tyr Ala Gly Asp Leu Arg Phe Cys
145                 150                 155


<210> 1495
<211> 372
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(349)
<223> RXN03140

<400> 1495
ctcaagcgat cggtggaaca tccactaacg gggttaccaa aaatccttcg cggacactcc 60

cgaaggaaca cttcttgcga gaaggaaagg aagaagcact gtg aag ggc att cat   115
                                              Val Lys Gly Ile His
                                                1               5

cag gaa att agc cgt atc gag cgt agc cac gat tat ctg tgg agc gtc   163
Gln Glu Ile Ser Arg Ile Glu Arg Ser His Asp Tyr Leu Trp Ser Val
                10                  15                  20

cga gaa gac ctg cat gca cga ttc gac aac caa ctg aag gca cac ttt   211
Arg Glu Asp Leu His Ala Arg Phe Asp Asn Gln Leu Lys Ala His Phe
            25                  30                  35

gta gac agt gtc ctg gat agc att gca gaa gga tat gaa ggc cga atc   259
Val Asp Ser Val Leu Asp Ser Ile Ala Glu Gly Tyr Glu Gly Arg Ile
        40                  45                  50

aac cga ttc cgc aaa atc ttc att gaa atg aaa gcg gtt gaa gag ctg   307
Asn Arg Phe Arg Lys Ile Phe Ile Glu Met Lys Ala Val Glu Glu Leu
    55                  60                  65

cgc acc atc gcc gcc acc cgc cca agc cac ctc ttg gct gca           349
Arg Thr Ile Ala Ala Thr Arg Pro Ser His Leu Leu Ala Ala
70                  75                  80

taagacactt aaaagttaaa taa                                        372


<210> 1496
```

<211> 83
<212> PRT
<213> Corynebacterium glutamicum

<400> 1496
Val Lys Gly Ile His Gln Glu Ile Ser Arg Ile Glu Arg Ser His Asp
1 5 10 15

Tyr Leu Trp Ser Val Arg Glu Asp Leu His Ala Arg Phe Asp Asn Gln
20 25 30

Leu Lys Ala His Phe Val Asp Ser Val Leu Asp Ser Ile Ala Glu Gly
35 40 45

Tyr Glu Gly Arg Ile Asn Arg Phe Arg Lys Ile Phe Ile Glu Met Lys
50 55 60

Ala Val Glu Glu Leu Arg Thr Ile Ala Ala Thr Arg Pro Ser His Leu
65 70 75 80

Leu Ala Ala

<210> 1497
<211> 453
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(430)
<223> RXN03141

<400> 1497
ggccctgctg cttcatgcgg tgagctgcgc gaccgaaagc gatctgtgag gaagcggtga 60

aatctgggtt tcggtccagc ttgaggatgt attccacggt gtg gtt gaa gcc acc 115
Val Val Glu Ala Thr
1 5

ggt gtc gcc ggt ggt aat cac gtg gcc acc gtg tgg cat gcc ggt gtg 163
Gly Val Ala Gly Gly Asn His Val Ala Thr Val Trp His Ala Gly Val
10 15 20

ctc gga gtc gaa ggt tgc ttc gtc gat gaa gtt gac ttc gac ttc gta 211
Leu Gly Val Glu Gly Cys Phe Val Asp Glu Val Asp Phe Asp Phe Val
25 30 35

gcc aac gaa gta atc agg cat ggt gcg gat gtc gtt ttc gat gcg ctc 259
Ala Asn Glu Val Ile Arg His Gly Ala Asp Val Val Phe Asp Ala Leu
40 45 50

gtg atc ggc cgc gtc ggc aac cac gaa gca ttg gcg ctt gtg ggt ttg 307
Val Ile Gly Arg Val Gly Asn His Glu Ala Leu Ala Leu Val Gly Leu
55 60 65

ctt tcc ggt aag gtc gcc ggc ttc gcc gcg gcg ggc ctt ttc cag ggc 355
Leu Ser Gly Lys Val Ala Gly Phe Ala Ala Ala Gly Leu Phe Gln Gly
70 75 80 85

```
gtc ttc gga tgg gag ggt gta ctg gac tgc ctt ttg aac gcc agg gat   403
Val Phe Gly Trp Glu Gly Val Leu Asp Cys Leu Leu Asn Ala Arg Asp
                 90                  95                 100

gcg tcg caa agc atc gga gtg gcc ctg tgacaaacct gggccccaga         450
Ala Ser Gln Ser Ile Gly Val Ala Leu
            105                 110

agg                                                               453
```

<210> 1498
<211> 110
<212> PRT
<213> Corynebacterium glutamicum

<400> 1498

```
Val Val Glu Ala Thr Gly Val Ala Gly Gly Asn His Val Ala Thr Val
  1               5                  10                  15

Trp His Ala Gly Val Leu Gly Val Glu Gly Cys Phe Val Asp Glu Val
             20                  25                  30

Asp Phe Asp Phe Val Ala Asn Glu Val Ile Arg His Gly Ala Asp Val
         35                  40                  45

Val Phe Asp Ala Leu Val Ile Gly Arg Val Gly Asn His Glu Ala Leu
     50                  55                  60

Ala Leu Val Gly Leu Leu Ser Gly Lys Val Ala Gly Phe Ala Ala Ala
 65                  70                  75                  80

Gly Leu Phe Gln Gly Val Phe Gly Trp Glu Gly Val Leu Asp Cys Leu
                 85                  90                  95

Leu Asn Ala Arg Asp Ala Ser Gln Ser Ile Gly Val Ala Leu
            100                 105                 110
```

<210> 1499
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXN03146

<400> 1499

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taacgtgggg gttttaagct tgcgtagaca tatcgttttt cgatagattt acatcttgaa 60

acgatacgcc catccacggc gcatgtctga aaggttcccc atg aat ccc cgc atc   115
                                              Met Asn Pro Arg Ile
                                                1               5

ctc atg ctg ctt cgc atc att ttc ggc gcg gcc ttc ctc gca ctg ttg   163
Leu Met Leu Leu Arg Ile Ile Phe Gly Ala Ala Phe Leu Ala Leu Leu
                10                  15                  20

gtg ctg caa gtc ctg ctc gcc atc aaa atc gtg cgc gat ggc ctc aac   211
```

```
Val Leu Gln Val Leu Leu Ala Ile Lys Ile Val Arg Asp Gly Leu Asn
             25                  30                  35

tcc ggc gag ctc tcc ccc atc ccg ctc acc att ctc gcg agc ttc gtg   259
Ser Gly Glu Leu Ser Pro Ile Pro Leu Thr Ile Leu Ala Ser Phe Val
         40                  45                  50

atc atc ggt ttc ggg ctc gtg cag ttc atc atc gtc tgt ctg ttc gcg   307
Ile Ile Gly Phe Gly Leu Val Gln Phe Ile Ile Val Cys Leu Phe Ala
     55                  60                  65

cta ctg cgt ctc gtg gaa gac gat gaa atc ttc gac gcc cac tcg ctc   355
Leu Leu Arg Leu Val Glu Asp Asp Glu Ile Phe Asp Ala His Ser Leu
 70                  75                  80                  85

gcc tgg gtt gat cga att gcc atc acc atc gca gcc ggc gcc gtt tta   403
Ala Trp Val Asp Arg Ile Ala Ile Thr Ile Ala Ala Gly Ala Val Leu
                 90                  95                 100

ctc ctc cca atg gcc tac atc gtc gca gaa gtc gac gac gcc ccc gga   451
Leu Leu Pro Met Ala Tyr Ile Val Ala Glu Val Asp Asp Ala Pro Gly
            105                 110                 115

gcc atc gtc ttc ggt ctc atc ctc gcg atg ctc atc acg ggc gta tcc   499
Ala Ile Val Phe Gly Leu Ile Leu Ala Met Leu Ile Thr Gly Val Ser
        120                 125                 130

ctg ctg gta aaa atc atg cgc gca ctc ctg gcc cgc gcc atc gga ttc   547
Leu Leu Val Lys Ile Met Arg Ala Leu Leu Ala Arg Ala Ile Gly Phe
    135                 140                 145

tcc acg gaa ctg gaa tcg gtg atc taaatggcca tcatcgtcga cat         594
Ser Thr Glu Leu Glu Ser Val Ile
150                 155


<210> 1500
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 1500
Met Asn Pro Arg Ile Leu Met Leu Leu Arg Ile Ile Phe Gly Ala Ala
  1               5                  10                  15

Phe Leu Ala Leu Leu Val Leu Gln Val Leu Leu Ala Ile Lys Ile Val
             20                  25                  30

Arg Asp Gly Leu Asn Ser Gly Glu Leu Ser Pro Ile Pro Leu Thr Ile
         35                  40                  45

Leu Ala Ser Phe Val Ile Ile Gly Phe Gly Leu Val Gln Phe Ile Ile
     50                  55                  60

Val Cys Leu Phe Ala Leu Leu Arg Leu Val Glu Asp Asp Glu Ile Phe
 65                  70                  75                  80

Asp Ala His Ser Leu Ala Trp Val Asp Arg Ile Ala Ile Thr Ile Ala
                 85                  90                  95

Ala Gly Ala Val Leu Leu Leu Pro Met Ala Tyr Ile Val Ala Glu Val
```

```
            100                 105                 110

Asp Asp Ala Pro Gly Ala Ile Val Phe Gly Leu Ile Leu Ala Met Leu
        115                 120                 125

Ile Thr Gly Val Ser Leu Leu Val Lys Ile Met Arg Ala Leu Leu Ala
    130                 135                 140

Arg Ala Ile Gly Phe Ser Thr Glu Leu Glu Ser Val Ile
145                 150                 155


<210> 1501
<211> 375
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(352)
<223> RXN03147

<400> 1501
ccctgatccc gaggacgatg accgccaaag cgatggcgcc tccaatcagg atgtactgca 60

gtgggattgg gcgggcgtca tcgatggcat cgatgcagtt ttg gaa atc ctc ttt   115
                                              Leu Glu Ile Leu Phe
                                                1               5

aag agc ggt ttg gga ttc gtt gta atc atc ggt gcg gtc ggc gaa tac   163
Lys Ser Gly Leu Gly Phe Val Val Ile Ile Gly Ala Val Gly Glu Tyr
                  10                  15                  20

ttc ggc gcg gat ttc tgc ggt gcg ggt gcc ggt ggt ggc ggc ttg ttg   211
Phe Gly Ala Asp Phe Cys Gly Ala Gly Ala Gly Gly Gly Gly Leu Leu
             25                  30                  35

aag ttg gct gag tac atc gct ggc tgg atc gct gga gaa tcc gct gat   259
Lys Leu Ala Glu Tyr Ile Ala Gly Trp Ile Ala Gly Glu Ser Ala Asp
         40                  45                  50

gat gtc ttt ggc ttc gtc gta tgt gta ctc cgt ttt gaa act ttc ctc   307
Asp Val Phe Gly Phe Val Val Cys Val Leu Arg Phe Glu Thr Phe Leu
     55                  60                  65

ggc gtt ggg gtc tgc cag cgt ggg atc gtc tgg gag gag cat ggc       352
Gly Val Gly Val Cys Gln Arg Gly Ile Val Trp Glu Glu His Gly
 70                  75                  80

taggccttcg ccggattcga tgg                                        375


<210> 1502
<211> 84
<212> PRT
<213> Corynebacterium glutamicum

<400> 1502
Leu Glu Ile Leu Phe Lys Ser Gly Leu Gly Phe Val Val Ile Ile Gly
  1               5                  10                  15
```

```
Ala Val Gly Glu Tyr Phe Gly Ala Asp Phe Cys Gly Ala Gly Ala Gly
             20                  25                  30

Gly Gly Gly Leu Leu Lys Leu Ala Glu Tyr Ile Ala Gly Trp Ile Ala
         35                  40                  45

Gly Glu Ser Ala Asp Asp Val Phe Gly Phe Val Val Cys Val Leu Arg
     50                  55                  60

Phe Glu Thr Phe Leu Gly Val Gly Val Cys Gln Arg Gly Ile Val Trp
 65                  70                  75                  80

Glu Glu His Gly
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<210> 1503
<211> 390
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(367)
<223> RXN03149

<400> 1503
gctttactag aaccagtgat cggtaaacta ccttttagtt cggctattag cagtacaatc 60

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tctgtggcgc tgggatttat tttagttacc gtatatcgat gtg gtt att ggc gaa   115
                                            Val Val Ile Gly Glu
                                              1               5

ctg ctt cct aag agc tat agt atc gtc aat acg gag aag gtc gtc ttg   163
Leu Leu Pro Lys Ser Tyr Ser Ile Val Asn Thr Glu Lys Val Val Leu
                 10                  15                  20

ttc gta gtt aaa cca ctt cat tat ttt tat aaa gta atg ttt cct ttt   211
Phe Val Val Lys Pro Leu His Tyr Phe Tyr Lys Val Met Phe Pro Phe
             25                  30                  35

att tgg gta ttg aat cat tca gct gca ggg cta ggg aag cta tta ggt   259
Ile Trp Val Leu Asn His Ser Ala Ala Gly Leu Gly Lys Leu Leu Gly
         40                  45                  50

gtg cgt ctc gta tct gaa gga gaa gag aca ttg tct caa gaa gag ctg   307
Val Arg Leu Val Ser Glu Gly Glu Glu Thr Leu Ser Gln Glu Glu Leu
     55                  60                  65

aca tta gtc gca ttg aat tct tat gaa aaa gga gag ttg cca aag aag   355
Thr Leu Val Ala Leu Asn Ser Tyr Glu Lys Gly Glu Leu Pro Lys Lys
 70                  75                  80                  85

aat atc att att tgaaaacgtg tttgaatttg atg                        390
Asn Ile Ile Ile
```

<210> 1504
<211> 89
<212> PRT

<213> Corynebacterium glutamicum

<400> 1504

```
Val Val Ile Gly Glu Leu Leu Pro Lys Ser Tyr Ser Ile Val Asn Thr
  1               5                  10                  15

Glu Lys Val Val Leu Phe Val Val Lys Pro Leu His Tyr Phe Tyr Lys
             20                  25                  30

Val Met Phe Pro Phe Ile Trp Val Leu Asn His Ser Ala Ala Gly Leu
         35                  40                  45

Gly Lys Leu Leu Gly Val Arg Leu Val Ser Glu Gly Glu Glu Thr Leu
     50                  55                  60

Ser Gln Glu Glu Leu Thr Leu Val Ala Leu Asn Ser Tyr Glu Lys Gly
 65                  70                  75                  80

Glu Leu Pro Lys Lys Asn Ile Ile Ile
                 85
```

<210> 1505
<211> 396
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(373)
<223> RXN03152

<400> 1505

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gcaaaatatc agctttgacc tgcacatata gttgcacaat ggtgaaagtg cacataaagt 60

aactttcgta ttcgaatatt taaacctaag gggtttagca atg aag cta ttt tct   115
                                              Met Lys Leu Phe Ser
                                                1               5

cgt act ccc ctc gtc gca ctc ggc aca gct gct gca atg gca gca acc   163
Arg Thr Pro Leu Val Ala Leu Gly Thr Ala Ala Ala Met Ala Ala Thr
                10                  15                  20

tcc atc tcc gtt cct gca cag gct gaa gaa gtc gca cca gca cag gtt   211
Ser Ile Ser Val Pro Ala Gln Ala Glu Glu Val Ala Pro Ala Gln Val
            25                  30                  35

gtg tac gtg gct gac acc gta gaa gaa gaa acg ggt agc tcc aac gga   259
Val Tyr Val Ala Asp Thr Val Glu Glu Glu Thr Gly Ser Ser Asn Gly
        40                  45                  50

tct tct gac att gac tct gac acc att ttg gat tac gtc gtc gtt att   307
Ser Ser Asp Ile Asp Ser Asp Thr Ile Leu Asp Tyr Val Val Val Ile
    55                  60                  65

act ggc atc gtt ggc gtc ctc agc gct ggt ttg acc ttc gct act gct   355
Thr Gly Ile Val Gly Val Leu Ser Ala Gly Leu Thr Phe Ala Thr Ala
70                  75                  80                  85

ttc cag cgt tca ttg cag taaatttcag cgttaatcac caa                 396
Phe Gln Arg Ser Leu Gln
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90

<210> 1506
<211> 91
<212> PRT
<213> Corynebacterium glutamicum

<400> 1506
Met Lys Leu Phe Ser Arg Thr Pro Leu Val Ala Leu Gly Thr Ala Ala
1 5 10 15

Ala Met Ala Ala Thr Ser Ile Ser Val Pro Ala Gln Ala Glu Glu Val
20 25 30

Ala Pro Ala Gln Val Val Tyr Val Ala Asp Thr Val Glu Glu Glu Thr
35 40 45

Gly Ser Ser Asn Gly Ser Ser Asp Ile Asp Ser Asp Thr Ile Leu Asp
50 55 60

Tyr Val Val Val Ile Thr Gly Ile Val Gly Val Leu Ser Ala Gly Leu
65 70 75 80

Thr Phe Ala Thr Ala Phe Gln Arg Ser Leu Gln
85 90

<210> 1507
<211> 687
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(664)
<223> RXN03153

<400> 1507
taatttgaat tttagggaac ctaccccgag cttttgcagt ctaacgctta tgagtgcctt 60

ttcacggccc tcgttacgac tacaaagatc ggggtatttt atg cga cga atc tgg 115
Met Arg Arg Ile Trp
1 5

ctg ctc gta tgc ggc atc gca ttg act gtc gcc ggc tgc acg agt gga 163
Leu Leu Val Cys Gly Ile Ala Leu Thr Val Ala Gly Cys Thr Ser Gly
10 15 20

tcc acc act ccc aca acc gtc acg gta acc gca acg cca acg tcg gag 211
Ser Thr Thr Pro Thr Thr Val Thr Val Thr Ala Thr Pro Thr Ser Glu
25 30 35

gag gct gca tcc acg gag ccg acc aac gac ata ctt gcc agc caa ttt 259
Glu Ala Ala Ser Thr Glu Pro Thr Asn Asp Ile Leu Ala Ser Gln Phe
40 45 50

cat ccg tgt gaa gta ctc acg cag gaa cag ttc gaa gaa gtc gga ttg 307
His Pro Cys Glu Val Leu Thr Gln Glu Gln Phe Glu Glu Val Gly Leu
55 60 65

```
gga gtc ttg att gtt gaa gac gct tac ctc ggc tcg aca ggt tta ggt   355
Gly Val Leu Ile Val Glu Asp Ala Tyr Leu Gly Ser Thr Gly Leu Gly
 70                  75                  80                  85

tgc agt ttc ggg aaa gca gac aga gag gat ttt tca ggt acg tgg ctc   403
Cys Ser Phe Gly Lys Ala Asp Arg Glu Asp Phe Ser Gly Thr Trp Leu
                 90                  95                 100

att tca act gac caa gca aac cga caa ttt gtt gaa aac caa gat cta   451
Ile Ser Thr Asp Gln Ala Asn Arg Gln Phe Val Glu Asn Gln Asp Leu
            105                 110                 115

gag aca ttg gat tgg gga tcc aat gac aat cca gat ctg tat gtg cat   499
Glu Thr Leu Asp Trp Gly Ser Asn Asp Asn Pro Asp Leu Tyr Val His
        120                 125                 130

caa atg tcc gag acg ggt cgt caa tgt gag gca gca gtt gac tat gac   547
Gln Met Ser Glu Thr Gly Arg Gln Cys Glu Ala Ala Val Asp Tyr Asp
    135                 140                 145

tgg ggc cgg ctt acg gtt gac tat ctc gaa tta ggt gag ggc tgg gag   595
Trp Gly Arg Leu Thr Val Asp Tyr Leu Glu Leu Gly Glu Gly Trp Glu
150                 155                 160                 165

cca gaa att ttg tgc tct gat gct gtt gaa att tta gaa aat ctc atc   643
Pro Glu Ile Leu Cys Ser Asp Ala Val Glu Ile Leu Glu Asn Leu Ile
                170                 175                 180

aag gaa cta agg gga att cca tgacattgaa aattgatccc tcg             687
Lys Glu Leu Arg Gly Ile Pro
            185
```

Sequence Listing

<210> 1508
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 1508

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Met Arg Arg Ile Trp Leu Leu Val Cys Gly Ile Ala Leu Thr Val Ala
  1               5                  10                  15

Gly Cys Thr Ser Gly Ser Thr Thr Pro Thr Thr Val Thr Val Thr Ala
             20                  25                  30

Thr Pro Thr Ser Glu Glu Ala Ala Ser Thr Glu Pro Thr Asn Asp Ile
         35                  40                  45

Leu Ala Ser Gln Phe His Pro Cys Glu Val Leu Thr Gln Glu Gln Phe
     50                  55                  60

Glu Glu Val Gly Leu Gly Val Leu Ile Val Glu Asp Ala Tyr Leu Gly
 65                  70                  75                  80

Ser Thr Gly Leu Gly Cys Ser Phe Gly Lys Ala Asp Arg Glu Asp Phe
                 85                  90                  95

Ser Gly Thr Trp Leu Ile Ser Thr Asp Gln Ala Asn Arg Gln Phe Val
            100                 105                 110

Glu Asn Gln Asp Leu Glu Thr Leu Asp Trp Gly Ser Asn Asp Asn Pro
```

```
        115                 120                 125

Asp Leu Tyr Val His Gln Met Ser Glu Thr Gly Arg Gln Cys Glu Ala
    130                 135                 140

Ala Val Asp Tyr Asp Trp Gly Arg Leu Thr Val Asp Tyr Leu Glu Leu
145                 150                 155                 160

Gly Glu Gly Trp Glu Pro Glu Ile Leu Cys Ser Asp Ala Val Glu Ile
                165                 170                 175

Leu Glu Asn Leu Ile Lys Glu Leu Arg Gly Ile Pro
            180                 185


<210> 1509
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> RXN03154

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aaagtgccct ctcctaaatc gtttctaagg gctcgtcaga ccccagttga tacaaacata 60

cattctgaaa attcagtcgc ttaaatgggc gcagcgggaa atg ctg aaa act aca   115
                                              Met Leu Lys Thr Thr
                                                1               5

tta atc acc gat acc cta ggg cac gtg acc tct act gaa ccc acc acc   163
Leu Ile Thr Asp Thr Leu Gly His Val Thr Ser Thr Glu Pro Thr Thr
                10                  15                  20

aca gcc cat gtt cca cta cct gat gga tct tcc act cca gtc caa att   211
Thr Ala His Val Pro Leu Pro Asp Gly Ser Ser Thr Pro Val Gln Ile
            25                  30                  35

tgg gcg tca gat aac aaa gac tcc caa ctg gtg atg ctg tgg cca ggt   259
Trp Ala Ser Asp Asn Lys Asp Ser Gln Leu Val Met Leu Trp Pro Gly
        40                  45                  50

ttc ggc atg ggt ggc tat tac tat cgt ccg ctt gcg gca gcg cta aat   307
Phe Gly Met Gly Gly Tyr Tyr Tyr Arg Pro Leu Ala Ala Ala Leu Asn
    55                  60                  65

aaa gct gga ttc cat gtg gcg att ggt gaa ctt cgt ggt cag ggg caa   355
Lys Ala Gly Phe His Val Ala Ile Gly Glu Leu Arg Gly Gln Gly Gln
70                  75                  80                  85

agt tcc gcg aag gct tct cgg aaa agt cag tgg gga tac cat gat ctc   403
Ser Ser Ala Lys Ala Ser Arg Lys Ser Gln Trp Gly Tyr His Asp Leu
                90                  95                  100

gca tcg gta gat ttt ccg ctg cag att gcc gct gcg aaa aag gcg ctt   451
Ala Ser Val Asp Phe Pro Leu Gln Ile Ala Ala Ala Lys Lys Ala Leu
            105                 110                 115

gac ctg gag gaa ggc cat ccc atg agg ttt ttg tcg cat tcg atg ggt   499
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```
Asp Leu Glu Glu Gly His Pro Met Arg Phe Leu Ser His Ser Met Gly
        120                 125                 130

ggg cag att tct tgt ctt ttc gca gcg agg ccg gag gct gag aaa tat   547
Gly Gln Ile Ser Cys Leu Phe Ala Ala Arg Pro Glu Ala Glu Lys Tyr
    135                 140                 145

aat ctt cgg gcg att ttc ggg gtg ggt gca ggg tcg ccg ttt agg cct   595
Asn Leu Arg Ala Ile Phe Gly Val Gly Ala Gly Ser Pro Phe Arg Pro
150                 155                 160                 165

acg ttt agt ccg aaa atg ggg aag cgt ttg gga ttg ggt gcg gtg ctg   643
Thr Phe Ser Pro Lys Met Gly Lys Arg Leu Gly Leu Gly Ala Val Leu
                170                 175                 180

ctt ggt ggg att ggt ggc cac att gtg gga ttt tgg ccc ggc aaa gtt   691
Leu Gly Gly Ile Gly Gly His Ile Val Gly Phe Trp Pro Gly Lys Val
            185                 190                 195

tta gga aaa gac ctg gtg ggt tat ggc cga caa tcg gga act cac atg   739
Leu Gly Lys Asp Leu Val Gly Tyr Gly Arg Gln Ser Gly Thr His Met
        200                 205                 210

agg gaa tgg cgt cga ttc cat aag cac aat tct ttg gac gat ctc acc   787
Arg Glu Trp Arg Arg Phe His Lys His Asn Ser Leu Asp Asp Leu Thr
    215                 220                 225

gcg cag gac atc aac tat gtg gag gtg atg aag aag gtg agc att cct   835
Ala Gln Asp Ile Asn Tyr Val Glu Val Met Lys Lys Val Ser Ile Pro
230                 235                 240                 245

att act ttt agt cgt tgt cct gat gat gag gac tgc ccg cag gca tcg   883
Ile Thr Phe Ser Arg Cys Pro Asp Asp Glu Asp Cys Pro Gln Ala Ser
                250                 255                 260

att gat ggg ttg gcg agt ttt gtt ccc gca gcg cag atc aaa atg ata   931
Ile Asp Gly Leu Ala Ser Phe Val Pro Ala Ala Gln Ile Lys Met Ile
            265                 270                 275

gaa att cca gaa gcc ctg gga cat aac cgg tgg gct cgg gaa cct gaa   979
Glu Ile Pro Glu Ala Leu Gly His Asn Arg Trp Ala Arg Glu Pro Glu
        280                 285                 290

tca aca gtg aaa ctc ttc ctg gaa caa gct ctt tagtgaccga tggagcggag 1032
Ser Thr Val Lys Leu Phe Leu Glu Gln Ala Leu
    295                 300

gta                                                               1035
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<210> 1510
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 1510

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Met Leu Lys Thr Thr Leu Ile Thr Asp Thr Leu Gly His Val Thr Ser
  1               5                  10                  15

Thr Glu Pro Thr Thr Thr Ala His Val Pro Leu Pro Asp Gly Ser Ser
             20                  25                  30
```

```
Thr Pro Val Gln Ile Trp Ala Ser Asp Asn Lys Asp Ser Gln Leu Val
         35                  40                  45

Met Leu Trp Pro Gly Phe Gly Met Gly Gly Tyr Tyr Tyr Arg Pro Leu
     50                  55                  60

Ala Ala Ala Leu Asn Lys Ala Gly Phe His Val Ala Ile Gly Glu Leu
 65                  70                  75                  80

Arg Gly Gln Gly Gln Ser Ser Ala Lys Ala Ser Arg Lys Ser Gln Trp
                 85                  90                  95

Gly Tyr His Asp Leu Ala Ser Val Asp Phe Pro Leu Gln Ile Ala Ala
            100                 105                 110

Ala Lys Lys Ala Leu Asp Leu Glu Glu Gly His Pro Met Arg Phe Leu
        115                 120                 125

Ser His Ser Met Gly Gly Gln Ile Ser Cys Leu Phe Ala Ala Arg Pro
    130                 135                 140

Glu Ala Glu Lys Tyr Asn Leu Arg Ala Ile Phe Gly Val Gly Ala Gly
145                 150                 155                 160

Ser Pro Phe Arg Pro Thr Phe Ser Pro Lys Met Gly Lys Arg Leu Gly
                165                 170                 175

Leu Gly Ala Val Leu Leu Gly Gly Ile Gly Gly His Ile Val Gly Phe
            180                 185                 190

Trp Pro Gly Lys Val Leu Gly Lys Asp Leu Val Gly Tyr Gly Arg Gln
        195                 200                 205

Ser Gly Thr His Met Arg Glu Trp Arg Arg Phe His Lys His Asn Ser
    210                 215                 220

Leu Asp Asp Leu Thr Ala Gln Asp Ile Asn Tyr Val Glu Val Met Lys
225                 230                 235                 240

Lys Val Ser Ile Pro Ile Thr Phe Ser Arg Cys Pro Asp Asp Glu Asp
                245                 250                 255

Cys Pro Gln Ala Ser Ile Asp Gly Leu Ala Ser Phe Val Pro Ala Ala
            260                 265                 270

Gln Ile Lys Met Ile Glu Ile Pro Glu Ala Leu Gly His Asn Arg Trp
        275                 280                 285

Ala Arg Glu Pro Glu Ser Thr Val Lys Leu Phe Leu Glu Gln Ala Leu
    290                 295                 300
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<210> 1511
<211> 303
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(280)
<223> RXN03156

<400> 1511
gtatcgacct cgatgatcgc gttgctgcag agatgaccat tttaggtcgc cctgtgccta 60

aagaaggata accaccacac cagaaaagaa gtacctcatt atg gct cga acc aca 115
Met Ala Arg Thr Thr
1 5

cct cca cca gct gat gta ctc gac atc atc att tcc acc gtg aag cag 163
Pro Pro Pro Ala Asp Val Leu Asp Ile Ile Ile Ser Thr Val Lys Gln
10 15 20

acc atc ggc att gat ctt gct gaa ctg att cag ggc cgt gca ctc ggc 211
Thr Ile Gly Ile Asp Leu Ala Glu Leu Ile Gln Gly Arg Ala Leu Gly
25 30 35

cag gct caa ggt gag gca caa ggc aaa gct agt gca gca gcc ctt gag 259
Gln Ala Gln Gly Glu Ala Gln Gly Lys Ala Ser Ala Ala Ala Leu Glu
40 45 50

cag gca cct cat aat gag cag taaataacac acaccacatg tgc 303
Gln Ala Pro His Asn Glu Gln
55 60

<210> 1512
<211> 60
<212> PRT
<213> Corynebacterium glutamicum

<400> 1512
Met Ala Arg Thr Thr Pro Pro Pro Ala Asp Val Leu Asp Ile Ile Ile
1 5 10 15

Ser Thr Val Lys Gln Thr Ile Gly Ile Asp Leu Ala Glu Leu Ile Gln
20 25 30

Gly Arg Ala Leu Gly Gln Ala Gln Gly Glu Ala Gln Gly Lys Ala Ser
35 40 45

Ala Ala Ala Leu Glu Gln Ala Pro His Asn Glu Gln
50 55 60

<210> 1513
<211> 182
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(159)
<223> FRXA00176

<400> 1513
cag ctg atg tac tcg aca tca tca ttt acc acc gtg aag cag acc atc 48
Gln Leu Met Tyr Ser Thr Ser Ser Phe Thr Thr Val Lys Gln Thr Ile

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  1               5                  10                  15

ggc att gat ctt gct gaa ctg att cag ggc cgt gca ctc ggc cag gct   96
Gly Ile Asp Leu Ala Glu Leu Ile Gln Gly Arg Ala Leu Gly Gln Ala
            20                  25                  30

caa ggt gag gca caa ggc aaa gct agt gca gca gcc ctt gag cag gca   144
Gln Gly Glu Ala Gln Gly Lys Ala Ser Ala Ala Ala Leu Glu Gln Ala
        35                  40                  45

cct cat aat gag cag taaataacac acaccacatg tgc                     182
Pro His Asn Glu Gln
    50


<210> 1514
<211> 53
<212> PRT
<213> Corynebacterium glutamicum

<400> 1514
Gln Leu Met Tyr Ser Thr Ser Ser Phe Thr Thr Val Lys Gln Thr Ile
  1               5                  10                  15

Gly Ile Asp Leu Ala Glu Leu Ile Gln Gly Arg Ala Leu Gly Gln Ala
            20                  25                  30

Gln Gly Glu Ala Gln Gly Lys Ala Ser Ala Ala Ala Leu Glu Gln Ala
        35                  40                  45

Pro His Asn Glu Gln
    50


<210> 1515
<211> 519
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(496)
<223> RXN03162

<400> 1515
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gggttgcgga gaagttgtcg ccgccttctg ctggcttctt gtg cac gac gaa cac   115
                                              Val His Asp Glu His
                                                1               5

tgg gtg tgg tcc gac gag aag gat gcg gat ttc gcc ttc gac gat gcg   163
Trp Val Trp Ser Asp Glu Lys Asp Ala Asp Phe Ala Phe Asp Asp Ala
                10                  15                  20

tgg cat gaa acg cat atc aac gag cat gcc gtt gtc gcc gat gat gta   211
Trp His Glu Thr His Ile Asn Glu His Ala Val Val Ala Asp Asp Val
            25                  30                  35

ctg gtc aca gaa atc cat gaa ctc gcc gag ctt gcg gac ttc agt gtg   259
Leu Val Thr Glu Ile His Glu Leu Ala Glu Leu Ala Asp Phe Ser Val
```

```
        40                  45                  50

gtt gtc gac tgc ttc ggt gca ctt gat ttc agt gtc caa tgg cag tgc   307
Val Val Asp Cys Phe Gly Ala Leu Asp Phe Ser Val Gln Trp Gln Cys
     55                  60                  65

ggt gcc tgg ctc gat gga tgc agc cag ttc ctt gtc tac caa ctg gac   355
Gly Ala Trp Leu Asp Gly Cys Ser Gln Phe Leu Val Tyr Gln Leu Asp
 70                  75                  80                  85

gcg cca aat gcc gga gcc ggt gga gcc acg gtt ttg ctt gag cac gcg   403
Ala Pro Asn Ala Gly Ala Gly Gly Ala Thr Val Leu Leu Glu His Ala
                 90                  95                 100

ctc acc gaa gga cag gga ggt tgg gaa aac ctt gtg gaa ggt ctc cac   451
Leu Thr Glu Gly Gln Gly Gly Trp Glu Asn Leu Val Glu Gly Leu His
            105                 110                 115

gtc gta gta cgc ctc ggt gtc gga tgg cac cag gtc ggt ttg gga        496
Val Val Val Arg Leu Gly Val Gly Trp His Gln Val Gly Leu Gly
        120                 125                 130

tagcttgacc agcgcatctt tcg                                         519


<210> 1516
<211> 132
<212> PRT
<213> Corynebacterium glutamicum

<400> 1516
Val His Asp Glu His Trp Val Trp Ser Asp Glu Lys Asp Ala Asp Phe
  1               5                  10                  15

Ala Phe Asp Asp Ala Trp His Glu Thr His Ile Asn Glu His Ala Val
             20                  25                  30

Val Ala Asp Asp Val Leu Val Thr Glu Ile His Glu Leu Ala Glu Leu
         35                  40                  45

Ala Asp Phe Ser Val Val Val Asp Cys Phe Gly Ala Leu Asp Phe Ser
     50                  55                  60

Val Gln Trp Gln Cys Gly Ala Trp Leu Asp Gly Cys Ser Gln Phe Leu
 65                  70                  75                  80

Val Tyr Gln Leu Asp Ala Pro Asn Ala Gly Ala Gly Gly Ala Thr Val
                 85                  90                  95

Leu Leu Glu His Ala Leu Thr Glu Gly Gln Gly Gly Trp Glu Asn Leu
            100                 105                 110

Val Glu Gly Leu His Val Val Val Arg Leu Gly Val Gly Trp His Gln
        115                 120                 125

Val Gly Leu Gly
    130


<210> 1517
<211> 730
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(730)
<223> RXN03167

<400> 1517
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cctgattccc aggtggtgcc acattgttta tggtggagat atg aac acg aac ttg 115
Met Asn Thr Asn Leu
1 5

ccg aac cta tac acc gca ttt gac ctt gat cga agt gaa tcc tcc gaa 163
Pro Asn Leu Tyr Thr Ala Phe Asp Leu Asp Arg Ser Glu Ser Ser Glu
10 15 20

gct tta ggt gtt tcc ctt tct gcc cgc gat ctt cgc tta gaa caa atg 211
Ala Leu Gly Val Ser Leu Ser Ala Arg Asp Leu Arg Leu Glu Gln Met
25 30 35

gga att gcc cag gac gat cct cga cgt gcc caa acc gtc caa gct ttc 259
Gly Ile Ala Gln Asp Asp Pro Arg Arg Ala Gln Thr Val Gln Ala Phe
40 45 50

gca gtg ctt gca gac cca gca aaa cgc gcc acc tac gat gct caa tta 307
Ala Val Leu Ala Asp Pro Ala Lys Arg Ala Thr Tyr Asp Ala Gln Leu
55 60 65

gaa gct gga gtt cca ctc acc tgg gcg cag att cag cat tta gga aac 355
Glu Ala Gly Val Pro Leu Thr Trp Ala Gln Ile Gln His Leu Gly Asn
70 75 80 85

ttc ggc acc ttg cct tcc acc cct act gcg cag ccg ttt gcg gca cct 403
Phe Gly Thr Leu Pro Ser Thr Pro Thr Ala Gln Pro Phe Ala Ala Pro
90 95 100

cag ccg gag ccg tcg ccg gaa ccg caa cag cag tgg aat agc gga caa 451
Gln Pro Glu Pro Ser Pro Glu Pro Gln Gln Gln Trp Asn Ser Gly Gln
105 110 115

aac tat gcg tat ggc aat ccg acc atg gat tac caa act cag cag agc 499
Asn Tyr Ala Tyr Gly Asn Pro Thr Met Asp Tyr Gln Thr Gln Gln Ser
120 125 130

tac aac ccg atg cag gac caa acc caa gcg tcg atg tat gcg caa cct 547
Tyr Asn Pro Met Gln Asp Gln Thr Gln Ala Ser Met Tyr Ala Gln Pro
135 140 145

ttc gcg aac acc cct gca ccg atg tac aac agc aat cag gtt ttt aac 595
Phe Ala Asn Thr Pro Ala Pro Met Tyr Asn Ser Asn Gln Val Phe Asn
150 155 160 165

agg cct act gcg ggt acg cgt ttg tgg atg gcg atc ctc gac agt att 643
Arg Pro Thr Ala Gly Thr Arg Leu Trp Met Ala Ile Leu Asp Ser Ile
170 175 180

ttt gcc ggc atc gct ggt gga att gtc tcc ggt att ttc ggc ttt gga 691
Phe Ala Gly Ile Ala Gly Gly Ile Val Ser Gly Ile Phe Gly Phe Gly

```
            185                 190                 195

tct gaa ttc ctc acc agt gtc atc atg att ttg gtg ctg                 730
Ser Glu Phe Leu Thr Ser Val Ile Met Ile Leu Val Leu
        200                 205                 210


<210> 1518
<211> 210
<212> PRT
<213> Corynebacterium glutamicum

<400> 1518
Met Asn Thr Asn Leu Pro Asn Leu Tyr Thr Ala Phe Asp Leu Asp Arg
  1               5                  10                  15

Ser Glu Ser Ser Glu Ala Leu Gly Val Ser Leu Ser Ala Arg Asp Leu
             20                  25                  30

Arg Leu Glu Gln Met Gly Ile Ala Gln Asp Asp Pro Arg Arg Ala Gln
         35                  40                  45

Thr Val Gln Ala Phe Ala Val Leu Ala Asp Pro Ala Lys Arg Ala Thr
     50                  55                  60

Tyr Asp Ala Gln Leu Glu Ala Gly Val Pro Leu Thr Trp Ala Gln Ile
 65                  70                  75                  80

Gln His Leu Gly Asn Phe Gly Thr Leu Pro Ser Thr Pro Thr Ala Gln
                 85                  90                  95

Pro Phe Ala Ala Pro Gln Pro Glu Pro Ser Pro Glu Pro Gln Gln Gln
            100                 105                 110

Trp Asn Ser Gly Gln Asn Tyr Ala Tyr Gly Asn Pro Thr Met Asp Tyr
        115                 120                 125

Gln Thr Gln Gln Ser Tyr Asn Pro Met Gln Asp Gln Thr Gln Ala Ser
    130                 135                 140

Met Tyr Ala Gln Pro Phe Ala Asn Thr Pro Ala Pro Met Tyr Asn Ser
145                 150                 155                 160

Asn Gln Val Phe Asn Arg Pro Thr Ala Gly Thr Arg Leu Trp Met Ala
                165                 170                 175

Ile Leu Asp Ser Ile Phe Ala Gly Ile Ala Gly Gly Ile Val Ser Gly
            180                 185                 190

Ile Phe Gly Phe Gly Ser Glu Phe Leu Thr Ser Val Ile Met Ile Leu
        195                 200                 205

Val Leu
    210


<210> 1519
<211> 736
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(736)
<223> FRXA02862

<400> 1519
gccgcgactg cgggtgcttt tgcgctgttg cgtaaaaaat agtttttatt aagggcattc 60

cctgattccc aggtggtgcc acattgttta tggtggagat atg aac acg aac ttg 115
Met Asn Thr Asn Leu
1 5

ccg aac cta tac acc gca ttt gac ctt gat cga agt gaa tcc tcc gaa 163
Pro Asn Leu Tyr Thr Ala Phe Asp Leu Asp Arg Ser Glu Ser Ser Glu
10 15 20

gct tta ggt gtt tcc ctt tct gcc cgc gat ctt cgc tta gaa caa atg 211
Ala Leu Gly Val Ser Leu Ser Ala Arg Asp Leu Arg Leu Glu Gln Met
25 30 35

gga att gcc cag gac gat cct cga cgt gcc caa acc gtc caa gct ttc 259
Gly Ile Ala Gln Asp Asp Pro Arg Arg Ala Gln Thr Val Gln Ala Phe
40 45 50

gca gtg ctt gca gac cca gca aaa cgc gcc acc tac gat gct caa tta 307
Ala Val Leu Ala Asp Pro Ala Lys Arg Ala Thr Tyr Asp Ala Gln Leu
55 60 65

gaa gct gga gtt cca ctc acc tgg gcg cag att cag cat tta gga aac 355
Glu Ala Gly Val Pro Leu Thr Trp Ala Gln Ile Gln His Leu Gly Asn
70 75 80 85

ttc ggc acc ttg cct tcc acc cct act gcg cag ccg ttt gcg gca cct 403
Phe Gly Thr Leu Pro Ser Thr Pro Thr Ala Gln Pro Phe Ala Ala Pro
90 95 100

cag ccg gag ccg tcg ccg gaa ccg caa cag cag tgg aat agc gga caa 451
Gln Pro Glu Pro Ser Pro Glu Pro Gln Gln Gln Trp Asn Ser Gly Gln
105 110 115

aac tat gcg tat ggc aat ccg acc atg gat tac caa act cag cag agc 499
Asn Tyr Ala Tyr Gly Asn Pro Thr Met Asp Tyr Gln Thr Gln Gln Ser
120 125 130

tac aac ccg atg cag gac caa acc caa gcg tcg atg tat gcg caa cct 547
Tyr Asn Pro Met Gln Asp Gln Thr Gln Ala Ser Met Tyr Ala Gln Pro
135 140 145

ttc gcg aac acc cct gca ccg atg tac aac agc aat cag gtt ttt aac 595
Phe Ala Asn Thr Pro Ala Pro Met Tyr Asn Ser Asn Gln Val Phe Asn
150 155 160 165

agg cct act gcg ggt acg cgt ttg tgg atg gcg atc ctc gac agt att 643
Arg Pro Thr Ala Gly Thr Arg Leu Trp Met Ala Ile Leu Asp Ser Ile
170 175 180

ttt gcc ggc atc gct ggt gga att gtc tcc ggt att ttc ggc ttt gga 691
Phe Ala Gly Ile Ala Gly Gly Ile Val Ser Gly Ile Phe Gly Phe Gly
185 190 195

tct gaa ttc ctc acc agt gtc atc atg att ttg gtg ctg atc gtc 736

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Ser Glu Phe Leu Thr Ser Val Ile Met Ile Leu Val Leu Ile Val
        200                 205                 210


<210> 1520
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 1520
Met Asn Thr Asn Leu Pro Asn Leu Tyr Thr Ala Phe Asp Leu Asp Arg
  1               5                  10                  15

Ser Glu Ser Ser Glu Ala Leu Gly Val Ser Leu Ser Ala Arg Asp Leu
             20                  25                  30

Arg Leu Glu Gln Met Gly Ile Ala Gln Asp Asp Pro Arg Arg Ala Gln
         35                  40                  45

Thr Val Gln Ala Phe Ala Val Leu Ala Asp Pro Ala Lys Arg Ala Thr
     50                  55                  60

Tyr Asp Ala Gln Leu Glu Ala Gly Val Pro Leu Thr Trp Ala Gln Ile
 65                  70                  75                  80

Gln His Leu Gly Asn Phe Gly Thr Leu Pro Ser Thr Pro Thr Ala Gln
                 85                  90                  95

Pro Phe Ala Ala Pro Gln Pro Glu Pro Ser Pro Glu Pro Gln Gln Gln
            100                 105                 110

Trp Asn Ser Gly Gln Asn Tyr Ala Tyr Gly Asn Pro Thr Met Asp Tyr
        115                 120                 125

Gln Thr Gln Gln Ser Tyr Asn Pro Met Gln Asp Gln Thr Gln Ala Ser
    130                 135                 140

Met Tyr Ala Gln Pro Phe Ala Asn Thr Pro Ala Pro Met Tyr Asn Ser
145                 150                 155                 160

Asn Gln Val Phe Asn Arg Pro Thr Ala Gly Thr Arg Leu Trp Met Ala
                165                 170                 175

Ile Leu Asp Ser Ile Phe Ala Gly Ile Ala Gly Gly Ile Val Ser Gly
            180                 185                 190

Ile Phe Gly Phe Gly Ser Glu Phe Leu Thr Ser Val Ile Met Ile Leu
        195                 200                 205

Val Leu Ile Val
    210


<210> 1521
<211> 372
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(349)
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<223> RXN03170

<400> 1521
gttaaatcat tgccgcccag aagaagaccg cgcgggcgaa tttgggcttg gagggaacca 60

aacggccact tttccagtcc aacaaagtat gaggattaat ttg ccc cac gcc aaa 115
Leu Pro His Ala Lys
1 5

gag ctc gcc cac gag ctg tgt ttg ttg ccc acc cct gct gtg ccc gcg 163
Glu Leu Ala His Glu Leu Cys Leu Leu Pro Thr Pro Ala Val Pro Ala
10 15 20

ctt ccc act gat tct ggc gcg cag ttt gat atc cac cag gca cta tcc 211
Leu Pro Thr Asp Ser Gly Ala Gln Phe Asp Ile His Gln Ala Leu Ser
25 30 35

gcc tcc ctt gcc acc tat gcc cgc aac ctc acc ttg ctg tcc cac acc 259
Ala Ser Leu Ala Thr Tyr Ala Arg Asn Leu Thr Leu Leu Ser His Thr
40 45 50

gcc gag aat tta gga aac cgc gcg ctg acg ggc ctc gct gaa atc gaa 307
Ala Glu Asn Leu Gly Asn Arg Ala Leu Thr Gly Leu Ala Glu Ile Glu
55 60 65

gac acc gac gac caa ctc gca cac gca ttg gag cgc ctg aca 349
Asp Thr Asp Asp Gln Leu Ala His Ala Leu Glu Arg Leu Thr
70 75 80

tgatcggtct gatcagcgcc ctt 372

<210> 1522
<211> 83
<212> PRT
<213> Corynebacterium glutamicum

<400> 1522
Leu Pro His Ala Lys Glu Leu Ala His Glu Leu Cys Leu Leu Pro Thr
1 5 10 15

Pro Ala Val Pro Ala Leu Pro Thr Asp Ser Gly Ala Gln Phe Asp Ile
20 25 30

His Gln Ala Leu Ser Ala Ser Leu Ala Thr Tyr Ala Arg Asn Leu Thr
35 40 45

Leu Leu Ser His Thr Ala Glu Asn Leu Gly Asn Arg Ala Leu Thr Gly
50 55 60

Leu Ala Glu Ile Glu Asp Thr Asp Asp Gln Leu Ala His Ala Leu Glu
65 70 75 80

Arg Leu Thr

<210> 1523
<211> 372
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(349)
<223> FRXA02856

<400> 1523
gttaaatcat tgccgcccag aagaagaccg cgcgggcgaa tttgggcttg gagggaacca 60

aacggccact tttccagtcc aacaaagtat gaggattaat ttg ccc cac gcc aaa 115
Leu Pro His Ala Lys
1 5

gag ctc gcc cac gag ctg tgt ttg ttg ccc acc cct gct gtg ccc gcg 163
Glu Leu Ala His Glu Leu Cys Leu Leu Pro Thr Pro Ala Val Pro Ala
10 15 20

ctt ccc act gat tct ggc gcg cag ttt gat atc cac cag gca cta tcc 211
Leu Pro Thr Asp Ser Gly Ala Gln Phe Asp Ile His Gln Ala Leu Ser
25 30 35

gcc tcc ctt gcc acc tat gcc cgc aac ctc acc ttg ctg tcc cac acc 259
Ala Ser Leu Ala Thr Tyr Ala Arg Asn Leu Thr Leu Leu Ser His Thr
40 45 50

gcc gag aat tta gga aac cgc gcg ctg acg ggc ctc gct gaa atc gaa 307
Ala Glu Asn Leu Gly Asn Arg Ala Leu Thr Gly Leu Ala Glu Ile Glu
55 60 65

gac acc gac gac caa ctc gca cac gca ttg gag cgc ctg aca 349
Asp Thr Asp Asp Gln Leu Ala His Ala Leu Glu Arg Leu Thr
70 75 80

tgatcggtct gatcagcgcc ctt 372

<210> 1524
<211> 83
<212> PRT
<213> Corynebacterium glutamicum

<400> 1524
Leu Pro His Ala Lys Glu Leu Ala His Glu Leu Cys Leu Leu Pro Thr
1 5 10 15

Pro Ala Val Pro Ala Leu Pro Thr Asp Ser Gly Ala Gln Phe Asp Ile
20 25 30

His Gln Ala Leu Ser Ala Ser Leu Ala Thr Tyr Ala Arg Asn Leu Thr
35 40 45

Leu Leu Ser His Thr Ala Glu Asn Leu Gly Asn Arg Ala Leu Thr Gly
50 55 60

Leu Ala Glu Ile Glu Asp Thr Asp Asp Gln Leu Ala His Ala Leu Glu
65 70 75 80

Arg Leu Thr

<210> 1525
<211> 1049
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1026)
<223> RXN03172

<400> 1525

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cca gag tgg aag aaa ttc aac tcc ggc gac gca gcc cgc gtt gtc cca   48
Pro Glu Trp Lys Lys Phe Asn Ser Gly Asp Ala Ala Arg Val Val Pro
  1               5                  10                  15

gac gcc aac gca gag ctc gac atc atc ggc gca cca gca ctt ctt gcc   96
Asp Ala Asn Ala Glu Leu Asp Ile Ile Gly Ala Pro Ala Leu Leu Ala
             20                  25                  30

gat cgc ccc tcc tac gca aac gtc aaa acc ctc tcc cgc atc ttc gct   144
Asp Arg Pro Ser Tyr Ala Asn Val Lys Thr Leu Ser Arg Ile Phe Ala
         35                  40                  45

gtc atg cgc agc ctc ggc cac gtc acc gct gcc tcc cca gtc acc gtg   192
Val Met Arg Ser Leu Gly His Val Thr Ala Ala Ser Pro Val Thr Val
     50                  55                  60

ttc ttc tcc tcc cac tcc gtg ctc agc aac gtt gac cgc gga tcc gag   240
Phe Phe Ser Ser His Ser Val Leu Ser Asn Val Asp Arg Gly Ser Glu
 65                  70                  75                  80

cac tac tcc gga ccc aac ggc ctg ggc gaa tgg acc tcc gtt ggt cgc   288
His Tyr Ser Gly Pro Asn Gly Leu Gly Glu Trp Thr Ser Val Gly Arg
                 85                  90                  95

gca gta gcc acc aac tgg aac ggc gtt gtc gac gcc ctc gac gaa gcc   336
Ala Val Ala Thr Asn Trp Asn Gly Val Val Asp Ala Leu Asp Glu Ala
            100                 105                 110

atc acc gtc aag gaa gta aac agc ctc ttt acc gaa gac gcc gca acc   384
Ile Thr Val Lys Glu Val Asn Ser Leu Phe Thr Glu Asp Ala Ala Thr
        115                 120                 125

cgc att caa gaa gca caa gca gct gtt cag gca gct cgc gag gct gaa   432
Arg Ile Gln Glu Ala Gln Ala Ala Val Gln Ala Ala Arg Glu Ala Glu
    130                 135                 140

gag caa atc gcc aag gaa gaa gcc gaa aag gtc gac cct tac gac aac   480
Glu Gln Ile Ala Lys Glu Glu Ala Glu Lys Val Asp Pro Tyr Asp Asn
145                 150                 155                 160

tcc cca tgg gct gca gca ggc atc gac ccc atc aag gtc tcc atc gac   528
Ser Pro Trp Ala Ala Ala Gly Ile Asp Pro Ile Lys Val Ser Ile Asp
                165                 170                 175

gga cgc acc atc tac acc ctg cgc acc tac ctc ggc gga cag cca gta   576
Gly Arg Thr Ile Tyr Thr Leu Arg Thr Tyr Leu Gly Gly Gln Pro Val
            180                 185                 190

ttc ctc gga aaa ttc ggc gaa atc tcc acc ttc aac agc caa aaa tcc   624
Phe Leu Gly Lys Phe Gly Glu Ile Ser Thr Phe Asn Ser Gln Lys Ser
```

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        195                 200                 205

ctc ctg cgc tgg ctc gtc gaa cac gat gac cac gac ctc gcc cgc gcc   672
Leu Leu Arg Trp Leu Val Glu His Asp Asp His Asp Leu Ala Arg Ala
    210                 215                 220

tcc acc tgg agc gac ctc atg ctc ggc atc aac gcc ggt gaa acc gaa   720
Ser Thr Trp Ser Asp Leu Met Leu Gly Ile Asn Ala Gly Glu Thr Glu
225                 230                 235                 240

ctc ctc gtc cac agc gac aac gtc tac tcc ttc aac ggc ctg gtc aaa   768
Leu Leu Val His Ser Asp Asn Val Tyr Ser Phe Asn Gly Leu Val Lys
                245                 250                 255

gac atc aac acc tcc gtc gac gcc gta gac acc caa caa atg gcc cgc   816
Asp Ile Asn Thr Ser Val Asp Ala Val Asp Thr Gln Gln Met Ala Arg
            260                 265                 270

gcc tac gaa ctc atg gca gac acc gcc gac tgg gcc gac gac gac tcc   864
Ala Tyr Glu Leu Met Ala Asp Thr Ala Asp Trp Ala Asp Asp Asp Ser
        275                 280                 285

atg aat tcc tac ttc ctg gcc aac cca cgc atg cag gac tac atc tcc   912
Met Asn Ser Tyr Phe Leu Ala Asn Pro Arg Met Gln Asp Tyr Ile Ser
    290                 295                 300

tac atg ctc ggc ggc agc gac acc tcc gga tat gtc cct cac gca cca   960
Tyr Met Leu Gly Gly Ser Asp Thr Ser Gly Tyr Val Pro His Ala Pro
305                 310                 315                 320

ttc aac gac cac tct gag agc tgg cgc gag ctg gag gag atg ctg atc  1008
Phe Asn Asp His Ser Glu Ser Trp Arg Glu Leu Glu Glu Met Leu Ile
                325                 330                 335

aag cga ttc agc aag ttc taggtcgcct atttggggtt cgt                1049
Lys Arg Phe Ser Lys Phe
            340
```

<210> 1526
<211> 342
<212> PRT
<213> Corynebacterium glutamicum

<400> 1526

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Pro Glu Trp Lys Lys Phe Asn Ser Gly Asp Ala Ala Arg Val Val Pro
  1               5                  10                  15

Asp Ala Asn Ala Glu Leu Asp Ile Ile Gly Ala Pro Ala Leu Leu Ala
             20                  25                  30

Asp Arg Pro Ser Tyr Ala Asn Val Lys Thr Leu Ser Arg Ile Phe Ala
         35                  40                  45

Val Met Arg Ser Leu Gly His Val Thr Ala Ala Ser Pro Val Thr Val
     50                  55                  60

Phe Phe Ser Ser His Ser Val Leu Ser Asn Val Asp Arg Gly Ser Glu
 65                  70                  75                  80

His Tyr Ser Gly Pro Asn Gly Leu Gly Glu Trp Thr Ser Val Gly Arg
```

```
                85                  90                  95

Ala Val Ala Thr Asn Trp Asn Gly Val Val Asp Ala Leu Asp Glu Ala
            100                 105                 110

Ile Thr Val Lys Glu Val Asn Ser Leu Phe Thr Glu Asp Ala Ala Thr
        115                 120                 125

Arg Ile Gln Glu Ala Gln Ala Ala Val Gln Ala Ala Arg Glu Ala Glu
    130                 135                 140

Glu Gln Ile Ala Lys Glu Glu Ala Glu Lys Val Asp Pro Tyr Asp Asn
145                 150                 155                 160

Ser Pro Trp Ala Ala Ala Gly Ile Asp Pro Ile Lys Val Ser Ile Asp
                165                 170                 175

Gly Arg Thr Ile Tyr Thr Leu Arg Thr Tyr Leu Gly Gly Gln Pro Val
            180                 185                 190

Phe Leu Gly Lys Phe Gly Glu Ile Ser Thr Phe Asn Ser Gln Lys Ser
        195                 200                 205

Leu Leu Arg Trp Leu Val Glu His Asp Asp His Asp Leu Ala Arg Ala
    210                 215                 220

Ser Thr Trp Ser Asp Leu Met Leu Gly Ile Asn Ala Gly Glu Thr Glu
225                 230                 235                 240

Leu Leu Val His Ser Asp Asn Val Tyr Ser Phe Asn Gly Leu Val Lys
                245                 250                 255

Asp Ile Asn Thr Ser Val Asp Ala Val Asp Thr Gln Gln Met Ala Arg
            260                 265                 270

Ala Tyr Glu Leu Met Ala Asp Thr Ala Asp Trp Ala Asp Asp Asp Ser
        275                 280                 285

Met Asn Ser Tyr Phe Leu Ala Asn Pro Arg Met Gln Asp Tyr Ile Ser
    290                 295                 300

Tyr Met Leu Gly Gly Ser Asp Thr Ser Gly Tyr Val Pro His Ala Pro
305                 310                 315                 320

Phe Asn Asp His Ser Glu Ser Trp Arg Glu Leu Glu Glu Met Leu Ile
                325                 330                 335

Lys Arg Phe Ser Lys Phe
            340
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<210> 1527
<211> 1049
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1026)
<223> FRXA02858

<400> 1527

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cca gag tgg aag aaa ttc aac tcc ggc gac gca gcc cgc gtt gtc cca   48
Pro Glu Trp Lys Lys Phe Asn Ser Gly Asp Ala Ala Arg Val Val Pro
  1               5                  10                  15

gac gcc aac gca gag ctc gac atc atc ggc gca cca gca ctt ctt gcc   96
Asp Ala Asn Ala Glu Leu Asp Ile Ile Gly Ala Pro Ala Leu Leu Ala
             20                  25                  30

gat cgc ccc tcc tac gca aac gtc aaa acc ctc tcc cgc atc ttc gct  144
Asp Arg Pro Ser Tyr Ala Asn Val Lys Thr Leu Ser Arg Ile Phe Ala
         35                  40                  45

gtc atg cgc agc ctc ggc cac gtc acc gct gcc tcc cca gtc acc gtg  192
Val Met Arg Ser Leu Gly His Val Thr Ala Ala Ser Pro Val Thr Val
     50                  55                  60

ttc ttc tcc tcc cac tcc gtg ctc agc aac gtt gac cgc gga tcc gag  240
Phe Phe Ser Ser His Ser Val Leu Ser Asn Val Asp Arg Gly Ser Glu
 65                  70                  75                  80

cac tac tcc gga ccc aac ggc ctg ggc gaa tgg acc tcc gtt ggt cgc  288
His Tyr Ser Gly Pro Asn Gly Leu Gly Glu Trp Thr Ser Val Gly Arg
                 85                  90                  95

gca gta gcc acc aac tgg aac ggc gtt gtc gac gcc ctc gac gaa gcc  336
Ala Val Ala Thr Asn Trp Asn Gly Val Val Asp Ala Leu Asp Glu Ala
            100                 105                 110

atc acc gtc aag gaa gta aac agc ctc ttt acc gaa gac gcc gca acc  384
Ile Thr Val Lys Glu Val Asn Ser Leu Phe Thr Glu Asp Ala Ala Thr
        115                 120                 125

cgc att caa gaa gca caa gca gct gtt cag gca gct cgc gag gct gaa  432
Arg Ile Gln Glu Ala Gln Ala Ala Val Gln Ala Ala Arg Glu Ala Glu
    130                 135                 140

gag caa atc gcc aag gaa gaa gcc gaa aag gtc gac cct tac gac aac  480
Glu Gln Ile Ala Lys Glu Glu Ala Glu Lys Val Asp Pro Tyr Asp Asn
145                 150                 155                 160

tcc cca tgg gct gca gca ggc atc gac ccc atc aag gtc tcc atc gac  528
Ser Pro Trp Ala Ala Ala Gly Ile Asp Pro Ile Lys Val Ser Ile Asp
                165                 170                 175

gga cgc acc atc tac acc ctg cgc acc tac ctc ggc gga cag cca gta  576
Gly Arg Thr Ile Tyr Thr Leu Arg Thr Tyr Leu Gly Gly Gln Pro Val
            180                 185                 190

ttc ctc gga aaa ttc ggc gaa atc ttc acc ttc aac agc caa aaa tcc  624
Phe Leu Gly Lys Phe Gly Glu Ile Phe Thr Phe Asn Ser Gln Lys Ser
        195                 200                 205

ctc ctg cgc tgg ctc gtc gaa cac gat gac cac gac ctc gcc cgc gcc  672
Leu Leu Arg Trp Leu Val Glu His Asp Asp His Asp Leu Ala Arg Ala
    210                 215                 220

tcc acc tgg agc gac ctc atg ctc ggc atc aac gcc ggt gaa acc gaa  720
Ser Thr Trp Ser Asp Leu Met Leu Gly Ile Asn Ala Gly Glu Thr Glu
225                 230                 235                 240
```

```
ctc ctc gtc cac agc gac aac gtc tac tcc ttc aac ggc ctg gtc aaa   768
Leu Leu Val His Ser Asp Asn Val Tyr Ser Phe Asn Gly Leu Val Lys
                245                 250                 255

gac atc aac acc tcc gtc gac gcc gta gac acc caa caa atg gcc cgc   816
Asp Ile Asn Thr Ser Val Asp Ala Val Asp Thr Gln Gln Met Ala Arg
            260                 265                 270

gcc tac gaa ctc atg gca gac acc gcc gac tgg gcc gac gac gac tcc   864
Ala Tyr Glu Leu Met Ala Asp Thr Ala Asp Trp Ala Asp Asp Asp Ser
        275                 280                 285

atg aat tcc tac ttc ctg gcc aac cca cgc atg cag gac tac atc tcc   912
Met Asn Ser Tyr Phe Leu Ala Asn Pro Arg Met Gln Asp Tyr Ile Ser
    290                 295                 300

tac atg ctc ggc ggc agc gac acc tcc gga tat gtc cct cac gca cca   960
Tyr Met Leu Gly Gly Ser Asp Thr Ser Gly Tyr Val Pro His Ala Pro
305                 310                 315                 320

ttc aac gac cac tct gag agc tgg cgc gag ctg gag gag atg ctg atc   1008
Phe Asn Asp His Ser Glu Ser Trp Arg Glu Leu Glu Glu Met Leu Ile
                325                 330                 335

aag cga ttc agc aag ttc taggtcgcct atttggggtt cgt                 1049
Lys Arg Phe Ser Lys Phe
            340
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<210> 1528
<211> 342
<212> PRT
<213> Corynebacterium glutamicum

<400> 1528

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Pro Glu Trp Lys Lys Phe Asn Ser Gly Asp Ala Ala Arg Val Val Pro
  1               5                  10                  15

Asp Ala Asn Ala Glu Leu Asp Ile Ile Gly Ala Pro Ala Leu Leu Ala
             20                  25                  30

Asp Arg Pro Ser Tyr Ala Asn Val Lys Thr Leu Ser Arg Ile Phe Ala
         35                  40                  45

Val Met Arg Ser Leu Gly His Val Thr Ala Ala Ser Pro Val Thr Val
     50                  55                  60

Phe Phe Ser Ser His Ser Val Leu Ser Asn Val Asp Arg Gly Ser Glu
 65                  70                  75                  80

His Tyr Ser Gly Pro Asn Gly Leu Gly Glu Trp Thr Ser Val Gly Arg
                 85                  90                  95

Ala Val Ala Thr Asn Trp Asn Gly Val Val Asp Ala Leu Asp Glu Ala
            100                 105                 110

Ile Thr Val Lys Glu Val Asn Ser Leu Phe Thr Glu Asp Ala Ala Thr
        115                 120                 125

Arg Ile Gln Glu Ala Gln Ala Ala Val Gln Ala Ala Arg Glu Ala Glu
    130                 135                 140
```

```
Glu Gln Ile Ala Lys Glu Glu Ala Glu Lys Val Asp Pro Tyr Asp Asn
145                 150                 155                 160

Ser Pro Trp Ala Ala Ala Gly Ile Asp Pro Ile Lys Val Ser Ile Asp
                165                 170                 175

Gly Arg Thr Ile Tyr Thr Leu Arg Thr Tyr Leu Gly Gly Gln Pro Val
            180                 185                 190

Phe Leu Gly Lys Phe Gly Glu Ile Phe Thr Phe Asn Ser Gln Lys Ser
        195                 200                 205

Leu Leu Arg Trp Leu Val Glu His Asp Asp His Asp Leu Ala Arg Ala
    210                 215                 220

Ser Thr Trp Ser Asp Leu Met Leu Gly Ile Asn Ala Gly Glu Thr Glu
225                 230                 235                 240

Leu Leu Val His Ser Asp Asn Val Tyr Ser Phe Asn Gly Leu Val Lys
                245                 250                 255

Asp Ile Asn Thr Ser Val Asp Ala Val Asp Thr Gln Gln Met Ala Arg
            260                 265                 270

Ala Tyr Glu Leu Met Ala Asp Thr Ala Asp Trp Ala Asp Asp Asp Ser
        275                 280                 285

Met Asn Ser Tyr Phe Leu Ala Asn Pro Arg Met Gln Asp Tyr Ile Ser
    290                 295                 300

Tyr Met Leu Gly Gly Ser Asp Thr Ser Gly Tyr Val Pro His Ala Pro
305                 310                 315                 320

Phe Asn Asp His Ser Glu Ser Trp Arg Glu Leu Glu Glu Met Leu Ile
                325                 330                 335

Lys Arg Phe Ser Lys Phe
            340
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US20050153417A1

<210> 1529
<211> 1121
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1098)
<223> RXN03173

<400> 1529

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ctc aac cgc gac acc cat cac ctg tgg gtc gtc tta acc acc gac tcc   48
Leu Asn Arg Asp Thr His His Leu Trp Val Val Leu Thr Thr Asp Ser
  1               5                  10                  15

gac gac ttc gac gca gac tcc ttt acc acc gaa gtc atc cgg atc acc   96
Asp Asp Phe Asp Ala Asp Ser Phe Thr Thr Glu Val Ile Arg Ile Thr
             20                  25                  30

ggc tac tcc cgc cac gaa gtc aac aac ggc ctt aac gcc atg gcc gcg   144
```

```
Gly Tyr Ser Arg His Glu Val Asn Asn Gly Leu Asn Ala Met Ala Ala
          35                  40                  45

atg acc aac ctc cca cac ctg cgc gcc atc caa gaa cgc tac tac ttc   192
Met Thr Asn Leu Pro His Leu Arg Ala Ile Gln Glu Arg Tyr Tyr Phe
      50                  55                  60

ctg agc atc cgc tac ctc gcc tcc atc atg atc gcc gtg gcc aaa gca   240
Leu Ser Ile Arg Tyr Leu Ala Ser Ile Met Ile Ala Val Ala Lys Ala
 65                  70                  75                  80

gac ccc acc ctg tgg gaa gaa ctc gac ctg cgc atc acc gac gcc tta   288
Asp Pro Thr Leu Trp Glu Glu Leu Asp Leu Arg Ile Thr Asp Ala Leu
                 85                  90                  95

aca cca gtc acc gca ggg gaa gtc atg atc caa tcc tcc acc ctg tcc   336
Thr Pro Val Thr Ala Gly Glu Val Met Ile Gln Ser Ser Thr Leu Ser
            100                 105                 110

aaa cgc atc gcc gcc tgg atc aaa gaa ctc gac ccc gaa ccc aca cca   384
Lys Arg Ile Ala Ala Trp Ile Lys Glu Leu Asp Pro Glu Pro Thr Pro
        115                 120                 125

gag ccc aca ccg aaa gag gac tat gtt cac gtc cac acc act gat gag   432
Glu Pro Thr Pro Lys Glu Asp Tyr Val His Val His Thr Thr Asp Glu
    130                 135                 140

gcg acc tat gtc cgc atc aaa atc agc ggc ccc aac cgc ctg atc ctc   480
Ala Thr Tyr Val Arg Ile Lys Ile Ser Gly Pro Asn Arg Leu Ile Leu
145                 150                 155                 160

aat gac atc atc acc caa ctc aaa gac aca gac acc gag gac agc ctg   528
Asn Asp Ile Ile Thr Gln Leu Lys Asp Thr Asp Thr Glu Asp Ser Leu
                165                 170                 175

cct gaa gcg ctc atg gcg ttc ctg aca gag aaa atc cag tta aag atc   576
Pro Glu Ala Leu Met Ala Phe Leu Thr Glu Lys Ile Gln Leu Lys Ile
            180                 185                 190

acc aaa tac ctc ttc acc cca cat aag cac cct gag cag gtg tgg tca   624
Thr Lys Tyr Leu Phe Thr Pro His Lys His Pro Glu Gln Val Trp Ser
        195                 200                 205

ccg gac tac ggt gac att gat ccc gaa gcc tat gcc aac gcc acc ctc   672
Pro Asp Tyr Gly Asp Ile Asp Pro Glu Ala Tyr Ala Asn Ala Thr Leu
    210                 215                 220

gtg tgc gcc aag gac tta gat gag ctc gct gga gcc acg gag aag agc   720
Val Cys Ala Lys Asp Leu Asp Glu Leu Ala Gly Ala Thr Glu Lys Ser
225                 230                 235                 240

tac acc ccg agt gag aag atg aaa gcc ctg atc aga gct cgg gat ggg   768
Tyr Thr Pro Ser Glu Lys Met Lys Ala Leu Ile Arg Ala Arg Asp Gly
                245                 250                 255

cat tgc cgc ttc cca ggg tgt tgc gtt ccg gcg agt aag tgc cag gtc   816
His Cys Arg Phe Pro Gly Cys Cys Val Pro Ala Ser Lys Cys Gln Val
            260                 265                 270

gat cac att atc ccg tgg gcg gag ggc ggc ccg aca gcg gcg tgg aac   864
Asp His Ile Ile Pro Trp Ala Glu Gly Gly Pro Thr Ala Ala Trp Asn
```

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        275                 280                 285

ctg cag ttg ttg tgc cag cgg cat cac aat atg aaa acc gat ggt cgc   912
Leu Gln Leu Leu Cys Gln Arg His His Asn Met Lys Thr Asp Gly Arg
    290                 295                 300

ttt act gct gat gct aat gga ttg gcg gag att aga tgg att ggg ccg   960
Phe Thr Ala Asp Ala Asn Gly Leu Ala Glu Ile Arg Trp Ile Gly Pro
305                 310                 315                 320

atg gat gta cca gcg gtg acc agg ccg acg ggt ccg ttg gtg aaa gcg   1008
Met Asp Val Pro Ala Val Thr Arg Pro Thr Gly Pro Leu Val Lys Ala
                325                 330                 335

atg ccg cgg ggg att tgg ggt cag gtg ttg agg gat cgg atc cag gct   1056
Met Pro Arg Gly Ile Trp Gly Gln Val Leu Arg Asp Arg Ile Gln Ala
            340                 345                 350

agg ttt gag cgg atc cgc gac cgc gcc ctc aac aaa gaa gac           1098
Arg Phe Glu Arg Ile Arg Asp Arg Ala Leu Asn Lys Glu Asp
        355                 360                 365

tagaagcgca caggtttttg cat                                        1121


<210> 1530
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

<400> 1530
Leu Asn Arg Asp Thr His His Leu Trp Val Val Leu Thr Thr Asp Ser
  1               5                  10                  15

Asp Asp Phe Asp Ala Asp Ser Phe Thr Thr Glu Val Ile Arg Ile Thr
             20                  25                  30

Gly Tyr Ser Arg His Glu Val Asn Asn Gly Leu Asn Ala Met Ala Ala
         35                  40                  45

Met Thr Asn Leu Pro His Leu Arg Ala Ile Gln Glu Arg Tyr Tyr Phe
     50                  55                  60

Leu Ser Ile Arg Tyr Leu Ala Ser Ile Met Ile Ala Val Ala Lys Ala
 65                  70                  75                  80

Asp Pro Thr Leu Trp Glu Glu Leu Asp Leu Arg Ile Thr Asp Ala Leu
                 85                  90                  95

Thr Pro Val Thr Ala Gly Glu Val Met Ile Gln Ser Ser Thr Leu Ser
            100                 105                 110

Lys Arg Ile Ala Ala Trp Ile Lys Glu Leu Asp Pro Glu Pro Thr Pro
        115                 120                 125

Glu Pro Thr Pro Lys Glu Asp Tyr Val His Val His Thr Thr Asp Glu
    130                 135                 140

Ala Thr Tyr Val Arg Ile Lys Ile Ser Gly Pro Asn Arg Leu Ile Leu
145                 150                 155                 160
```

```
Asn Asp Ile Ile Thr Gln Leu Lys Asp Thr Asp Thr Glu Asp Ser Leu
                165                 170                 175

Pro Glu Ala Leu Met Ala Phe Leu Thr Glu Lys Ile Gln Leu Lys Ile
            180                 185                 190

Thr Lys Tyr Leu Phe Thr Pro His Lys His Pro Glu Gln Val Trp Ser
        195                 200                 205

Pro Asp Tyr Gly Asp Ile Asp Pro Glu Ala Tyr Ala Asn Ala Thr Leu
    210                 215                 220

Val Cys Ala Lys Asp Leu Asp Glu Leu Ala Gly Ala Thr Glu Lys Ser
225                 230                 235                 240

Tyr Thr Pro Ser Glu Lys Met Lys Ala Leu Ile Arg Ala Arg Asp Gly
                245                 250                 255

His Cys Arg Phe Pro Gly Cys Cys Val Pro Ala Ser Lys Cys Gln Val
            260                 265                 270

Asp His Ile Ile Pro Trp Ala Glu Gly Gly Pro Thr Ala Ala Trp Asn
        275                 280                 285

Leu Gln Leu Leu Cys Gln Arg His His Asn Met Lys Thr Asp Gly Arg
    290                 295                 300

Phe Thr Ala Asp Ala Asn Gly Leu Ala Glu Ile Arg Trp Ile Gly Pro
305                 310                 315                 320

Met Asp Val Pro Ala Val Thr Arg Pro Thr Gly Pro Leu Val Lys Ala
                325                 330                 335

Met Pro Arg Gly Ile Trp Gly Gln Val Leu Arg Asp Arg Ile Gln Ala
            340                 345                 350

Arg Phe Glu Arg Ile Arg Asp Arg Ala Leu Asn Lys Glu Asp
        355                 360                 365
```

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<210> 1531
<211> 503
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(480)
<223> FRXA02874

<400> 1531

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acc gaa ctc aac cgc gac acc cat cac ctg tgg gtc gtc tta acc acc   48
Thr Glu Leu Asn Arg Asp Thr His His Leu Trp Val Val Leu Thr Thr
  1               5                  10                  15

gac tcc gac gac ttc gac gca gac tcc ttt acc acc gaa gtc atc cgg   96
Asp Ser Asp Asp Phe Asp Ala Asp Ser Phe Thr Thr Glu Val Ile Arg
             20                  25                  30

atc acc ggc tac tcc cgc cac gaa gtc aac aac ggc ctt aac gcc atg   144
Ile Thr Gly Tyr Ser Arg His Glu Val Asn Asn Gly Leu Asn Ala Met
```

```
         35                  40                  45

gcc gcg atg acc aac ctc cca cac ctg cgc gcc atc caa gaa cgc tac   192
Ala Ala Met Thr Asn Leu Pro His Leu Arg Ala Ile Gln Glu Arg Tyr
     50                  55                  60

tac ttc ctg agc atc cgc tac ctc gcc tcc atc atg atc gcc gtg gcc   240
Tyr Phe Leu Ser Ile Arg Tyr Leu Ala Ser Ile Met Ile Ala Val Ala
 65                  70                  75                  80

aaa gca gac ccc acc ctg tgg gaa gaa ctc gac ctg cgc atc acc gac   288
Lys Ala Asp Pro Thr Leu Trp Glu Glu Leu Asp Leu Arg Ile Thr Asp
                 85                  90                  95

gcc tta aca cca gtc acc gca ggg gaa gtc atg atc caa tcc tcc acc   336
Ala Leu Thr Pro Val Thr Ala Gly Glu Val Met Ile Gln Ser Ser Thr
            100                 105                 110

ctg tcc aaa cng cat cgc cng cct gga tca aag aac tcg acc ccg aac   384
Leu Ser Lys Xaa His Arg Xaa Pro Gly Ser Lys Asn Ser Thr Pro Asn
        115                 120                 125

cca cac cag agc cca cac cga aag agg act atg ttc acg tcc aca cca   432
Pro His Gln Ser Pro His Arg Lys Arg Thr Met Phe Thr Ser Thr Pro
    130                 135                 140

ctg atg agg cga cct atg tcc gca tca aaa tca gcg gcc cca acc gcc   480
Leu Met Arg Arg Pro Met Ser Ala Ser Lys Ser Ala Ala Pro Thr Ala
145                 150                 155                 160

tgatcctcaa tgacatcatc acc                                        503


<210> 1532
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 1532
Thr Glu Leu Asn Arg Asp Thr His His Leu Trp Val Val Leu Thr Thr
  1               5                  10                  15

Asp Ser Asp Asp Phe Asp Ala Asp Ser Phe Thr Thr Glu Val Ile Arg
             20                  25                  30

Ile Thr Gly Tyr Ser Arg His Glu Val Asn Asn Gly Leu Asn Ala Met
         35                  40                  45

Ala Ala Met Thr Asn Leu Pro His Leu Arg Ala Ile Gln Glu Arg Tyr
     50                  55                  60

Tyr Phe Leu Ser Ile Arg Tyr Leu Ala Ser Ile Met Ile Ala Val Ala
 65                  70                  75                  80

Lys Ala Asp Pro Thr Leu Trp Glu Glu Leu Asp Leu Arg Ile Thr Asp
                 85                  90                  95

Ala Leu Thr Pro Val Thr Ala Gly Glu Val Met Ile Gln Ser Ser Thr
            100                 105                 110

Leu Ser Lys Xaa His Arg Xaa Pro Gly Ser Lys Asn Ser Thr Pro Asn
```

```
        115                 120                 125

Pro His Gln Ser Pro His Arg Lys Arg Thr Met Phe Thr Ser Thr Pro
    130                 135                 140

Leu Met Arg Arg Pro Met Ser Ala Ser Lys Ser Ala Ala Pro Thr Ala
145                 150                 155                 160
```

<210> 1533
<211> 556
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXN03174

Sequence Listing

<400> 1533

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gcgatgctcg aacgcgcaga acgctcctgg gtagacaaag ccgctgcata cgatttgcgc 60

tggtcagatc actcaccact gaacgtgatc tactcctaaa atg ctg ctg aca att   115
                                              Met Leu Leu Thr Ile
                                                1               5

cta tgg gcc atc ggc atc acc gcc gaa ggc atg aca ggc gcg ctg gcc   163
Leu Trp Ala Ile Gly Ile Thr Ala Glu Gly Met Thr Gly Ala Leu Ala
                  10                  15                  20

gca ggc cga caa aaa atg gat ctc ttc gga gta tcc gtc atc gca tgc   211
Ala Gly Arg Gln Lys Met Asp Leu Phe Gly Val Ser Val Ile Ala Cys
              25                  30                  35

gtt acc gcg atc ggc ggc gga tcc atc cgc gac atg ctg ctg gga cat   259
Val Thr Ala Ile Gly Gly Gly Ser Ile Arg Asp Met Leu Leu Gly His
          40                  45                  50

tac ccg ctg gtg tgg gtg gaa aag cca ctg tat cta ctg ctg atc att   307
Tyr Pro Leu Val Trp Val Glu Lys Pro Leu Tyr Leu Leu Leu Ile Ile
      55                  60                  65

ggc gca gcc att ttg aca gtg tcc att tcc ttc ctg atg gag cac ttc   355
Gly Ala Ala Ile Leu Thr Val Ser Ile Ser Phe Leu Met Glu His Phe
  70                  75                  80                  85

cgt gtg ttg ttc ctc gtg ctc gac gcc gtg ggt ctt tct gca ttc gct   403
Arg Val Leu Phe Leu Val Leu Asp Ala Val Gly Leu Ser Ala Phe Ala
                  90                  95                 100

gtg atc ggc aca caa atc gca ctg gaa atg ggc tac gga ttc atc atc   451
Val Ile Gly Thr Gln Ile Ala Leu Glu Met Gly Tyr Gly Phe Ile Ile
             105                 110                 115

gca gta gtg gca tca gtg ctc aca ggt gta ttc ggc ggc gtc atg cgt   499
Ala Val Val Ala Ser Val Leu Thr Gly Val Phe Gly Gly Val Met Arg
         120                 125                 130
```

```
gac ctt ttg tgt gac cgc atc cca ctg gta ttt caa aaa gag ctc tac   547
Asp Leu Leu Cys Asp Arg Ile Pro Leu Val Phe Gln Lys Glu Leu Tyr
    135                 140                 145

gca tca atc                                                       556
Ala Ser Ile
150
```

<210> 1534
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 1534

```
Met Leu Leu Thr Ile Leu Trp Ala Ile Gly Ile Thr Ala Glu Gly Met
  1               5                  10                  15

Thr Gly Ala Leu Ala Ala Gly Arg Gln Lys Met Asp Leu Phe Gly Val
             20                  25                  30

Ser Val Ile Ala Cys Val Thr Ala Ile Gly Gly Gly Ser Ile Arg Asp
         35                  40                  45

Met Leu Leu Gly His Tyr Pro Leu Val Trp Val Glu Lys Pro Leu Tyr
     50                  55                  60

Leu Leu Leu Ile Ile Gly Ala Ala Ile Leu Thr Val Ser Ile Ser Phe
 65                  70                  75                  80

Leu Met Glu His Phe Arg Val Leu Phe Leu Val Leu Asp Ala Val Gly
                85                  90                  95

Leu Ser Ala Phe Ala Val Ile Gly Thr Gln Ile Ala Leu Glu Met Gly
            100                 105                 110

Tyr Gly Phe Ile Ile Ala Val Val Ala Ser Val Leu Thr Gly Val Phe
        115                 120                 125

Gly Gly Val Met Arg Asp Leu Leu Cys Asp Arg Ile Pro Leu Val Phe
    130                 135                 140

Gln Lys Glu Leu Tyr Ala Ser Ile
145                 150
```

<210> 1535
<211> 562
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> FRXA02884

<400> 1535

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gcgatgctcg aacgcgcaga acgctcctgg gtagacaaag ccgctgcata cgatttgcgc 60

tggtcagatc actcaccact gaacgtgatc tactcctaaa atg ctg ctg aca att   115
                                                Met Leu Leu Thr Ile
```

```
                                                    1               5

cta tgg gcc atc ggc atc acc gcc gaa ggc atg aca ggc gcg ctg gcc   163
Leu Trp Ala Ile Gly Ile Thr Ala Glu Gly Met Thr Gly Ala Leu Ala
                 10                  15                  20

gca ggc cga caa aaa atg gat ctc ttc gga gta tcc gtc atc gca tgc   211
Ala Gly Arg Gln Lys Met Asp Leu Phe Gly Val Ser Val Ile Ala Cys
             25                  30                  35

gtt acc gcg atc ggc ggc gga tcc atc cgc gac atg ctg ctg gga cat   259
Val Thr Ala Ile Gly Gly Gly Ser Ile Arg Asp Met Leu Leu Gly His
         40                  45                  50

tac ccg ctg gtg tgg gtg gaa aag cca ctg tat cta ctg ctg atc att   307
Tyr Pro Leu Val Trp Val Glu Lys Pro Leu Tyr Leu Leu Leu Ile Ile
     55                  60                  65

ggc gca gcc att ttg aca gtg tcc att tcc ttc ctg atg gag cac ttc   355
Gly Ala Ala Ile Leu Thr Val Ser Ile Ser Phe Leu Met Glu His Phe
 70                  75                  80                  85

cgt gtg ttg ttc ctc gtg ctc gac gcc gtg ggt ctt tct gca ttc gct   403
Arg Val Leu Phe Leu Val Leu Asp Ala Val Gly Leu Ser Ala Phe Ala
                 90                  95                 100

gtg atc ggc aca caa atc gca ctg gaa atg ggc tac gga ttc atc atc   451
Val Ile Gly Thr Gln Ile Ala Leu Glu Met Gly Tyr Gly Phe Ile Ile
             105                 110                 115

gca gta gtg gca tca gtg ctc aca ggt gta ttc ggc ggc gtc atg cgt   499
Ala Val Val Ala Ser Val Leu Thr Gly Val Phe Gly Gly Val Met Arg
         120                 125                 130

gac ctt ttg tgt gac cgc atc cca ctg gta ttt caa aaa gag ctc tac   547
Asp Leu Leu Cys Asp Arg Ile Pro Leu Val Phe Gln Lys Glu Leu Tyr
     135                 140                 145

gca tca atc gca ttc                                               562
Ala Ser Ile Ala Phe
150
```

<210> 1536
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 1536

```
Met Leu Leu Thr Ile Leu Trp Ala Ile Gly Ile Thr Ala Glu Gly Met
  1               5                  10                  15

Thr Gly Ala Leu Ala Ala Gly Arg Gln Lys Met Asp Leu Phe Gly Val
             20                  25                  30

Ser Val Ile Ala Cys Val Thr Ala Ile Gly Gly Gly Ser Ile Arg Asp
         35                  40                  45

Met Leu Leu Gly His Tyr Pro Leu Val Trp Val Glu Lys Pro Leu Tyr
     50                  55                  60
```

```
Leu Leu Leu Ile Ile Gly Ala Ala Ile Leu Thr Val Ser Ile Ser Phe
 65                  70                  75                  80

Leu Met Glu His Phe Arg Val Leu Phe Leu Val Leu Asp Ala Val Gly
                 85                  90                  95

Leu Ser Ala Phe Ala Val Ile Gly Thr Gln Ile Ala Leu Glu Met Gly
            100                 105                 110

Tyr Gly Phe Ile Ile Ala Val Val Ala Ser Val Leu Thr Gly Val Phe
        115                 120                 125

Gly Gly Val Met Arg Asp Leu Leu Cys Asp Arg Ile Pro Leu Val Phe
    130                 135                 140

Gln Lys Glu Leu Tyr Ala Ser Ile Ala Phe
145                 150


<210> 1537
<211> 781
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (93)..(758)
<223> RXN03177

<400> 1537
ctgcccgatt tatgttttcc gacggcacca tctgcaaaga acgagtgtga ccggtagctt 60

tatgggctga acaattctaa ggagaattat ccgtg aaa aag aag ctt atg ttg    113
                                  Val Lys Lys Lys Leu Met Leu
                                    1               5

cct ttg att gtt gca gct ttg ggg tta agt gcc tgc agc tcc gaa cct   161
Pro Leu Ile Val Ala Ala Leu Gly Leu Ser Ala Cys Ser Ser Glu Pro
         10                  15                  20

gca gca gcc cca ctc gaa gca gag cca tta cat aac ctg ctc att gat   209
Ala Ala Ala Pro Leu Glu Ala Glu Pro Leu His Asn Leu Leu Ile Asp
     25                  30                  35

ggt tca gag tcc ggc ttg gac aat gcc act gaa gga aac gac acc tca   257
Gly Ser Glu Ser Gly Leu Asp Asn Ala Thr Glu Gly Asn Asp Thr Ser
 40                  45                  50                  55

tta agt ggc caa ccc atc aat ctt aca gtg gtc aac ggt gcc tta gat   305
Leu Ser Gly Gln Pro Ile Asn Leu Thr Val Val Asn Gly Ala Leu Asp
                 60                  65                  70

atc gat ggc tcc tgc gga aaa gcc ctc caa gct gta gag gac gtc aat   353
Ile Asp Gly Ser Cys Gly Lys Ala Leu Gln Ala Val Glu Asp Val Asn
             75                  80                  85

ctg gac agc gta gct agc gca tcc agg gca ctg gca tcc ggc gac aaa   401
Leu Asp Ser Val Ala Ser Ala Ser Arg Ala Leu Ala Ser Gly Asp Lys
         90                  95                  100

caa gta ggc atc gcc atg tac tca acc gcc gaa gac aac gac atc tca   449
```

```
Gln Val Gly Ile Ala Met Tyr Ser Thr Ala Glu Asp Asn Asp Ile Ser
    105                 110                 115

cca atg gac ctc tac gca gac atc gcg aat gct tgc gaa gac ccc gtc   497
Pro Met Asp Leu Tyr Ala Asp Ile Ala Asn Ala Cys Glu Asp Pro Val
120                 125                 130                 135

gtc gat tct tcc gac acc acc tac acc ttc ggc aaa ctc gat gat gct   545
Val Asp Ser Ser Asp Thr Thr Tyr Thr Phe Gly Lys Leu Asp Asp Ala
                140                 145                 150

ccc gac ggc gcc gtt gga ttc acc ctc gac att gaa gtc acc cct gac   593
Pro Asp Gly Ala Val Gly Phe Thr Leu Asp Ile Glu Val Thr Pro Asp
            155                 160                 165

aat caa ggc tcc acc gtg atg atg atc caa gaa tta gga aac cac cac   641
Asn Gln Gly Ser Thr Val Met Met Ile Gln Glu Leu Gly Asn His His
        170                 175                 180

atc atc gtc gca gga ctt gaa acc acc cca gaa gaa acc gcc act gtc   689
Ile Ile Val Ala Gly Leu Glu Thr Thr Pro Glu Glu Thr Ala Thr Val
    185                 190                 195

ttc gaa gca caa cgc acc aaa ctc gaa gaa ggc ttg cag ctt aaa cag   737
Phe Glu Ala Gln Arg Thr Lys Leu Glu Glu Gly Leu Gln Leu Lys Gln
200                 205                 210                 215

aat tgg cag ctt ggg tgg gtt taaatgcgcc caacctaaga aaa             781
Asn Trp Gln Leu Gly Trp Val
                220
```

Sequence Listing

<210> 1538
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 1538

```
Val Lys Lys Lys Leu Met Leu Pro Leu Ile Val Ala Ala Leu Gly Leu
  1               5                  10                  15

Ser Ala Cys Ser Ser Glu Pro Ala Ala Ala Pro Leu Glu Ala Glu Pro
             20                  25                  30

Leu His Asn Leu Leu Ile Asp Gly Ser Glu Ser Gly Leu Asp Asn Ala
         35                  40                  45

Thr Glu Gly Asn Asp Thr Ser Leu Ser Gly Gln Pro Ile Asn Leu Thr
     50                  55                  60

Val Val Asn Gly Ala Leu Asp Ile Asp Gly Ser Cys Gly Lys Ala Leu
 65                  70                  75                  80

Gln Ala Val Glu Asp Val Asn Leu Asp Ser Val Ala Ser Ala Ser Arg
                 85                  90                  95

Ala Leu Ala Ser Gly Asp Lys Gln Val Gly Ile Ala Met Tyr Ser Thr
            100                 105                 110

Ala Glu Asp Asn Asp Ile Ser Pro Met Asp Leu Tyr Ala Asp Ile Ala
        115                 120                 125
```

```
Asn Ala Cys Glu Asp Pro Val Val Asp Ser Ser Asp Thr Thr Tyr Thr
    130                 135                 140

Phe Gly Lys Leu Asp Asp Ala Pro Asp Gly Ala Val Gly Phe Thr Leu
145                 150                 155                 160

Asp Ile Glu Val Thr Pro Asp Asn Gln Gly Ser Thr Val Met Met Ile
                165                 170                 175

Gln Glu Leu Gly Asn His His Ile Ile Val Ala Gly Leu Glu Thr Thr
            180                 185                 190

Pro Glu Glu Thr Ala Thr Val Phe Glu Ala Gln Arg Thr Lys Leu Glu
        195                 200                 205

Glu Gly Leu Gln Leu Lys Gln Asn Trp Gln Leu Gly Trp Val
    210                 215                 220


<210> 1539
<211> 782
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (94)..(759)
<223> FRXA02881

<400> 1539
ctgcccgatt tcatgttttc cgacggcacc atctgcaaag aacgagtgtg accggtagct 60

ttatgggctg aacaattcta aggagaatta tccgtg aaa aag aag ctt atg ttg   114
                                    Val Lys Lys Lys Leu Met Leu
                                      1               5

cct ttg att gtt gca gct ttg ggg tta agt gcc tgc agc tcc gaa cct   162
Pro Leu Ile Val Ala Ala Leu Gly Leu Ser Ala Cys Ser Ser Glu Pro
         10                  15                  20

gca gca gcc cca ctc gaa gca gag cca tta cat aac ctg ctc att gat   210
Ala Ala Ala Pro Leu Glu Ala Glu Pro Leu His Asn Leu Leu Ile Asp
     25                  30                  35

ggt tca gag tcc ggc ttg gac aat gcc act gaa gga aac gac acc tca   258
Gly Ser Glu Ser Gly Leu Asp Asn Ala Thr Glu Gly Asn Asp Thr Ser
 40                  45                  50                  55

tta agt ggc caa ccc atc aat ctt aca gtg gtc aac ggt gcc tta gat   306
Leu Ser Gly Gln Pro Ile Asn Leu Thr Val Val Asn Gly Ala Leu Asp
                 60                  65                  70

atc gat ggc tcc tgc gga aaa gcc ctc caa gct gta gag gac gtc aat   354
Ile Asp Gly Ser Cys Gly Lys Ala Leu Gln Ala Val Glu Asp Val Asn
             75                  80                  85

ctg gac agc gta gct agc gca tcc agg gca ctg gca tcc ggc gac aaa   402
Leu Asp Ser Val Ala Ser Ala Ser Arg Ala Leu Ala Ser Gly Asp Lys
         90                  95                  100
```

```
caa gta ggc atc gcc atg tac tca acc gcc gaa gac aac gac atc tca   450
Gln Val Gly Ile Ala Met Tyr Ser Thr Ala Glu Asp Asn Asp Ile Ser
    105                 110                 115

cca atg gac ctc tac gca gac atc gcg aat gct tgc gaa gac ccc gtc   498
Pro Met Asp Leu Tyr Ala Asp Ile Ala Asn Ala Cys Glu Asp Pro Val
120                 125                 130                 135

gtc gat tct tcc gac acc acc tac acc ttc ggc aaa ctc gat gat gct   546
Val Asp Ser Ser Asp Thr Thr Tyr Thr Phe Gly Lys Leu Asp Asp Ala
                140                 145                 150

ccc gac ggc gcc gtt gga ttc acc ctc gac att gaa gtc acc cct gac   594
Pro Asp Gly Ala Val Gly Phe Thr Leu Asp Ile Glu Val Thr Pro Asp
            155                 160                 165

aat caa ggc tcc acc gtg atg atg atc caa gaa tta gga aac cac cac   642
Asn Gln Gly Ser Thr Val Met Met Ile Gln Glu Leu Gly Asn His His
        170                 175                 180

atc atc gtc gca gga ctt gaa acc acc cca gaa gaa acc gcc act gtc   690
Ile Ile Val Ala Gly Leu Glu Thr Thr Pro Glu Glu Thr Ala Thr Val
    185                 190                 195

ttc gaa gca caa cgc acc aaa ctc gaa gaa ggc ttg cag ctt aaa cag   738
Phe Glu Ala Gln Arg Thr Lys Leu Glu Glu Gly Leu Gln Leu Lys Gln
200                 205                 210                 215

aat tgg cag ctt ggg tgg gtt taaatgcgcc caacctaaga aaa             782
Asn Trp Gln Leu Gly Trp Val
                220
```

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<210> 1540
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 1540

```
Val Lys Lys Lys Leu Met Leu Pro Leu Ile Val Ala Ala Leu Gly Leu
  1               5                  10                  15

Ser Ala Cys Ser Ser Glu Pro Ala Ala Ala Pro Leu Glu Ala Glu Pro
             20                  25                  30

Leu His Asn Leu Leu Ile Asp Gly Ser Glu Ser Gly Leu Asp Asn Ala
         35                  40                  45

Thr Glu Gly Asn Asp Thr Ser Leu Ser Gly Gln Pro Ile Asn Leu Thr
     50                  55                  60

Val Val Asn Gly Ala Leu Asp Ile Asp Gly Ser Cys Gly Lys Ala Leu
 65                  70                  75                  80

Gln Ala Val Glu Asp Val Asn Leu Asp Ser Val Ala Ser Ala Ser Arg
                 85                  90                  95

Ala Leu Ala Ser Gly Asp Lys Gln Val Gly Ile Ala Met Tyr Ser Thr
            100                 105                 110

Ala Glu Asp Asn Asp Ile Ser Pro Met Asp Leu Tyr Ala Asp Ile Ala
```

```
        115                 120                 125

Asn Ala Cys Glu Asp Pro Val Val Asp Ser Ser Asp Thr Thr Tyr Thr
    130                 135                 140

Phe Gly Lys Leu Asp Asp Ala Pro Asp Gly Ala Val Gly Phe Thr Leu
145                 150                 155                 160

Asp Ile Glu Val Thr Pro Asp Asn Gln Gly Ser Thr Val Met Met Ile
                165                 170                 175

Gln Glu Leu Gly Asn His His Ile Ile Val Ala Gly Leu Glu Thr Thr
            180                 185                 190

Pro Glu Glu Thr Ala Thr Val Phe Glu Ala Gln Arg Thr Lys Leu Glu
        195                 200                 205

Glu Gly Leu Gln Leu Lys Gln Asn Trp Gln Leu Gly Trp Val
    210                 215                 220
```

<210> 1541
<211> 373
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(373)
<223> RXN03182

<400> 1541

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actcgacacc accgtcacca acttcatgat ggtcatcgca ctcttaggat tcatcagctc 60

tgtatccgta gcccgcttcc gcaagaggga tggtgcctaa atg acc ctg caa cta   115
                                               Met Thr Leu Gln Leu
                                                 1               5

ttc acc gac atc gtg tct ctg gtg ttc att ctc agc ggc gca ttc ttg   163
Phe Thr Asp Ile Val Ser Leu Val Phe Ile Leu Ser Gly Ala Phe Leu
                 10                  15                  20

tca ttc tcc gca tcc atc ggc ctc ata cga ttc aaa gac acc atg tcc   211
Ser Phe Ser Ala Ser Ile Gly Leu Ile Arg Phe Lys Asp Thr Met Ser
             25                  30                  35

aga gtc cac gcc atg acc aaa ccc caa aca acc ggc ctt atc ctc acc   259
Arg Val His Ala Met Thr Lys Pro Gln Thr Thr Gly Leu Ile Leu Thr
         40                  45                  50

gtt gta ggc gca atc atc cgc atc tta ggc cac gaa cac ttc gat caa   307
Val Val Gly Ala Ile Ile Arg Ile Leu Gly His Glu His Phe Asp Gln
     55                  60                  65

tca caa cgc agt gac ctc gga gtc ctt gtt ctc ctc gta ctg ttt gca   355
Ser Gln Arg Ser Asp Leu Gly Val Leu Val Leu Leu Val Leu Phe Ala
 70                  75                  80                  85

ctg ctc acc agc cca gtg                                         373
Leu Leu Thr Ser Pro Val
                 90
```

<210> 1542
<211> 91
<212> PRT
<213> Corynebacterium glutamicum

<400> 1542
Met Thr Leu Gln Leu Phe Thr Asp Ile Val Ser Leu Val Phe Ile Leu
1 5 10 15

Ser Gly Ala Phe Leu Ser Phe Ser Ala Ser Ile Gly Leu Ile Arg Phe
20 25 30

Lys Asp Thr Met Ser Arg Val His Ala Met Thr Lys Pro Gln Thr Thr
35 40 45

Gly Leu Ile Leu Thr Val Val Gly Ala Ile Ile Arg Ile Leu Gly His
50 55 60

Glu His Phe Asp Gln Ser Gln Arg Ser Asp Leu Gly Val Leu Val Leu
65 70 75 80

Leu Val Leu Phe Ala Leu Leu Thr Ser Pro Val
85 90

<210> 1543
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (87)..(584)
<223> RXN03184

<400> 1543
gcacaacgtc gctggtcagt gccattagtc acgcaagaaa tgggcgggtc cggtggaaga 60

ctggcctgct gtttggtgcc gcgggcatg gtt ggc gcg ttt ggc ggt ggc gtt 113
Met Val Gly Ala Phe Gly Gly Gly Val
1 5

ctc ggg ggc tac att cct ggc acg att ttg atg atc gcg ttt gcg ctc 161
Leu Gly Gly Tyr Ile Pro Gly Thr Ile Leu Met Ile Ala Phe Ala Leu
10 15 20 25

atg atg atc gcc acg tcg act gcg atg ttg cgg ggg cgt aag cag aag 209
Met Met Ile Ala Thr Ser Thr Ala Met Leu Arg Gly Arg Lys Gln Lys
30 35 40

aag ggg gcg tcg aaa agc tct ctt tgg cgc gtc ctt gtt gat ggc ctg 257
Lys Gly Ala Ser Lys Ser Ser Leu Trp Arg Val Leu Val Asp Gly Leu
45 50 55

gtg gtc ggc gcg gtg acc ggg ctt gtt ggt gcg ggc ggc ggc ttt ttg 305
Val Val Gly Ala Val Thr Gly Leu Val Gly Ala Gly Gly Gly Phe Leu
60 65 70

gtg gtg ccg gcg ctg gcg ctg ctc ggc ggg ctg tcg atg ccg gtg gct 353

```
Val Val Pro Ala Leu Ala Leu Leu Gly Gly Leu Ser Met Pro Val Ala
     75                  80                  85

gtg ggc acg tcg ttg gtg gtg atc acg atg aag tcg ttt gcg ggg ctt   401
Val Gly Thr Ser Leu Val Val Ile Thr Met Lys Ser Phe Ala Gly Leu
 90                  95                 100                 105

gcc ggg tat ctg acc agc gtg cag ctg gat tgg ggg ctg gtg ctg atg   449
Ala Gly Tyr Leu Thr Ser Val Gln Leu Asp Trp Gly Leu Val Leu Met
                110                 115                 120

gtg act gcg gcc gcc atc gtc ggt tcg ctt gcc ggt tcg cgc ctt gcg   497
Val Thr Ala Ala Ala Ile Val Gly Ser Leu Ala Gly Ser Arg Leu Ala
            125                 130                 135

ggg cgc gtg cct gag act ttg ctc cgc aaa ggg ttc ggg gtg ttc gtg   545
Gly Arg Val Pro Glu Thr Leu Leu Arg Lys Gly Phe Gly Val Phe Val
        140                 145                 150

ctg gtc atg ggc gtg ttc gtg ctc ggc ttg gag ctt tta taagcttttc    594
Leu Val Met Gly Val Phe Val Leu Gly Leu Glu Leu Leu
    155                 160                 165

gacgtctcc                                                         603


<210> 1544
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

<400> 1544
Met Val Gly Ala Phe Gly Gly Gly Val Leu Gly Gly Tyr Ile Pro Gly
  1               5                  10                  15

Thr Ile Leu Met Ile Ala Phe Ala Leu Met Met Ile Ala Thr Ser Thr
             20                  25                  30

Ala Met Leu Arg Gly Arg Lys Gln Lys Lys Gly Ala Ser Lys Ser Ser
         35                  40                  45

Leu Trp Arg Val Leu Val Asp Gly Leu Val Val Gly Ala Val Thr Gly
     50                  55                  60

Leu Val Gly Ala Gly Gly Gly Phe Leu Val Val Pro Ala Leu Ala Leu
 65                  70                  75                  80

Leu Gly Gly Leu Ser Met Pro Val Ala Val Gly Thr Ser Leu Val Val
                 85                  90                  95

Ile Thr Met Lys Ser Phe Ala Gly Leu Ala Gly Tyr Leu Thr Ser Val
            100                 105                 110

Gln Leu Asp Trp Gly Leu Val Leu Met Val Thr Ala Ala Ala Ile Val
        115                 120                 125

Gly Ser Leu Ala Gly Ser Arg Leu Ala Gly Arg Val Pro Glu Thr Leu
    130                 135                 140

Leu Arg Lys Gly Phe Gly Val Phe Val Leu Val Met Gly Val Phe Val
145                 150                 155                 160
```

```
Leu Gly Leu Glu Leu Leu
                165


<210> 1545
<211> 295
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (84)..(272)
<223> RXN03185

<400> 1545
agcgcccaac cgttcagacc agcggtttct ctgaggatgc aaagtccatg atgggtnagg 60

tcactgagct gtccgaaacc accatg aat gat ctt gca gct gaa ggt gaa aac  113
                        Met Asn Asp Leu Ala Ala Glu Gly Glu Asn
                          1               5                  10

gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctc tct cgc ttc   161
Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe
                 15                  20                  25

gtc gag cag aag tgg aag cgc cag ccg gtc atc atg cca acc gtc att   209
Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile
             30                  35                  40

ccg atg act gcg gaa acc acg cac atc ggt gac gat gag gtt cgc gct   257
Pro Met Thr Ala Glu Thr Thr His Ile Gly Asp Asp Glu Val Arg Ala
         45                  50                  55

tca cgc gag tcc ctg taaaagcatt tcgcttttcg acg                    295
Ser Arg Glu Ser Leu
     60


<210> 1546
<211> 63
<212> PRT
<213> Corynebacterium glutamicum

<400> 1546
Met Asn Asp Leu Ala Ala Glu Gly Glu Asn Asp Pro Tyr Arg Met Val
  1               5                  10                  15

Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe Val Glu Gln Lys Trp Lys
             20                  25                  30

Arg Gln Pro Val Ile Met Pro Thr Val Ile Pro Met Thr Ala Glu Thr
         35                  40                  45

Thr His Ile Gly Asp Asp Glu Val Arg Ala Ser Arg Glu Ser Leu
     50                  55                  60


<210> 1547
<211> 864
<212> DNA
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<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(841)
<223> RXA00003

<400> 1547
catccatttc gcacagaaca tggtaatcct tctctaggcc ccactcgaag ccggcgatat 60

aagcgccaag aaggccaccc ttgccttcgc ggtgcagcac gtg cag gtg aga atc 115
Val Gln Val Arg Ile
1 5

ctc agc agc gag ctt gtc tgc agc ctc tcc ggt gcc atc cgg ggc gtg 163
Leu Ser Ser Glu Leu Val Cys Ser Leu Ser Gly Ala Ile Arg Gly Val
10 15 20

aac cta gat att gca gca ccg aag ccc aag aag tca ggc cgc cgc aca 211
Asn Leu Asp Ile Ala Ala Pro Lys Pro Lys Lys Ser Gly Arg Arg Thr
25 30 35

ctc aca aaa ccc gaa tgg gat gcc gtc att aag cat ctg tta acg cgg 259
Leu Thr Lys Pro Glu Trp Asp Ala Val Ile Lys His Leu Leu Thr Arg
40 45 50

gat acc gag cca ctg tta acc ccc acc aag cac aag aac atc cga caa 307
Asp Thr Glu Pro Leu Leu Thr Pro Thr Lys His Lys Asn Ile Arg Gln
55 60 65

agc acc aag aac atc cat gcc cgc att gtg cgg ctc act ctc ctc caa 355
Ser Thr Lys Asn Ile His Ala Arg Ile Val Arg Leu Thr Leu Leu Gln
70 75 80 85

gcc gtt tca ggg ctg aga att gcc gaa gcc aat caa ttg cag tgg aag 403
Ala Val Ser Gly Leu Arg Ile Ala Glu Ala Asn Gln Leu Gln Trp Lys
90 95 100

cac atc atc gac ggt gac gat ggc atg ctc att aat gcc agc gcc gat 451
His Ile Ile Asp Gly Asp Asp Gly Met Leu Ile Asn Ala Ser Ala Asp
105 110 115

att gtc aag ggg cga aaa ggc aag gaa aga ggg cgg tat atc cct atc 499
Ile Val Lys Gly Arg Lys Gly Lys Glu Arg Gly Arg Tyr Ile Pro Ile
120 125 130

ctg agg gcc gac gta gcg gaa tac ctg cgt aca cac cgc gag gac gac 547
Leu Arg Ala Asp Val Ala Glu Tyr Leu Arg Thr His Arg Glu Asp Asp
135 140 145

gag cat ttc atc gta ggc tca ccg acg acg acc gcg agg ccc tgg gac 595
Glu His Phe Ile Val Gly Ser Pro Thr Thr Thr Ala Arg Pro Trp Asp
150 155 160 165

gcg acg aac gca gat gac aag gtg ccc gag cta tac cgg caa att gca 643
Ala Thr Asn Ala Asp Asp Lys Val Pro Glu Leu Tyr Arg Gln Ile Ala
170 175 180

gaa gct aca ggc gtg aag act ctt caa gac ctc cga agc cac tcc tgg 691
Glu Ala Thr Gly Val Lys Thr Leu Gln Asp Leu Arg Ser His Ser Trp
185 190 195

```
cgt gcg acg ctg cac ggt gtg tac gcg gac gtg atg gac cca gct aca   739
Arg Ala Thr Leu His Gly Val Tyr Ala Asp Val Met Asp Pro Ala Thr
        200                 205                 210

cgc gcc gcc att ttc ggc cac acc gag cag gta gct gag gag tac tac   787
Arg Ala Ala Ile Phe Gly His Thr Glu Gln Val Ala Glu Glu Tyr Tyr
    215                 220                 225

aac gac cgc caa aat att gaa tca ctc atg aga caa gtc aag cgc gcc   835
Asn Asp Arg Gln Asn Ile Glu Ser Leu Met Arg Gln Val Lys Arg Ala
230                 235                 240                 245

tac gcg taactacgct taagactacg cgt                                 864
Tyr Ala
```

<210> 1548
<211> 247
<212> PRT
<213> Corynebacterium glutamicum

<400> 1548

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Val Gln Val Arg Ile Leu Ser Ser Glu Leu Val Cys Ser Leu Ser Gly
  1               5                  10                  15

Ala Ile Arg Gly Val Asn Leu Asp Ile Ala Ala Pro Lys Pro Lys Lys
             20                  25                  30

Ser Gly Arg Arg Thr Leu Thr Lys Pro Glu Trp Asp Ala Val Ile Lys
         35                  40                  45

His Leu Leu Thr Arg Asp Thr Glu Pro Leu Leu Thr Pro Thr Lys His
     50                  55                  60

Lys Asn Ile Arg Gln Ser Thr Lys Asn Ile His Ala Arg Ile Val Arg
 65                  70                  75                  80

Leu Thr Leu Leu Gln Ala Val Ser Gly Leu Arg Ile Ala Glu Ala Asn
                 85                  90                  95

Gln Leu Gln Trp Lys His Ile Ile Asp Gly Asp Asp Gly Met Leu Ile
            100                 105                 110

Asn Ala Ser Ala Asp Ile Val Lys Gly Arg Lys Gly Lys Glu Arg Gly
        115                 120                 125

Arg Tyr Ile Pro Ile Leu Arg Ala Asp Val Ala Glu Tyr Leu Arg Thr
    130                 135                 140

His Arg Glu Asp Asp Glu His Phe Ile Val Gly Ser Pro Thr Thr Thr
145                 150                 155                 160

Ala Arg Pro Trp Asp Ala Thr Asn Ala Asp Asp Lys Val Pro Glu Leu
                165                 170                 175

Tyr Arg Gln Ile Ala Glu Ala Thr Gly Val Lys Thr Leu Gln Asp Leu
            180                 185                 190

Arg Ser His Ser Trp Arg Ala Thr Leu His Gly Val Tyr Ala Asp Val
```

```
        195                 200                 205

Met Asp Pro Ala Thr Arg Ala Ala Ile Phe Gly His Thr Glu Gln Val
    210                 215                 220

Ala Glu Glu Tyr Tyr Asn Asp Arg Gln Asn Ile Glu Ser Leu Met Arg
225                 230                 235                 240

Gln Val Lys Arg Ala Tyr Ala
                245
```

<210> 1549
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(592)
<223> RXA00008

<400> 1549

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cattggcgtg gtgatcgccg gcattatcgc acaactcacc ctgcgcttct acgtgaggaa 60

ataagactat tgaactcctt gccgtagact tagaaagact atg gcc aag aag aaa   115
                                        Met Ala Lys Lys Lys
                                          1               5

aag aaa gtc gac gaa aac aac tca gtt ctc gcg acc aat cgc aag gcc   163
Lys Lys Val Asp Glu Asn Asn Ser Val Leu Ala Thr Asn Arg Lys Ala
                 10                  15                  20

cgc cat gac tac cac atc att gat acg tgg gag gcg ggc gtg gtg ctc   211
Arg His Asp Tyr His Ile Ile Asp Thr Trp Glu Ala Gly Val Val Leu
             25                  30                  35

tta ggc acc gaa atc aaa tca ctg cgc gaa ggt aag gta tcc ctc gtg   259
Leu Gly Thr Glu Ile Lys Ser Leu Arg Glu Gly Lys Val Ser Leu Val
         40                  45                  50

gat tcc ttt gcc acc att gat aac gga gaa atc tgg ctt cag cat ctc   307
Asp Ser Phe Ala Thr Ile Asp Asn Gly Glu Ile Trp Leu Gln His Leu
     55                  60                  65

cac atc ccg cag tat tcc atg ggc tcc tgg aca aac cac acg ccc aag   355
His Ile Pro Gln Tyr Ser Met Gly Ser Trp Thr Asn His Thr Pro Lys
 70                  75                  80                  85

cgc acc cgc aaa ctt ttg ctg cac cgc aac gag att gat tcc ctg atg   403
Arg Thr Arg Lys Leu Leu Leu His Arg Asn Glu Ile Asp Ser Leu Met
                 90                  95                 100

ggt aaa gtc cgc gac ggc aac cgc acg ttg gtt ccg ctc aag ctt tac   451
Gly Lys Val Arg Asp Gly Asn Arg Thr Leu Val Pro Leu Lys Leu Tyr
            105                 110                 115

ctc aaa aac ggt cgc gtc aaa ctc gaa ctc gga ctc gca caa ggt aag   499
Leu Lys Asn Gly Arg Val Lys Leu Glu Leu Gly Leu Ala Gln Gly Lys
        120                 125                 130
```

```
cag gat tac gac aag cgc caa gat atc aag cgt cgc acc gaa gaa cgc   547
Gln Asp Tyr Asp Lys Arg Gln Asp Ile Lys Arg Arg Thr Glu Glu Arg
    135                 140                 145

gaa gtc acc cgt gag ctc ggc cgt cgc att aag gga atc aac gcg       592
Glu Val Thr Arg Glu Leu Gly Arg Arg Ile Lys Gly Ile Asn Ala
150                 155                 160

taaatgagta ttcacatcgc aaa                                        615
```

<210> 1550
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 1550

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Met Ala Lys Lys Lys Lys Lys Val Asp Glu Asn Asn Ser Val Leu Ala
  1               5                  10                  15

Thr Asn Arg Lys Ala Arg His Asp Tyr His Ile Ile Asp Thr Trp Glu
             20                  25                  30

Ala Gly Val Val Leu Leu Gly Thr Glu Ile Lys Ser Leu Arg Glu Gly
         35                  40                  45

Lys Val Ser Leu Val Asp Ser Phe Ala Thr Ile Asp Asn Gly Glu Ile
     50                  55                  60

Trp Leu Gln His Leu His Ile Pro Gln Tyr Ser Met Gly Ser Trp Thr
 65                  70                  75                  80

Asn His Thr Pro Lys Arg Thr Arg Lys Leu Leu Leu His Arg Asn Glu
                 85                  90                  95

Ile Asp Ser Leu Met Gly Lys Val Arg Asp Gly Asn Arg Thr Leu Val
            100                 105                 110

Pro Leu Lys Leu Tyr Leu Lys Asn Gly Arg Val Lys Leu Glu Leu Gly
        115                 120                 125

Leu Ala Gln Gly Lys Gln Asp Tyr Asp Lys Arg Gln Asp Ile Lys Arg
    130                 135                 140

Arg Thr Glu Glu Arg Glu Val Thr Arg Glu Leu Gly Arg Arg Ile Lys
145                 150                 155                 160

Gly Ile Asn Ala
```

<210> 1551
<211> 432
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(409)
<223> RXA00015

<400> 1551
aagacgcaca gaagctacac acatagctac atcgtcagca ccaaagccgg aacaagaact 60

acagcaaccg acgacactca acgagcgcga cctccaagac atg att gat atg tgc 115
Met Ile Asp Met Cys
1 5

acc act cct cga caa gag atc atg atc cgc gag caa ttt aag gag atc 163
Thr Thr Pro Arg Gln Glu Ile Met Ile Arg Glu Gln Phe Lys Glu Ile
10 15 20

aac aac ggt agg gtt gta cct cat tac gat cag ctt gaa cag ctc gca 211
Asn Asn Gly Arg Val Val Pro His Tyr Asp Gln Leu Glu Gln Leu Ala
25 30 35

gag att ttt tca act aaa gac tca atc gac atg gtc aac gag ata ctc 259
Glu Ile Phe Ser Thr Lys Asp Ser Ile Asp Met Val Asn Glu Ile Leu
40 45 50

aat cgc gat acg gat ttt ctc agt aat gaa ggc aca att ttt atg gaa 307
Asn Arg Asp Thr Asp Phe Leu Ser Asn Glu Gly Thr Ile Phe Met Glu
55 60 65

tac att ttc aac ggt gga ttc cat acg gac aac ggc tat caa ccg ttg 355
Tyr Ile Phe Asn Gly Gly Phe His Thr Asp Asn Gly Tyr Gln Pro Leu
70 75 80 85

tcc tat gca tat gtt gaa cga ggc tta gcg atc cgc cct cca cgc ata 403
Ser Tyr Ala Tyr Val Glu Arg Gly Leu Ala Ile Arg Pro Pro Arg Ile
90 95 100

gtg ctc tagatatgac acaaatcggt att 432
Val Leu

<210> 1552
<211> 103
<212> PRT
<213> Corynebacterium glutamicum

<400> 1552
Met Ile Asp Met Cys Thr Thr Pro Arg Gln Glu Ile Met Ile Arg Glu
1 5 10 15

Gln Phe Lys Glu Ile Asn Asn Gly Arg Val Val Pro His Tyr Asp Gln
20 25 30

Leu Glu Gln Leu Ala Glu Ile Phe Ser Thr Lys Asp Ser Ile Asp Met
35 40 45

Val Asn Glu Ile Leu Asn Arg Asp Thr Asp Phe Leu Ser Asn Glu Gly
50 55 60

Thr Ile Phe Met Glu Tyr Ile Phe Asn Gly Gly Phe His Thr Asp Asn
65 70 75 80

Gly Tyr Gln Pro Leu Ser Tyr Ala Tyr Val Glu Arg Gly Leu Ala Ile
85 90 95

Arg Pro Pro Arg Ile Val Leu

100

<210> 1553
<211> 1422
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1399)
<223> RXA00018

<400> 1553
caacccgccc cacaaacaca tacaattaac ttctatattt agtaaataaa taactagtat 60

ttttaatgac ttacaaatat caagaaagaa tctattcctt atg tcc gca tta tct 115
Met Ser Ala Leu Ser
1 5

aga ccg cac aag atc gcc acc ggc gtt gct gtc gca act ctt acc ctc 163
Arg Pro His Lys Ile Ala Thr Gly Val Ala Val Ala Thr Leu Thr Leu
10 15 20

acc ttg tgt acc tct gct gcc ggc gtt gtc cat gca gcg caa caa tcc 211
Thr Leu Cys Thr Ser Ala Ala Gly Val Val His Ala Ala Gln Gln Ser
25 30 35

atc agc ggt cca gaa tcc tcc tgt gct ttt aat caa cag cgt tgg gat 259
Ile Ser Gly Pro Glu Ser Ser Cys Ala Phe Asn Gln Gln Arg Trp Asp
40 45 50

gac agc aaa gtt aag ctt gac gac acc atc gct acg gcc aaa aac tca 307
Asp Ser Lys Val Lys Leu Asp Asp Thr Ile Ala Thr Ala Lys Asn Ser
55 60 65

ttg gta caa aca ggc gaa ctg cac cgc aac gaa cag gat cta ctt act 355
Leu Val Gln Thr Gly Glu Leu His Arg Asn Glu Gln Asp Leu Leu Thr
70 75 80 85

ggc tat ctt ttc cag caa ccg cac agc agc aat tac ctt gca ctc aac 403
Gly Tyr Leu Phe Gln Gln Pro His Ser Ser Asn Tyr Leu Ala Leu Asn
90 95 100

aac gct tat gcc gat gcc gta gca atc aaa gac agc ttt gtc cgc cca 451
Asn Ala Tyr Ala Asp Ala Val Ala Ile Lys Asp Ser Phe Val Arg Pro
105 110 115

aca tgt gac ggt tct aaa gag tcc aag att gcc agc gaa cac gcc gtg 499
Thr Cys Asp Gly Ser Lys Glu Ser Lys Ile Ala Ser Glu His Ala Val
120 125 130

tct gag gtt gtg ggt gca gtg aat gta ctc gcc cga gca caa aaa gcg 547
Ser Glu Val Val Gly Ala Val Asn Val Leu Ala Arg Ala Gln Lys Ala
135 140 145

ctg cag att aac tcc gac acc tac gaa cag caa cgt cgt tgt gat gcc 595
Leu Gln Ile Asn Ser Asp Thr Tyr Glu Gln Gln Arg Arg Cys Asp Ala
150 155 160 165

ctt cgt cta gca agc cga gat gaa tca gat gtt ctt atg cgc att gat 643

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Leu Arg Leu Ala Ser Arg Asp Glu Ser Asp Val Leu Met Arg Ile Asp
                170                 175                 180

cgc acc atg ctg cag ctt cgt cgc aca cta gct gac att gac cag gcg   691
Arg Thr Met Leu Gln Leu Arg Arg Thr Leu Ala Asp Ile Asp Gln Ala
            185                 190                 195

tcc aca gac att cgc gat att cgg gct caa aca aca agc ttt gaa cgt   739
Ser Thr Asp Ile Arg Asp Ile Arg Ala Gln Thr Thr Ser Phe Glu Arg
        200                 205                 210

gat ctt gcc cgc gag caa aaa gag gcc gac gca gca gca cgt gct caa   787
Asp Leu Ala Arg Glu Gln Lys Glu Ala Asp Ala Ala Ala Arg Ala Gln
    215                 220                 225

gct gta gac act tcg acc aca cca aca tca agc aca gaa gat cgt gtc   835
Ala Val Asp Thr Ser Thr Thr Pro Thr Ser Ser Thr Glu Asp Arg Val
230                 235                 240                 245

aac gac att ctt aaa gag tcc cgt acc gat cac agt ggc gac agt tac   883
Asn Asp Ile Leu Lys Glu Ser Arg Thr Asp His Ser Gly Asp Ser Tyr
                250                 255                 260

acg cgc tca acg aca acg agc gca caa agc act gag ccg gat tct gca   931
Thr Arg Ser Thr Thr Thr Ser Ala Gln Ser Thr Glu Pro Asp Ser Ala
            265                 270                 275

acc aac acc tca tat ctg tca cgt cgt ctc gac agc ctg gaa cgc agt   979
Thr Asn Thr Ser Tyr Leu Ser Arg Arg Leu Asp Ser Leu Glu Arg Ser
        280                 285                 290

gcg cag cat att gat ctc aat acc cag tgc gac aac ctc gat gat ctt   1027
Ala Gln His Ile Asp Leu Asn Thr Gln Cys Asp Asn Leu Asp Asp Leu
    295                 300                 305

cgt gaa ctc acc aac aat gac acg cgt gat cac acc ggc tcc gtc att   1075
Arg Glu Leu Thr Asn Asn Asp Thr Arg Asp His Thr Gly Ser Val Ile
310                 315                 320                 325

tcc att gcc gat caa ctc aca gac atc acc aat gaa atc aat gaa tta   1123
Ser Ile Ala Asp Gln Leu Thr Asp Ile Thr Asn Glu Ile Asn Glu Leu
                330                 335                 340

cgc gat agc act ttt gcc acc aga gac agt gcc caa caa gca cag gat   1171
Arg Asp Ser Thr Phe Ala Thr Arg Asp Ser Ala Gln Gln Ala Gln Asp
            345                 350                 355

cag gta att gct caa cgt gaa gaa ctg caa cga gca aag gaa gca cga   1219
Gln Val Ile Ala Gln Arg Glu Glu Leu Gln Arg Ala Lys Glu Ala Arg
        360                 365                 370

cta gaa gaa cag cga ctc gcc aaa gaa gca gaa gag ggc gct cgc aac   1267
Leu Glu Glu Gln Arg Leu Ala Lys Glu Ala Glu Glu Gly Ala Arg Asn
    375                 380                 385

gca gca att cag gaa cgt gac gcg gcc gaa gca gca ctg cgt gaa gca   1315
Ala Ala Ile Gln Glu Arg Asp Ala Ala Glu Ala Ala Leu Arg Glu Ala
390                 395                 400                 405

caa gac ctc ctc agt cgc ctc gat gac aca ggc aac gca acc agt gat   1363
Gln Asp Leu Leu Ser Arg Leu Asp Asp Thr Gly Asn Ala Thr Ser Asp
```

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                410                 415                 420

gac aca gca gcg cta gta gac ggt ctt ctc aat aac taacaatcag        1409
Asp Thr Ala Ala Leu Val Asp Gly Leu Leu Asn Asn
            425                 430

caacaccgct cac                                                   1422


<210> 1554
<211> 433
<212> PRT
<213> Corynebacterium glutamicum

<400> 1554
Met Ser Ala Leu Ser Arg Pro His Lys Ile Ala Thr Gly Val Ala Val
  1               5                  10                  15

Ala Thr Leu Thr Leu Thr Leu Cys Thr Ser Ala Ala Gly Val Val His
             20                  25                  30

Ala Ala Gln Gln Ser Ile Ser Gly Pro Glu Ser Ser Cys Ala Phe Asn
         35                  40                  45

Gln Gln Arg Trp Asp Asp Ser Lys Val Lys Leu Asp Asp Thr Ile Ala
     50                  55                  60

Thr Ala Lys Asn Ser Leu Val Gln Thr Gly Glu Leu His Arg Asn Glu
 65                  70                  75                  80

Gln Asp Leu Leu Thr Gly Tyr Leu Phe Gln Gln Pro His Ser Ser Asn
                 85                  90                  95

Tyr Leu Ala Leu Asn Asn Ala Tyr Ala Asp Ala Val Ala Ile Lys Asp
            100                 105                 110

Ser Phe Val Arg Pro Thr Cys Asp Gly Ser Lys Glu Ser Lys Ile Ala
        115                 120                 125

Ser Glu His Ala Val Ser Glu Val Val Gly Ala Val Asn Val Leu Ala
    130                 135                 140

Arg Ala Gln Lys Ala Leu Gln Ile Asn Ser Asp Thr Tyr Glu Gln Gln
145                 150                 155                 160

Arg Arg Cys Asp Ala Leu Arg Leu Ala Ser Arg Asp Glu Ser Asp Val
                165                 170                 175

Leu Met Arg Ile Asp Arg Thr Met Leu Gln Leu Arg Arg Thr Leu Ala
            180                 185                 190

Asp Ile Asp Gln Ala Ser Thr Asp Ile Arg Asp Ile Arg Ala Gln Thr
        195                 200                 205

Thr Ser Phe Glu Arg Asp Leu Ala Arg Glu Gln Lys Glu Ala Asp Ala
    210                 215                 220

Ala Ala Arg Ala Gln Ala Val Asp Thr Ser Thr Thr Pro Thr Ser Ser
225                 230                 235                 240

Thr Glu Asp Arg Val Asn Asp Ile Leu Lys Glu Ser Arg Thr Asp His
```

```
                245                 250                 255

Ser Gly Asp Ser Tyr Thr Arg Ser Thr Thr Thr Ser Ala Gln Ser Thr
            260                 265                 270

Glu Pro Asp Ser Ala Thr Asn Thr Ser Tyr Leu Ser Arg Arg Leu Asp
        275                 280                 285

Ser Leu Glu Arg Ser Ala Gln His Ile Asp Leu Asn Thr Gln Cys Asp
    290                 295                 300

Asn Leu Asp Asp Leu Arg Glu Leu Thr Asn Asn Asp Thr Arg Asp His
305                 310                 315                 320

Thr Gly Ser Val Ile Ser Ile Ala Asp Gln Leu Thr Asp Ile Thr Asn
                325                 330                 335

Glu Ile Asn Glu Leu Arg Asp Ser Thr Phe Ala Thr Arg Asp Ser Ala
            340                 345                 350

Gln Gln Ala Gln Asp Gln Val Ile Ala Gln Arg Glu Glu Leu Gln Arg
        355                 360                 365

Ala Lys Glu Ala Arg Leu Glu Glu Gln Arg Leu Ala Lys Glu Ala Glu
    370                 375                 380

Glu Gly Ala Arg Asn Ala Ala Ile Gln Glu Arg Asp Ala Ala Glu Ala
385                 390                 395                 400

Ala Leu Arg Glu Ala Gln Asp Leu Leu Ser Arg Leu Asp Asp Thr Gly
                405                 410                 415

Asn Ala Thr Ser Asp Asp Thr Ala Ala Leu Val Asp Gly Leu Leu Asn
            420                 425                 430

Asn
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<210> 1555
<211> 903
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(880)
<223> RXA00020

<400> 1555
taggagaact acctttcttg ctggtgttac ctagctttaa gtttgttaga gtaattaatg 60

aataactaag taatgtaagt aaagggactt ttaaataact atg act gtg acc acc 115
                                            Met Thr Val Thr Thr
                                              1   5

gca caa cga atc gct gac gaa ttt caa cgt ggc att agt atc ggc ccg 163
Ala Gln Arg Ile Ala Asp Glu Phe Gln Arg Gly Ile Ser Ile Gly Pro
                 10   15   20

tgg gat ctg tgc gaa gta cca gca ggc gat gac tat tta gag cac acc 211

```
Trp Asp Leu Cys Glu Val Pro Ala Gly Asp Asp Tyr Leu Glu His Thr
             25                  30                  35

acc aag gtc agg cga cgc cac agc acg gct gta gag att cac act gac   259
Thr Lys Val Arg Arg Arg His Ser Thr Ala Val Glu Ile His Thr Asp
         40                  45                  50

tct ttg atc att tgt gcg cct gaa ggc agt acg tac agc cac aac cgc   307
Ser Leu Ile Ile Cys Ala Pro Glu Gly Ser Thr Tyr Ser His Asn Arg
     55                  60                  65

act aag gct ggt ctt gcg tcc acg ggc aca gtc act gtg cca gtg aag   355
Thr Lys Ala Gly Leu Ala Ser Thr Gly Thr Val Thr Val Pro Val Lys
 70                  75                  80                  85

ggg ctt tct gag cct gtg aag ctt agt ctc aat ctt ctt gct gat tat   403
Gly Leu Ser Glu Pro Val Lys Leu Ser Leu Asn Leu Leu Ala Asp Tyr
                 90                  95                 100

gga aac tcc ttt gac act gtg cac gac gat ctg tgg caa cga gag ctg   451
Gly Asn Ser Phe Asp Thr Val His Asp Asp Leu Trp Gln Arg Glu Leu
            105                 110                 115

cgt gag cag acg cgg ggg cag tta ctc aca ctt aat gca gtc tcc ggt   499
Arg Glu Gln Thr Arg Gly Gln Leu Leu Thr Leu Asn Ala Val Ser Gly
        120                 125                 130

ctt ggg gat gac agc gtg gcg att atg ggc acg cca tgg ggc gat ggt   547
Leu Gly Asp Asp Ser Val Ala Ile Met Gly Thr Pro Trp Gly Asp Gly
    135                 140                 145

ctc acc ggg gag gcc aac acc att aaa ggt cgt gag cat ttt gtc atg   595
Leu Thr Gly Glu Ala Asn Thr Ile Lys Gly Arg Glu His Phe Val Met
150                 155                 160                 165

tgg gct gca ggg tgc cgc ttt gaa gac ggt tat ggt cgt cac gca ctt   643
Trp Ala Ala Gly Cys Arg Phe Glu Asp Gly Tyr Gly Arg His Ala Leu
                170                 175                 180

cga gag gat cgc cat gtg cga cac cag gca cgt gcg ggt gag gat tcc   691
Arg Glu Asp Arg His Val Arg His Gln Ala Arg Ala Gly Glu Asp Ser
            185                 190                 195

act gca cat cac ggt tgg ttg ctt aaa ggc aca gtg ttc ggg aaa gaa   739
Thr Ala His His Gly Trp Leu Leu Lys Gly Thr Val Phe Gly Lys Glu
        200                 205                 210

ctc acc ggt gat gct gtg acg gca gcc atg aca gtt ttt agt gat gtg   787
Leu Thr Gly Asp Ala Val Thr Ala Ala Met Thr Val Phe Ser Asp Val
    215                 220                 225

gtg gtc act gtc gat gag ggg cgt atc cct ggc atg aaa tca gga caa   835
Val Val Thr Val Asp Glu Gly Arg Ile Pro Gly Met Lys Ser Gly Gln
230                 235                 240                 245

ccg ttt tct atg gca acc cgt tta cgc gca tca tct gcg cct gtg       880
Pro Phe Ser Met Ala Thr Arg Leu Arg Ala Ser Ser Ala Pro Val
                250                 255                 260

tagagacttt ttcagacctt aac                                        903
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<210> 1556
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

<400> 1556
Met Thr Val Thr Thr Ala Gln Arg Ile Ala Asp Glu Phe Gln Arg Gly
1 5 10 15

Ile Ser Ile Gly Pro Trp Asp Leu Cys Glu Val Pro Ala Gly Asp Asp
20 25 30

Tyr Leu Glu His Thr Thr Lys Val Arg Arg Arg His Ser Thr Ala Val
35 40 45

Glu Ile His Thr Asp Ser Leu Ile Ile Cys Ala Pro Glu Gly Ser Thr
50 55 60

Tyr Ser His Asn Arg Thr Lys Ala Gly Leu Ala Ser Thr Gly Thr Val
65 70 75 80

Thr Val Pro Val Lys Gly Leu Ser Glu Pro Val Lys Leu Ser Leu Asn
85 90 95

Leu Leu Ala Asp Tyr Gly Asn Ser Phe Asp Thr Val His Asp Asp Leu
100 105 110

Trp Gln Arg Glu Leu Arg Glu Gln Thr Arg Gly Gln Leu Leu Thr Leu
115 120 125

Asn Ala Val Ser Gly Leu Gly Asp Asp Ser Val Ala Ile Met Gly Thr
130 135 140

Pro Trp Gly Asp Gly Leu Thr Gly Glu Ala Asn Thr Ile Lys Gly Arg
145 150 155 160

Glu His Phe Val Met Trp Ala Ala Gly Cys Arg Phe Glu Asp Gly Tyr
165 170 175

Gly Arg His Ala Leu Arg Glu Asp Arg His Val Arg His Gln Ala Arg
180 185 190

Ala Gly Glu Asp Ser Thr Ala His His Gly Trp Leu Leu Lys Gly Thr
195 200 205

Val Phe Gly Lys Glu Leu Thr Gly Asp Ala Val Thr Ala Ala Met Thr
210 215 220

Val Phe Ser Asp Val Val Val Thr Val Asp Glu Gly Arg Ile Pro Gly
225 230 235 240

Met Lys Ser Gly Gln Pro Phe Ser Met Ala Thr Arg Leu Arg Ala Ser
245 250 255

Ser Ala Pro Val
260

<210> 1557
<211> 1896

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1873)
<223> RXA00021

<400> 1557
aaaagcaact cacttcgtgc ttttttcacc gaccccggct gtgtggatgc cacccactta 60

caccgcacaa tcgaaaataa aagtaaagga tgttcacctt atg tct gac acc aca 115
Met Ser Asp Thr Thr
1 5

gac agc cac gac cca gca acc tcc cct aca gtc gat tca gcc gca tcc 163
Asp Ser His Asp Pro Ala Thr Ser Pro Thr Val Asp Ser Ala Ala Ser
10 15 20

ggt act tct gac ccc aac cag caa ccc aag aag aaa ttc acc atc att 211
Gly Thr Ser Asp Pro Asn Gln Gln Pro Lys Lys Lys Phe Thr Ile Ile
25 30 35

aag cag gtg aac atg att gcg cgt act gcc att gat gac tgc att aat 259
Lys Gln Val Asn Met Ile Ala Arg Thr Ala Ile Asp Asp Cys Ile Asn
40 45 50

cga cta ggc cca gat gtt gtc acc atg tcc agc gaa gac att gct gat 307
Arg Leu Gly Pro Asp Val Val Thr Met Ser Ser Glu Asp Ile Ala Asp
55 60 65

caa gtg gtc aac tcc att aac gtt gct att gcc aga gaa aac aca cgt 355
Gln Val Val Asn Ser Ile Asn Val Ala Ile Ala Arg Glu Asn Thr Arg
70 75 80 85

gcc caa gat gcc aat gct gcg gtg cgt tac aca cct atc ttt aag ctc 403
Ala Gln Asp Ala Asn Ala Ala Val Arg Tyr Thr Pro Ile Phe Lys Leu
90 95 100

gat ttc tcc cat gtc gct gtc ctt atg cgc aga ctg cat gtg att atc 451
Asp Phe Ser His Val Ala Val Leu Met Arg Arg Leu His Val Ile Ile
105 110 115

aac atc gcg cca tcg cat aac tct gat cct gac agc gat atg ttg gct 499
Asn Ile Ala Pro Ser His Asn Ser Asp Pro Asp Ser Asp Met Leu Ala
120 125 130

att tac gac ccc aac cca cgc agc gag cat tac ggg atc tat cgc acc 547
Ile Tyr Asp Pro Asn Pro Arg Ser Glu His Tyr Gly Ile Tyr Arg Thr
135 140 145

tca gag gct gaa ata cgc cgc gta gcc cgt gaa tac tgc cct gac ctc 595
Ser Glu Ala Glu Ile Arg Arg Val Ala Arg Glu Tyr Cys Pro Asp Leu
150 155 160 165

acc tca gcg cag ttt aga gaa ctg cag atg gca ctc tca gat gct gca 643
Thr Ser Ala Gln Phe Arg Glu Leu Gln Met Ala Leu Ser Asp Ala Ala
170 175 180

cct cgt aaa gtc cgc cac aag cag cgt gac ttg att ccc gtg aaa aac 691
Pro Arg Lys Val Arg His Lys Gln Arg Asp Leu Ile Pro Val Lys Asn

```
                185                 190                 195

ggc atc ttt aat tac tcg act aaa caa cta gaa ccg ttt tct caa gag   739
Gly Ile Phe Asn Tyr Ser Thr Lys Gln Leu Glu Pro Phe Ser Gln Glu
        200                 205                 210

ttt gtc ttt ctt gct aaa tct gca gtg aac tac aac cca aat gca caa   787
Phe Val Phe Leu Ala Lys Ser Ala Val Asn Tyr Asn Pro Asn Ala Gln
    215                 220                 225

aac cct gtc atc act cat ccc cag gat ggc tct gtc tgg gat gtt gaa   835
Asn Pro Val Ile Thr His Pro Gln Asp Gly Ser Val Trp Asp Val Glu
230                 235                 240                 245

tca tgg atg aac gat ctc tcc gat gac cct gaa gtc gtt aac ctg ctg   883
Ser Trp Met Asn Asp Leu Ser Asp Asp Pro Glu Val Val Asn Leu Leu
                250                 255                 260

tgg gag att atc ggc gct atc gtg cgc ccc tat gtg tcc tgg aac aag   931
Trp Glu Ile Ile Gly Ala Ile Val Arg Pro Tyr Val Ser Trp Asn Lys
            265                 270                 275

tct gcc tgg ttc tac tca gag gcc ggc aac aac ggt aaa ggc acg ctc   979
Ser Ala Trp Phe Tyr Ser Glu Ala Gly Asn Asn Gly Lys Gly Thr Leu
        280                 285                 290

gtt gag ctc atg cgc aac atc ttg ggc gca gag gcc tat acc agt atc  1027
Val Glu Leu Met Arg Asn Ile Leu Gly Ala Glu Ala Tyr Thr Ser Ile
    295                 300                 305

cag ctc tcg gac ttc tct aaa gag ttc cac ctt gaa tca ctg act cgt  1075
Gln Leu Ser Asp Phe Ser Lys Glu Phe His Leu Glu Ser Leu Thr Arg
310                 315                 320                 325

gca caa gca atc ctt gtt gat gag aac gat gtc ggc gcc ttc tta gaa  1123
Ala Gln Ala Ile Leu Val Asp Glu Asn Asp Val Gly Ala Phe Leu Glu
                330                 335                 340

aag tca gca aac ctt aaa gcg att gtc acc aat gac gtc atc tcc att  1171
Lys Ser Ala Asn Leu Lys Ala Ile Val Thr Asn Asp Val Ile Ser Ile
            345                 350                 355

aac cgc aag cac aaa acc atg ctc agc tat cag ttt tat ggc ttt atg  1219
Asn Arg Lys His Lys Thr Met Leu Ser Tyr Gln Phe Tyr Gly Phe Met
        360                 365                 370

gtg cag tgt att aac ggc ttc ccc aag gtc aaa gac cag tcg gag tca  1267
Val Gln Cys Ile Asn Gly Phe Pro Lys Val Lys Asp Gln Ser Glu Ser
    375                 380                 385

ttt ttc agg cgc caa ctc ttt gtg ccg ttt gag aaa agc ttc acc ggt  1315
Phe Phe Arg Arg Gln Leu Phe Val Pro Phe Glu Lys Ser Phe Thr Gly
390                 395                 400                 405

gcc gag cgc aag tac atc aaa gac gac tac atg tcg cgc act gat gtc  1363
Ala Glu Arg Lys Tyr Ile Lys Asp Asp Tyr Met Ser Arg Thr Asp Val
                410                 415                 420

ctc gaa tat gta ctg cac cgc gta ctg cat atg aac tac gac aat ctc  1411
Leu Glu Tyr Val Leu His Arg Val Leu His Met Asn Tyr Asp Asn Leu
            425                 430                 435
```

```
tcc acc cct gct gca gct ctc gct gtg ctg gat gaa tac aaa gag ttt   1459
Ser Thr Pro Ala Ala Ala Leu Ala Val Leu Asp Glu Tyr Lys Glu Phe
        440                 445                 450

gtc gat cct gtg cgc gca ttc tgg aat gaa ttc agc gat caa ttt gtc   1507
Val Asp Pro Val Arg Ala Phe Trp Asn Glu Phe Ser Asp Gln Phe Val
    455                 460                 465

tgg gat ctt ctt ccc ctg caa ttc ctc tac gag ttt tat cgc aag tgg   1555
Trp Asp Leu Leu Pro Leu Gln Phe Leu Tyr Glu Phe Tyr Arg Lys Trp
470                 475                 480                 485

ttt gac cgt gac agc cca tcc ggg tct gtg ctc ggc aaa cgc agc ttc   1603
Phe Asp Arg Asp Ser Pro Ser Gly Ser Val Leu Gly Lys Arg Ser Phe
                490                 495                 500

att caa aaa atc acc acc atc gcc gtt gat agc ggt cag tgg gag tat   1651
Ile Gln Lys Ile Thr Thr Ile Ala Val Asp Ser Gly Gln Trp Glu Tyr
            505                 510                 515

ccg ctg aca gca cag cgt ccc ggt ggc gat atg gcc gtt cct gag cca   1699
Pro Leu Thr Ala Gln Arg Pro Gly Gly Asp Met Ala Val Pro Glu Pro
        520                 525                 530

tta gtc att gat tat gac ctc acc gag tgg caa aac gcc act gta cct   1747
Leu Val Ile Asp Tyr Asp Leu Thr Glu Trp Gln Asn Ala Thr Val Pro
    535                 540                 545

aaa ggt cac gtc aac aag ggg ctc cct cta cca ctc aag gct aat tat   1795
Lys Gly His Val Asn Lys Gly Leu Pro Leu Pro Leu Lys Ala Asn Tyr
550                 555                 560                 565

cga gga ctg ctc cgc aaa cct cta aca aca cct gct act ccc cct gca   1843
Arg Gly Leu Leu Arg Lys Pro Leu Thr Thr Pro Ala Thr Pro Pro Ala
                570                 575                 580

gcg ccg gtc aac ccc aca cca ccc acc cct taacaaccac aagaaagatt     1893
Ala Pro Val Asn Pro Thr Pro Pro Thr Pro
            585                 590

tat                                                               1896
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<210> 1558
<211> 591
<212> PRT
<213> Corynebacterium glutamicum

<400> 1558

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Met Ser Asp Thr Thr Asp Ser His Asp Pro Ala Thr Ser Pro Thr Val
  1               5                  10                  15

Asp Ser Ala Ala Ser Gly Thr Ser Asp Pro Asn Gln Gln Pro Lys Lys
             20                  25                  30

Lys Phe Thr Ile Ile Lys Gln Val Asn Met Ile Ala Arg Thr Ala Ile
         35                  40                  45

Asp Asp Cys Ile Asn Arg Leu Gly Pro Asp Val Val Thr Met Ser Ser
     50                  55                  60
```

```
Glu Asp Ile Ala Asp Gln Val Val Asn Ser Ile Asn Val Ala Ile Ala
 65                  70                  75                  80

Arg Glu Asn Thr Arg Ala Gln Asp Ala Asn Ala Ala Val Arg Tyr Thr
                 85                  90                  95

Pro Ile Phe Lys Leu Asp Phe Ser His Val Ala Val Leu Met Arg Arg
            100                 105                 110

Leu His Val Ile Ile Asn Ile Ala Pro Ser His Asn Ser Asp Pro Asp
        115                 120                 125

Ser Asp Met Leu Ala Ile Tyr Asp Pro Asn Pro Arg Ser Glu His Tyr
    130                 135                 140

Gly Ile Tyr Arg Thr Ser Glu Ala Glu Ile Arg Arg Val Ala Arg Glu
145                 150                 155                 160

Tyr Cys Pro Asp Leu Thr Ser Ala Gln Phe Arg Glu Leu Gln Met Ala
                165                 170                 175

Leu Ser Asp Ala Ala Pro Arg Lys Val Arg His Lys Gln Arg Asp Leu
            180                 185                 190

Ile Pro Val Lys Asn Gly Ile Phe Asn Tyr Ser Thr Lys Gln Leu Glu
        195                 200                 205

Pro Phe Ser Gln Glu Phe Val Phe Leu Ala Lys Ser Ala Val Asn Tyr
    210                 215                 220

Asn Pro Asn Ala Gln Asn Pro Val Ile Thr His Pro Gln Asp Gly Ser
225                 230                 235                 240

Val Trp Asp Val Glu Ser Trp Met Asn Asp Leu Ser Asp Asp Pro Glu
                245                 250                 255

Val Val Asn Leu Leu Trp Glu Ile Ile Gly Ala Ile Val Arg Pro Tyr
            260                 265                 270

Val Ser Trp Asn Lys Ser Ala Trp Phe Tyr Ser Glu Ala Gly Asn Asn
        275                 280                 285

Gly Lys Gly Thr Leu Val Glu Leu Met Arg Asn Ile Leu Gly Ala Glu
    290                 295                 300

Ala Tyr Thr Ser Ile Gln Leu Ser Asp Phe Ser Lys Glu Phe His Leu
305                 310                 315                 320

Glu Ser Leu Thr Arg Ala Gln Ala Ile Leu Val Asp Glu Asn Asp Val
                325                 330                 335

Gly Ala Phe Leu Glu Lys Ser Ala Asn Leu Lys Ala Ile Val Thr Asn
            340                 345                 350

Asp Val Ile Ser Ile Asn Arg Lys His Lys Thr Met Leu Ser Tyr Gln
        355                 360                 365

Phe Tyr Gly Phe Met Val Gln Cys Ile Asn Gly Phe Pro Lys Val Lys
    370                 375                 380
```

```
Asp Gln Ser Glu Ser Phe Phe Arg Arg Gln Leu Phe Val Pro Phe Glu
385                 390                 395                 400

Lys Ser Phe Thr Gly Ala Glu Arg Lys Tyr Ile Lys Asp Asp Tyr Met
                405                 410                 415

Ser Arg Thr Asp Val Leu Glu Tyr Val Leu His Arg Val Leu His Met
            420                 425                 430

Asn Tyr Asp Asn Leu Ser Thr Pro Ala Ala Ala Leu Ala Val Leu Asp
        435                 440                 445

Glu Tyr Lys Glu Phe Val Asp Pro Val Arg Ala Phe Trp Asn Glu Phe
    450                 455                 460

Ser Asp Gln Phe Val Trp Asp Leu Leu Pro Leu Gln Phe Leu Tyr Glu
465                 470                 475                 480

Phe Tyr Arg Lys Trp Phe Asp Arg Asp Ser Pro Ser Gly Ser Val Leu
                485                 490                 495

Gly Lys Arg Ser Phe Ile Gln Lys Ile Thr Thr Ile Ala Val Asp Ser
            500                 505                 510

Gly Gln Trp Glu Tyr Pro Leu Thr Ala Gln Arg Pro Gly Gly Asp Met
        515                 520                 525

Ala Val Pro Glu Pro Leu Val Ile Asp Tyr Asp Leu Thr Glu Trp Gln
    530                 535                 540

Asn Ala Thr Val Pro Lys Gly His Val Asn Lys Gly Leu Pro Leu Pro
545                 550                 555                 560

Leu Lys Ala Asn Tyr Arg Gly Leu Leu Arg Lys Pro Leu Thr Thr Pro
                565                 570                 575

Ala Thr Pro Pro Ala Ala Pro Val Asn Pro Thr Pro Pro Thr Pro
            580                 585                 590
```

CCA GTG TCC GAC GTC AGC

<210> 1559
<211> 1560
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1537)
<223> RXA00025

<400> 1559

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taaatttctc aatggtgtgg aaacacttgg aaacaagctg cccacaccat ttacgctttt 60

cttgatactt ttcctgatca cggcgctggc ttcatcgatc atg gcg tgg atg aac   115
                                              Met Ala Trp Met Asn
                                                1               5

gta tcc gtg att gtt cca ggc tct gat gag gaa cta ttt gta aaa ggc   163
Val Ser Val Ile Val Pro Gly Ser Asp Glu Glu Leu Phe Val Lys Gly
                 10                  15                  20
```

```
ctg ttc acc ggt gaa ggc cta acc tgg ttg act acg aat ctc ggg gca   211
Leu Phe Thr Gly Glu Gly Leu Thr Trp Leu Thr Thr Asn Leu Gly Ala
            25                  30                  35

aac tac atc ggg ttc ccg ccg ttg ctc acc gtg ttg cca att ctg ttg   259
Asn Tyr Ile Gly Phe Pro Pro Leu Leu Thr Val Leu Pro Ile Leu Leu
        40                  45                  50

gca gtg ggt gtt gct gaa cgt tcc ggc atg ttg gct gcg ctg att agg   307
Ala Val Gly Val Ala Glu Arg Ser Gly Met Leu Ala Ala Leu Ile Arg
    55                  60                  65

aaa ctt ttt ggt tcg gcg aaa aag atc gtt ttg cca tat gca gtc ggt   355
Lys Leu Phe Gly Ser Ala Lys Lys Ile Val Leu Pro Tyr Ala Val Gly
70                  75                  80                  85

gtg att ggc gtg acc gcg tcg atc atg gcg gac gct gcc ttc gtg gtg   403
Val Ile Gly Val Thr Ala Ser Ile Met Ala Asp Ala Ala Phe Val Val
                90                  95                  100

gtg cca cct ttg gcc gcg atg gtg ttt aaa gct gct ggt cgg cac cct   451
Val Pro Pro Leu Ala Ala Met Val Phe Lys Ala Ala Gly Arg His Pro
            105                 110                 115

gtg gct ggg cta ttg ggt tcg ttt gca gct gtg ggt gca gga tat tcc   499
Val Ala Gly Leu Leu Gly Ser Phe Ala Ala Val Gly Ala Gly Tyr Ser
        120                 125                 130

aca gcg att gtg ccc acc agc ctt gat gca ctt ttt gcg gga att acc   547
Thr Ala Ile Val Pro Thr Ser Leu Asp Ala Leu Phe Ala Gly Ile Thr
    135                 140                 145

aac gcc gtg atg gag aca ctt cca ggc att gcg aca act gaa gtc aat   595
Asn Ala Val Met Glu Thr Leu Pro Gly Ile Ala Thr Thr Glu Val Asn
150                 155                 160                 165

ccg gtt tct aac tat tac ttc aat att gca tcc tcg att gtg ttg ggt   643
Pro Val Ser Asn Tyr Tyr Phe Asn Ile Ala Ser Ser Ile Val Leu Gly
                170                 175                 180

ctg tta tgt ggt ttc ctc att gat aag gtg ctg gaa cct cgg atg tgg   691
Leu Leu Cys Gly Phe Leu Ile Asp Lys Val Leu Glu Pro Arg Met Trp
            185                 190                 195

cgt cag aaa atc gct acg gag tat gca gaa agc att gaa ccc acc agc   739
Arg Gln Lys Ile Ala Thr Glu Tyr Ala Glu Ser Ile Glu Pro Thr Ser
        200                 205                 210

gca gca gat gat gag gaa atc tct gca acc cta acc gca cag gaa aac   787
Ala Ala Asp Asp Glu Glu Ile Ser Ala Thr Leu Thr Ala Gln Glu Asn
    215                 220                 225

cgc gcg ctg aca att tcc atg tgg acc acc ctg gcg acg gcc atc atc   835
Arg Ala Leu Thr Ile Ser Met Trp Thr Thr Leu Ala Thr Ala Ile Ile
230                 235                 240                 245

gtg ctg gtt gtg gtg ctg att ccg gga tcc cca tgg aga aat gag gat   883
Val Leu Val Val Val Leu Ile Pro Gly Ser Pro Trp Arg Asn Glu Asp
                250                 255                 260

ggt gga ttc ttg cct acc tcg cca ctg ctg agc tct gtg gtg ttt att   931
```

```
Gly Gly Phe Leu Pro Thr Ser Pro Leu Leu Ser Ser Val Val Phe Ile
            265                 270                 275

gta ttt ttg ttt ttc atg gtg atg ggc ctg gcc tac ggc atg gtg gtg   979
Val Phe Leu Phe Phe Met Val Met Gly Leu Ala Tyr Gly Met Val Val
        280                 285                 290

ggc acg atc aag aac atg gat gat gtc gtg aac atg atg ggc gaa gca   1027
Gly Thr Ile Lys Asn Met Asp Asp Val Val Asn Met Met Gly Glu Ala
    295                 300                 305

atc aag gac atg att ggt ttc ttg gtt ttg gcc ttc att ttg gga cag   1075
Ile Lys Asp Met Ile Gly Phe Leu Val Leu Ala Phe Ile Leu Gly Gln
310                 315                 320                 325

ttt gtg gcg ctg ttt aac tgg acg ggc atc ggt acc tgg act gct gtt   1123
Phe Val Ala Leu Phe Asn Trp Thr Gly Ile Gly Thr Trp Thr Ala Val
                330                 335                 340

cag ggt gct gcg gga ttg gaa gcg atc ggg ctt acc gga ttc cct gcg   1171
Gln Gly Ala Ala Gly Leu Glu Ala Ile Gly Leu Thr Gly Phe Pro Ala
            345                 350                 355

atc att gca ttt att att ttg gcg tca tgt ttg aac ctg ctg att att   1219
Ile Ile Ala Phe Ile Ile Leu Ala Ser Cys Leu Asn Leu Leu Ile Ile
        360                 365                 370

tcc ggc tct gcg atg tgg acg ctg atg gct gcg gtg ttc gtc ccg atg   1267
Ser Gly Ser Ala Met Trp Thr Leu Met Ala Ala Val Phe Val Pro Met
    375                 380                 385

ttc gct ctg ctt ggc tat gaa cca tca ttc att cag gca gca ttc cgc   1315
Phe Ala Leu Leu Gly Tyr Glu Pro Ser Phe Ile Gln Ala Ala Phe Arg
390                 395                 400                 405

gtg ggt gac tcg gca act cag gtg atc aca ccg ctg aat ccg tac atg   1363
Val Gly Asp Ser Ala Thr Gln Val Ile Thr Pro Leu Asn Pro Tyr Met
                410                 415                 420

att gtg atc ctc ggt ttg ctc cgt cga tac gaa ccg gat gca ggt tta   1411
Ile Val Ile Leu Gly Leu Leu Arg Arg Tyr Glu Pro Asp Ala Gly Leu
            425                 430                 435

ggc acc ttg atg tca agg ctt atc cca ttt gtg atc cct ttc tgg cta   1459
Gly Thr Leu Met Ser Arg Leu Ile Pro Phe Val Ile Pro Phe Trp Leu
        440                 445                 450

gcc tgg gct aca ttg ttg gca att tgg ttc tac gcc gat ttg ccg ctt   1507
Ala Trp Ala Thr Leu Leu Ala Ile Trp Phe Tyr Ala Asp Leu Pro Leu
    455                 460                 465

gga cct ggc tct gcg atc ttc ctc gaa gga taagttttca tgagtactga     1557
Gly Pro Gly Ser Ala Ile Phe Leu Glu Gly
470                 475

caa                                                               1560
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US 20050009050 A1

<210> 1560
<211> 479
<212> PRT

<213> Corynebacterium glutamicum

<400> 1560

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Met Ala Trp Met Asn Val Ser Val Ile Val Pro Gly Ser Asp Glu Glu
  1               5                  10                  15

Leu Phe Val Lys Gly Leu Phe Thr Gly Glu Gly Leu Thr Trp Leu Thr
             20                  25                  30

Thr Asn Leu Gly Ala Asn Tyr Ile Gly Phe Pro Pro Leu Leu Thr Val
         35                  40                  45

Leu Pro Ile Leu Leu Ala Val Gly Val Ala Glu Arg Ser Gly Met Leu
     50                  55                  60

Ala Ala Leu Ile Arg Lys Leu Phe Gly Ser Ala Lys Lys Ile Val Leu
 65                  70                  75                  80

Pro Tyr Ala Val Gly Val Ile Gly Val Thr Ala Ser Ile Met Ala Asp
                 85                  90                  95

Ala Ala Phe Val Val Val Pro Pro Leu Ala Ala Met Val Phe Lys Ala
            100                 105                 110

Ala Gly Arg His Pro Val Ala Gly Leu Leu Gly Ser Phe Ala Ala Val
        115                 120                 125

Gly Ala Gly Tyr Ser Thr Ala Ile Val Pro Thr Ser Leu Asp Ala Leu
    130                 135                 140

Phe Ala Gly Ile Thr Asn Ala Val Met Glu Thr Leu Pro Gly Ile Ala
145                 150                 155                 160

Thr Thr Glu Val Asn Pro Val Ser Asn Tyr Tyr Phe Asn Ile Ala Ser
                165                 170                 175

Ser Ile Val Leu Gly Leu Leu Cys Gly Phe Leu Ile Asp Lys Val Leu
            180                 185                 190

Glu Pro Arg Met Trp Arg Gln Lys Ile Ala Thr Glu Tyr Ala Glu Ser
        195                 200                 205

Ile Glu Pro Thr Ser Ala Ala Asp Asp Glu Glu Ile Ser Ala Thr Leu
    210                 215                 220

Thr Ala Gln Glu Asn Arg Ala Leu Thr Ile Ser Met Trp Thr Thr Leu
225                 230                 235                 240

Ala Thr Ala Ile Ile Val Leu Val Val Val Leu Ile Pro Gly Ser Pro
                245                 250                 255

Trp Arg Asn Glu Asp Gly Gly Phe Leu Pro Thr Ser Pro Leu Leu Ser
            260                 265                 270

Ser Val Val Phe Ile Val Phe Leu Phe Phe Met Val Met Gly Leu Ala
        275                 280                 285

Tyr Gly Met Val Val Gly Thr Ile Lys Asn Met Asp Asp Val Val Asn
    290                 295                 300

Met Met Gly Glu Ala Ile Lys Asp Met Ile Gly Phe Leu Val Leu Ala
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305                 310                 315                 320

Phe Ile Leu Gly Gln Phe Val Ala Leu Phe Asn Trp Thr Gly Ile Gly
                325                 330                 335

Thr Trp Thr Ala Val Gln Gly Ala Ala Gly Leu Glu Ala Ile Gly Leu
            340                 345                 350

Thr Gly Phe Pro Ala Ile Ile Ala Phe Ile Ile Leu Ala Ser Cys Leu
        355                 360                 365

Asn Leu Leu Ile Ile Ser Gly Ser Ala Met Trp Thr Leu Met Ala Ala
    370                 375                 380

Val Phe Val Pro Met Phe Ala Leu Leu Gly Tyr Glu Pro Ser Phe Ile
385                 390                 395                 400

Gln Ala Ala Phe Arg Val Gly Asp Ser Ala Thr Gln Val Ile Thr Pro
                405                 410                 415

Leu Asn Pro Tyr Met Ile Val Ile Leu Gly Leu Leu Arg Arg Tyr Glu
            420                 425                 430

Pro Asp Ala Gly Leu Gly Thr Leu Met Ser Arg Leu Ile Pro Phe Val
        435                 440                 445

Ile Pro Phe Trp Leu Ala Trp Ala Thr Leu Leu Ala Ile Trp Phe Tyr
    450                 455                 460

Ala Asp Leu Pro Leu Gly Pro Gly Ser Ala Ile Phe Leu Glu Gly
465                 470                 475


<210> 1561
<211> 525
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(502)
<223> RXA00031

<400> 1561
cacacatcgc ctcgtcatcc ttagacacgc caaatcttcc tggtccaccg gagtactcga 60

ccataaacgc ccacttaatc aacgtgggct tcgcgatggc gtg gca gct ggc caa   115
                                              Val Ala Ala Gly Gln
                                                1               5

tgg cta gct ggc aac atc ggc gaa att gat cat gtg ctg tgt tca gat   163
Trp Leu Ala Gly Asn Ile Gly Glu Ile Asp His Val Leu Cys Ser Asp
                10                  15                  20

gcc acc cgc aca caa tta acg tgg gaa cgc gtc cag ctt ggt ggc gca   211
Ala Thr Arg Thr Gln Leu Thr Trp Glu Arg Val Gln Leu Gly Gly Ala
            25                  30                  35

acc gcc aaa ggc tct agc ttc cac aat gac atc tat gaa aac caa gtg   259
Thr Ala Lys Gly Ser Ser Phe His Asn Asp Ile Tyr Glu Asn Gln Val
        40                  45                  50
```

```
tct gaa ttt aaa cat tta ata aca ggg ctc cca gat gta gtt ggt acc   307
Ser Glu Phe Lys His Leu Ile Thr Gly Leu Pro Asp Val Val Gly Thr
     55                  60                  65

gcc cta ctc atc ggg cac tgg cca ggc gtg gaa gaa cta gcc cat tat   355
Ala Leu Leu Ile Gly His Trp Pro Gly Val Glu Glu Leu Ala His Tyr
 70                  75                  80                  85

ttt ggc atc cgc gat gaa cat ccc ggt tgg gat cag atg gaa gaa aag   403
Phe Gly Ile Arg Asp Glu His Pro Gly Trp Asp Gln Met Glu Glu Lys
                 90                  95                 100

ttt ccc acc agc gcc att gcg gtg ttg gaa ttt aac acc cct tgg tca   451
Phe Pro Thr Ser Ala Ile Ala Val Leu Glu Phe Asn Thr Pro Trp Ser
            105                 110                 115

aaa ctt gag aga aac tct gct cgg ttg aca gat ttt gtc att cca cgg   499
Lys Leu Glu Arg Asn Ser Ala Arg Leu Thr Asp Phe Val Ile Pro Arg
        120                 125                 130

ggt tagttctgct tcaattgaac aat                                    525
Gly
```

<210> 1562
<211> 134
<212> PRT
<213> Corynebacterium glutamicum

<400> 1562

```
Val Ala Ala Gly Gln Trp Leu Ala Gly Asn Ile Gly Glu Ile Asp His
  1               5                  10                  15

Val Leu Cys Ser Asp Ala Thr Arg Thr Gln Leu Thr Trp Glu Arg Val
             20                  25                  30

Gln Leu Gly Gly Ala Thr Ala Lys Gly Ser Ser Phe His Asn Asp Ile
         35                  40                  45

Tyr Glu Asn Gln Val Ser Glu Phe Lys His Leu Ile Thr Gly Leu Pro
     50                  55                  60

Asp Val Val Gly Thr Ala Leu Leu Ile Gly His Trp Pro Gly Val Glu
 65                  70                  75                  80

Glu Leu Ala His Tyr Phe Gly Ile Arg Asp Glu His Pro Gly Trp Asp
                 85                  90                  95

Gln Met Glu Glu Lys Phe Pro Thr Ser Ala Ile Ala Val Leu Glu Phe
            100                 105                 110

Asn Thr Pro Trp Ser Lys Leu Glu Arg Asn Ser Ala Arg Leu Thr Asp
        115                 120                 125

Phe Val Ile Pro Arg Gly
    130
```

<210> 1563

<211> 810
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(787)
<223> RXA00049

<400> 1563
ctgaatcatg attcataaat gaacaagggt tcagatttta caataccccc attccacccc 60

cttatattta agtcaccgca gatcagctaa ggttttccct atg ccc acg cct tcg 115
Met Pro Thr Pro Ser
1 5

cag cac aag gac gct tca aca gca caa acc gac aac cag gta cca act 163
Gln His Lys Asp Ala Ser Thr Ala Gln Thr Asp Asn Gln Val Pro Thr
10 15 20

ggc cgc cgt gca caa aaa cgc gaa caa acc cgc gcg cgc ctg atc act 211
Gly Arg Arg Ala Gln Lys Arg Glu Gln Thr Arg Ala Arg Leu Ile Thr
25 30 35

tcc gct cgc aca ctc atg gca gaa cgg ggt gtc gac aat gta gga ata 259
Ser Ala Arg Thr Leu Met Ala Glu Arg Gly Val Asp Asn Val Gly Ile
40 45 50

gct gaa atc acc gaa ggc gca aac atc gga acg gga acc ttc tac aac 307
Ala Glu Ile Thr Glu Gly Ala Asn Ile Gly Thr Gly Thr Phe Tyr Asn
55 60 65

tac ttc cca gac cgt gaa caa cta ctc caa gct gtc gca gaa gat gcc 355
Tyr Phe Pro Asp Arg Glu Gln Leu Leu Gln Ala Val Ala Glu Asp Ala
70 75 80 85

ttt gaa tcc gtg gga att gcc ctc gac cag gtg cta acc aaa tta gac 403
Phe Glu Ser Val Gly Ile Ala Leu Asp Gln Val Leu Thr Lys Leu Asp
90 95 100

gat ccg gct gaa gta ttt gca ggg tcg ctt cga cat cta gta cgg cac 451
Asp Pro Ala Glu Val Phe Ala Gly Ser Leu Arg His Leu Val Arg His
105 110 115

tcg tta gaa gat cgg att tgg ggc gga ttt ttc ata caa atg ggt gct 499
Ser Leu Glu Asp Arg Ile Trp Gly Gly Phe Phe Ile Gln Met Gly Ala
120 125 130

gct cat ccc gta ctc atg cgc atc cta gga ccc cgc gca cgc cga gat 547
Ala His Pro Val Leu Met Arg Ile Leu Gly Pro Arg Ala Arg Arg Asp
135 140 145

cta ctt cat ggt tta gaa act ggc cga ttc acc atc gaa gat ctg gac 595
Leu Leu His Gly Leu Glu Thr Gly Arg Phe Thr Ile Glu Asp Leu Asp
150 155 160 165

cta gca acc aca tgc act ttt ggt tca ctc atc gca gcg atc caa atg 643
Leu Ala Thr Thr Cys Thr Phe Gly Ser Leu Ile Ala Ala Ile Gln Met
170 175 180

gcg ctt tct gca gat caa gat tcc aac gat gac aaa gat cag att ttc 691

```
Ala Leu Ser Ala Asp Gln Asp Ser Asn Asp Asp Lys Asp Gln Ile Phe
            185                 190                 195

gca gcc gcg atg ctc cgg atg gtg ggt gtt caa gca gca gaa gcc cgg   739
Ala Ala Ala Met Leu Arg Met Val Gly Val Gln Ala Ala Glu Ala Arg
        200                 205                 210

gag atc gct tcg cgt cca ctc ccc gaa ata tcc cca gtc aaa ccg cag   787
Glu Ile Ala Ser Arg Pro Leu Pro Glu Ile Ser Pro Val Lys Pro Gln
    215                 220                 225

tagtgatcgg gcctcaaata aac                                        810


<210> 1564
<211> 229
<212> PRT
<213> Corynebacterium glutamicum

<400> 1564
Met Pro Thr Pro Ser Gln His Lys Asp Ala Ser Thr Ala Gln Thr Asp
  1               5                  10                  15

Asn Gln Val Pro Thr Gly Arg Arg Ala Gln Lys Arg Glu Gln Thr Arg
             20                  25                  30

Ala Arg Leu Ile Thr Ser Ala Arg Thr Leu Met Ala Glu Arg Gly Val
         35                  40                  45

Asp Asn Val Gly Ile Ala Glu Ile Thr Glu Gly Ala Asn Ile Gly Thr
     50                  55                  60

Gly Thr Phe Tyr Asn Tyr Phe Pro Asp Arg Glu Gln Leu Leu Gln Ala
 65                  70                  75                  80

Val Ala Glu Asp Ala Phe Glu Ser Val Gly Ile Ala Leu Asp Gln Val
                 85                  90                  95

Leu Thr Lys Leu Asp Asp Pro Ala Glu Val Phe Ala Gly Ser Leu Arg
            100                 105                 110

His Leu Val Arg His Ser Leu Glu Asp Arg Ile Trp Gly Gly Phe Phe
        115                 120                 125

Ile Gln Met Gly Ala Ala His Pro Val Leu Met Arg Ile Leu Gly Pro
    130                 135                 140

Arg Ala Arg Arg Asp Leu Leu His Gly Leu Glu Thr Gly Arg Phe Thr
145                 150                 155                 160

Ile Glu Asp Leu Asp Leu Ala Thr Thr Cys Thr Phe Gly Ser Leu Ile
                165                 170                 175

Ala Ala Ile Gln Met Ala Leu Ser Ala Asp Gln Asp Ser Asn Asp Asp
            180                 185                 190

Lys Asp Gln Ile Phe Ala Ala Ala Met Leu Arg Met Val Gly Val Gln
        195                 200                 205

Ala Ala Glu Ala Arg Glu Ile Ala Ser Arg Pro Leu Pro Glu Ile Ser
    210                 215                 220
```

```
Pro Val Lys Pro Gln
225


<210> 1565
<211> 834
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(811)
<223> RXA00052

<400> 1565
agctaaagtt ctaatttcct aaattggtaa agatcggaac tcaaaaatgt cgcttcgaaa 60

gctcacaagc ttaattggca tactggctgt tgttggccta gtg gcg ttt atc ctt   115
                                            Val Ala Phe Ile Leu
                                              1               5

ttc aac ttc gtg aaa aca aac gac gaa aca tcg aat gtc tct cag agc   163
Phe Asn Phe Val Lys Thr Asn Asp Glu Thr Ser Asn Val Ser Gln Ser
                  10                  15                  20

gag tca act gca gag aca gtc agc gaa aca aat ggc gtg ctc tcc gac   211
Glu Ser Thr Ala Glu Thr Val Ser Glu Thr Asn Gly Val Leu Ser Asp
              25                  30                  35

ggc gca gaa aac atc gct tct caa tct gat gag agt aaa tcg ggt gta   259
Gly Ala Glu Asn Ile Ala Ser Gln Ser Asp Glu Ser Lys Ser Gly Val
          40                  45                  50

gag att att gat tct gga ttt ggg cag agc tca aat tcg gcg atg gca   307
Glu Ile Ile Asp Ser Gly Phe Gly Gln Ser Ser Asn Ser Ala Met Ala
      55                  60                  65

att gtt att gcc aaa act tct ggt gga agc ctc gca ggg gaa ttt gtt   355
Ile Val Ile Ala Lys Thr Ser Gly Gly Ser Leu Ala Gly Glu Phe Val
  70                  75                  80                  85

acg gcg acg gtg aat ttc ctc gat gaa agt ggc gcc gtt gta gcg act   403
Thr Ala Thr Val Asn Phe Leu Asp Glu Ser Gly Ala Val Val Ala Thr
                  90                  95                 100

gaa gat caa gta gaa aca ctc agt tgg gaa gac cag gaa ttg gta ttg   451
Glu Asp Gln Val Glu Thr Leu Ser Trp Glu Asp Gln Glu Leu Val Leu
              105                 110                 115

cca gta tct cac tac aag gag gat tca agc cgc cca gaa att aca agc   499
Pro Val Ser His Tyr Lys Glu Asp Ser Ser Arg Pro Glu Ile Thr Ser
          120                 125                 130

att gag gct ttt ctt tca gta acg gat tac ggt tca gga caa cca gat   547
Ile Glu Ala Phe Leu Ser Val Thr Asp Tyr Gly Ser Gly Gln Pro Asp
      135                 140                 145

gaa act gca ttg ccg gtg ttg gaa acc acc gat att tcc aac cca tac   595
Glu Thr Ala Leu Pro Val Leu Glu Thr Thr Asp Ile Ser Asn Pro Tyr
150                 155                 160                 165
```

```
gct ggt agt tac aat gcc tca ttt gcg ttg aaa aat gac tcc tca gat   643
Ala Gly Ser Tyr Asn Ala Ser Phe Ala Leu Lys Asn Asp Ser Ser Asp
                170                 175                 180

gat ttt aag aac ctg aga gtt ggt att gtt tgc tac aac gag caa act   691
Asp Phe Lys Asn Leu Arg Val Gly Ile Val Cys Tyr Asn Glu Gln Thr
            185                 190                 195

gac atc att ggt ggt ggt ttc aaa ttt ccg aac ctg gtt cca gcg ggt   739
Asp Ile Ile Gly Gly Gly Phe Lys Phe Pro Asn Leu Val Pro Ala Gly
        200                 205                 210

ggg agt att cga atg gac gct agt gtg acg gtc tcc gaa atg cca gct   787
Gly Ser Ile Arg Met Asp Ala Ser Val Thr Val Ser Glu Met Pro Ala
    215                 220                 225

tct tgt aag gca tat tta aat cac taatagattc ttaaaaggca gca         834
Ser Cys Lys Ala Tyr Leu Asn His
230                 235
```

<210> 1566
<211> 237
<212> PRT
<213> Corynebacterium glutamicum

<400> 1566

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Val Ala Phe Ile Leu Phe Asn Phe Val Lys Thr Asn Asp Glu Thr Ser
  1               5                  10                  15

Asn Val Ser Gln Ser Glu Ser Thr Ala Glu Thr Val Ser Glu Thr Asn
             20                  25                  30

Gly Val Leu Ser Asp Gly Ala Glu Asn Ile Ala Ser Gln Ser Asp Glu
         35                  40                  45

Ser Lys Ser Gly Val Glu Ile Ile Asp Ser Gly Phe Gly Gln Ser Ser
     50                  55                  60

Asn Ser Ala Met Ala Ile Val Ile Ala Lys Thr Ser Gly Gly Ser Leu
 65                  70                  75                  80

Ala Gly Glu Phe Val Thr Ala Thr Val Asn Phe Leu Asp Glu Ser Gly
                 85                  90                  95

Ala Val Val Ala Thr Glu Asp Gln Val Glu Thr Leu Ser Trp Glu Asp
            100                 105                 110

Gln Glu Leu Val Leu Pro Val Ser His Tyr Lys Glu Asp Ser Ser Arg
        115                 120                 125

Pro Glu Ile Thr Ser Ile Glu Ala Phe Leu Ser Val Thr Asp Tyr Gly
    130                 135                 140

Ser Gly Gln Pro Asp Glu Thr Ala Leu Pro Val Leu Glu Thr Thr Asp
145                 150                 155                 160

Ile Ser Asn Pro Tyr Ala Gly Ser Tyr Asn Ala Ser Phe Ala Leu Lys
                165                 170                 175
```

```
Asn Asp Ser Ser Asp Asp Phe Lys Asn Leu Arg Val Gly Ile Val Cys
            180                 185                 190

Tyr Asn Glu Gln Thr Asp Ile Ile Gly Gly Gly Phe Lys Phe Pro Asn
        195                 200                 205

Leu Val Pro Ala Gly Gly Ser Ile Arg Met Asp Ala Ser Val Thr Val
    210                 215                 220

Ser Glu Met Pro Ala Ser Cys Lys Ala Tyr Leu Asn His
225                 230                 235


<210> 1567
<211> 3036
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(3013)
<223> RXA00054

<400> 1567
atgctgagat ccgctgggtg gcaccacacg aattggaatc tttggagtgg gcacctgctg 60

atattcctgc ggtgaaactt ctcgtcgagc agcttgctta atg agc cca ttc gat   115
                                        Met Ser Pro Phe Asp
                                          1               5

tca aag ctt ggt cgc gat acc cat ttt gga ttc ctc gat aag acc act   163
Ser Lys Leu Gly Arg Asp Thr His Phe Gly Phe Leu Asp Lys Thr Thr
                  10                  15                  20

gct tcg caa caa ctg ctg aat cct tca ttg att tct aat gag gat ccg   211
Ala Ser Gln Gln Leu Leu Asn Pro Ser Leu Ile Ser Asn Glu Asp Pro
              25                  30                  35

cac acc atg ttg cag gcg atc aag tta gag ctt cgt acc gca cag tct   259
His Thr Met Leu Gln Ala Ile Lys Leu Glu Leu Arg Thr Ala Gln Ser
          40                  45                  50

ttt aca ttt tca gtc gct ttt att tcc agt cgc ggt atc gcg ttg ttg   307
Phe Thr Phe Ser Val Ala Phe Ile Ser Ser Arg Gly Ile Ala Leu Leu
      55                  60                  65

aaa cag gca ttg ttg gac ttc aag ggt aaa gga cga att atc acg tcc   355
Lys Gln Ala Leu Leu Asp Phe Lys Gly Lys Gly Arg Ile Ile Thr Ser
  70                  75                  80                  85

cgc tac ctg gat ttc aat gat cca acg atg ttt cgt gag ctt ctt act   403
Arg Tyr Leu Asp Phe Asn Asp Pro Thr Met Phe Arg Glu Leu Leu Thr
                  90                  95                 100

ttg gag aac gtg gaa gtc ctc ata cat caa ggc gat ggt ttc cac tcc   451
Leu Glu Asn Val Glu Val Leu Ile His Gln Gly Asp Gly Phe His Ser
            105                 110                 115

aag ggc tac gtt ttc cat cac gac gtg gga atc acc gca gta gtg ggt   499
Lys Gly Tyr Val Phe His His Asp Val Gly Ile Thr Ala Val Val Gly
        120                 125                 130
```

```
agt tcc aac ctc aca gat aat gct ctg ttg gta aac cgg gaa tgg aat   547
Ser Ser Asn Leu Thr Asp Asn Ala Leu Leu Val Asn Arg Glu Trp Asn
    135                 140                 145

ctg aag ttc tct gcc agc aag aat ggc gac att gct ttt caa ctt gat   595
Leu Lys Phe Ser Ala Ser Lys Asn Gly Asp Ile Ala Phe Gln Leu Asp
150                 155                 160                 165

gat gcg att aat cgc caa att gaa cga tcc acg cca ctg acg cct gaa   643
Asp Ala Ile Asn Arg Gln Ile Glu Arg Ser Thr Pro Leu Thr Pro Glu
                170                 175                 180

tgg atc tca gag tat gag gca acc aga cgt gta cct gag cgt ttg gtg   691
Trp Ile Ser Glu Tyr Glu Ala Thr Arg Arg Val Pro Glu Arg Leu Val
            185                 190                 195

tct cag aat att cct ctc gag gat caa agt aac gcc gga aca att gtt   739
Ser Gln Asn Ile Pro Leu Glu Asp Gln Ser Asn Ala Gly Thr Ile Val
        200                 205                 210

cca aac gtc atg cag gaa gag gcc ctc gac gct cta ctt tct ttg acg   787
Pro Asn Val Met Gln Glu Glu Ala Leu Asp Ala Leu Leu Ser Leu Thr
    215                 220                 225

gag aag gga gag aaa cgt ggt gtc att att tct gcg aca gga act ggc   835
Glu Lys Gly Glu Lys Arg Gly Val Ile Ile Ser Ala Thr Gly Thr Gly
230                 235                 240                 245

aag act atc ctg gct gct cta gct aca aga atg ctc aag cct gaa cga   883
Lys Thr Ile Leu Ala Ala Leu Ala Thr Arg Met Leu Lys Pro Glu Arg
                250                 255                 260

gtt ttg ttt gtc gtg cac cgc gaa caa att ctg gat aag gcg cga tcc   931
Val Leu Phe Val Val His Arg Glu Gln Ile Leu Asp Lys Ala Arg Ser
            265                 270                 275

gag ttc atc aaa gtt ctt gaa cgt ccc gct gtt gat ttc gga aaa atg   979
Glu Phe Ile Lys Val Leu Glu Arg Pro Ala Val Asp Phe Gly Lys Met
        280                 285                 290

tct ggc tcg acc aag gag cta gat aag ccg ttt gtg ttt ggc acc atc   1027
Ser Gly Ser Thr Lys Glu Leu Asp Lys Pro Phe Val Phe Gly Thr Ile
    295                 300                 305

caa acg ctg aca aag gaa gct aca ctt tcc cag atc tcc cct act gac   1075
Gln Thr Leu Thr Lys Glu Ala Thr Leu Ser Gln Ile Ser Pro Thr Asp
310                 315                 320                 325

ttt gat tta gtc atc gtc gat gaa gtc cat cgc gcc ggt gcc gaa tcc   1123
Phe Asp Leu Val Ile Val Asp Glu Val His Arg Ala Gly Ala Glu Ser
                330                 335                 340

tat ttg gca ttg ctc aat cat ctg cag cca cag ttt tta ttg ggc ctg   1171
Tyr Leu Ala Leu Leu Asn His Leu Gln Pro Gln Phe Leu Leu Gly Leu
            345                 350                 355

act gct acc cca gag cga act gat gga ttc aat att tat gag ttg ttc   1219
Thr Ala Thr Pro Glu Arg Thr Asp Gly Phe Asn Ile Tyr Glu Leu Phe
        360                 365                 370
```

```
gat ttc aac gtg cca tat gag atc cga ctt caa gct gct tta gaa tcc   1267
Asp Phe Asn Val Pro Tyr Glu Ile Arg Leu Gln Ala Ala Leu Glu Ser
    375                 380                 385

aac atg ctc gta ccg ttt cac tat tac ggt gtc aca gac ttc acg ctt   1315
Asn Met Leu Val Pro Phe His Tyr Tyr Gly Val Thr Asp Phe Thr Leu
390                 395                 400                 405

gat tct gaa aca acg gtg act gat acc tcc aaa cta agt gcc ttg gtg   1363
Asp Ser Glu Thr Thr Val Thr Asp Thr Ser Lys Leu Ser Ala Leu Val
                410                 415                 420

agc gaa gag aga gtc cat cac att ctg gag gcc ctc aaa act tat ggt   1411
Ser Glu Glu Arg Val His His Ile Leu Glu Ala Leu Lys Thr Tyr Gly
            425                 430                 435

cat cca gaa aat gtt cgt gga ctg atc ttc tgt tcc aag act gaa gag   1459
His Pro Glu Asn Val Arg Gly Leu Ile Phe Cys Ser Lys Thr Glu Glu
        440                 445                 450

gct gag gag ctg tca aaa ctt ctc gac cag tcg ttg ttt aat ggc agc   1507
Ala Glu Glu Leu Ser Lys Leu Leu Asp Gln Ser Leu Phe Asn Gly Ser
    455                 460                 465

ttg ctt aaa acc aag gcg ctc tct gcg aag gac tca att ccc tac cgc   1555
Leu Leu Lys Thr Lys Ala Leu Ser Ala Lys Asp Ser Ile Pro Tyr Arg
470                 475                 480                 485

gaa gag gtt gta gct gag ctg gag tcc ggc gac ctg gac tac atc ttg   1603
Glu Glu Val Val Ala Glu Leu Glu Ser Gly Asp Leu Asp Tyr Ile Leu
                490                 495                 500

acg gtt gac atc ttc aat gaa ggc att gat att cct tcg gtg aat caa   1651
Thr Val Asp Ile Phe Asn Glu Gly Ile Asp Ile Pro Ser Val Asn Gln
            505                 510                 515

atc gta atg att cgt agt act caa tca agc att gtg ttt acg cag cag   1699
Ile Val Met Ile Arg Ser Thr Gln Ser Ser Ile Val Phe Thr Gln Gln
        520                 525                 530

ctc ggg cgt gga ctc cga aaa gct gct ggc aaa gac cat ctg cgc gtt   1747
Leu Gly Arg Gly Leu Arg Lys Ala Ala Gly Lys Asp His Leu Arg Val
    535                 540                 545

att gat ttc att ggc aac tac gcg aac aac tat ctc att ccc atc gca   1795
Ile Asp Phe Ile Gly Asn Tyr Ala Asn Asn Tyr Leu Ile Pro Ile Ala
550                 555                 560                 565

ttg ttt ggc gat aat tct cgc aat aag aac agc atc aga cgc cgc ctg   1843
Leu Phe Gly Asp Asn Ser Arg Asn Lys Asn Ser Ile Arg Arg Arg Leu
                570                 575                 580

att gag agc gat att gat gga aca atc tca ggt gtt tca agt gtt aac   1891
Ile Glu Ser Asp Ile Asp Gly Thr Ile Ser Gly Val Ser Ser Val Asn
            585                 590                 595

ttt gat ccc atc gcg cag gag aga att ttt gct gcg ttg aag gct gcg   1939
Phe Asp Pro Ile Ala Gln Glu Arg Ile Phe Ala Ala Leu Lys Ala Ala
        600                 605                 610

aag ttg gac tca aaa gca caa ttc aag cag gat att gtt cag ctt caa   1987
```

```
Lys Leu Asp Ser Lys Ala Gln Phe Lys Gln Asp Ile Val Gln Leu Gln
    615                 620                 625

gat cga ctc aat cat gtg cca gca ctg tta gac ttc gct cgc ttc aat   2035
Asp Arg Leu Asn His Val Pro Ala Leu Leu Asp Phe Ala Arg Phe Asn
630                 635                 640                 645

act gtt gat ccg ttt atc ctt gcc acg cat tct ggc aac tac tgg tcg   2083
Thr Val Asp Pro Phe Ile Leu Ala Thr His Ser Gly Asn Tyr Trp Ser
                650                 655                 660

ctg ctc agt tca gtg aag ttt gtc gat cac gct ccc agc gaa tcg gag   2131
Leu Leu Ser Ser Val Lys Phe Val Asp His Ala Pro Ser Glu Ser Glu
            665                 670                 675

aag tac ttt ctg gat ttc ctt acc gga gag ctt ctt aac ggc aag cga   2179
Lys Tyr Phe Leu Asp Phe Leu Thr Gly Glu Leu Leu Asn Gly Lys Arg
        680                 685                 690

cct cat gag ctg ttg ctg atc cag gaa cta atg aaa cag cct gaa act   2227
Pro His Glu Leu Leu Leu Ile Gln Glu Leu Met Lys Gln Pro Glu Thr
    695                 700                 705

tct act gaa gaa ttc cgt aag ctc ttg cag gcc caa tcg act agt tca   2275
Ser Thr Glu Glu Phe Arg Lys Leu Leu Gln Ala Gln Ser Thr Ser Ser
710                 715                 720                 725

gat gag caa aca atc aac tcg gtt gaa agg att ttg agc caa gaa ttc   2323
Asp Glu Gln Thr Ile Asn Ser Val Glu Arg Ile Leu Ser Gln Glu Phe
                730                 735                 740

tat acg gga cca aac cgc aag aag ttt ggc gaa cat ccg atc ctc tct   2371
Tyr Thr Gly Pro Asn Arg Lys Lys Phe Gly Glu His Pro Ile Leu Ser
            745                 750                 755

gtt caa aac cgc acc tac tct ttt act ccc gag ttc cga cgt gcc ctc   2419
Val Gln Asn Arg Thr Tyr Ser Phe Thr Pro Glu Phe Arg Arg Ala Leu
        760                 765                 770

gac gaa agc cta gaa gtg acg gac cga gat gag gct gct cag aat ttt   2467
Asp Glu Ser Leu Glu Val Thr Asp Arg Asp Glu Ala Ala Gln Asn Phe
    775                 780                 785

aag ttt cac gtc caa gac atc atc gac act ggt ttg ttt atc gcc aga   2515
Lys Phe His Val Gln Asp Ile Ile Asp Thr Gly Leu Phe Ile Ala Arg
790                 795                 800                 805

aac aat gga ttt tgg caa gga aac ctc gtt gtt ggc gag aga tac tcc   2563
Asn Asn Gly Phe Trp Gln Gly Asn Leu Val Val Gly Glu Arg Tyr Ser
                810                 815                 820

cga cga gat gtc tgc cga att ctc aat tgg gaa cga aac aac gag agc   2611
Arg Arg Asp Val Cys Arg Ile Leu Asn Trp Glu Arg Asn Asn Glu Ser
            825                 830                 835

acg att tat gga tac aaa gtg gac agt tac aca tct act tgc cca atc   2659
Thr Ile Tyr Gly Tyr Lys Val Asp Ser Tyr Thr Ser Thr Cys Pro Ile
        840                 845                 850

ttt gtg acc tat cac aag gct gat gat gta tcc gaa agt act cgt tac   2707
Phe Val Thr Tyr His Lys Ala Asp Asp Val Ser Glu Ser Thr Arg Tyr
```

```
    855                 860                 865

cag gat gaa ctc gtc gat ccg aat acc ctt cat tgg tat tcc cgc ggc   2755
Gln Asp Glu Leu Val Asp Pro Asn Thr Leu His Trp Tyr Ser Arg Gly
870                 875                 880                 885

aac cga aag atc acg tct aat gag atc aag ccc atc gct gcg aat gct   2803
Asn Arg Lys Ile Thr Ser Asn Glu Ile Lys Pro Ile Ala Ala Asn Ala
                890                 895                 900

gtg gat ctt cat gtt ttt gtg aag aag gac gat gcc gaa ggc ctt gat   2851
Val Asp Leu His Val Phe Val Lys Lys Asp Asp Ala Glu Gly Leu Asp
            905                 910                 915

ttc ttc tac ctt ggt caa gcg cat tca gaa aac agc aaa cag tca tcg   2899
Phe Phe Tyr Leu Gly Gln Ala His Ser Glu Asn Ser Lys Gln Ser Ser
        920                 925                 930

atg ccc gga aac aaa gga gtt gtg caa ccg gtg gtc aca atg gat cta   2947
Met Pro Gly Asn Lys Gly Val Val Gln Pro Val Val Thr Met Asp Leu
    935                 940                 945

cag ttc gac aca ccc gtc gaa caa agc ctg ttt gag tac ctg agc aca   2995
Gln Phe Asp Thr Pro Val Glu Gln Ser Leu Phe Glu Tyr Leu Ser Thr
950                 955                 960                 965

aat ctc gcc gta acg gag taaccaccgc aaccaagcgt cga                 3036
Asn Leu Ala Val Thr Glu
                970
```

<210> 1568
<211> 971
<212> PRT
<213> Corynebacterium glutamicum

<400> 1568

```
Met Ser Pro Phe Asp Ser Lys Leu Gly Arg Asp Thr His Phe Gly Phe
  1               5                  10                  15

Leu Asp Lys Thr Thr Ala Ser Gln Gln Leu Leu Asn Pro Ser Leu Ile
             20                  25                  30

Ser Asn Glu Asp Pro His Thr Met Leu Gln Ala Ile Lys Leu Glu Leu
         35                  40                  45

Arg Thr Ala Gln Ser Phe Thr Phe Ser Val Ala Phe Ile Ser Ser Arg
     50                  55                  60

Gly Ile Ala Leu Leu Lys Gln Ala Leu Leu Asp Phe Lys Gly Lys Gly
 65                  70                  75                  80

Arg Ile Ile Thr Ser Arg Tyr Leu Asp Phe Asn Asp Pro Thr Met Phe
                 85                  90                  95

Arg Glu Leu Leu Thr Leu Glu Asn Val Glu Val Leu Ile His Gln Gly
            100                 105                 110

Asp Gly Phe His Ser Lys Gly Tyr Val Phe His His Asp Val Gly Ile
        115                 120                 125
```

```
Thr Ala Val Val Gly Ser Ser Asn Leu Thr Asp Asn Ala Leu Leu Val
    130                 135                 140

Asn Arg Glu Trp Asn Leu Lys Phe Ser Ala Ser Lys Asn Gly Asp Ile
145                 150                 155                 160

Ala Phe Gln Leu Asp Asp Ala Ile Asn Arg Gln Ile Glu Arg Ser Thr
                165                 170                 175

Pro Leu Thr Pro Glu Trp Ile Ser Glu Tyr Glu Ala Thr Arg Arg Val
            180                 185                 190

Pro Glu Arg Leu Val Ser Gln Asn Ile Pro Leu Glu Asp Gln Ser Asn
        195                 200                 205

Ala Gly Thr Ile Val Pro Asn Val Met Gln Glu Glu Ala Leu Asp Ala
    210                 215                 220

Leu Leu Ser Leu Thr Glu Lys Gly Glu Lys Arg Gly Val Ile Ile Ser
225                 230                 235                 240

Ala Thr Gly Thr Gly Lys Thr Ile Leu Ala Ala Leu Ala Thr Arg Met
                245                 250                 255

Leu Lys Pro Glu Arg Val Leu Phe Val Val His Arg Glu Gln Ile Leu
            260                 265                 270

Asp Lys Ala Arg Ser Glu Phe Ile Lys Val Leu Glu Arg Pro Ala Val
        275                 280                 285

Asp Phe Gly Lys Met Ser Gly Ser Thr Lys Glu Leu Asp Lys Pro Phe
    290                 295                 300

Val Phe Gly Thr Ile Gln Thr Leu Thr Lys Glu Ala Thr Leu Ser Gln
305                 310                 315                 320

Ile Ser Pro Thr Asp Phe Asp Leu Val Ile Val Asp Glu Val His Arg
                325                 330                 335

Ala Gly Ala Glu Ser Tyr Leu Ala Leu Leu Asn His Leu Gln Pro Gln
            340                 345                 350

Phe Leu Leu Gly Leu Thr Ala Thr Pro Glu Arg Thr Asp Gly Phe Asn
        355                 360                 365

Ile Tyr Glu Leu Phe Asp Phe Asn Val Pro Tyr Glu Ile Arg Leu Gln
    370                 375                 380

Ala Ala Leu Glu Ser Asn Met Leu Val Pro Phe His Tyr Tyr Gly Val
385                 390                 395                 400

Thr Asp Phe Thr Leu Asp Ser Glu Thr Thr Val Thr Asp Thr Ser Lys
                405                 410                 415

Leu Ser Ala Leu Val Ser Glu Glu Arg Val His His Ile Leu Glu Ala
            420                 425                 430

Leu Lys Thr Tyr Gly His Pro Glu Asn Val Arg Gly Leu Ile Phe Cys
        435                 440                 445

Ser Lys Thr Glu Glu Ala Glu Glu Leu Ser Lys Leu Leu Asp Gln Ser
```

```
    450                 455                 460

Leu Phe Asn Gly Ser Leu Leu Lys Thr Lys Ala Leu Ser Ala Lys Asp
465                 470                 475                 480

Ser Ile Pro Tyr Arg Glu Glu Val Val Ala Glu Leu Glu Ser Gly Asp
                485                 490                 495

Leu Asp Tyr Ile Leu Thr Val Asp Ile Phe Asn Glu Gly Ile Asp Ile
            500                 505                 510

Pro Ser Val Asn Gln Ile Val Met Ile Arg Ser Thr Gln Ser Ser Ile
        515                 520                 525

Val Phe Thr Gln Gln Leu Gly Arg Gly Leu Arg Lys Ala Ala Gly Lys
    530                 535                 540

Asp His Leu Arg Val Ile Asp Phe Ile Gly Asn Tyr Ala Asn Asn Tyr
545                 550                 555                 560

Leu Ile Pro Ile Ala Leu Phe Gly Asp Asn Ser Arg Asn Lys Asn Ser
                565                 570                 575

Ile Arg Arg Arg Leu Ile Glu Ser Asp Ile Asp Gly Thr Ile Ser Gly
            580                 585                 590

Val Ser Ser Val Asn Phe Asp Pro Ile Ala Gln Glu Arg Ile Phe Ala
        595                 600                 605

Ala Leu Lys Ala Ala Lys Leu Asp Ser Lys Ala Gln Phe Lys Gln Asp
    610                 615                 620

Ile Val Gln Leu Gln Asp Arg Leu Asn His Val Pro Ala Leu Leu Asp
625                 630                 635                 640

Phe Ala Arg Phe Asn Thr Val Asp Pro Phe Ile Leu Ala Thr His Ser
                645                 650                 655

Gly Asn Tyr Trp Ser Leu Leu Ser Ser Val Lys Phe Val Asp His Ala
            660                 665                 670

Pro Ser Glu Ser Glu Lys Tyr Phe Leu Asp Phe Leu Thr Gly Glu Leu
        675                 680                 685

Leu Asn Gly Lys Arg Pro His Glu Leu Leu Leu Ile Gln Glu Leu Met
    690                 695                 700

Lys Gln Pro Glu Thr Ser Thr Glu Glu Phe Arg Lys Leu Leu Gln Ala
705                 710                 715                 720

Gln Ser Thr Ser Ser Asp Glu Gln Thr Ile Asn Ser Val Glu Arg Ile
                725                 730                 735

Leu Ser Gln Glu Phe Tyr Thr Gly Pro Asn Arg Lys Lys Phe Gly Glu
            740                 745                 750

His Pro Ile Leu Ser Val Gln Asn Arg Thr Tyr Ser Phe Thr Pro Glu
        755                 760                 765

Phe Arg Arg Ala Leu Asp Glu Ser Leu Glu Val Thr Asp Arg Asp Glu
    770                 775                 780
```

```
Ala Ala Gln Asn Phe Lys Phe His Val Gln Asp Ile Ile Asp Thr Gly
785                 790                 795                 800

Leu Phe Ile Ala Arg Asn Asn Gly Phe Trp Gln Gly Asn Leu Val Val
                805                 810                 815

Gly Glu Arg Tyr Ser Arg Arg Asp Val Cys Arg Ile Leu Asn Trp Glu
            820                 825                 830

Arg Asn Asn Glu Ser Thr Ile Tyr Gly Tyr Lys Val Asp Ser Tyr Thr
        835                 840                 845

Ser Thr Cys Pro Ile Phe Val Thr Tyr His Lys Ala Asp Asp Val Ser
    850                 855                 860

Glu Ser Thr Arg Tyr Gln Asp Glu Leu Val Asp Pro Asn Thr Leu His
865                 870                 875                 880

Trp Tyr Ser Arg Gly Asn Arg Lys Ile Thr Ser Asn Glu Ile Lys Pro
                885                 890                 895

Ile Ala Ala Asn Ala Val Asp Leu His Val Phe Val Lys Lys Asp Asp
            900                 905                 910

Ala Glu Gly Leu Asp Phe Phe Tyr Leu Gly Gln Ala His Ser Glu Asn
        915                 920                 925

Ser Lys Gln Ser Ser Met Pro Gly Asn Lys Gly Val Val Gln Pro Val
    930                 935                 940

Val Thr Met Asp Leu Gln Phe Asp Thr Pro Val Glu Gln Ser Leu Phe
945                 950                 955                 960

Glu Tyr Leu Ser Thr Asn Leu Ala Val Thr Glu
                965                 970
```

CONFIDENTIAL

<210> 1569
<211> 687
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(664)
<223> RXA00058

<400> 1569

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atcactaggc tatcttccgg ttcacctgaa gttagtaaca caccggtcac agaagttccg 60

gctcgtgtaa tctccgctta tctagctcaa aggaatactt atg aag ttc ttc ggg   115
                                            Met Lys Phe Phe Gly
                                              1               5

ttt tat cgt cct att gct tta att gct ggc att acc gtt tca gca tct   163
Phe Tyr Arg Pro Ile Ala Leu Ile Ala Gly Ile Thr Val Ser Ala Ser
                 10                  15                  20

att ctc aca tcc gta gct act gca gct gaa tct cca act agc ttt caa   211
Ile Leu Thr Ser Val Ala Thr Ala Ala Glu Ser Pro Thr Ser Phe Gln
```

```
            25                  30                  35

gcg att aca cct gca ttc tct tca tca tcg gct cca gaa gca gac gca   259
Ala Ile Thr Pro Ala Phe Ser Ser Ser Ser Ala Pro Glu Ala Asp Ala
         40                  45                  50

gaa gca aac acc agt gaa gct acc gca gac ctg ctt tac gtg gca gaa   307
Glu Ala Asn Thr Ser Glu Ala Thr Ala Asp Leu Leu Tyr Val Ala Glu
     55                  60                  65

aac caa cta ctt att aag ctt tct aac gcc gtc gtc gaa gat gtt aac   355
Asn Gln Leu Leu Ile Lys Leu Ser Asn Ala Val Val Glu Asp Val Asn
 70                  75                  80                  85

ggc gaa atc tta atg aaa gat aat aag ggc act ctt ctg gag aat ttg   403
Gly Glu Ile Leu Met Lys Asp Asn Lys Gly Thr Leu Leu Glu Asn Leu
                90                  95                 100

aca gct gaa ctt caa gcc caa cca ggc ttc tca atc gag aaa gtc gat   451
Thr Ala Glu Leu Gln Ala Gln Pro Gly Phe Ser Ile Glu Lys Val Asp
            105                 110                 115

tcc cat act gct ttg ttg acc atg aat cca gat gag gtg cca gat tta   499
Ser His Thr Ala Leu Leu Thr Met Asn Pro Asp Glu Val Pro Asp Leu
        120                 125                 130

cag gac tgg cga tgc gga gtc ggc gct ttg tca ggc ggg gta gca ggt   547
Gln Asp Trp Arg Cys Gly Val Gly Ala Leu Ser Gly Gly Val Ala Gly
    135                 140                 145

gtg gtg gca act ggt cta gct ctc gcc gct ttg gga gtt gcc aca ggt   595
Val Val Ala Thr Gly Leu Ala Leu Ala Ala Leu Gly Val Ala Thr Gly
150                 155                 160                 165

ggc acg ggg ttt gct gtg ctt gca gca ggg gga ctt gct gga tat ggc   643
Gly Thr Gly Phe Ala Val Leu Ala Ala Gly Gly Leu Ala Gly Tyr Gly
                170                 175                 180

act ggc gct gtc gcc aac tgc taaggagaaa taatgggaat tgt             687
Thr Gly Ala Val Ala Asn Cys
            185
```

<210> 1570
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 1570

```
Met Lys Phe Phe Gly Phe Tyr Arg Pro Ile Ala Leu Ile Ala Gly Ile
  1               5                  10                  15

Thr Val Ser Ala Ser Ile Leu Thr Ser Val Ala Thr Ala Ala Glu Ser
             20                  25                  30

Pro Thr Ser Phe Gln Ala Ile Thr Pro Ala Phe Ser Ser Ser Ser Ala
         35                  40                  45

Pro Glu Ala Asp Ala Glu Ala Asn Thr Ser Glu Ala Thr Ala Asp Leu
     50                  55                  60
```

```
Leu Tyr Val Ala Glu Asn Gln Leu Leu Ile Lys Leu Ser Asn Ala Val
 65                  70                  75                  80

Val Glu Asp Val Asn Gly Glu Ile Leu Met Lys Asp Asn Lys Gly Thr
                 85                  90                  95

Leu Leu Glu Asn Leu Thr Ala Glu Leu Gln Ala Gln Pro Gly Phe Ser
            100                 105                 110

Ile Glu Lys Val Asp Ser His Thr Ala Leu Leu Thr Met Asn Pro Asp
        115                 120                 125

Glu Val Pro Asp Leu Gln Asp Trp Arg Cys Gly Val Gly Ala Leu Ser
    130                 135                 140

Gly Gly Val Ala Gly Val Val Ala Thr Gly Leu Ala Leu Ala Ala Leu
145                 150                 155                 160

Gly Val Ala Thr Gly Gly Thr Gly Phe Ala Val Leu Ala Ala Gly Gly
                165                 170                 175

Leu Ala Gly Tyr Gly Thr Gly Ala Val Ala Asn Cys
            180                 185
```

<210> 1571
<211> 405
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(382)
<223> RXA00059

<400> 1571

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ctggcaggcg attgttctct tactacttgc gctaggtaca ggtggtgcct atctgctggc 60

cggtggtgat gtcactcaaa ctgcccgact ggtgttgtgg gtg ttg acc gga atc   115
                                              Val Leu Thr Gly Ile
                                                1               5

tta ctg gct atg gtc tct acc gcc cta cga atc cgc ttc gga tca ggg   163
Leu Leu Ala Met Val Ser Thr Ala Leu Arg Ile Arg Phe Gly Ser Gly
                10                  15                  20

gta gct atc gct gca acc gtg ctg tgg aca gtt atc tca ata acc ttg   211
Val Ala Ile Ala Ala Thr Val Leu Trp Thr Val Ile Ser Ile Thr Leu
            25                  30                  35

ggc gga gat gtg cta gcc gag acc atg ctc tgg ctt gta gca gta cca   259
Gly Gly Asp Val Leu Ala Glu Thr Met Leu Trp Leu Val Ala Val Pro
        40                  45                  50

tcc tgg cca gaa aca gcg gat act act acc cgc ttc ctt att gcg atg   307
Ser Trp Pro Glu Thr Ala Asp Thr Thr Thr Arg Phe Leu Ile Ala Met
    55                  60                  65

cta ctg cag gca gtt ctt atc acc ggc agc act atc tgg gct atc cga   355
Leu Leu Gln Ala Val Leu Ile Thr Gly Ser Thr Ile Trp Ala Ile Arg
70                  75                  80                  85
```

```
gag atc cgg gat tca gag cgc cgt ggc taagttcagc acctccgaca          402
Glu Ile Arg Asp Ser Glu Arg Arg Gly
                 90

acg                                                                405


<210> 1572
<211> 94
<212> PRT
<213> Corynebacterium glutamicum

<400> 1572
Val Leu Thr Gly Ile Leu Leu Ala Met Val Ser Thr Ala Leu Arg Ile
  1               5                  10                  15

Arg Phe Gly Ser Gly Val Ala Ile Ala Ala Thr Val Leu Trp Thr Val
             20                  25                  30

Ile Ser Ile Thr Leu Gly Gly Asp Val Leu Ala Glu Thr Met Leu Trp
         35                  40                  45

Leu Val Ala Val Pro Ser Trp Pro Glu Thr Ala Asp Thr Thr Thr Arg
     50                  55                  60

Phe Leu Ile Ala Met Leu Leu Gln Ala Val Leu Ile Thr Gly Ser Thr
 65                  70                  75                  80

Ile Trp Ala Ile Arg Glu Ile Arg Asp Ser Glu Arg Arg Gly
                 85                  90


<210> 1573
<211> 396
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(373)
<223> RXA00065

<400> 1573
atgcttctca gacgcctccc tctccttcaa atccgccacc gattccagcg tcactcccat  60

gcatgcccaa ccgggacaga tcttgccgtg cgtaggaatt atg gcg aat ctt ccc    115
                                        Met Ala Asn Leu Pro
                                          1               5

caa gag ggt ttt tct gtg gtg cac gga att ttg gcg gat ccc cgc att    163
Gln Glu Gly Phe Ser Val Val His Gly Ile Leu Ala Asp Pro Arg Ile
                 10                  15                  20

tgg ggc ccg gag att ccg tat gtt cgt gaa gaa gca ggt caa gta aat    211
Trp Gly Pro Glu Ile Pro Tyr Val Arg Glu Glu Ala Gly Gln Val Asn
             25                  30                  35

gtg gaa gca ccc gac gag gct ggc gat cta gcc cga ttg acg ttg cct    259
Val Glu Ala Pro Asp Glu Ala Gly Asp Leu Ala Arg Leu Thr Leu Pro
         40                  45                  50
```

```
ctg cag ttg atc ctg ctc acg gag gaa gag ttt gcc atc gct ctc aac   307
Leu Gln Leu Ile Leu Leu Thr Glu Glu Glu Phe Ala Ile Ala Leu Asn
     55                  60                  65

gag ggc agc gac gtc atg ttc gaa cga atg gcg gag caa gaa gtc gat   355
Glu Gly Ser Asp Val Met Phe Glu Arg Met Ala Glu Gln Glu Val Asp
 70                  75                  80                  85

ctt ctg gat ctg aaa cgt taagacggta ggctcaattc cgt                 396
Leu Leu Asp Leu Lys Arg
                 90


<210> 1574
<211> 91
<212> PRT
<213> Corynebacterium glutamicum

<400> 1574
Met Ala Asn Leu Pro Gln Glu Gly Phe Ser Val Val His Gly Ile Leu
  1               5                  10                  15

Ala Asp Pro Arg Ile Trp Gly Pro Glu Ile Pro Tyr Val Arg Glu Glu
             20                  25                  30

Ala Gly Gln Val Asn Val Glu Ala Pro Asp Glu Ala Gly Asp Leu Ala
         35                  40                  45

Arg Leu Thr Leu Pro Leu Gln Leu Ile Leu Leu Thr Glu Glu Glu Phe
     50                  55                  60

Ala Ile Ala Leu Asn Glu Gly Ser Asp Val Met Phe Glu Arg Met Ala
 65                  70                  75                  80

Glu Gln Glu Val Asp Leu Leu Asp Leu Lys Arg
                 85                  90


<210> 1575
<211> 705
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(682)
<223> RXA00068

<400> 1575
ggctgctaaa cggcaaccaa tagagcgata attcgctaag gcgaatgtaa tcgcagcaac 60

atatagcacc ggcttaacag gccggtgcta ttctgttcgc atg act tcg aag gat   115
                                           Met Thr Ser Lys Asp
                                             1               5

ctg att gtg acc tcc tat acg tct tgg ggc aag cgt ttc aag aat gac   163
Leu Ile Val Thr Ser Tyr Thr Ser Trp Gly Lys Arg Phe Lys Asn Asp
                 10                  15                  20

ggg aag ctt ttt att aac cta ctt cgc agc acc act gat agt gct gat   211
```

```
Gly Lys Leu Phe Ile Asn Leu Leu Arg Ser Thr Thr Asp Ser Ala Asp
             25                  30                  35

gaa aag gtt tta gcc act ttc ggt gaa gtt ccc agc aaa tca ttt gaa   259
Glu Lys Val Leu Ala Thr Phe Gly Glu Val Pro Ser Lys Ser Phe Glu
         40                  45                  50

acc acc gca acg gtt gat gag cag cag tgg gaa ctg tcc ttc agt att   307
Thr Thr Ala Thr Val Asp Glu Gln Gln Trp Glu Leu Ser Phe Ser Ile
     55                  60                  65

gat gga acg gca act gcc aag ctt cct gat ggt cgt gtg ttc agc gcg   355
Asp Gly Thr Ala Thr Ala Lys Leu Pro Asp Gly Arg Val Phe Ser Ala
 70                  75                  80                  85

aat gca ggt gag aag acc ttt acc aag tcc aag cgg att gaa atc gac   403
Asn Ala Gly Glu Lys Thr Phe Thr Lys Ser Lys Arg Ile Glu Ile Asp
                 90                  95                 100

atg gac ggc acc gcg atg gct gct gtt aat gaa gat aaa aac aat tgg   451
Met Asp Gly Thr Ala Met Ala Ala Val Asn Glu Asp Lys Asn Asn Trp
            105                 110                 115

att atc gac gat tct gaa gag aat aaa gtc gct cag ttt acc ggt atg   499
Ile Ile Asp Asp Ser Glu Glu Asn Lys Val Ala Gln Phe Thr Gly Met
        120                 125                 130

aac aac ggt gtg cgt cgc gcg att gtg gag ttt gag cct gac gta gaa   547
Asn Asn Gly Val Arg Arg Ala Ile Val Glu Phe Glu Pro Asp Val Glu
    135                 140                 145

gtc acc cag gag cag gaa att ttc ttg tcg tgg gtt gct cgg aaa act   595
Val Thr Gln Glu Gln Glu Ile Phe Leu Ser Trp Val Ala Arg Lys Thr
150                 155                 160                 165

ctg gaa tcc cgc atg ttg ggc tcc agt tgg gga ctg act ctg ttt ttg   643
Leu Glu Ser Arg Met Leu Gly Ser Ser Trp Gly Leu Thr Leu Phe Leu
                170                 175                 180

atc att ttg acg cca atc att att ttc ctc act ttc agc taaaaggacc    692
Ile Ile Leu Thr Pro Ile Ile Ile Phe Leu Thr Phe Ser
            185                 190

atgcaatggt aga                                                   705


<210> 1576
<211> 194
<212> PRT
<213> Corynebacterium glutamicum

<400> 1576
Met Thr Ser Lys Asp Leu Ile Val Thr Ser Tyr Thr Ser Trp Gly Lys
  1               5                  10                  15

Arg Phe Lys Asn Asp Gly Lys Leu Phe Ile Asn Leu Leu Arg Ser Thr
             20                  25                  30

Thr Asp Ser Ala Asp Glu Lys Val Leu Ala Thr Phe Gly Glu Val Pro
         35                  40                  45
```

```
Ser Lys Ser Phe Glu Thr Thr Ala Thr Val Asp Glu Gln Gln Trp Glu
     50                  55                  60

Leu Ser Phe Ser Ile Asp Gly Thr Ala Thr Ala Lys Leu Pro Asp Gly
 65                  70                  75                  80

Arg Val Phe Ser Ala Asn Ala Gly Glu Lys Thr Phe Thr Lys Ser Lys
                 85                  90                  95

Arg Ile Glu Ile Asp Met Asp Gly Thr Ala Met Ala Ala Val Asn Glu
            100                 105                 110

Asp Lys Asn Asn Trp Ile Ile Asp Asp Ser Glu Glu Asn Lys Val Ala
        115                 120                 125

Gln Phe Thr Gly Met Asn Asn Gly Val Arg Arg Ala Ile Val Glu Phe
    130                 135                 140

Glu Pro Asp Val Glu Val Thr Gln Glu Gln Glu Ile Phe Leu Ser Trp
145                 150                 155                 160

Val Ala Arg Lys Thr Leu Glu Ser Arg Met Leu Gly Ser Ser Trp Gly
                165                 170                 175

Leu Thr Leu Phe Leu Ile Ile Leu Thr Pro Ile Ile Ile Phe Leu Thr
            180                 185                 190

Phe Ser
```

<210> 1577
<211> 345
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(322)
<223> RXA00079

<400> 1577

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gatagcgcgc gatcttccta ggctgcccgc ttgggcttca ggtttagcaa gcgggacgct 60

ttcgcttatc gacgccaact ccctccattt ggaatccccc atg ggc cta gtt cac   115
                                              Met Gly Leu Val His
                                                1               5

acc gaa ttc acc cca ata aac acc tac gga atc ctc gac cac gta gtc   163
Thr Glu Phe Thr Pro Ile Asn Thr Tyr Gly Ile Leu Asp His Val Val
                10                  15                  20

acc ctc ccc gac gga act aaa gtg ctc aac cct ttc cga gtc atc ccc   211
Thr Leu Pro Asp Gly Thr Lys Val Leu Asn Pro Phe Arg Val Ile Pro
            25                  30                  35

cac gac acc ggc tcc gaa ctc att ttc acc gtc cgc ccc aac gaa aac   259
His Asp Thr Gly Ser Glu Leu Ile Phe Thr Val Arg Pro Asn Glu Asn
        40                  45                  50

ttc gaa gaa gat tgc caa gca gtc gca gca gac ctc gaa agg ctg gtc   307
```

```
Phe Glu Glu Asp Cys Gln Ala Val Ala Ala Asp Leu Glu Arg Leu Val
     55                  60                  65

gca ctg gcc gaa aaa tgaccccaca gaatggtctc taa                    345
Ala Leu Ala Glu Lys
 70


<210> 1578
<211> 74
<212> PRT
<213> Corynebacterium glutamicum

<400> 1578
Met Gly Leu Val His Thr Glu Phe Thr Pro Ile Asn Thr Tyr Gly Ile
  1               5                  10                  15

Leu Asp His Val Val Thr Leu Pro Asp Gly Thr Lys Val Leu Asn Pro
             20                  25                  30

Phe Arg Val Ile Pro His Asp Thr Gly Ser Glu Leu Ile Phe Thr Val
         35                  40                  45

Arg Pro Asn Glu Asn Phe Glu Glu Asp Cys Gln Ala Val Ala Ala Asp
     50                  55                  60

Leu Glu Arg Leu Val Ala Leu Ala Glu Lys
 65                  70


<210> 1579
<211> 666
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (80)..(643)
<223> RXA00082

<400> 1579
cacttgaagg cgaagaactc gaccagtttg ttgaagatga aattgaccga attgatcagc 60

tattcaagaa gatgggctagtg aac gtc act gaa caa tcc ggc gag tcc cat   112
                    Val Asn Val Thr Glu Gln Ser Gly Glu Ser His
                      1               5                  10

atc gac atc ccg gaa tca cac cag ctg ccc gga cct cgt cca gtt ggc   160
Ile Asp Ile Pro Glu Ser His Gln Leu Pro Gly Pro Arg Pro Val Gly
             15                  20                  25

gag ggc act ttc tgg gaa ggc cgc tcc ggg ctc atc atg ccc gca att   208
Glu Gly Thr Phe Trp Glu Gly Arg Ser Gly Leu Ile Met Pro Ala Ile
         30                  35                  40

ctt acg gca ttt agt ttg tat ttg ctc atc ggt gtt tta aac atg gat   256
Leu Thr Ala Phe Ser Leu Tyr Leu Leu Ile Gly Val Leu Asn Met Asp
     45                  50                  55

gtg ggc aat gca gca ttc cca gga cct cga ttc ttc cca aca atc ctc   304
Val Gly Asn Ala Ala Phe Pro Gly Pro Arg Phe Phe Pro Thr Ile Leu
```

```
 60                  65                  70                  75

ggc atc gcg ggt ttg ttg gtg gca gtg gca ttg acc att caa acc atc   352
Gly Ile Ala Gly Leu Leu Val Ala Val Ala Leu Thr Ile Gln Thr Ile
                 80                  85                  90

aag tac ccc atg cat cca gaa aat gaa tct ggc cga agc tgg aaa ttc   400
Lys Tyr Pro Met His Pro Glu Asn Glu Ser Gly Arg Ser Trp Lys Phe
             95                 100                 105

cac tct gat tac gtc tca ctc gcg tgg gcg atc ggt ggc ttc ttc gcc   448
His Ser Asp Tyr Val Ser Leu Ala Trp Ala Ile Gly Gly Phe Phe Ala
        110                 115                 120

ttt gca gtc ttg ctt cca tat ctt ggc tgg gtc ctt gct ggc tcc ttg   496
Phe Ala Val Leu Leu Pro Tyr Leu Gly Trp Val Leu Ala Gly Ser Leu
    125                 130                 135

ttg ttc tgg aca atg acc agg gct ttc ggt tcc aaa cgc cca ggt ttc   544
Leu Phe Trp Thr Met Thr Arg Ala Phe Gly Ser Lys Arg Pro Gly Phe
140                 145                 150                 155

gat gtt ctt gtt tcc ctc atg atg agc tcc gtg gtc tac ctc gca ttc   592
Asp Val Leu Val Ser Leu Met Met Ser Ser Val Val Tyr Leu Ala Phe
                160                 165                 170

gat gtg ggc ttg gga ctt aat ctt cct tcc gga ctt ttg ggt ggt ggc   640
Asp Val Gly Leu Gly Leu Asn Leu Pro Ser Gly Leu Leu Gly Gly Gly
            175                 180                 185

ttt taatggatat tttgtccctc ttg                                    666
Phe
```

20050070160

```
<210> 1580
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 1580
Val Asn Val Thr Glu Gln Ser Gly Glu Ser His Ile Asp Ile Pro Glu
  1               5                  10                  15

Ser His Gln Leu Pro Gly Pro Arg Pro Val Gly Glu Gly Thr Phe Trp
             20                  25                  30

Glu Gly Arg Ser Gly Leu Ile Met Pro Ala Ile Leu Thr Ala Phe Ser
         35                  40                  45

Leu Tyr Leu Leu Ile Gly Val Leu Asn Met Asp Val Gly Asn Ala Ala
     50                  55                  60

Phe Pro Gly Pro Arg Phe Phe Pro Thr Ile Leu Gly Ile Ala Gly Leu
 65                  70                  75                  80

Leu Val Ala Val Ala Leu Thr Ile Gln Thr Ile Lys Tyr Pro Met His
                 85                  90                  95

Pro Glu Asn Glu Ser Gly Arg Ser Trp Lys Phe His Ser Asp Tyr Val
            100                 105                 110
```

```
Ser Leu Ala Trp Ala Ile Gly Gly Phe Phe Ala Phe Ala Val Leu Leu
        115                 120                 125

Pro Tyr Leu Gly Trp Val Leu Ala Gly Ser Leu Leu Phe Trp Thr Met
    130                 135                 140

Thr Arg Ala Phe Gly Ser Lys Arg Pro Gly Phe Asp Val Leu Val Ser
145                 150                 155                 160

Leu Met Met Ser Ser Val Val Tyr Leu Ala Phe Asp Val Gly Leu Gly
                165                 170                 175

Leu Asn Leu Pro Ser Gly Leu Leu Gly Gly Gly Phe
            180                 185


<210> 1581
<211> 423
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(400)
<223> RXA00083

<400> 1581
gaagatacag ggggccacgg tggggtggtg aacaagagca ggcacgaggc ctggtagata 60

cggattcgac caagaaaacg tacaccactc aggagcactc gtg ctt gcc ctt cca   115
                                            Val Leu Ala Leu Pro
                                              1               5

tcc tct atc atc gac ccc ctc tgg tgc cag ttc gcc gcg ctg atc cca   163
Ser Ser Ile Ile Asp Pro Leu Trp Cys Gln Phe Ala Ala Leu Ile Pro
                  10                  15                  20

ccc gtg acc gac acc cac cca ctt cgg tgc cac cgc cca cgc atc ccg   211
Pro Val Thr Asp Thr His Pro Leu Arg Cys His Arg Pro Arg Ile Pro
             25                  30                  35

gac cgg atc atc ttc gac aag ctc atc cag gtc ctc gtc ctc ggc gcc   259
Asp Arg Ile Ile Phe Asp Lys Leu Ile Gln Val Leu Val Leu Gly Ala
         40                  45                  50

tcc tat gcc aag atc gcc gac acg aca tgc tcg gcc acc acc ttg cgc   307
Ser Tyr Ala Lys Ile Ala Asp Thr Thr Cys Ser Ala Thr Thr Leu Arg
     55                  60                  65

acc cgc cgg gac gag tgg atc acc gct ggc atc ttc gag cag ctg gaa   355
Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile Phe Glu Gln Leu Glu
 70                  75                  80                  85

cag atc tgt ttg gaa ttc tac gac cgt atc gtc gga ctc gat ctc       400
Gln Ile Cys Leu Glu Phe Tyr Asp Arg Ile Val Gly Leu Asp Leu
                 90                  95                 100

taagttcgga ttggctcgaa ttg                                        423
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<210> 1582
<211> 100
<212> PRT
<213> Corynebacterium glutamicum

<400> 1582
Val Leu Ala Leu Pro Ser Ser Ile Ile Asp Pro Leu Trp Cys Gln Phe
1 5 10 15

Ala Ala Leu Ile Pro Pro Val Thr Asp Thr His Pro Leu Arg Cys His
20 25 30

Arg Pro Arg Ile Pro Asp Arg Ile Ile Phe Asp Lys Leu Ile Gln Val
35 40 45

Leu Val Leu Gly Ala Ser Tyr Ala Lys Ile Ala Asp Thr Thr Cys Ser
50 55 60

Ala Thr Thr Leu Arg Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile
65 70 75 80

Phe Glu Gln Leu Glu Gln Ile Cys Leu Glu Phe Tyr Asp Arg Ile Val
85 90 95

Gly Leu Asp Leu
100

<210> 1583
<211> 2346
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2323)
<223> RXA00093

<400> 1583
aaagaatcga ttccggtgcc gcaggcctcc ttgtcaccca cgaaccccgc ttcgccgcgt 60

gggcagaccg aacaatcatg cttagggatg gtgaaatcca gtg acc aca ctt cta 115
Val Thr Thr Leu Leu
1 5

gca gca acc cgc ccc acc ctg cgc gat gcc ttt aaa cac cca tgg cga 163
Ala Ala Thr Arg Pro Thr Leu Arg Asp Ala Phe Lys His Pro Trp Arg
10 15 20

tcg ctg gca gcc atc ttg ttg gtg gcc gta ccg atg ttc ctg gtg agt 211
Ser Leu Ala Ala Ile Leu Leu Val Ala Val Pro Met Phe Leu Val Ser
25 30 35

ttc ttt ctt acc tat gat caa tca atc aac aat gca gct agc tat cct 259
Phe Phe Leu Thr Tyr Asp Gln Ser Ile Asn Asn Ala Ala Ser Tyr Pro
40 45 50

ggt tcc cag gta caa gct cac tat gac gga gaa gga gcc tac caa ctc 307
Gly Ser Gln Val Gln Ala His Tyr Asp Gly Glu Gly Ala Tyr Gln Leu
55 60 65

```
ctc caa gaa aac ctt cca gaa gac ttc cac ctg gaa ctc ttt gcc aat   355
Leu Gln Glu Asn Leu Pro Glu Asp Phe His Leu Glu Leu Phe Ala Asn
 70                  75                  80                  85

ggt tat cca gaa gtc tcc ttc ggt gat gaa gaa gtc aat ttc ttt gtt   403
Gly Tyr Pro Glu Val Ser Phe Gly Asp Glu Glu Val Asn Phe Phe Val
                 90                  95                 100

gtg caa tca aca aac gta caa caa gcc tca ttt ccc gcc gat gca ctc   451
Val Gln Ser Thr Asn Val Gln Gln Ala Ser Phe Pro Ala Asp Ala Leu
            105                 110                 115

gat gtt tta ggt gcc aca atc ggt gat acc gtg acc att cac ggc acc   499
Asp Val Leu Gly Ala Thr Ile Gly Asp Thr Val Thr Ile His Gly Thr
        120                 125                 130

ccg gtg gaa gtt cag tcg att tct ccc aca aat atc tta ttg ccc gaa   547
Pro Val Glu Val Gln Ser Ile Ser Pro Thr Asn Ile Leu Leu Pro Glu
    135                 140                 145

ggt act ctg ttt tct ctt gag aat ttc tcc gaa tca gaa act ttt tcc   595
Gly Thr Leu Phe Ser Leu Glu Asn Phe Ser Glu Ser Glu Thr Phe Ser
150                 155                 160                 165

ggc acc tgg tac ttc ccc gga tcg aat ttc acc gaa gaa aac cga caa   643
Gly Thr Trp Tyr Phe Pro Gly Ser Asn Phe Thr Glu Glu Asn Arg Gln
                170                 175                 180

gca cta gaa gca gtt ggc ttt gaa gtt aat gaa tat cgg cgc ggc ccc   691
Ala Leu Glu Ala Val Gly Phe Glu Val Asn Glu Tyr Arg Arg Gly Pro
            185                 190                 195

ata tcc gtc gac cca aat ttg atc cca agc tac atc atg gga ttt tta   739
Ile Ser Val Asp Pro Asn Leu Ile Pro Ser Tyr Ile Met Gly Phe Leu
        200                 205                 210

tcg acg aca att ctc gcc gtc gtt gca ctc atg ctg atc tca cca gta   787
Ser Thr Thr Ile Leu Ala Val Val Ala Leu Met Leu Ile Ser Pro Val
    215                 220                 225

ttt aca att tcc gcc tca agg caa acc aga act ttc gca ctg ctc gcc   835
Phe Thr Ile Ser Ala Ser Arg Gln Thr Arg Thr Phe Ala Leu Leu Ala
230                 235                 240                 245

tca cag ggt gcc aca cct aga cac att cgg tgg gca gtg ctt aca tat   883
Ser Gln Gly Ala Thr Pro Arg His Ile Arg Trp Ala Val Leu Thr Tyr
                250                 255                 260

ggg ctc ttc gca ggt ctt gtt ggg gca tcc att ggt tta gtt ctg ggg   931
Gly Leu Phe Ala Gly Leu Val Gly Ala Ser Ile Gly Leu Val Leu Gly
            265                 270                 275

caa ata ggc atc tac ggc tgg tgg aaa tac acc tat cct gaa ttc tcc   979
Gln Ile Gly Ile Tyr Gly Trp Trp Lys Tyr Thr Tyr Pro Glu Phe Ser
        280                 285                 290

ctc acc acc ccc tgg cta gtt ctt gta ggt ttt tgg gcg ctg gca atc   1027
Leu Thr Thr Pro Trp Leu Val Leu Val Gly Phe Trp Ala Leu Ala Ile
    295                 300                 305

atc gct tca acg att gct gca ttc tta ccg gca gtt ttt gtc agt aga   1075
```

```
Ile Ala Ser Thr Ile Ala Ala Phe Leu Pro Ala Val Phe Val Ser Arg
310                 315                 320                 325

tca agc atc atc aac gga atc tac gga gga atc tcc gac aaa atc atc   1123
Ser Ser Ile Ile Asn Gly Ile Tyr Gly Gly Ile Ser Asp Lys Ile Ile
                330                 335                 340

cgg tgg agc cct cga atg ctc atc ggg cca atc gtc tta att gca gct   1171
Arg Trp Ser Pro Arg Met Leu Ile Gly Pro Ile Val Leu Ile Ala Ala
            345                 350                 355

gcg gta atc gcc ttg ttt atc ggt gac gga gag tgg gga ggc gtc gtc   1219
Ala Val Ile Ala Leu Phe Ile Gly Asp Gly Glu Trp Gly Gly Val Val
        360                 365                 370

aag caa tta tgc ttc ctg gca gcc gtc atc gcc ctg ccg gcc tca gtg   1267
Lys Gln Leu Cys Phe Leu Ala Ala Val Ile Ala Leu Pro Ala Ser Val
    375                 380                 385

cct gcg gtg ttg tgg gcg ctt ggg cgc ctg cct ggt ttg aca ttc aaa   1315
Pro Ala Val Leu Trp Ala Leu Gly Arg Leu Pro Gly Leu Thr Phe Lys
390                 395                 400                 405

cta gct acg cgc gat atg ctg cgc cga tca atg cac tcc att cct gcg   1363
Leu Ala Thr Arg Asp Met Leu Arg Arg Ser Met His Ser Ile Pro Ala
                410                 415                 420

att ggt gcg ctg gcg gca gtg att atg ctt ggt aca ttt atg caa aca   1411
Ile Gly Ala Leu Ala Ala Val Ile Met Leu Gly Thr Phe Met Gln Thr
            425                 430                 435

act gga ctt gca acc caa gcc agc gat aga gaa gct acc gcc tcg gtg   1459
Thr Gly Leu Ala Thr Gln Ala Ser Asp Arg Glu Ala Thr Ala Ser Val
        440                 445                 450

tat cct gag gcc gta ttc tta cgc ggt gac aca caa atc cct gga ctc   1507
Tyr Pro Glu Ala Val Phe Leu Arg Gly Asp Thr Gln Ile Pro Gly Leu
    455                 460                 465

atg ggg caa aaa atc gat gta tac ggt gat aac cat ggc ttt ggt atc   1555
Met Gly Gln Lys Ile Asp Val Tyr Gly Asp Asn His Gly Phe Gly Ile
470                 475                 480                 485

tat gaa cta gat gta gat ttt tac tcg gcc aac tat gtg ccc gca ctg   1603
Tyr Glu Leu Asp Val Asp Phe Tyr Ser Ala Asn Tyr Val Pro Ala Leu
                490                 495                 500

acc tca ttt ttt ggc gga cca gtt att gcc acg ccc aag att tta gac   1651
Thr Ser Phe Phe Gly Gly Pro Val Ile Ala Thr Pro Lys Ile Leu Asp
            505                 510                 515

atg ttc ggt gtc cac gaa caa gcc gac atc tac gcg cca tca acc tat   1699
Met Phe Gly Val His Glu Gln Ala Asp Ile Tyr Ala Pro Ser Thr Tyr
        520                 525                 530

aat tcc ggg ctg caa gaa tac gca ata tac ccc ggc gat gaa acc tac   1747
Asn Ser Gly Leu Gln Glu Tyr Ala Ile Tyr Pro Gly Asp Glu Thr Tyr
    535                 540                 545

atg cta gac acc gct gct gtt tta ccg ccg ctg tac tca cat gtt tta   1795
Met Leu Asp Thr Ala Ala Val Leu Pro Pro Leu Tyr Ser His Val Leu
```

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550                 555                 560                 565

tta agc cca gaa act ttt gaa gaa atc gga gga caa aca gaa ttc ttg   1843
Leu Ser Pro Glu Thr Phe Glu Glu Ile Gly Gly Gln Thr Glu Phe Leu
                570                 575                 580

gga aca atc gtg ctt ccc caa gaa cta gat gac caa act gta caa gca   1891
Gly Thr Ile Val Leu Pro Gln Glu Leu Asp Asp Gln Thr Val Gln Ala
            585                 590                 595

atc aat cgg tca aga gat gcg cat ttc agc cac gac ggc cat aat tct   1939
Ile Asn Arg Ser Arg Asp Ala His Phe Ser His Asp Gly His Asn Ser
        600                 605                 610

tca ctt gct tcc agt gct gca cta act gcg gtg gca att gtg gtc gtt   1987
Ser Leu Ala Ser Ser Ala Ala Leu Thr Ala Val Ala Ile Val Val Val
    615                 620                 625

tcc ctt gtg atc gtg ctg gct aat cgc aaa ctc caa cag cac gca ttg   2035
Ser Leu Val Ile Val Leu Ala Asn Arg Lys Leu Gln Gln His Ala Leu
630                 635                 640                 645

att gcc atc gga gca aca cct gga aca atc tac aaa gtc aat gcc tta   2083
Ile Ala Ile Gly Ala Thr Pro Gly Thr Ile Tyr Lys Val Asn Ala Leu
                650                 655                 660

aat gca gcg ttg ctt gcc ctt gtc gga ggc atc atg ggc ctt gtc tcc   2131
Asn Ala Ala Leu Leu Ala Leu Val Gly Gly Ile Met Gly Leu Val Ser
            665                 670                 675

gga tgg att gca gcg ctg ctg aca ggc acc act gat gaa att gtt gat   2179
Gly Trp Ile Ala Ala Leu Leu Thr Gly Thr Thr Asp Glu Ile Val Asp
        680                 685                 690

gga gca att ttg aac tac ggc acg ctt gaa cac atg atg ctg ccg tgg   2227
Gly Ala Ile Leu Asn Tyr Gly Thr Leu Glu His Met Met Leu Pro Trp
    695                 700                 705

cct ctg ttg gta agc ctc ctc gtt gtg gcg ccg ctg gtg tgc gcc gtg   2275
Pro Leu Leu Val Ser Leu Leu Val Val Ala Pro Leu Val Cys Ala Val
710                 715                 720                 725

att ggg gct ata gct tct cca tcg gga cgc cac caa gaa gca tca atc   2323
Ile Gly Ala Ile Ala Ser Pro Ser Gly Arg His Gln Glu Ala Ser Ile
                730                 735                 740

taaccttgcc ggaggaaccg aaa                                       2346
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<210> 1584
<211> 741
<212> PRT
<213> Corynebacterium glutamicum

<400> 1584

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Val Thr Thr Leu Leu Ala Ala Thr Arg Pro Thr Leu Arg Asp Ala Phe
  1               5                  10                  15

Lys His Pro Trp Arg Ser Leu Ala Ala Ile Leu Leu Val Ala Val Pro
             20                  25                  30
```

```
Met Phe Leu Val Ser Phe Phe Leu Thr Tyr Asp Gln Ser Ile Asn Asn
          35                  40                  45

Ala Ala Ser Tyr Pro Gly Ser Gln Val Gln Ala His Tyr Asp Gly Glu
      50                  55                  60

Gly Ala Tyr Gln Leu Leu Gln Glu Asn Leu Pro Glu Asp Phe His Leu
 65                  70                  75                  80

Glu Leu Phe Ala Asn Gly Tyr Pro Glu Val Ser Phe Gly Asp Glu Glu
                 85                  90                  95

Val Asn Phe Phe Val Val Gln Ser Thr Asn Val Gln Gln Ala Ser Phe
            100                 105                 110

Pro Ala Asp Ala Leu Asp Val Leu Gly Ala Thr Ile Gly Asp Thr Val
        115                 120                 125

Thr Ile His Gly Thr Pro Val Glu Val Gln Ser Ile Ser Pro Thr Asn
    130                 135                 140

Ile Leu Leu Pro Glu Gly Thr Leu Phe Ser Leu Glu Asn Phe Ser Glu
145                 150                 155                 160

Ser Glu Thr Phe Ser Gly Thr Trp Tyr Phe Pro Gly Ser Asn Phe Thr
                165                 170                 175

Glu Glu Asn Arg Gln Ala Leu Glu Ala Val Gly Phe Glu Val Asn Glu
            180                 185                 190

Tyr Arg Arg Gly Pro Ile Ser Val Asp Pro Asn Leu Ile Pro Ser Tyr
        195                 200                 205

Ile Met Gly Phe Leu Ser Thr Thr Ile Leu Ala Val Val Ala Leu Met
    210                 215                 220

Leu Ile Ser Pro Val Phe Thr Ile Ser Ala Ser Arg Gln Thr Arg Thr
225                 230                 235                 240

Phe Ala Leu Leu Ala Ser Gln Gly Ala Thr Pro Arg His Ile Arg Trp
                245                 250                 255

Ala Val Leu Thr Tyr Gly Leu Phe Ala Gly Leu Val Gly Ala Ser Ile
            260                 265                 270

Gly Leu Val Leu Gly Gln Ile Gly Ile Tyr Gly Trp Trp Lys Tyr Thr
        275                 280                 285

Tyr Pro Glu Phe Ser Leu Thr Thr Pro Trp Leu Val Leu Val Gly Phe
    290                 295                 300

Trp Ala Leu Ala Ile Ile Ala Ser Thr Ile Ala Ala Phe Leu Pro Ala
305                 310                 315                 320

Val Phe Val Ser Arg Ser Ser Ile Ile Asn Gly Ile Tyr Gly Gly Ile
                325                 330                 335

Ser Asp Lys Ile Ile Arg Trp Ser Pro Arg Met Leu Ile Gly Pro Ile
            340                 345                 350

Val Leu Ile Ala Ala Ala Val Ile Ala Leu Phe Ile Gly Asp Gly Glu
```

```
        355                 360                 365

Trp Gly Gly Val Val Lys Gln Leu Cys Phe Leu Ala Ala Val Ile Ala
    370                 375                 380

Leu Pro Ala Ser Val Pro Ala Val Leu Trp Ala Leu Gly Arg Leu Pro
385                 390                 395                 400

Gly Leu Thr Phe Lys Leu Ala Thr Arg Asp Met Leu Arg Arg Ser Met
                405                 410                 415

His Ser Ile Pro Ala Ile Gly Ala Leu Ala Ala Val Ile Met Leu Gly
            420                 425                 430

Thr Phe Met Gln Thr Thr Gly Leu Ala Thr Gln Ala Ser Asp Arg Glu
        435                 440                 445

Ala Thr Ala Ser Val Tyr Pro Glu Ala Val Phe Leu Arg Gly Asp Thr
    450                 455                 460

Gln Ile Pro Gly Leu Met Gly Gln Lys Ile Asp Val Tyr Gly Asp Asn
465                 470                 475                 480

His Gly Phe Gly Ile Tyr Glu Leu Asp Val Asp Phe Tyr Ser Ala Asn
                485                 490                 495

Tyr Val Pro Ala Leu Thr Ser Phe Phe Gly Gly Pro Val Ile Ala Thr
            500                 505                 510

Pro Lys Ile Leu Asp Met Phe Gly Val His Glu Gln Ala Asp Ile Tyr
        515                 520                 525

Ala Pro Ser Thr Tyr Asn Ser Gly Leu Gln Glu Tyr Ala Ile Tyr Pro
    530                 535                 540

Gly Asp Glu Thr Tyr Met Leu Asp Thr Ala Ala Val Leu Pro Pro Leu
545                 550                 555                 560

Tyr Ser His Val Leu Leu Ser Pro Glu Thr Phe Glu Glu Ile Gly Gly
                565                 570                 575

Gln Thr Glu Phe Leu Gly Thr Ile Val Leu Pro Gln Glu Leu Asp Asp
            580                 585                 590

Gln Thr Val Gln Ala Ile Asn Arg Ser Arg Asp Ala His Phe Ser His
        595                 600                 605

Asp Gly His Asn Ser Ser Leu Ala Ser Ser Ala Ala Leu Thr Ala Val
    610                 615                 620

Ala Ile Val Val Val Ser Leu Val Ile Val Leu Ala Asn Arg Lys Leu
625                 630                 635                 640

Gln Gln His Ala Leu Ile Ala Ile Gly Ala Thr Pro Gly Thr Ile Tyr
                645                 650                 655

Lys Val Asn Ala Leu Asn Ala Ala Leu Leu Ala Leu Val Gly Gly Ile
            660                 665                 670

Met Gly Leu Val Ser Gly Trp Ile Ala Ala Leu Leu Thr Gly Thr Thr
        675                 680                 685
```

```
Asp Glu Ile Val Asp Gly Ala Ile Leu Asn Tyr Gly Thr Leu Glu His
    690                 695                 700

Met Met Leu Pro Trp Pro Leu Leu Val Ser Leu Leu Val Val Ala Pro
705                 710                 715                 720

Leu Val Cys Ala Val Ile Gly Ala Ile Ala Ser Pro Ser Gly Arg His
                725                 730                 735

Gln Glu Ala Ser Ile
            740


<210> 1585
<211> 531
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> RXA00101

<400> 1585
taaaccgtgc aggagatgcc gaaccccaat cgtgaaagcc gagttggggg agcgaataat 60

ctggtggtgt ccgcgctgcc aaccgctaaa ctcgtgaagc atg aga cta ata ctc   115
                                            Met Arg Leu Ile Leu
                                              1               5

aac ctg att tgg tta ttc ttc ggt ggc att tgg ctc gcg ttg gga tac   163
Asn Leu Ile Trp Leu Phe Phe Gly Gly Ile Trp Leu Ala Leu Gly Tyr
                 10                  15                  20

gta ttc ttc gga atc atc gca tgt atc ttc atc gtg acg att ccc gcc   211
Val Phe Phe Gly Ile Ile Ala Cys Ile Phe Ile Val Thr Ile Pro Ala
             25                  30                  35

ggt atc gca agc ttc cgc atg gct aac tac gcg ctg tgg ccg ttt ggt   259
Gly Ile Ala Ser Phe Arg Met Ala Asn Tyr Ala Leu Trp Pro Phe Gly
         40                  45                  50

agg acg gtt gtt cgt aat cct aaa gcc gga ggg ttt tct gcc ctg agc   307
Arg Thr Val Val Arg Asn Pro Lys Ala Gly Gly Phe Ser Ala Leu Ser
     55                  60                  65

aac gga ctg tgg ttt atc att gct gga ctg tgg ctg gcg atc ggg cac   355
Asn Gly Leu Trp Phe Ile Ile Ala Gly Leu Trp Leu Ala Ile Gly His
 70                  75                  80                  85

ctc acc acc gcg gct gcc cag gcg atc acc atc atc gga att cca ctg   403
Leu Thr Thr Ala Ala Ala Gln Ala Ile Thr Ile Ile Gly Ile Pro Leu
                 90                  95                 100

gcg atc gca aac atc cga atg atc ccc gtg acg tgt ttc ccg ttc ggc   451
Ala Ile Ala Asn Ile Arg Met Ile Pro Val Thr Cys Phe Pro Phe Gly
            105                 110                 115

aaa gaa atc tat gac agc aac cgc att ccc ttc ggc tac gaa ccg atg   499
Lys Glu Ile Tyr Asp Ser Asn Arg Ile Pro Phe Gly Tyr Glu Pro Met
```

```
        120                 125                 130

gtt aag ttt taattcggcg acggactaaa cca                                  531
Val Lys Phe
    135


<210> 1586
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 1586
Met Arg Leu Ile Leu Asn Leu Ile Trp Leu Phe Phe Gly Gly Ile Trp
  1               5                  10                  15

Leu Ala Leu Gly Tyr Val Phe Phe Gly Ile Ile Ala Cys Ile Phe Ile
             20                  25                  30

Val Thr Ile Pro Ala Gly Ile Ala Ser Phe Arg Met Ala Asn Tyr Ala
         35                  40                  45

Leu Trp Pro Phe Gly Arg Thr Val Val Arg Asn Pro Lys Ala Gly Gly
     50                  55                  60

Phe Ser Ala Leu Ser Asn Gly Leu Trp Phe Ile Ile Ala Gly Leu Trp
 65                  70                  75                  80

Leu Ala Ile Gly His Leu Thr Thr Ala Ala Ala Gln Ala Ile Thr Ile
                 85                  90                  95

Ile Gly Ile Pro Leu Ala Ile Ala Asn Ile Arg Met Ile Pro Val Thr
            100                 105                 110

Cys Phe Pro Phe Gly Lys Glu Ile Tyr Asp Ser Asn Arg Ile Pro Phe
        115                 120                 125

Gly Tyr Glu Pro Met Val Lys Phe
    130                 135


<210> 1587
<211> 643
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(643)
<223> RXA00108

<400> 1587
gaattgggtt ttgagcatcg tggcggtgct tgttgttgca agtgccatcg tcatgatgat 60

tgcaaagaat cgtaaccaga ataagaggg tttattcacc atg aag aag ttt ttt   115
                                            Met Lys Lys Phe Phe
                                              1               5

gtc gca ggt gct gta ctg agc agt gcg ttg gtt atg gcg gcg tgt tcg   163
Val Ala Gly Ala Val Leu Ser Ser Ala Leu Val Met Ala Ala Cys Ser
                 10                  15                  20
```

```
cct gct aat caa agt gat tcc acc tcc acg agc gtg gag act act tcc   211
Pro Ala Asn Gln Ser Asp Ser Thr Ser Thr Ser Val Glu Thr Thr Ser
             25                  30                  35

tcc agc agc acg cag gta agc gat gct gtg atc acc acg gaa aac gct   259
Ser Ser Ser Thr Gln Val Ser Asp Ala Val Ile Thr Thr Glu Asn Ala
         40                  45                  50

gtt gtt cgt gcg tct gtg gag gac agc gac atg acg gca gtg ttc gct   307
Val Val Arg Ala Ser Val Glu Asp Ser Asp Met Thr Ala Val Phe Ala
     55                  60                  65

acg ttg gtg aac aat tct gat gat gag atc aac gtt tct ggc ttt act   355
Thr Leu Val Asn Asn Ser Asp Asp Glu Ile Asn Val Ser Gly Phe Thr
 70                  75                  80                  85

gct gat gtt gat gct gcc agc ttt gag gtc cat gag gtt gtt gat ggc   403
Ala Asp Val Asp Ala Ala Ser Phe Glu Val His Glu Val Val Asp Gly
                 90                  95                 100

gtc atg cag gaa aag cca ggt ggt ttt gtg atc cct gca ggg gag agc   451
Val Met Gln Glu Lys Pro Gly Gly Phe Val Ile Pro Ala Gly Glu Ser
             105                 110                 115

atc gag ctg gca cca ggt ggc gat cat ttg atg atc atg ggg ctt gcg   499
Ile Glu Leu Ala Pro Gly Gly Asp His Leu Met Ile Met Gly Leu Ala
         120                 125                 130

aac cca atc gag gct ggc gat gaa gtg acg gtc act ctt gaa ttg gct   547
Asn Pro Ile Glu Ala Gly Asp Glu Val Thr Val Thr Leu Glu Leu Ala
     135                 140                 145

gat ggt tct gaa gtt aag ctt gat ccg atc ccg gcg cgc acc att gct   595
Asp Gly Ser Glu Val Lys Leu Asp Pro Ile Pro Ala Arg Thr Ile Ala
150                 155                 160                 165

gct ggt gat gag gat tat ggc gat ctg gga act gaa ggc cac gag ggc   643
Ala Gly Asp Glu Asp Tyr Gly Asp Leu Gly Thr Glu Gly His Glu Gly
                170                 175                 180
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<210> 1588
<211> 181
<212> PRT
<213> Corynebacterium glutamicum

<400> 1588

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Met Lys Lys Phe Phe Val Ala Gly Ala Val Leu Ser Ser Ala Leu Val
  1               5                  10                  15

Met Ala Ala Cys Ser Pro Ala Asn Gln Ser Asp Ser Thr Ser Thr Ser
             20                  25                  30

Val Glu Thr Thr Ser Ser Ser Ser Thr Gln Val Ser Asp Ala Val Ile
         35                  40                  45

Thr Thr Glu Asn Ala Val Val Arg Ala Ser Val Glu Asp Ser Asp Met
     50                  55                  60

Thr Ala Val Phe Ala Thr Leu Val Asn Asn Ser Asp Asp Glu Ile Asn
```

```
 65                  70                  75                  80

Val Ser Gly Phe Thr Ala Asp Val Asp Ala Ala Ser Phe Glu Val His
                 85                  90                  95

Glu Val Val Asp Gly Val Met Gln Glu Lys Pro Gly Gly Phe Val Ile
            100                 105                 110

Pro Ala Gly Glu Ser Ile Glu Leu Ala Pro Gly Gly Asp His Leu Met
        115                 120                 125

Ile Met Gly Leu Ala Asn Pro Ile Glu Ala Gly Asp Glu Val Thr Val
    130                 135                 140

Thr Leu Glu Leu Ala Asp Gly Ser Glu Val Lys Leu Asp Pro Ile Pro
145                 150                 155                 160

Ala Arg Thr Ile Ala Ala Gly Asp Glu Asp Tyr Gly Asp Leu Gly Thr
                165                 170                 175

Glu Gly His Glu Gly
            180
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<210> 1589
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
<223> RXA00110

<400> 1589

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aataacgaac gctaatttta aacactggag gagcttccac gtg agc aac aaa gac   115
                                              Val Ser Asn Lys Asp
                                                1               5

ggc ctt ttt act gac ggt aac agc acg ttt gca cct aag gtg gat tca   163
Gly Leu Phe Thr Asp Gly Asn Ser Thr Phe Ala Pro Lys Val Asp Ser
                 10                  15                  20

att ccc ctc agc gat gtg gat acc agc gtt agc ggt gaa gcc tcc atc   211
Ile Pro Leu Ser Asp Val Asp Thr Ser Val Ser Gly Glu Ala Ser Ile
             25                  30                  35

ggc acg ctg atc tcc aac gca acc tcc caa atg tcc agc ctt ttc cgc   259
Gly Thr Leu Ile Ser Asn Ala Thr Ser Gln Met Ser Ser Leu Phe Arg
         40                  45                  50

gca gaa gtt gag ctg gcg aag act gaa ctc gca ggc gaa gcc aag aaa   307
Ala Glu Val Glu Leu Ala Lys Thr Glu Leu Ala Gly Glu Ala Lys Lys
     55                  60                  65

gct gcc atc ggc ggc ggc gca ttc agc gtt gct ggc gta atc gca ctg   355
Ala Ala Ile Gly Gly Gly Ala Phe Ser Val Ala Gly Val Ile Ala Leu
 70                  75                  80                  85
```

```
tac agc tcc ttc ttc ttt ttc ttc ttc gtc gca gca ctg ctg agc gag   403
Tyr Ser Ser Phe Phe Phe Phe Phe Phe Val Ala Ala Leu Leu Ser Glu
                 90                  95                 100

tgg att aag cct tgg gca gca ttc ctc atc gtg ttc ctc ttc atg ctg   451
Trp Ile Lys Pro Trp Ala Ala Phe Leu Ile Val Phe Leu Phe Met Leu
            105                 110                 115

gtc atc gcc gca gct ctc gca ctg ttc ggc tgg cgc aag gtg aag aag   499
Val Ile Ala Ala Ala Leu Ala Leu Phe Gly Trp Arg Lys Val Lys Lys
        120                 125                 130

atg ggc gct ccg aag aac acc atc caa tcg gtc aac caa ctg aag aac   547
Met Gly Ala Pro Lys Asn Thr Ile Gln Ser Val Asn Gln Leu Lys Asn
    135                 140                 145

ctg gtc cca ggt cag gca tcc gag aag ctg gag aag gcc aac aag cgt   595
Leu Val Pro Gly Gln Ala Ser Glu Lys Leu Glu Lys Ala Asn Lys Arg
150                 155                 160                 165

ggc ctc tac acc tcc gcg tcc ttc cac agc ccc ggc gcc atc act ggc   643
Gly Leu Tyr Thr Ser Ala Ser Phe His Ser Pro Gly Ala Ile Thr Gly
                170                 175                 180

gac cac taaaaaagga gacttcgatg gcc                                672
Asp His
```

<210> 1590
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 1590

```
Val Ser Asn Lys Asp Gly Leu Phe Thr Asp Gly Asn Ser Thr Phe Ala
  1               5                  10                  15

Pro Lys Val Asp Ser Ile Pro Leu Ser Asp Val Asp Thr Ser Val Ser
             20                  25                  30

Gly Glu Ala Ser Ile Gly Thr Leu Ile Ser Asn Ala Thr Ser Gln Met
         35                  40                  45

Ser Ser Leu Phe Arg Ala Glu Val Glu Leu Ala Lys Thr Glu Leu Ala
     50                  55                  60

Gly Glu Ala Lys Lys Ala Ala Ile Gly Gly Gly Ala Phe Ser Val Ala
 65                  70                  75                  80

Gly Val Ile Ala Leu Tyr Ser Ser Phe Phe Phe Phe Phe Phe Val Ala
                 85                  90                  95

Ala Leu Leu Ser Glu Trp Ile Lys Pro Trp Ala Ala Phe Leu Ile Val
            100                 105                 110

Phe Leu Phe Met Leu Val Ile Ala Ala Ala Leu Ala Leu Phe Gly Trp
        115                 120                 125

Arg Lys Val Lys Lys Met Gly Ala Pro Lys Asn Thr Ile Gln Ser Val
    130                 135                 140
```

```
Asn Gln Leu Lys Asn Leu Val Pro Gly Gln Ala Ser Glu Lys Leu Glu
145                 150                 155                 160

Lys Ala Asn Lys Arg Gly Leu Tyr Thr Ser Ala Ser Phe His Ser Pro
                165                 170                 175

Gly Ala Ile Thr Gly Asp His
            180
```

<210> 1591
<211> 714
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(691)
<223> RXA00117

<400> 1591

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gttgatccca cagtataccc ccacccctat cttgaatacc ccccagggta tatggcacac 60

ttggaatcgc ccatcacttt gagattgaaa aggacaaggt atg act tcc gct caa   115
                                            Met Thr Ser Ala Gln
                                              1               5

ccg att act tcc gta gat gca cag act cta aaa tcg tgg atc gat aag   163
Pro Ile Thr Ser Val Asp Ala Gln Thr Leu Lys Ser Trp Ile Asp Lys
                10                  15                  20

cat gaa gga ctc acc gtc att gac gtc cgc act gca cat gag ttt tca   211
His Glu Gly Leu Thr Val Ile Asp Val Arg Thr Ala His Glu Phe Ser
            25                  30                  35

aat ttg cac att aaa ggc tct tac aac gtg cct cta act aca ctt gct   259
Asn Leu His Ile Lys Gly Ser Tyr Asn Val Pro Leu Thr Thr Leu Ala
        40                  45                  50

gag cat tcc gaa gag att tcc tct cgt gtt gga gaa cat gtt gtt ttg   307
Glu His Ser Glu Glu Ile Ser Ser Arg Val Gly Glu His Val Val Leu
    55                  60                  65

gtg tgt caa tcc ggc att cga gca ggt cag gca caa caa aag ctg gca   355
Val Cys Gln Ser Gly Ile Arg Ala Gly Gln Ala Gln Gln Lys Leu Ala
70                  75                  80                  85

cct ttg gga att tcc acc gtg gct gtt ttg gag ggt ggc atc aat agt   403
Pro Leu Gly Ile Ser Thr Val Ala Val Leu Glu Gly Gly Ile Asn Ser
                90                  95                  100

ttt gct aag gct gac ggt gat gtg gtc cgc gga acc cag gtg tgg gat   451
Phe Ala Lys Ala Asp Gly Asp Val Val Arg Gly Thr Gln Val Trp Asp
            105                 110                 115

atc gaa cgt cag gtg cgt ttt gcc gct gga tca ttg gtg ctc gca ggg   499
Ile Glu Arg Gln Val Arg Phe Ala Ala Gly Ser Leu Val Leu Ala Gly
        120                 125                 130

ctt gcg gga ggt aaa ttc ctt tca cca aaa gtt cgc acc ctg tcg gga   547
```

```
Leu Ala Gly Gly Lys Phe Leu Ser Pro Lys Val Arg Thr Leu Ser Gly
    135                 140                 145

att att ggt gcg ggt ctg aca ttt tct ggc gtt tcc aac acc tgt gcc   595
Ile Ile Gly Ala Gly Leu Thr Phe Ser Gly Val Ser Asn Thr Cys Ala
150                 155                 160                 165

atg ggc aaa gct ctg tcc gcc ttg ccg tgg aat aaa act aag cca gtt   643
Met Gly Lys Ala Leu Ser Ala Leu Pro Trp Asn Lys Thr Lys Pro Val
                170                 175                 180

cct acc gaa acc gag aca ttg agc aag ctt cca agc cct aag gag aac   691
Pro Thr Glu Thr Glu Thr Leu Ser Lys Leu Pro Ser Pro Lys Glu Asn
            185                 190                 195

taaatgtcta tcaccattac tga                                        714


<210> 1592
<211> 197
<212> PRT
<213> Corynebacterium glutamicum

<400> 1592
Met Thr Ser Ala Gln Pro Ile Thr Ser Val Asp Ala Gln Thr Leu Lys
  1               5                  10                  15

Ser Trp Ile Asp Lys His Glu Gly Leu Thr Val Ile Asp Val Arg Thr
             20                  25                  30

Ala His Glu Phe Ser Asn Leu His Ile Lys Gly Ser Tyr Asn Val Pro
         35                  40                  45

Leu Thr Thr Leu Ala Glu His Ser Glu Glu Ile Ser Ser Arg Val Gly
     50                  55                  60

Glu His Val Val Leu Val Cys Gln Ser Gly Ile Arg Ala Gly Gln Ala
 65                  70                  75                  80

Gln Gln Lys Leu Ala Pro Leu Gly Ile Ser Thr Val Ala Val Leu Glu
                 85                  90                  95

Gly Gly Ile Asn Ser Phe Ala Lys Ala Asp Gly Asp Val Val Arg Gly
            100                 105                 110

Thr Gln Val Trp Asp Ile Glu Arg Gln Val Arg Phe Ala Ala Gly Ser
        115                 120                 125

Leu Val Leu Ala Gly Leu Ala Gly Gly Lys Phe Leu Ser Pro Lys Val
    130                 135                 140

Arg Thr Leu Ser Gly Ile Ile Gly Ala Gly Leu Thr Phe Ser Gly Val
145                 150                 155                 160

Ser Asn Thr Cys Ala Met Gly Lys Ala Leu Ser Ala Leu Pro Trp Asn
                165                 170                 175

Lys Thr Lys Pro Val Pro Thr Glu Thr Glu Thr Leu Ser Lys Leu Pro
            180                 185                 190

Ser Pro Lys Glu Asn
```

195

<210> 1593
<211> 378
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(355)
<223> RXA00118

<400> 1593
atgggcgatt ccaagtgtgc catataccct ggggggtatt caagataggg gtgggggtat 60

actgtgggat caacgttcca gggcaacaaa aggagaaaaa atg caa ctc aat cct 115
Met Gln Leu Asn Pro
1 5

gat gag atc acc cca gtg ctc aac cga ctc aag cgc gcc caa ggt caa 163
Asp Glu Ile Thr Pro Val Leu Asn Arg Leu Lys Arg Ala Gln Gly Gln
10 15 20

ctc acc gga gta atc cga atg ctt gat gaa ggc gaa gac tgt aaa gcc 211
Leu Thr Gly Val Ile Arg Met Leu Asp Glu Gly Glu Asp Cys Lys Ala
25 30 35

gta gtc acc caa ctt gcc gca gtc aca aaa gcg ctg gac agg gca ggc 259
Val Val Thr Gln Leu Ala Ala Val Thr Lys Ala Leu Asp Arg Ala Gly
40 45 50

ttc gcc atc att gcc aca ggt ttg gaa cag tgc ctc acc aac cct gat 307
Phe Ala Ile Ile Ala Thr Gly Leu Glu Gln Cys Leu Thr Asn Pro Asp
55 60 65

ggc gac atg gac aaa aag gaa cta gaa aaa ctg ttc ctg tcg ctg gct 355
Gly Asp Met Asp Lys Lys Glu Leu Glu Lys Leu Phe Leu Ser Leu Ala
70 75 80 85

taactatggc ctagttcagg gcg 378

<210> 1594
<211> 85
<212> PRT
<213> Corynebacterium glutamicum

<400> 1594
Met Gln Leu Asn Pro Asp Glu Ile Thr Pro Val Leu Asn Arg Leu Lys
1 5 10 15

Arg Ala Gln Gly Gln Leu Thr Gly Val Ile Arg Met Leu Asp Glu Gly
20 25 30

Glu Asp Cys Lys Ala Val Val Thr Gln Leu Ala Ala Val Thr Lys Ala
35 40 45

Leu Asp Arg Ala Gly Phe Ala Ile Ile Ala Thr Gly Leu Glu Gln Cys
50 55 60

```
Leu Thr Asn Pro Asp Gly Asp Met Asp Lys Lys Glu Leu Glu Lys Leu
 65                  70                  75                  80

Phe Leu Ser Leu Ala
                 85
```

<210> 1595
<211> 882
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(859)
<223> RXA00119

<400> 1595

```
actaatgaga actgtttttc aattggtgca ggatttccac aaggaagcta ggggagaggg 60

gcttccaatc aagtggggtc catcgcgtgg agaatttggc atg ctg gag ttt cct   115
                                              Met Leu Glu Phe Pro
                                                1               5

gca gat gtc att ccc gag aac atc aaa cac att gcg cag aca aag ttc   163
Ala Asp Val Ile Pro Glu Asn Ile Lys His Ile Ala Gln Thr Lys Phe
                 10                  15                  20

cag act gaa gca act tcg gtg gag gat att cgt cgt gcg att aac ctg   211
Gln Thr Glu Ala Thr Ser Val Glu Asp Ile Arg Arg Ala Ile Asn Leu
             25                  30                  35

ctg agt gat cag gcg gag cgt gcg ggt gcg tcc ttt aat cct ggt ttc   259
Leu Ser Asp Gln Ala Glu Arg Ala Gly Ala Ser Phe Asn Pro Gly Phe
         40                  45                  50

att ctt gcg cag gtg ggc tcc acc atc gtg gag gtt tat ggc ggt gct   307
Ile Leu Ala Gln Val Gly Ser Thr Ile Val Glu Val Tyr Gly Gly Ala
     55                  60                  65

ccg gtt gct tgg ctg gat gcg gtt gag ctg ttg att agt cct gat gtg   355
Pro Val Ala Trp Leu Asp Ala Val Glu Leu Leu Ile Ser Pro Asp Val
 70                  75                  80                  85

gag tgg gtt ggg gtt cat ggc tca agg aag ctc gat att aat gtc agc   403
Glu Trp Val Gly Val His Gly Ser Arg Lys Leu Asp Ile Asn Val Ser
                 90                  95                 100

gga gaa ttg tcc ggg gtg att tct gct ggt gac aag ttg ggt gaa ctg   451
Gly Glu Leu Ser Gly Val Ile Ser Ala Gly Asp Lys Leu Gly Glu Leu
            105                 110                 115

ctt ggc gat gat tgg aca atc aac att gtt cac ggc gag tac aaa atc   499
Leu Gly Asp Asp Trp Thr Ile Asn Ile Val His Gly Glu Tyr Lys Ile
        120                 125                 130

cag atc gaa gat gct cga cca agt act gca ttc ctt gcg gac gcg act   547
Gln Ile Glu Asp Ala Arg Pro Ser Thr Ala Phe Leu Ala Asp Ala Thr
    135                 140                 145

gaa ctg att aat cag gca aac tct gag att gtt ccg ttc cat gtt cgg   595
```

```
Glu Leu Ile Asn Gln Ala Asn Ser Glu Ile Val Pro Phe His Val Arg
150                 155                 160                 165

atg ctc agc aac tcg aaa att gtg atg tct ggc ttt agt gat tat tca   643
Met Leu Ser Asn Ser Lys Ile Val Met Ser Gly Phe Ser Asp Tyr Ser
                170                 175                 180

cta gcg ggt gat gcg att aca tct gcg gga aaa ctg gct gaa ttg gcg   691
Leu Ala Gly Asp Ala Ile Thr Ser Ala Gly Lys Leu Ala Glu Leu Ala
            185                 190                 195

agg cct ttt gcc cac tgg aaa gaa aac gtc att cct acg ata gaa ata   739
Arg Pro Phe Ala His Trp Lys Glu Asn Val Ile Pro Thr Ile Glu Ile
        200                 205                 210

gcc atg gac tat gaa cca tca ccg gtg gca gat ctt tgg cag gga gat   787
Ala Met Asp Tyr Glu Pro Ser Pro Val Ala Asp Leu Trp Gln Gly Asp
    215                 220                 225

tct tcg gag aca cct gag cct ttc gac gat ttt gag cgc tta ttg cgg   835
Ser Ser Glu Thr Pro Glu Pro Phe Asp Asp Phe Glu Arg Leu Leu Arg
230                 235                 240                 245

gaa gaa atg ctt att cct gag att tagctggtca tagacctgct gtt         882
Glu Glu Met Leu Ile Pro Glu Ile
                250
```

US20050009150A1

<210> 1596
<211> 253
<212> PRT
<213> Corynebacterium glutamicum

<400> 1596

```
Met Leu Glu Phe Pro Ala Asp Val Ile Pro Glu Asn Ile Lys His Ile
  1               5                  10                  15

Ala Gln Thr Lys Phe Gln Thr Glu Ala Thr Ser Val Glu Asp Ile Arg
             20                  25                  30

Arg Ala Ile Asn Leu Leu Ser Asp Gln Ala Glu Arg Ala Gly Ala Ser
         35                  40                  45

Phe Asn Pro Gly Phe Ile Leu Ala Gln Val Gly Ser Thr Ile Val Glu
     50                  55                  60

Val Tyr Gly Gly Ala Pro Val Ala Trp Leu Asp Ala Val Glu Leu Leu
 65                  70                  75                  80

Ile Ser Pro Asp Val Glu Trp Val Gly Val His Gly Ser Arg Lys Leu
                 85                  90                  95

Asp Ile Asn Val Ser Gly Glu Leu Ser Gly Val Ile Ser Ala Gly Asp
            100                 105                 110

Lys Leu Gly Glu Leu Leu Gly Asp Asp Trp Thr Ile Asn Ile Val His
        115                 120                 125

Gly Glu Tyr Lys Ile Gln Ile Glu Asp Ala Arg Pro Ser Thr Ala Phe
    130                 135                 140
```

```
Leu Ala Asp Ala Thr Glu Leu Ile Asn Gln Ala Asn Ser Glu Ile Val
145                 150                 155                 160

Pro Phe His Val Arg Met Leu Ser Asn Ser Lys Ile Val Met Ser Gly
                165                 170                 175

Phe Ser Asp Tyr Ser Leu Ala Gly Asp Ala Ile Thr Ser Ala Gly Lys
            180                 185                 190

Leu Ala Glu Leu Ala Arg Pro Phe Ala His Trp Lys Glu Asn Val Ile
        195                 200                 205

Pro Thr Ile Glu Ile Ala Met Asp Tyr Glu Pro Ser Pro Val Ala Asp
    210                 215                 220

Leu Trp Gln Gly Asp Ser Ser Glu Thr Pro Glu Pro Phe Asp Asp Phe
225                 230                 235                 240

Glu Arg Leu Leu Arg Glu Glu Met Leu Ile Pro Glu Ile
                245                 250
```

<210> 1597
<211> 834
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(811)
<223> RXA00121

<400> 1597

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gatgtccaaa tactgcgaaa ccatcgaagc gtttcacaac cgtccggcat cagctttcgg 60

cgctgtcgac cccatcttct aaacaagaaa ggcccctcca atg ttg agc gat ctg   115
                                            Met Leu Ser Asp Leu
                                              1               5

agc tcc att ttt gac ttc caa gac ctc tcc ggc acc ttc tct gtc gtc   163
Ser Ser Ile Phe Asp Phe Gln Asp Leu Ser Gly Thr Phe Ser Val Val
                 10                  15                  20

gac gtt ctc atc act ttg gtc ttg tcc ttc gtc ctg acc tcc atc gtg   211
Asp Val Leu Ile Thr Leu Val Leu Ser Phe Val Leu Thr Ser Ile Val
             25                  30                  35

ggt gtg gtg tac caa aag acc cac cgc cac atc tcc tac agc cag tca   259
Gly Val Val Tyr Gln Lys Thr His Arg His Ile Ser Tyr Ser Gln Ser
         40                  45                  50

ttc gta caa acg ttg gtg ctg gtg gga atg gtc att gca atc atc atg   307
Phe Val Gln Thr Leu Val Leu Val Gly Met Val Ile Ala Ile Ile Met
     55                  60                  65

ctg gtg gtc ggc tcc aac att gca cgt gca ttc gcc ctg gtt ggc gcg   355
Leu Val Val Gly Ser Asn Ile Ala Arg Ala Phe Ala Leu Val Gly Ala
 70                  75                  80                  85

ctt tcg gtg att cga ttc cgc aac gca gtg aaa gaa acc cga gat gtg   403
Leu Ser Val Ile Arg Phe Arg Asn Ala Val Lys Glu Thr Arg Asp Val
```

```
                  90                  95                 100

ggc ttc ctt ttc ctt gcc atg gca atc ggc atg act tgc ggt acc cgc   451
Gly Phe Leu Phe Leu Ala Met Ala Ile Gly Met Thr Cys Gly Thr Arg
            105                 110                 115

ttc tac gtt ctg gcg atc gct gca acc atc gtt gtc tgt ggc gtt ctg   499
Phe Tyr Val Leu Ala Ile Ala Ala Thr Ile Val Val Cys Gly Val Leu
        120                 125                 130

ttc atc atg tac cgc ttc gac tgg ttc aag gct gat atc cag cgc cag   547
Phe Ile Met Tyr Arg Phe Asp Trp Phe Lys Ala Asp Ile Gln Arg Gln
    135                 140                 145

gtc atc aag gtg cag gtc cca gcc gat gga caa gct gat tcc ggc agg   595
Val Ile Lys Val Gln Val Pro Ala Asp Gly Gln Ala Asp Ser Gly Arg
150                 155                 160                 165

tcc tac gca gaa gaa gtt gaa ctg atc ctc gca cag tac tgc act tcc   643
Ser Tyr Ala Glu Glu Val Glu Leu Ile Leu Ala Gln Tyr Cys Thr Ser
                170                 175                 180

ttt gag atg atg tcc gct gaa tct gtc cgc ggc gga gcc ctg acc gag   691
Phe Glu Met Met Ser Ala Glu Ser Val Arg Gly Gly Ala Leu Thr Glu
            185                 190                 195

ttc tcc tac acc gct caa atg cgc aag aac gtg aag cca cat gag ctg   739
Phe Ser Tyr Thr Ala Gln Met Arg Lys Asn Val Lys Pro His Glu Leu
        200                 205                 210

gtc gcc aag atg cgc gat gtg aac tac ggc caa aaa gcg act gtc ctg   787
Val Ala Lys Met Arg Asp Val Asn Tyr Gly Gln Lys Ala Thr Val Leu
    215                 220                 225

acc ggt cac gat caa acg gat gta tagaaaatgc ctagctttaa atc         834
Thr Gly His Asp Gln Thr Asp Val
230                 235
```

US20050009150A1

<210> 1598
<211> 237
<212> PRT
<213> Corynebacterium glutamicum

<400> 1598

```
Met Leu Ser Asp Leu Ser Ser Ile Phe Asp Phe Gln Asp Leu Ser Gly
  1               5                  10                  15

Thr Phe Ser Val Val Asp Val Leu Ile Thr Leu Val Leu Ser Phe Val
             20                  25                  30

Leu Thr Ser Ile Val Gly Val Val Tyr Gln Lys Thr His Arg His Ile
         35                  40                  45

Ser Tyr Ser Gln Ser Phe Val Gln Thr Leu Val Leu Val Gly Met Val
     50                  55                  60

Ile Ala Ile Ile Met Leu Val Val Gly Ser Asn Ile Ala Arg Ala Phe
 65                  70                  75                  80

Ala Leu Val Gly Ala Leu Ser Val Ile Arg Phe Arg Asn Ala Val Lys
```

```
                85                  90                  95

Glu Thr Arg Asp Val Gly Phe Leu Phe Leu Ala Met Ala Ile Gly Met
            100                 105                 110

Thr Cys Gly Thr Arg Phe Tyr Val Leu Ala Ile Ala Ala Thr Ile Val
        115                 120                 125

Val Cys Gly Val Leu Phe Ile Met Tyr Arg Phe Asp Trp Phe Lys Ala
    130                 135                 140

Asp Ile Gln Arg Gln Val Ile Lys Val Gln Val Pro Ala Asp Gly Gln
145                 150                 155                 160

Ala Asp Ser Gly Arg Ser Tyr Ala Glu Glu Val Glu Leu Ile Leu Ala
                165                 170                 175

Gln Tyr Cys Thr Ser Phe Glu Met Met Ser Ala Glu Ser Val Arg Gly
            180                 185                 190

Gly Ala Leu Thr Glu Phe Ser Tyr Thr Ala Gln Met Arg Lys Asn Val
        195                 200                 205

Lys Pro His Glu Leu Val Ala Lys Met Arg Asp Val Asn Tyr Gly Gln
    210                 215                 220

Lys Ala Thr Val Leu Thr Gly His Asp Gln Thr Asp Val
225                 230                 235


<210> 1599
<211> 1746
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1723)
<223> RXA00122

<400> 1599
gatgcgcgat gtgaactacg gccaaaaagc gactgtcctg accggtcacg atcaaacgga 60

tgtatagaaa atgcctagct ttaaatctgc tcgatggagg atg aac aga cgc ctc   115
                                              Met Asn Arg Arg Leu
                                                1               5

ttc cta gga act tcc gca gct atc atc gct gtc ggt ggc gtg ctc ggt   163
Phe Leu Gly Thr Ser Ala Ala Ile Ile Ala Val Gly Gly Val Leu Gly
                10                  15                  20

gga gtg cag gtt gta cct tat att tcc tct ggt gaa atc caa acg tca   211
Gly Val Gln Val Val Pro Tyr Ile Ser Ser Gly Glu Ile Gln Thr Ser
            25                  30                  35

gca tca tcg act gcc acg atc gat gtc ggt gca ggc aat gtc gat att   259
Ala Ser Ser Thr Ala Thr Ile Asp Val Gly Ala Gly Asn Val Asp Ile
        40                  45                  50

ttt gat acc tcc gtt tcc cat gaa atc agc ctg cag gtt tcg cag gaa   307
Phe Asp Thr Ser Val Ser His Glu Ile Ser Leu Gln Val Ser Gln Glu
```

```
     55                  60                  65

agc ctc gat gag atg ctc gcg gac tat caa gaa gac ggt tcc aaa acc   355
Ser Leu Asp Glu Met Leu Ala Asp Tyr Gln Glu Asp Gly Ser Lys Thr
 70                  75                  80                  85

tgg gtg aaa gca acc atc acg att gat ggc gtg acc att gaa aac gtc   403
Trp Val Lys Ala Thr Ile Thr Ile Asp Gly Val Thr Ile Glu Asn Val
                 90                  95                 100

ggc atc cgc ctc aag ggc aac tcc acg ctg tcc ggg ttg ggt cga aca   451
Gly Ile Arg Leu Lys Gly Asn Ser Thr Leu Ser Gly Leu Gly Arg Thr
            105                 110                 115

tct gaa gaa ggc gga cct cag gca cca gaa ggc gtc gaa gag ttt aca   499
Ser Glu Glu Gly Gly Pro Gln Ala Pro Glu Gly Val Glu Glu Phe Thr
        120                 125                 130

gat ctc agt gaa gag gaa atc gcc cag ttt gag gaa cag ttc gcg gcg   547
Asp Leu Ser Glu Glu Glu Ile Ala Gln Phe Glu Glu Gln Phe Ala Ala
    135                 140                 145

cag caa gag act act gac gct tca gag acc ggt gaa act gcg gaa aat   595
Gln Gln Glu Thr Thr Asp Ala Ser Glu Thr Gly Glu Thr Ala Glu Asn
150                 155                 160                 165

gaa gag act cgc ggc ccc ggc ggt ggc atg ggt ggt ggc ggc atg ggt   643
Glu Glu Thr Arg Gly Pro Gly Gly Gly Met Gly Gly Gly Gly Met Gly
                170                 175                 180

ggc atg act tcg gtc gat gcc gac gat gtc agc acc tgg cca ctt ctg   691
Gly Met Thr Ser Val Asp Ala Asp Asp Val Ser Thr Trp Pro Leu Leu
            185                 190                 195

atc agc ttc gac aaa tac gaa gac ggc cgc gtc tac caa ggc atg acc   739
Ile Ser Phe Asp Lys Tyr Glu Asp Gly Arg Val Tyr Gln Gly Met Thr
        200                 205                 210

caa ctg gca cta cgc ccc ggc acc acc gtg gtc aac gaa gca atg gcg   787
Gln Leu Ala Leu Arg Pro Gly Thr Thr Val Val Asn Glu Ala Met Ala
    215                 220                 225

ctg gcc ctg acc gca gaa acc ggc cag gtc tcg cag caa tcc agc ttc   835
Leu Ala Leu Thr Ala Glu Thr Gly Gln Val Ser Gln Gln Ser Ser Phe
230                 235                 240                 245

aca acg ttt tcg ctt aac gac gag ccc tcc acc act cga ctc ctt ttg   883
Thr Thr Phe Ser Leu Asn Asp Glu Pro Ser Thr Thr Arg Leu Leu Leu
                250                 255                 260

aag cac ccc gat gaa aat tat gcc gac gcg ctc ggc aac gga gtc ctc   931
Lys His Pro Asp Glu Asn Tyr Ala Asp Ala Leu Gly Asn Gly Val Leu
            265                 270                 275

ttc aaa gca gat tcc aac agt tcc ttc acc tac caa ggc gaa gac caa   979
Phe Lys Ala Asp Ser Asn Ser Ser Phe Thr Tyr Gln Gly Glu Asp Gln
        280                 285                 290

act gaa tac gac gga cag ttc aag cag atc aac ggt gac ggc aac gga   1027
Thr Glu Tyr Asp Gly Gln Phe Lys Gln Ile Asn Gly Asp Gly Asn Gly
    295                 300                 305
```

```
gac atc caa ccg atc atc aac ctg ctg aaa tgg ctc gac acc gca agc   1075
Asp Ile Gln Pro Ile Ile Asn Leu Leu Lys Trp Leu Asp Thr Ala Ser
310                 315                 320                 325

gat gaa gag ttt gct gaa cac ctc tct gac tac gtc gat gtg gaa agc   1123
Asp Glu Glu Phe Ala Glu His Leu Ser Asp Tyr Val Asp Val Glu Ser
                330                 335                 340

ttt gct cgc tac gtt gcc act caa aac ctg ttg gta aat tcc gac gac   1171
Phe Ala Arg Tyr Val Ala Thr Gln Asn Leu Leu Val Asn Ser Asp Asp
            345                 350                 355

atg gct ggt ccc ggt agt aat tac tac ctg tgg tac gac tac gac acc   1219
Met Ala Gly Pro Gly Ser Asn Tyr Tyr Leu Trp Tyr Asp Tyr Asp Thr
        360                 365                 370

ggc ctg atc agc gtg atc tct tgg gat ttg aac ctc gca atg tcc ggc   1267
Gly Leu Ile Ser Val Ile Ser Trp Asp Leu Asn Leu Ala Met Ser Gly
    375                 380                 385

tca act gat gct ggc cca gat gat gaa atc tcc atg ggc gga ggt ggc   1315
Ser Thr Asp Ala Gly Pro Asp Asp Glu Ile Ser Met Gly Gly Gly Gly
390                 395                 400                 405

ggt ggc gga atg cgt cct ggt gga acg acc gac act gaa att gaa ggt   1363
Gly Gly Gly Met Arg Pro Gly Gly Thr Thr Asp Thr Glu Ile Glu Gly
                410                 415                 420

act gcg acc gag gat atg cct gac atg ggc aat atg cag caa cgt gaa   1411
Thr Ala Thr Glu Asp Met Pro Asp Met Gly Asn Met Gln Gln Arg Glu
            425                 430                 435

cgc cct gaa gga atg cca gac atg ggt gag atg cct gat atg ggt gac   1459
Arg Pro Glu Gly Met Pro Asp Met Gly Glu Met Pro Asp Met Gly Asp
        440                 445                 450

cgg gaa ggc ggt gga tcg atg gga gga aac cag ctc aag gaa cgt ttc   1507
Arg Glu Gly Gly Gly Ser Met Gly Gly Asn Gln Leu Lys Glu Arg Phe
    455                 460                 465

ctc gct tcc gat gca ttc acg gaa atc tat gag cag gtg tac tgg gag   1555
Leu Ala Ser Asp Ala Phe Thr Glu Ile Tyr Glu Gln Val Tyr Trp Glu
470                 475                 480                 485

ctg tat gaa gaa atg tat ggt tcc gga act gcc atc gag ttg ttg gat   1603
Leu Tyr Glu Glu Met Tyr Gly Ser Gly Thr Ala Ile Glu Leu Leu Asp
                490                 495                 500

gag att gca gcg tca att cca gaa act gat gcg gtg act gca gat gag   1651
Glu Ile Ala Ala Ser Ile Pro Glu Thr Asp Ala Val Thr Ala Asp Glu
            505                 510                 515

atc gct acg gaa gtg gcg tca atg cgg gaa tgg atc act gcc cgc aca   1699
Ile Ala Thr Glu Val Ala Ser Met Arg Glu Trp Ile Thr Ala Arg Thr
        520                 525                 530

gaa gcg ttg gct gct ttg caa gag tgatcaaact agaaaaccaa caa         1746
Glu Ala Leu Ala Ala Leu Gln Glu
    535                 540
```

<210> 1600
<211> 541
<212> PRT
<213> Corynebacterium glutamicum

<400> 1600
Met Asn Arg Arg Leu Phe Leu Gly Thr Ser Ala Ala Ile Ile Ala Val
1 5 10 15

Gly Gly Val Leu Gly Gly Val Gln Val Val Pro Tyr Ile Ser Ser Gly
20 25 30

Glu Ile Gln Thr Ser Ala Ser Ser Thr Ala Thr Ile Asp Val Gly Ala
35 40 45

Gly Asn Val Asp Ile Phe Asp Thr Ser Val Ser His Glu Ile Ser Leu
50 55 60

Gln Val Ser Gln Glu Ser Leu Asp Glu Met Leu Ala Asp Tyr Gln Glu
65 70 75 80

Asp Gly Ser Lys Thr Trp Val Lys Ala Thr Ile Thr Ile Asp Gly Val
85 90 95

Thr Ile Glu Asn Val Gly Ile Arg Leu Lys Gly Asn Ser Thr Leu Ser
100 105 110

Gly Leu Gly Arg Thr Ser Glu Glu Gly Gly Pro Gln Ala Pro Glu Gly
115 120 125

Val Glu Glu Phe Thr Asp Leu Ser Glu Glu Glu Ile Ala Gln Phe Glu
130 135 140

Glu Gln Phe Ala Ala Gln Gln Glu Thr Thr Asp Ala Ser Glu Thr Gly
145 150 155 160

Glu Thr Ala Glu Asn Glu Glu Thr Arg Gly Pro Gly Gly Gly Met Gly
165 170 175

Gly Gly Gly Met Gly Gly Met Thr Ser Val Asp Ala Asp Asp Val Ser
180 185 190

Thr Trp Pro Leu Leu Ile Ser Phe Asp Lys Tyr Glu Asp Gly Arg Val
195 200 205

Tyr Gln Gly Met Thr Gln Leu Ala Leu Arg Pro Gly Thr Thr Val Val
210 215 220

Asn Glu Ala Met Ala Leu Ala Leu Thr Ala Glu Thr Gly Gln Val Ser
225 230 235 240

Gln Gln Ser Ser Phe Thr Thr Phe Ser Leu Asn Asp Glu Pro Ser Thr
245 250 255

Thr Arg Leu Leu Leu Lys His Pro Asp Glu Asn Tyr Ala Asp Ala Leu
260 265 270

Gly Asn Gly Val Leu Phe Lys Ala Asp Ser Asn Ser Ser Phe Thr Tyr
275 280 285

```
Gln Gly Glu Asp Gln Thr Glu Tyr Asp Gly Gln Phe Lys Gln Ile Asn
    290                 295                 300

Gly Asp Gly Asn Gly Asp Ile Gln Pro Ile Ile Asn Leu Leu Lys Trp
305                 310                 315                 320

Leu Asp Thr Ala Ser Asp Glu Glu Phe Ala Glu His Leu Ser Asp Tyr
                325                 330                 335

Val Asp Val Glu Ser Phe Ala Arg Tyr Val Ala Thr Gln Asn Leu Leu
            340                 345                 350

Val Asn Ser Asp Asp Met Ala Gly Pro Gly Ser Asn Tyr Tyr Leu Trp
        355                 360                 365

Tyr Asp Tyr Asp Thr Gly Leu Ile Ser Val Ile Ser Trp Asp Leu Asn
    370                 375                 380

Leu Ala Met Ser Gly Ser Thr Asp Ala Gly Pro Asp Asp Glu Ile Ser
385                 390                 395                 400

Met Gly Gly Gly Gly Gly Gly Gly Met Arg Pro Gly Gly Thr Thr Asp
                405                 410                 415

Thr Glu Ile Glu Gly Thr Ala Thr Glu Asp Met Pro Asp Met Gly Asn
            420                 425                 430

Met Gln Gln Arg Glu Arg Pro Glu Gly Met Pro Asp Met Gly Glu Met
        435                 440                 445

Pro Asp Met Gly Asp Arg Glu Gly Gly Gly Ser Met Gly Gly Asn Gln
    450                 455                 460

Leu Lys Glu Arg Phe Leu Ala Ser Asp Ala Phe Thr Glu Ile Tyr Glu
465                 470                 475                 480

Gln Val Tyr Trp Glu Leu Tyr Glu Glu Met Tyr Gly Ser Gly Thr Ala
                485                 490                 495

Ile Glu Leu Leu Asp Glu Ile Ala Ala Ser Ile Pro Glu Thr Asp Ala
            500                 505                 510

Val Thr Ala Asp Glu Ile Ala Thr Glu Val Ala Ser Met Arg Glu Trp
        515                 520                 525

Ile Thr Ala Arg Thr Glu Ala Leu Ala Ala Leu Gln Glu
    530                 535                 540
```

<210> 1601
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXA00127

<400> 1601
ttgtggggcg ccgggggcgt cgttatgcag tgactgccag cgtgtgtgga ggaagccgcc 60

```
aacattggcg cggcttgatt tagatttacc ggtgtggacg ttg tcg ccg tat gac   115
                                              Leu Ser Pro Tyr Asp
                                                1               5

ggc ccg cat cgc aac gtg ctc att gcg ctg aag gag cac ggc cgt gca   163
Gly Pro His Arg Asn Val Leu Ile Ala Leu Lys Glu His Gly Arg Ala
                10                  15                  20

gac ctt gtg gcg ttt gtg ggc gcg gtg gtg ggg gcg tcg ata agc tat   211
Asp Leu Val Ala Phe Val Gly Ala Val Val Gly Ala Ser Ile Ser Tyr
            25                  30                  35

ctg gcg gct cag ggg gaa att gag cac gac atc acg ctg gtt ccg gcg   259
Leu Ala Ala Gln Gly Glu Ile Glu His Asp Ile Thr Leu Val Pro Ala
        40                  45                  50

ccc acc cgc gcc acc tcg cga cgc cgg cgg ggc ggc gat ccg gtt gag   307
Pro Thr Arg Ala Thr Ser Arg Arg Arg Arg Gly Gly Asp Pro Val Glu
    55                  60                  65

cgg gtg tgc aat gca tca cgc tta tcg acg ttt ccc tgc ctt caa atc   355
Arg Val Cys Asn Ala Ser Arg Leu Ser Thr Phe Pro Cys Leu Gln Ile
70                  75                  80                  85

tca tcc cgc aca cca gac tcc gtc ggt caa act gcg caa cag cga aga   403
Ser Ser Arg Thr Pro Asp Ser Val Gly Gln Thr Ala Gln Gln Arg Arg
                90                  95                  100

ctc aat atg cga gtg gag tta gtc cga caa cct cgg ggt tct gtc ttg   451
Leu Asn Met Arg Val Glu Leu Val Arg Gln Pro Arg Gly Ser Val Leu
            105                 110                 115

atc atc gac gat gtg gta aca acg ggg gca act att tcc gca tct gca   499
Ile Ile Asp Asp Val Val Thr Thr Gly Ala Thr Ile Ser Ala Ser Ala
        120                 125                 130

aac gtt ctt cgc gca gcg ggt gtg cag gtc aga gga gct tta act tat   547
Asn Val Leu Arg Ala Ala Gly Val Gln Val Arg Gly Ala Leu Thr Tyr
    135                 140                 145

tgc caa gcg tgatcttgga tataaaaggg gcc                            579
Cys Gln Ala
150
```

<210> 1602
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 1602

```
Leu Ser Pro Tyr Asp Gly Pro His Arg Asn Val Leu Ile Ala Leu Lys
  1               5                  10                  15

Glu His Gly Arg Ala Asp Leu Val Ala Phe Val Gly Ala Val Val Gly
            20                  25                  30

Ala Ser Ile Ser Tyr Leu Ala Ala Gln Gly Glu Ile Glu His Asp Ile
        35                  40                  45
```

```
Thr Leu Val Pro Ala Pro Thr Arg Ala Thr Ser Arg Arg Arg Arg Gly
     50                  55                  60

Gly Asp Pro Val Glu Arg Val Cys Asn Ala Ser Arg Leu Ser Thr Phe
 65                  70                  75                  80

Pro Cys Leu Gln Ile Ser Ser Arg Thr Pro Asp Ser Val Gly Gln Thr
                 85                  90                  95

Ala Gln Gln Arg Arg Leu Asn Met Arg Val Glu Leu Val Arg Gln Pro
            100                 105                 110

Arg Gly Ser Val Leu Ile Ile Asp Asp Val Val Thr Thr Gly Ala Thr
        115                 120                 125

Ile Ser Ala Ser Ala Asn Val Leu Arg Ala Ala Gly Val Gln Val Arg
    130                 135                 140

Gly Ala Leu Thr Tyr Cys Gln Ala
145                 150
```

<210> 1603
<211> 693
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(670)
<223> RXA00134

<400> 1603

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gcagctgtgc tccaccagtg actaaaaact tgtctttcac gtgccccacc ttatccgtgt 60

tccccacccc tgtgcgtaac gacagctaga atctcaagtt atg gcc gtt cat tta   115
                                            Met Ala Val His Leu
                                              1               5

acc aag atc tat acg cga acc ggg gac gat gga acc acg ggg ctc tca   163
Thr Lys Ile Tyr Thr Arg Thr Gly Asp Asp Gly Thr Thr Gly Leu Ser
                 10                  15                  20

aat ttt gag cga gtt ccc aag gac gat ccc cgc ctt att gca tac gcc   211
Asn Phe Glu Arg Val Pro Lys Asp Asp Pro Arg Leu Ile Ala Tyr Ala
             25                  30                  35

gac tcc gat gaa gca aac tgt gcg att ggc caa gtg ctt gca ctc agc   259
Asp Ser Asp Glu Ala Asn Cys Ala Ile Gly Gln Val Leu Ala Leu Ser
         40                  45                  50

agc cct acg gaa gat atg gca acc tta ttg cgg act att caa aat gaa   307
Ser Pro Thr Glu Asp Met Ala Thr Leu Leu Arg Thr Ile Gln Asn Glu
     55                  60                  65

ctt ttt gat gtg ggc gca gac tta gca acc ccg att gag gag aat ccg   355
Leu Phe Asp Val Gly Ala Asp Leu Ala Thr Pro Ile Glu Glu Asn Pro
 70                  75                  80                  85

aag tat ccc cca ctt cga gtt ctt ccg gaa tat atc gaa cga ctt gag   403
Lys Tyr Pro Pro Leu Arg Val Leu Pro Glu Tyr Ile Glu Arg Leu Glu
```

```
                90                  95                  100

aag gag tgc gat aaa tgg aac gag gat gtg ccg gcg ttg gat tcc ttc   451
Lys Glu Cys Asp Lys Trp Asn Glu Asp Val Pro Ala Leu Asp Ser Phe
            105                 110                 115

att ttg ccg ggt ggc acg cca gca gcg gca ctc ttg cac acc gca agg   499
Ile Leu Pro Gly Gly Thr Pro Ala Ala Ala Leu Leu His Thr Ala Arg
        120                 125                 130

gta att acg agg cgc gcg gag aga gca gct tgg ata gcg gtg cgg gaa   547
Val Ile Thr Arg Arg Ala Glu Arg Ala Ala Trp Ile Ala Val Arg Glu
    135                 140                 145

ttt ccg agc acc acc tct acc ttg cca gcc caa tac ctg aat cgt ctt   595
Phe Pro Ser Thr Thr Ser Thr Leu Pro Ala Gln Tyr Leu Asn Arg Leu
150                 155                 160                 165

agc gat ctg ctg ttt att ctt tcc cgt gtt gcc aac aat ggc aat gat   643
Ser Asp Leu Leu Phe Ile Leu Ser Arg Val Ala Asn Asn Gly Asn Asp
                170                 175                 180

gtg aag tgg gtt ccg ggc gga aaa aga tgaaaaccac cctgcgaccg         690
Val Lys Trp Val Pro Gly Gly Lys Arg
            185                 190

tga                                                              693


<210> 1604
<211> 190
<212> PRT
<213> Corynebacterium glutamicum

<400> 1604
Met Ala Val His Leu Thr Lys Ile Tyr Thr Arg Thr Gly Asp Asp Gly
  1               5                  10                  15

Thr Thr Gly Leu Ser Asn Phe Glu Arg Val Pro Lys Asp Asp Pro Arg
             20                  25                  30

Leu Ile Ala Tyr Ala Asp Ser Asp Glu Ala Asn Cys Ala Ile Gly Gln
         35                  40                  45

Val Leu Ala Leu Ser Ser Pro Thr Glu Asp Met Ala Thr Leu Leu Arg
     50                  55                  60

Thr Ile Gln Asn Glu Leu Phe Asp Val Gly Ala Asp Leu Ala Thr Pro
 65                  70                  75                  80

Ile Glu Glu Asn Pro Lys Tyr Pro Pro Leu Arg Val Leu Pro Glu Tyr
                 85                  90                  95

Ile Glu Arg Leu Glu Lys Glu Cys Asp Lys Trp Asn Glu Asp Val Pro
            100                 105                 110

Ala Leu Asp Ser Phe Ile Leu Pro Gly Gly Thr Pro Ala Ala Ala Leu
        115                 120                 125

Leu His Thr Ala Arg Val Ile Thr Arg Arg Ala Glu Arg Ala Ala Trp
    130                 135                 140
```

```
Ile Ala Val Arg Glu Phe Pro Ser Thr Thr Ser Thr Leu Pro Ala Gln
145                 150                 155                 160

Tyr Leu Asn Arg Leu Ser Asp Leu Leu Phe Ile Leu Ser Arg Val Ala
                165                 170                 175

Asn Asn Gly Asn Asp Val Lys Trp Val Pro Gly Gly Lys Arg
            180                 185                 190


<210> 1605
<211> 309
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(286)
<223> RXA00140

<400> 1605
ctcaacgata ttcagctttc cgcaatgctg aaaaacgcca tcgatcacgt cctcgcgatt 60

caagatgccg tagccaatgc aggcaaggaa atcggctaac atg tcg gac gag tcc   115
                                            Met Ser Asp Glu Ser
                                              1               5

atc gaa gag cag gaa aaa gaa ctc gcg gcg ctg aag gct caa atc gat   163
Ile Glu Glu Gln Glu Lys Glu Leu Ala Ala Leu Lys Ala Gln Ile Asp
                  10                  15                  20

gaa ctg gaa aag aaa gac aag cag aac aag cta atc atc gag att ttg   211
Glu Leu Glu Lys Lys Asp Lys Gln Asn Lys Leu Ile Ile Glu Ile Leu
              25                  30                  35

tcc aag gcc gtc gaa aag aat gtg gca gag gca gaa gcg aaa aga gcc   259
Ser Lys Ala Val Glu Lys Asn Val Ala Glu Ala Glu Ala Lys Arg Ala
          40                  45                  50

cgc aaa tat ccg ccc aat ccc ctg tgg tgaattctaa ggcgtcgaac        306
Arg Lys Tyr Pro Pro Asn Pro Leu Trp
     55                  60

ttt                                                              309


<210> 1606
<211> 62
<212> PRT
<213> Corynebacterium glutamicum

<400> 1606
Met Ser Asp Glu Ser Ile Glu Glu Gln Glu Lys Glu Leu Ala Ala Leu
  1               5                  10                  15

Lys Ala Gln Ile Asp Glu Leu Glu Lys Lys Asp Lys Gln Asn Lys Leu
             20                  25                  30

Ile Ile Glu Ile Leu Ser Lys Ala Val Glu Lys Asn Val Ala Glu Ala
         35                  40                  45
```

```
Glu Ala Lys Arg Ala Arg Lys Tyr Pro Pro Asn Pro Leu Trp
     50                  55                  60


<210> 1607
<211> 585
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> RXA00141

<400> 1607
gtcggctcct acgttatgag ctccatcgaa tccgctgttc agtgcttcga atggcttgag 60

cagcaattcc cagatctagt cacctggaag gacgaacacc atg acc act gat tcc   115
                                           Met Thr Thr Asp Ser
                                             1               5

aat tct gcg aca atc cca acc cca aag ccg att cca gtg acc atc gac   163
Asn Ser Ala Thr Ile Pro Thr Pro Lys Pro Ile Pro Val Thr Ile Asp
                 10                  15                  20

cga atc tcc ctc atc atg aaa gaa ttc ggc att gac cta tcc atc gcc   211
Arg Ile Ser Leu Ile Met Lys Glu Phe Gly Ile Asp Leu Ser Ile Ala
             25                  30                  35

gat gaa caa ggc acc gga tcc caa gta gcc agc gcc aac ctc aac ggc   259
Asp Glu Gln Gly Thr Gly Ser Gln Val Ala Ser Ala Asn Leu Asn Gly
         40                  45                  50

cat cac gtc atg ttc gct gtc atc ggt tca gtc ctg atc gtt cgt gcc   307
His His Val Met Phe Ala Val Ile Gly Ser Val Leu Ile Val Arg Ala
     55                  60                  65

gat cgc gcc acc gaa atg cca gtc tcc gac ggc aac ccc gca tgg cat   355
Asp Arg Ala Thr Glu Met Pro Val Ser Asp Gly Asn Pro Ala Trp His
 70                  75                  80                  85

ctc gcc tgc aac caa gtc aac tgt ttc aac ttc gct gcc aag gct gtc   403
Leu Ala Cys Asn Gln Val Asn Cys Phe Asn Phe Ala Ala Lys Ala Val
                 90                  95                 100

gta gtt gat cgc acc gac aac atc gtg atc cgc gcc gag aag gat gtc   451
Val Val Asp Arg Thr Asp Asn Ile Val Ile Arg Ala Glu Lys Asp Val
            105                 110                 115

ccc atc gcc gct ggg ctc aac gat att cag ctt tcc gca atg ctg aaa   499
Pro Ile Ala Ala Gly Leu Asn Asp Ile Gln Leu Ser Ala Met Leu Lys
        120                 125                 130

aac gcc atc gat cac gtc ctc gcg att caa gat gcc gta gcc aat gca   547
Asn Ala Ile Asp His Val Leu Ala Ile Gln Asp Ala Val Ala Asn Ala
    135                 140                 145

ggc aag gaa atc ggc taacatgtcg gacgagtcca tcg                    585
Gly Lys Glu Ile Gly
150
```

<210> 1608
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 1608
Met Thr Thr Asp Ser Asn Ser Ala Thr Ile Pro Thr Pro Lys Pro Ile
1 5 10 15

Pro Val Thr Ile Asp Arg Ile Ser Leu Ile Met Lys Glu Phe Gly Ile
20 25 30

Asp Leu Ser Ile Ala Asp Glu Gln Gly Thr Gly Ser Gln Val Ala Ser
35 40 45

Ala Asn Leu Asn Gly His His Val Met Phe Ala Val Ile Gly Ser Val
50 55 60

Leu Ile Val Arg Ala Asp Arg Ala Thr Glu Met Pro Val Ser Asp Gly
65 70 75 80

Asn Pro Ala Trp His Leu Ala Cys Asn Gln Val Asn Cys Phe Asn Phe
85 90 95

Ala Ala Lys Ala Val Val Val Asp Arg Thr Asp Asn Ile Val Ile Arg
100 105 110

Ala Glu Lys Asp Val Pro Ile Ala Ala Gly Leu Asn Asp Ile Gln Leu
115 120 125

Ser Ala Met Leu Lys Asn Ala Ile Asp His Val Leu Ala Ile Gln Asp
130 135 140

Ala Val Ala Asn Ala Gly Lys Glu Ile Gly
145 150

<210> 1609
<211> 600
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(577)
<223> RXA00142

<400> 1609
atcctcaatt tccgccgtaa gcgcaacgac taaaaccacc atctgtagtg tggtggaaaa 60

gttactttta aaaggatttt ggaaggactg aaactcccca gtg cct caa tca ccc 115
Val Pro Gln Ser Pro
1 5

aca gca cac gac ccc aac gac atc cag gaa ttt aac ctc gat gcc gtt 163
Thr Ala His Asp Pro Asn Asp Ile Gln Glu Phe Asn Leu Asp Ala Val
10 15 20

gca ggg att ctc cag gac gaa aaa ctg gac tac cgc atc gat gaa cac 211

```
Ala Gly Ile Leu Gln Asp Glu Lys Leu Asp Tyr Arg Ile Asp Glu His
             25                  30                  35

gac ggc gaa aaa gta atc cgc acc gga ttc atc aac gcc gcc atc agc   259
Asp Gly Glu Lys Val Ile Arg Thr Gly Phe Ile Asn Ala Ala Ile Ser
         40                  45                  50

ttc atc ctc tta gac ggc agc tta acc atg gaa gcc atg tgg cga gga   307
Phe Ile Leu Leu Asp Gly Ser Leu Thr Met Glu Ala Met Trp Arg Gly
     55                  60                  65

gcc ccc tcc acc gat gct gcc gca caa gtt ctc gcg gcc acc aac gaa   355
Ala Pro Ser Thr Asp Ala Ala Ala Gln Val Leu Ala Ala Thr Asn Glu
 70                  75                  80                  85

tgg aac ctc acc cag ttc gca ccc acc att cga ttc ttc gaa ctc aac   403
Trp Asn Leu Thr Gln Phe Ala Pro Thr Ile Arg Phe Phe Glu Leu Asn
                 90                  95                 100

gaa ggc acc ctc gcc atc aat gca ctg cga cac gtc gtt gtt tcc gca   451
Glu Gly Thr Leu Ala Ile Asn Ala Leu Arg His Val Val Val Ser Ala
            105                 110                 115

ggc atg agc cac aac caa gtc ggc tcc tac gtt atg agc tcc atc gaa   499
Gly Met Ser His Asn Gln Val Gly Ser Tyr Val Met Ser Ser Ile Glu
        120                 125                 130

tcc gct gtt cag tgc ttc gaa tgg ctt gag cag caa ttc cca gat cta   547
Ser Ala Val Gln Cys Phe Glu Trp Leu Glu Gln Gln Phe Pro Asp Leu
    135                 140                 145

gtc acc tgg aag gac gaa cac cat gac cac tgattccaat tctgcgacaa     597
Val Thr Trp Lys Asp Glu His His Asp His
150                 155

tcc                                                               600
```

```
<210> 1610
<211> 159
<212> PRT
<213> Corynebacterium glutamicum

<400> 1610
Val Pro Gln Ser Pro Thr Ala His Asp Pro Asn Asp Ile Gln Glu Phe
  1               5                  10                  15

Asn Leu Asp Ala Val Ala Gly Ile Leu Gln Asp Glu Lys Leu Asp Tyr
             20                  25                  30

Arg Ile Asp Glu His Asp Gly Glu Lys Val Ile Arg Thr Gly Phe Ile
         35                  40                  45

Asn Ala Ala Ile Ser Phe Ile Leu Leu Asp Gly Ser Leu Thr Met Glu
     50                  55                  60

Ala Met Trp Arg Gly Ala Pro Ser Thr Asp Ala Ala Ala Gln Val Leu
 65                  70                  75                  80

Ala Ala Thr Asn Glu Trp Asn Leu Thr Gln Phe Ala Pro Thr Ile Arg
                 85                  90                  95
```

```
Phe Phe Glu Leu Asn Glu Gly Thr Leu Ala Ile Asn Ala Leu Arg His
            100                 105                 110

Val Val Val Ser Ala Gly Met Ser His Asn Gln Val Gly Ser Tyr Val
        115                 120                 125

Met Ser Ser Ile Glu Ser Ala Val Gln Cys Phe Glu Trp Leu Glu Gln
    130                 135                 140

Gln Phe Pro Asp Leu Val Thr Trp Lys Asp Glu His His Asp His
145                 150                 155
```

<210> 1611
<211> 897
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> RXA00150

<400> 1611

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agctgagcag ggatcggcac tagcttctac tacgataacg agaactttgt ttcaatacat 60

tcaaaatggc ggaatatttt gatcacgggg gtgcaactgt atg gtg ttt tct atg   115
                                            Met Val Phe Ser Met
                                              1               5

cat gac aaa ggt gag acc cag gag aat cct gcg gac atg tca gga cgc   163
His Asp Lys Gly Glu Thr Gln Glu Asn Pro Ala Asp Met Ser Gly Arg
                 10                  15                  20

cta aac aca cca att tcc acg gtc ttt cac ttc ttt agc tca ctt ttc   211
Leu Asn Thr Pro Ile Ser Thr Val Phe His Phe Phe Ser Ser Leu Phe
             25                  30                  35

cat gac gct ctg cgc agt gtt gcc cag tgg agt gcg tgg aag aaa atc   259
His Asp Ala Leu Arg Ser Val Ala Gln Trp Ser Ala Trp Lys Lys Ile
         40                  45                  50

gct gta tcg gtt gtc atc gtc gca att att tcc gta act ttt ctt gtc   307
Ala Val Ser Val Val Ile Val Ala Ile Ile Ser Val Thr Phe Leu Val
     55                  60                  65

gat gtc ccc ccg att tcg gtt tat cgt gac tgg gca aac aac gcc ggc   355
Asp Val Pro Pro Ile Ser Val Tyr Arg Asp Trp Ala Asn Asn Ala Gly
 70                  75                  80                  85

gac gct ttt gtc tta gtt ttt tgc gcc ttt tat atc ctc att act cag   403
Asp Ala Phe Val Leu Val Phe Cys Ala Phe Tyr Ile Leu Ile Thr Gln
                 90                  95                 100

ttc cct atc ccc cgc aca gtt ctc aca ctg gcc tcc ggc gtg ctg ttc   451
Phe Pro Ile Pro Arg Thr Val Leu Thr Leu Ala Ser Gly Val Leu Phe
            105                 110                 115

ggg ccg gtt ctt gga tca gtc gtg gcg ctg ggt tcc acc aca gtg tca   499
Gly Pro Val Leu Gly Ser Val Val Ala Leu Gly Ser Thr Thr Val Ser
```

```
        120                 125                 130

gcg gta atc tcg ctc ctc att gtt cgg ggt ctg ctt ggc gat tgg atg   547
Ala Val Ile Ser Leu Leu Ile Val Arg Gly Leu Leu Gly Asp Trp Met
    135                 140                 145

gcg cca cgt tta acg cac ccc gca gtc tca cgc atc aat acc cga ctt   595
Ala Pro Arg Leu Thr His Pro Ala Val Ser Arg Ile Asn Thr Arg Leu
150                 155                 160                 165

gag caa cgt gga tgg ctg gcg att acc tct tta aga atg atc gcc gct   643
Glu Gln Arg Gly Trp Leu Ala Ile Thr Ser Leu Arg Met Ile Ala Ala
                170                 175                 180

atc ccc ttt tcc atc ctc aac tat gtt gca gcc ttg act agc gtt cct   691
Ile Pro Phe Ser Ile Leu Asn Tyr Val Ala Ala Leu Thr Ser Val Pro
            185                 190                 195

gtt ttt tct ttt gcc atc gct acc ttg atc gga tct gca cca gga acc   739
Val Phe Ser Phe Ala Ile Ala Thr Leu Ile Gly Ser Ala Pro Gly Thr
        200                 205                 210

atc gtc acc gtc gtt ttg gga gat gca gtc aca ggt tct gga aac tgg   787
Ile Val Thr Val Val Leu Gly Asp Ala Val Thr Gly Ser Gly Asn Trp
    215                 220                 225

act gcc gtt gca ttc acg gta ttt tta gcg att ttg ggt gtt tta ggt   835
Thr Ala Val Ala Phe Thr Val Phe Leu Ala Ile Leu Gly Val Leu Gly
230                 235                 240                 245

atc ttt tta gat caa aag atg cca gtc aag cct gga aag tagacaatat    884
Ile Phe Leu Asp Gln Lys Met Pro Val Lys Pro Gly Lys
                250                 255

aaggtagggt tgg                                                   897


<210> 1612
<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 1612
Met Val Phe Ser Met His Asp Lys Gly Glu Thr Gln Glu Asn Pro Ala
  1               5                  10                  15

Asp Met Ser Gly Arg Leu Asn Thr Pro Ile Ser Thr Val Phe His Phe
             20                  25                  30

Phe Ser Ser Leu Phe His Asp Ala Leu Arg Ser Val Ala Gln Trp Ser
         35                  40                  45

Ala Trp Lys Lys Ile Ala Val Ser Val Val Ile Val Ala Ile Ile Ser
     50                  55                  60

Val Thr Phe Leu Val Asp Val Pro Pro Ile Ser Val Tyr Arg Asp Trp
 65                  70                  75                  80

Ala Asn Asn Ala Gly Asp Ala Phe Val Leu Val Phe Cys Ala Phe Tyr
                 85                  90                  95
```

```
Ile Leu Ile Thr Gln Phe Pro Ile Pro Arg Thr Val Leu Thr Leu Ala
            100                 105                 110

Ser Gly Val Leu Phe Gly Pro Val Leu Gly Ser Val Val Ala Leu Gly
        115                 120                 125

Ser Thr Thr Val Ser Ala Val Ile Ser Leu Leu Ile Val Arg Gly Leu
    130                 135                 140

Leu Gly Asp Trp Met Ala Pro Arg Leu Thr His Pro Ala Val Ser Arg
145                 150                 155                 160

Ile Asn Thr Arg Leu Glu Gln Arg Gly Trp Leu Ala Ile Thr Ser Leu
                165                 170                 175

Arg Met Ile Ala Ala Ile Pro Phe Ser Ile Leu Asn Tyr Val Ala Ala
            180                 185                 190

Leu Thr Ser Val Pro Val Phe Ser Phe Ala Ile Ala Thr Leu Ile Gly
        195                 200                 205

Ser Ala Pro Gly Thr Ile Val Thr Val Val Leu Gly Asp Ala Val Thr
    210                 215                 220

Gly Ser Gly Asn Trp Thr Ala Val Ala Phe Thr Val Phe Leu Ala Ile
225                 230                 235                 240

Leu Gly Val Leu Gly Ile Phe Leu Asp Gln Lys Met Pro Val Lys Pro
                245                 250                 255

Gly Lys
```

09/05/2005 09:56:56 AM

<210> 1613
<211> 720
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(697)
<223> RXA00151

<400> 1613

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aagtagacaa tataaggtag ggttggagaa gattctttac ttcttcactc attcgccctg 60

acagcgaatc cactacaata aacaaagggg gcagccaccc atg tgg gca ctg cat   115
                                              Met Trp Ala Leu His
                                                1               5

gcc aga tac cgc ggc cga gac aca cga cga gcc gaa ttg gtt aaa aga   163
Ala Arg Tyr Arg Gly Arg Asp Thr Arg Arg Ala Glu Leu Val Lys Arg
                10                  15                  20

ttt gca gaa gct ttg tcc acc ctc gaa ggt gct ggc cag ttt gaa gtc   211
Phe Ala Glu Ala Leu Ser Thr Leu Glu Gly Ala Gly Gln Phe Glu Val
            25                  30                  35

att ggt gtc gaa gac atc cga gca cac atc acc tca ccg tta acc aca   259
Ile Gly Val Glu Asp Ile Arg Ala His Ile Thr Ser Pro Leu Thr Thr
```

```
         40                  45                  50

tgt gat gtt gtc atg gcg cta ctc gca gct ggc gat tgg gca atc gga   307
Cys Asp Val Val Met Ala Leu Leu Ala Ala Gly Asp Trp Ala Ile Gly
     55                  60                  65

att ggt gtt atc ccc acc gtt gac gga aca gtc gat gaa tcg gat gag   355
Ile Gly Val Ile Pro Thr Val Asp Gly Thr Val Asp Glu Ser Asp Glu
 70                  75                  80                  85

gcc atc atc gaa cag gta aag aaa att tcc tct gat gct ctg cgc ccc   403
Ala Ile Ile Glu Gln Val Lys Lys Ile Ser Ser Asp Ala Leu Arg Pro
                 90                  95                 100

acc gcc aag gcg gga acg gtc aaa gtt agg atc gcc gga acc aaa cgg   451
Thr Ala Lys Ala Gly Thr Val Lys Val Arg Ile Ala Gly Thr Lys Arg
            105                 110                 115

gac aat act caa gcc ttc aac atc tcc gct gca ttc acg ttg att ggg   499
Asp Asn Thr Gln Ala Phe Asn Ile Ser Ala Ala Phe Thr Leu Ile Gly
        120                 125                 130

caa gtt ctg tca aag cgc acc atc gaa gga cgc gaa gcc acc gca ctc   547
Gln Val Leu Ser Lys Arg Thr Ile Glu Gly Arg Glu Ala Thr Ala Leu
    135                 140                 145

gtc cgt tct gga ctg aat caa aat gag gca gcc caa gag ctc ggt att   595
Val Arg Ser Gly Leu Asn Gln Asn Glu Ala Ala Gln Glu Leu Gly Ile
150                 155                 160                 165

tcc aag cag gca atg tcg cag cga ttg cag gcg gca ggt tgg cag gcg   643
Ser Lys Gln Ala Met Ser Gln Arg Leu Gln Ala Ala Gly Trp Gln Ala
                170                 175                 180

gaa tct gct ggt tgg caa ttg gcc gta aac ctc atc gag cag gct ggc   691
Glu Ser Ala Gly Trp Gln Leu Ala Val Asn Leu Ile Glu Gln Ala Gly
            185                 190                 195

aag cgc tagcaggcga tttaagagcc tga                                720
Lys Arg
```

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<210> 1614
<211> 199
<212> PRT
<213> Corynebacterium glutamicum

<400> 1614

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Met Trp Ala Leu His Ala Arg Tyr Arg Gly Arg Asp Thr Arg Arg Ala
  1               5                  10                  15

Glu Leu Val Lys Arg Phe Ala Glu Ala Leu Ser Thr Leu Glu Gly Ala
             20                  25                  30

Gly Gln Phe Glu Val Ile Gly Val Glu Asp Ile Arg Ala His Ile Thr
         35                  40                  45

Ser Pro Leu Thr Thr Cys Asp Val Val Met Ala Leu Leu Ala Ala Gly
     50                  55                  60
```

```
Asp Trp Ala Ile Gly Ile Gly Val Ile Pro Thr Val Asp Gly Thr Val
 65                  70                  75                  80

Asp Glu Ser Asp Glu Ala Ile Ile Glu Gln Val Lys Lys Ile Ser Ser
                 85                  90                  95

Asp Ala Leu Arg Pro Thr Ala Lys Ala Gly Thr Val Lys Val Arg Ile
            100                 105                 110

Ala Gly Thr Lys Arg Asp Asn Thr Gln Ala Phe Asn Ile Ser Ala Ala
        115                 120                 125

Phe Thr Leu Ile Gly Gln Val Leu Ser Lys Arg Thr Ile Glu Gly Arg
    130                 135                 140

Glu Ala Thr Ala Leu Val Arg Ser Gly Leu Asn Gln Asn Glu Ala Ala
145                 150                 155                 160

Gln Glu Leu Gly Ile Ser Lys Gln Ala Met Ser Gln Arg Leu Gln Ala
                165                 170                 175

Ala Gly Trp Gln Ala Glu Ser Ala Gly Trp Gln Leu Ala Val Asn Leu
            180                 185                 190

Ile Glu Gln Ala Gly Lys Arg
        195
```

EP 2 336 350 A1

<210> 1615
<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(526)
<223> RXA00153

<400> 1615

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cctcgatttg agtaaagagg acgtcctcgc ctgatttttc gggtgtgttt ttgcgtggcg 60

agccctgcct ggcccttcca aattatgtag ggtggcctgc gtg gga gca ata att   115
                                            Val Gly Ala Ile Ile
                                              1               5

tgg ttt atc gga gca ttg gtt ctt gct ggc ttg gaa ttg gca gta ggt   163
Trp Phe Ile Gly Ala Leu Val Leu Ala Gly Leu Glu Leu Ala Val Gly
                 10                  15                  20

gag ttc acc tta ttg atg ctc ggc ggt gca gct ttg gca acc gcc ggc   211
Glu Phe Thr Leu Leu Met Leu Gly Gly Ala Ala Leu Ala Thr Ala Gly
             25                  30                  35

gtg gca ctc atc ggt gtc cca gta tgg gct gaa ttt gtc acc ttc gcg   259
Val Ala Leu Ile Gly Val Pro Val Trp Ala Glu Phe Val Thr Phe Ala
         40                  45                  50

gtg gcc tca gct gct cta ctg atg ttc att agg ccg gcc att aga aag   307
Val Ala Ser Ala Ala Leu Leu Met Phe Ile Arg Pro Ala Ile Arg Lys
     55                  60                  65
```

```
cgt ctg ctg aaa cca aag gtt ctg gac tct tca cca cga gca ctt gtt   355
Arg Leu Leu Lys Pro Lys Val Leu Asp Ser Ser Pro Arg Ala Leu Val
 70                  75                  80                  85

ggc cac cgt gct gaa gtg ctc gaa gat gtc gga gcg acc agc ggg cag   403
Gly His Arg Ala Glu Val Leu Glu Asp Val Gly Ala Thr Ser Gly Gln
                 90                  95                 100

gtc cgc ctg gat ggt tca att tgg tcc gcc cgc agc atg gat ccc aca   451
Val Arg Leu Asp Gly Ser Ile Trp Ser Ala Arg Ser Met Asp Pro Thr
            105                 110                 115

cac acc ttc gcg gaa ggt gaa att gtc agt gtc att gat atc caa ggc   499
His Thr Phe Ala Glu Gly Glu Ile Val Ser Val Ile Asp Ile Gln Gly
        120                 125                 130

acg acc gcg att gta tgg aaa gaa gcc taaattttta acaatcaaat         546
Thr Thr Ala Ile Val Trp Lys Glu Ala
    135                 140

agt                                                               549
```

<210> 1616
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 1616

```
Val Gly Ala Ile Ile Trp Phe Ile Gly Ala Leu Val Leu Ala Gly Leu
  1               5                  10                  15

Glu Leu Ala Val Gly Glu Phe Thr Leu Leu Met Leu Gly Gly Ala Ala
             20                  25                  30

Leu Ala Thr Ala Gly Val Ala Leu Ile Gly Val Pro Val Trp Ala Glu
         35                  40                  45

Phe Val Thr Phe Ala Val Ala Ser Ala Ala Leu Leu Met Phe Ile Arg
     50                  55                  60

Pro Ala Ile Arg Lys Arg Leu Leu Lys Pro Lys Val Leu Asp Ser Ser
 65                  70                  75                  80

Pro Arg Ala Leu Val Gly His Arg Ala Glu Val Leu Glu Asp Val Gly
                 85                  90                  95

Ala Thr Ser Gly Gln Val Arg Leu Asp Gly Ser Ile Trp Ser Ala Arg
            100                 105                 110

Ser Met Asp Pro Thr His Thr Phe Ala Glu Gly Glu Ile Val Ser Val
        115                 120                 125

Ile Asp Ile Gln Gly Thr Thr Ala Ile Val Trp Lys Glu Ala
    130                 135                 140
```

<210> 1617
<211> 906
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(883)
<223> RXA00155

<400> 1617
gttgcgggag tgtccaccaa aaatattgcc tgcatagggg tctgaaaaac tcatagctca 60

ccaccctagt caaagcactg cactacactt ccctaacact atg gaa att cga gca 115
Met Glu Ile Arg Ala
1 5

aac gtt tat tca ccg ctt caa aat act gcc gtc tgg cta ggt gcg tgg 163
Asn Val Tyr Ser Pro Leu Gln Asn Thr Ala Val Trp Leu Gly Ala Trp
10 15 20

ctc tat gaa tta gtg ccc acc gaa gat gtc atc gat gcg ttc gtc gat 211
Leu Tyr Glu Leu Val Pro Thr Glu Asp Val Ile Asp Ala Phe Val Asp
25 30 35

ctc ggc ggc ccg cac acc ttc ggc gac ggc ggg ctg ctc gat atg ctg 259
Leu Gly Gly Pro His Thr Phe Gly Asp Gly Gly Leu Leu Asp Met Leu
40 45 50

cga act tta aaa gaa tta aca agc acg ctt atc gac gcc ccc ttc cac 307
Arg Thr Leu Lys Glu Leu Thr Ser Thr Leu Ile Asp Ala Pro Phe His
55 60 65

ggt ccg att tta act ctc gca ctc agc ggc cca ggc caa gtg ccg gcg 355
Gly Pro Ile Leu Thr Leu Ala Leu Ser Gly Pro Gly Gln Val Pro Ala
70 75 80 85

ttg ccg gca ggt tca cgc gct gcg gtc ttg gcc tcc gcc tcg aag gag 403
Leu Pro Ala Gly Ser Arg Ala Ala Val Leu Ala Ser Ala Ser Lys Glu
90 95 100

ggg gcg ttg gtg ctg ggc ggc gtc gat aag cag cat tct tgg gcg ctt 451
Gly Ala Leu Val Leu Gly Gly Val Asp Lys Gln His Ser Trp Ala Leu
105 110 115

att cct acg cgc ggt aag gat gcc act gag tgg aat ttg gtg gag gtg 499
Ile Pro Thr Arg Gly Lys Asp Ala Thr Glu Trp Asn Leu Val Glu Val
120 125 130

gag ggc ttt ttg ccg gcg att gcg act gtc tcg ccc ggt gag gcg gat 547
Glu Gly Phe Leu Pro Ala Ile Ala Thr Val Ser Pro Gly Glu Ala Asp
135 140 145

cag ctg ctc cgt cag gcg aca gat cag gcg gca aat atc att gag tta 595
Gln Leu Leu Arg Gln Ala Thr Asp Gln Ala Ala Asn Ile Ile Glu Leu
150 155 160 165

agt ggc tac gct tca ctt gcg ccg aaa tct ttg aag aat ccg cga cta 643
Ser Gly Tyr Ala Ser Leu Ala Pro Lys Ser Leu Lys Asn Pro Arg Leu
170 175 180

acc gtg ggc atg ctg tca gat ttt tac gac acc ccg ggg ctt ccc tat 691
Thr Val Gly Met Leu Ser Asp Phe Tyr Asp Thr Pro Gly Leu Pro Tyr
185 190 195

```
gca gtc cca gag agg tcg gcg aag ctt ttt gcg cgc gca gat cgc gtg   739
Ala Val Pro Glu Arg Ser Ala Lys Leu Phe Ala Arg Ala Asp Arg Val
        200                 205                 210

gct gcc atc gca gag acc gtg cag gaa acc atc ggc gat cac agc ctg   787
Ala Ala Ile Ala Glu Thr Val Gln Glu Thr Ile Gly Asp His Ser Leu
    215                 220                 225

gat cca cag ttg att ttc ctg tgg agc cat att cgg acc gcg cgc atg   835
Asp Pro Gln Leu Ile Phe Leu Trp Ser His Ile Arg Thr Ala Arg Met
230                 235                 240                 245

gct ggg gtg agt tat gcc ctc gca gag ttt gcg agg gac tat cac tcc   883
Ala Gly Val Ser Tyr Ala Leu Ala Glu Phe Ala Arg Asp Tyr His Ser
                250                 255                 260

tagttggcag ctggcgccgc tga                                        906


<210> 1618
<211> 261
<212> PRT
<213> Corynebacterium glutamicum

<400> 1618
Met Glu Ile Arg Ala Asn Val Tyr Ser Pro Leu Gln Asn Thr Ala Val
  1               5                  10                  15

Trp Leu Gly Ala Trp Leu Tyr Glu Leu Val Pro Thr Glu Asp Val Ile
             20                  25                  30

Asp Ala Phe Val Asp Leu Gly Gly Pro His Thr Phe Gly Asp Gly Gly
         35                  40                  45

Leu Leu Asp Met Leu Arg Thr Leu Lys Glu Leu Thr Ser Thr Leu Ile
     50                  55                  60

Asp Ala Pro Phe His Gly Pro Ile Leu Thr Leu Ala Leu Ser Gly Pro
 65                  70                  75                  80

Gly Gln Val Pro Ala Leu Pro Ala Gly Ser Arg Ala Ala Val Leu Ala
                 85                  90                  95

Ser Ala Ser Lys Glu Gly Ala Leu Val Leu Gly Gly Val Asp Lys Gln
            100                 105                 110

His Ser Trp Ala Leu Ile Pro Thr Arg Gly Lys Asp Ala Thr Glu Trp
        115                 120                 125

Asn Leu Val Glu Val Glu Gly Phe Leu Pro Ala Ile Ala Thr Val Ser
    130                 135                 140

Pro Gly Glu Ala Asp Gln Leu Leu Arg Gln Ala Thr Asp Gln Ala Ala
145                 150                 155                 160

Asn Ile Ile Glu Leu Ser Gly Tyr Ala Ser Leu Ala Pro Lys Ser Leu
                165                 170                 175

Lys Asn Pro Arg Leu Thr Val Gly Met Leu Ser Asp Phe Tyr Asp Thr
            180                 185                 190
```

```
Pro Gly Leu Pro Tyr Ala Val Pro Glu Arg Ser Ala Lys Leu Phe Ala
        195                 200                 205

Arg Ala Asp Arg Val Ala Ala Ile Ala Glu Thr Val Gln Glu Thr Ile
    210                 215                 220

Gly Asp His Ser Leu Asp Pro Gln Leu Ile Phe Leu Trp Ser His Ile
225                 230                 235                 240

Arg Thr Ala Arg Met Ala Gly Val Ser Tyr Ala Leu Ala Glu Phe Ala
                245                 250                 255

Arg Asp Tyr His Ser
            260


<210> 1619
<211> 1305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1282)
<223> RXA00159

<400> 1619
cttagggggt aaccccaccc ctgtacaagt tttcgtgcta ccaaacacgc cgtgctaggg 60

gtgtcgcatg gtgcaatgat ccccgctaac ctgggattcc atg gag aat gtt agt   115
                                            Met Glu Asn Val Ser
                                              1               5

tcc gtc acg tcg gat ggt tcg gta gcg gat gtg cat gcc gaa cgg tgg   163
Ser Val Thr Ser Asp Gly Ser Val Ala Asp Val His Ala Glu Arg Trp
                10                  15                  20

caa gaa ttg ctc gca cgt ttg gat gcc gat gcg ccg gat att gcg gag   211
Gln Glu Leu Leu Ala Arg Leu Asp Ala Asp Ala Pro Asp Ile Ala Glu
            25                  30                  35

ggc acc gcc gca aag ttg ctc gct acg atc ccg ggc tat gag ctc gtt   259
Gly Thr Ala Ala Lys Leu Leu Ala Thr Ile Pro Gly Tyr Glu Leu Val
        40                  45                  50

gac gcg ggg ccg atc agg gag tcg tcg ata cgc aat acg gcc ttg att   307
Asp Ala Gly Pro Ile Arg Glu Ser Ser Ile Arg Asn Thr Ala Leu Ile
    55                  60                  65

att cgc gtg att aac gcg ggc acc gag cca aag gcc gag gac ttg cct   355
Ile Arg Val Ile Asn Ala Gly Thr Glu Pro Lys Ala Glu Asp Leu Pro
70                  75                  80                  85

gag gct tta agg ctt gcc gac gaa cgt ata gcg caa aat gtg ccg ctg   403
Glu Ala Leu Arg Leu Ala Asp Glu Arg Ile Ala Gln Asn Val Pro Leu
                90                  95                  100

gga agt gtg ctg cac ggt ttt cgg atg tct ctg ggg gaa att ctg gag   451
Gly Ser Val Leu His Gly Phe Arg Met Ser Leu Gly Glu Ile Leu Glu
            105                 110                 115
```

```
cat ttg gtg cag ttg ggc ccg gaa tac aat att gat ccc ggc aga atg   499
His Leu Val Gln Leu Gly Pro Glu Tyr Asn Ile Asp Pro Gly Arg Met
        120                 125                 130

ctg cgc tgg tcc aca ctg atg tgg gcg gtc aat gat gcc ttt tct acg   547
Leu Arg Trp Ser Thr Leu Met Trp Ala Val Asn Asp Ala Phe Ser Thr
    135                 140                 145

cgt gcc aca agg gtg tac cgc gat cac gag gtc gcc acg gcg atc gcc   595
Arg Ala Thr Arg Val Tyr Arg Asp His Glu Val Ala Thr Ala Ile Ala
150                 155                 160                 165

gat tcg gtg cga agg tca gaa tgg atc ggc aaa gcg gtc tcg gaa ggc   643
Asp Ser Val Arg Arg Ser Glu Trp Ile Gly Lys Ala Val Ser Glu Gly
                170                 175                 180

tct gaa ctg tca gag ctt tta tgg ggt gct gcg atg tat gac gtt ccc   691
Ser Glu Leu Ser Glu Leu Leu Trp Gly Ala Ala Met Tyr Asp Val Pro
            185                 190                 195

gcc gac act cct cta aga gca ttg gca gcc acc tca cct gat cat gcg   739
Ala Asp Thr Pro Leu Arg Ala Leu Ala Ala Thr Ser Pro Asp His Ala
        200                 205                 210

aaa gct gaa aca cag atc cag aag tgg act cag cgc gcc gga gtg cgg   787
Lys Ala Glu Thr Gln Ile Gln Lys Trp Thr Gln Arg Ala Gly Val Arg
    215                 220                 225

gtg ctg gca tcg gtg cag cca agc gtg atc gtg ggg atc gtg att ggg   835
Val Leu Ala Ser Val Gln Pro Ser Val Ile Val Gly Ile Val Ile Gly
230                 235                 240                 245

gag ccg aag cga aac gtg gac ggc cct ggt ttt gct gtg ggt ttg ggt   883
Glu Pro Lys Arg Asn Val Asp Gly Pro Gly Phe Ala Val Gly Leu Gly
                250                 255                 260

agg gca gag gtg ctc tca aag ctg gcg gac tca tat aag gat gca tcc   931
Arg Ala Glu Val Leu Ser Lys Leu Ala Asp Ser Tyr Lys Asp Ala Ser
            265                 270                 275

ctt gta ttg aag gct gcc gat aat ctg aaa ctt aat gag gtg cag cgg   979
Leu Val Leu Lys Ala Ala Asp Asn Leu Lys Leu Asn Glu Val Gln Arg
        280                 285                 290

gca caa gat ttg tca tgg aag ttg gct atc cat gca agc cca cgg gtg   1027
Ala Gln Asp Leu Ser Trp Lys Leu Ala Ile His Ala Ser Pro Arg Val
    295                 300                 305

acg gag att ctt gcg cag aaa tat gtg aag cca cta agg gaa tct ggc   1075
Thr Glu Ile Leu Ala Gln Lys Tyr Val Lys Pro Leu Arg Glu Ser Gly
310                 315                 320                 325

gag ttt gct cat gag atc gtg gaa tct ttg cgg gca tat gtg gac aac   1123
Glu Phe Ala His Glu Ile Val Glu Ser Leu Arg Ala Tyr Val Asp Asn
                330                 335                 340

cag atg aat att cct gct gct gcg cgc agt att cct gtg cat gtg aat   1171
Gln Met Asn Ile Pro Ala Ala Ala Arg Ser Ile Pro Val His Val Asn
            345                 350                 355

acg ctt cgc tat cgg ttg cgc cgg ttt gag gag tta acg ggc tgc tat   1219
```

```
Thr Leu Arg Tyr Arg Leu Arg Arg Phe Glu Glu Leu Thr Gly Cys Tyr
        360                 365                 370

ttg gag gat aca tcc acg gtc att gaa gtg tcg tgg gtg ctg gaa gtc   1267
Leu Glu Asp Thr Ser Thr Val Ile Glu Val Ser Trp Val Leu Glu Val
    375                 380                 385

ttt ggc cgg gag ctg tagaaaattg cacctatata tat                   1305
Phe Gly Arg Glu Leu
390
```

<210> 1620
<211> 394
<212> PRT
<213> Corynebacterium glutamicum

<400> 1620

```
Met Glu Asn Val Ser Ser Val Thr Ser Asp Gly Ser Val Ala Asp Val
  1               5                  10                  15

His Ala Glu Arg Trp Gln Glu Leu Leu Ala Arg Leu Asp Ala Asp Ala
             20                  25                  30

Pro Asp Ile Ala Glu Gly Thr Ala Ala Lys Leu Leu Ala Thr Ile Pro
         35                  40                  45

Gly Tyr Glu Leu Val Asp Ala Gly Pro Ile Arg Glu Ser Ser Ile Arg
     50                  55                  60

Asn Thr Ala Leu Ile Ile Arg Val Ile Asn Ala Gly Thr Glu Pro Lys
 65                  70                  75                  80

Ala Glu Asp Leu Pro Glu Ala Leu Arg Leu Ala Asp Glu Arg Ile Ala
                 85                  90                  95

Gln Asn Val Pro Leu Gly Ser Val Leu His Gly Phe Arg Met Ser Leu
            100                 105                 110

Gly Glu Ile Leu Glu His Leu Val Gln Leu Gly Pro Glu Tyr Asn Ile
        115                 120                 125

Asp Pro Gly Arg Met Leu Arg Trp Ser Thr Leu Met Trp Ala Val Asn
    130                 135                 140

Asp Ala Phe Ser Thr Arg Ala Thr Arg Val Tyr Arg Asp His Glu Val
145                 150                 155                 160

Ala Thr Ala Ile Ala Asp Ser Val Arg Arg Ser Glu Trp Ile Gly Lys
                165                 170                 175

Ala Val Ser Glu Gly Ser Glu Leu Ser Glu Leu Leu Trp Gly Ala Ala
            180                 185                 190

Met Tyr Asp Val Pro Ala Asp Thr Pro Leu Arg Ala Leu Ala Ala Thr
        195                 200                 205

Ser Pro Asp His Ala Lys Ala Glu Thr Gln Ile Gln Lys Trp Thr Gln
    210                 215                 220

Arg Ala Gly Val Arg Val Leu Ala Ser Val Gln Pro Ser Val Ile Val
```

```
225                 230                 235                 240

Gly Ile Val Ile Gly Glu Pro Lys Arg Asn Val Asp Gly Pro Gly Phe
                245                 250                 255

Ala Val Gly Leu Gly Arg Ala Glu Val Leu Ser Lys Leu Ala Asp Ser
            260                 265                 270

Tyr Lys Asp Ala Ser Leu Val Leu Lys Ala Ala Asp Asn Leu Lys Leu
        275                 280                 285

Asn Glu Val Gln Arg Ala Gln Asp Leu Ser Trp Lys Leu Ala Ile His
    290                 295                 300

Ala Ser Pro Arg Val Thr Glu Ile Leu Ala Gln Lys Tyr Val Lys Pro
305                 310                 315                 320

Leu Arg Glu Ser Gly Glu Phe Ala His Glu Ile Val Glu Ser Leu Arg
                325                 330                 335

Ala Tyr Val Asp Asn Gln Met Asn Ile Pro Ala Ala Ala Arg Ser Ile
            340                 345                 350

Pro Val His Val Asn Thr Leu Arg Tyr Arg Leu Arg Arg Phe Glu Glu
        355                 360                 365

Leu Thr Gly Cys Tyr Leu Glu Asp Thr Ser Thr Val Ile Glu Val Ser
    370                 375                 380

Trp Val Leu Glu Val Phe Gly Arg Glu Leu
385                 390


<210> 1621
<211> 585
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> RXA00161

<400> 1621
ttactataca tggtgtagtc ccaaattaac taatgcgggt gaccaactgc accgtaaaaa 60

aaattcgctt atcgtaaatc agcaggtaga ataacactct atg agc gag cca ggg   115
                                              Met Ser Glu Pro Gly
                                                1               5

cca tcc ggg gtt aaa gaa aag aag aaa gta aag gca agt cac att gtc   163
Pro Ser Gly Val Lys Glu Lys Lys Lys Val Lys Ala Ser His Ile Val
                10                  15                  20

ttt ctt ctc att tgt ttt atc gca gcc tgc gcg ttg gcg tgg tgg cag   211
Phe Leu Leu Ile Cys Phe Ile Ala Ala Cys Ala Leu Ala Trp Trp Gln
            25                  30                  35

tgg tca aga ttc cag tcc ggg tct gga act ttc caa aac ctt ggc tat   259
Trp Ser Arg Phe Gln Ser Gly Ser Gly Thr Phe Gln Asn Leu Gly Tyr
        40                  45                  50
```

```
gcc ttc cag tgg cct ctt atc gga gca ttc ttt gtt tat gcc tac cgc   307
Ala Phe Gln Trp Pro Leu Ile Gly Ala Phe Phe Val Tyr Ala Tyr Arg
     55                  60                  65

aag tat ttg cag tat gag aat gag tcc att gag tta gaa aac atg gaa   355
Lys Tyr Leu Gln Tyr Glu Asn Glu Ser Ile Glu Leu Glu Asn Met Glu
 70                  75                  80                  85

gcc aaa atg atg gcg gag caa ggc aaa aca cca gtt gcg caa tca gag   403
Ala Lys Met Met Ala Glu Gln Gly Lys Thr Pro Val Ala Gln Ser Glu
                 90                  95                 100

cag gaa gat agc ttc gtt cag ctc tct cac cgt ccg agc ctg gtg gaa   451
Gln Glu Asp Ser Phe Val Gln Leu Ser His Arg Pro Ser Leu Val Glu
            105                 110                 115

gat gac agc gtc aag gaa atc gac gaa tcc ttc ctg ccg tct cgc ccg   499
Asp Asp Ser Val Lys Glu Ile Asp Glu Ser Phe Leu Pro Ser Arg Pro
        120                 125                 130

acg atg gat gtg gaa gag ttc aac agg ttg aat gat ccg cat gca cgg   547
Thr Met Asp Val Glu Glu Phe Asn Arg Leu Asn Asp Pro His Ala Arg
    135                 140                 145

aga cgt cga aaa gca taaacctgga acttttccgg gcc                    585
Arg Arg Arg Lys Ala
150
```

EFS Web 2.0.1.0

<210> 1622
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 1622

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Met Ser Glu Pro Gly Pro Ser Gly Val Lys Glu Lys Lys Lys Val Lys
  1               5                  10                  15

Ala Ser His Ile Val Phe Leu Leu Ile Cys Phe Ile Ala Ala Cys Ala
             20                  25                  30

Leu Ala Trp Trp Gln Trp Ser Arg Phe Gln Ser Gly Ser Gly Thr Phe
         35                  40                  45

Gln Asn Leu Gly Tyr Ala Phe Gln Trp Pro Leu Ile Gly Ala Phe Phe
     50                  55                  60

Val Tyr Ala Tyr Arg Lys Tyr Leu Gln Tyr Glu Asn Glu Ser Ile Glu
 65                  70                  75                  80

Leu Glu Asn Met Glu Ala Lys Met Met Ala Glu Gln Gly Lys Thr Pro
                 85                  90                  95

Val Ala Gln Ser Glu Gln Glu Asp Ser Phe Val Gln Leu Ser His Arg
            100                 105                 110

Pro Ser Leu Val Glu Asp Asp Ser Val Lys Glu Ile Asp Glu Ser Phe
        115                 120                 125

Leu Pro Ser Arg Pro Thr Met Asp Val Glu Glu Phe Asn Arg Leu Asn
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    130                 135                 140

Asp Pro His Ala Arg Arg Arg Arg Lys Ala
145                 150


<210> 1623
<211> 2196
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2173)
<223> RXA00169

<400> 1623
tttgctgtgt ctaagtgtgt ggggtaattg taatataatt ggtagaattt tctctaatta 60

atattttatt aacttacgga gaaagtttat gataaatatg atg tcg ttg ggt aat   115
                                        Met Ser Leu Gly Asn
                                          1               5

cca gca gca atg ctc gct gcg tac aac acc agc acg cag gtg gca ccg   163
Pro Ala Ala Met Leu Ala Ala Tyr Asn Thr Ser Thr Gln Val Ala Pro
                  10                  15                  20

cag cca cag ctg gga cca cgt gct gga gaa gtt caa ctc agt agc gaa   211
Gln Pro Gln Leu Gly Pro Arg Ala Gly Glu Val Gln Leu Ser Ser Glu
              25                  30                  35

cag caa gcc atg att gat tat gta ctt gct ggc aaa gat gtc att gtt   259
Gln Gln Ala Met Ile Asp Tyr Val Leu Ala Gly Lys Asp Val Ile Val
          40                  45                  50

gat gcc acc gta ggc tcg ggc aaa act acc gct att caa cga ctg tgt   307
Asp Ala Thr Val Gly Ser Gly Lys Thr Thr Ala Ile Gln Arg Leu Cys
      55                  60                  65

tcg atc atg ggt gca gac cat gac gtg ctg tat ttg acg tat tcg aag   355
Ser Ile Met Gly Ala Asp His Asp Val Leu Tyr Leu Thr Tyr Ser Lys
  70                  75                  80                  85

ttg ttg aag gtc gat gca cag cag cgc gtt cgt ggc gcc aag gtg cag   403
Leu Leu Lys Val Asp Ala Gln Gln Arg Val Arg Gly Ala Lys Val Gln
                  90                  95                 100

aac tat cac ggc att gtc tat ccg cat cta ctc aag gcc ggc atc aag   451
Asn Tyr His Gly Ile Val Tyr Pro His Leu Leu Lys Ala Gly Ile Lys
             105                 110                 115

tgt ggt att agc gag tcg att cgg gag ttt aac aag aac ttc aaa cac   499
Cys Gly Ile Ser Glu Ser Ile Arg Glu Phe Asn Lys Asn Phe Lys His
         120                 125                 130

att tct cgc acg ttc ccc agt tac gac ctg ctg gtt att gat gag tac   547
Ile Ser Arg Thr Phe Pro Ser Tyr Asp Leu Leu Val Ile Asp Glu Tyr
     135                 140                 145

cag gac atc aat gag gac tat gca gaa ctg ctg cgc aac att aag tct   595
Gln Asp Ile Asn Glu Asp Tyr Ala Glu Leu Leu Arg Asn Ile Lys Ser
```

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150                 155                 160                 165

gtg aat ccg ctt atg cag att gtc atg gtg ggt gat ttg gaa caa aaa   643
Val Asn Pro Leu Met Gln Ile Val Met Val Gly Asp Leu Glu Gln Lys
                170                 175                 180

gtc cgg tct gac acc acg tta gat cca caa gaa ttt gca gca caa ttg   691
Val Arg Ser Asp Thr Thr Leu Asp Pro Gln Glu Phe Ala Ala Gln Leu
            185                 190                 195

tgt gaa gat cca gtc ttc gcg ccg ttt aca cag tcg ttt cga att ggc   739
Cys Glu Asp Pro Val Phe Ala Pro Phe Thr Gln Ser Phe Arg Ile Gly
        200                 205                 210

gag gct atg gca gcg ggt ttg gct gat gcc tgg aat aaa ccg att gtg   787
Glu Ala Met Ala Ala Gly Leu Ala Asp Ala Trp Asn Lys Pro Ile Val
    215                 220                 225

ggt gcc aat acc gca cag cag att gaa tat agg tct ttc gct gag gca   835
Gly Ala Asn Thr Ala Gln Gln Ile Glu Tyr Arg Ser Phe Ala Glu Ala
230                 235                 240                 245

gtg gtg ttg atc caa agc acc gag ccg agc aaa ctg ttg tgt ttg ggt   883
Val Val Leu Ile Gln Ser Thr Glu Pro Ser Lys Leu Leu Cys Leu Gly
                250                 255                 260

agc cgc aat ggg cag atg tca gat gcg ctt aat gtc gtg gag agg aag   931
Ser Arg Asn Gly Gln Met Ser Asp Ala Leu Asn Val Val Glu Arg Lys
            265                 270                 275

tcg ccg gca aag ttc aat aag aaa act gtg ttc gcc tct att cgc gat   979
Ser Pro Ala Lys Phe Asn Lys Lys Thr Val Phe Ala Ser Ile Arg Asp
        280                 285                 290

ggt gat tcc cag att gca cac cct aat gac gct gcg gtg ttt acc acc   1027
Gly Asp Ser Gln Ile Ala His Pro Asn Asp Ala Ala Val Phe Thr Thr
    295                 300                 305

ttt gat tcc agt aaa ggt cta gag cgc gat acc tgc gtg gtc ttt gac   1075
Phe Asp Ser Ser Lys Gly Leu Glu Arg Asp Thr Cys Val Val Phe Asp
310                 315                 320                 325

tat gac gaa gaa ttc tgg gac atg cgt ctt ggt tac ccc aat gtt gat   1123
Tyr Asp Glu Glu Phe Trp Asp Met Arg Leu Gly Tyr Pro Asn Val Asp
                330                 335                 340

cca gtg gtc atg cgc aat gtg ttt ttg gtg gca gca tca cgc ggt aaa   1171
Pro Val Val Met Arg Asn Val Phe Leu Val Ala Ala Ser Arg Gly Lys
            345                 350                 355

aac aag gtt gtt ttt gta cgt agc gat tct ctt caa gca gcg tat gag   1219
Asn Lys Val Val Phe Val Arg Ser Asp Ser Leu Gln Ala Ala Tyr Glu
        360                 365                 370

gct ggt gcg gac tgg gct gca ggg ctc gct gtg ggt gtg gtg gac aac   1267
Ala Gly Ala Asp Trp Ala Ala Gly Leu Ala Val Gly Val Val Asp Asn
    375                 380                 385

aat act gag gtt gca cct gag gta gat gcc cat acg ccg gca gaa gaa   1315
Asn Thr Glu Val Ala Pro Glu Val Asp Ala His Thr Pro Ala Glu Glu
390                 395                 400                 405
```

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agt aag ggt gat gtg ggt gag gtt cag tca cag att gag cgc atg atg   1363
Ser Lys Gly Asp Val Gly Glu Val Gln Ser Gln Ile Glu Arg Met Met
                410                 415                 420

ggt ttt atc cct gtt tca gtg ttt aaa gaa cta cct gag ttg gcg ccg   1411
Gly Phe Ile Pro Val Ser Val Phe Lys Glu Leu Pro Glu Leu Ala Pro
            425                 430                 435

agc gaa tat gcg cga ccg atc tct gtg act gaa gcc ttt gat ttt aag   1459
Ser Glu Tyr Ala Arg Pro Ile Ser Val Thr Glu Ala Phe Asp Phe Lys
        440                 445                 450

tac gca gag aat gtc gaa gca tgt ttt gac ctg ctt gat gtc aag cgt   1507
Tyr Ala Glu Asn Val Glu Ala Cys Phe Asp Leu Leu Asp Val Lys Arg
    455                 460                 465

ctc gac aac ggc aag ggt gca gcc att gag gtc aat cgc agt gac ggg   1555
Leu Asp Asn Gly Lys Gly Ala Ala Ile Glu Val Asn Arg Ser Asp Gly
470                 475                 480                 485

ctt att gat ctc tca ccc aca gtg gga aac ttt cag gaa gca gtg ttc   1603
Leu Ile Asp Leu Ser Pro Thr Val Gly Asn Phe Gln Glu Ala Val Phe
                490                 495                 500

ttc aag gac tac aac gtt cat aca gca cta tcg gcg tac ccg agt cag   1651
Phe Lys Asp Tyr Asn Val His Thr Ala Leu Ser Ala Tyr Pro Ser Gln
            505                 510                 515

ttc gcg aaa aat ctt aaa cgt ttg gtg aag aaa aac aat agc gta tgg   1699
Phe Ala Lys Asn Leu Lys Arg Leu Val Lys Lys Asn Asn Ser Val Trp
        520                 525                 530

cgt aac tgc ctt att gtc aca gca gcg tcc aca gag cag atg cgg tat   1747
Arg Asn Cys Leu Ile Val Thr Ala Ala Ser Thr Glu Gln Met Arg Tyr
    535                 540                 545

gtc gat cag gtg cgc agc tct atc ccg gtt gct gcg gag aag gca ttg   1795
Val Asp Gln Val Arg Ser Ser Ile Pro Val Ala Ala Glu Lys Ala Leu
550                 555                 560                 565

gtc tca cgg ctg agt acg agg ctg aat gct gat tca cgt aat cag att   1843
Val Ser Arg Leu Ser Thr Arg Leu Asn Ala Asp Ser Arg Asn Gln Ile
                570                 575                 580

cca ctg atc ctt gac ggc gag gca gta cag agc aaa gta gtg cgc acg   1891
Pro Leu Ile Leu Asp Gly Glu Ala Val Gln Ser Lys Val Val Arg Thr
            585                 590                 595

cca atg tct ttt gca ggt gtc gca gat gcg gtg cac aag ggt gtg ctt   1939
Pro Met Ser Phe Ala Gly Val Ala Asp Ala Val His Lys Gly Val Leu
        600                 605                 610

tat gaa ttg aaa ttc gtc tct gag ttg aca cat ccg atg ttt ttg cag   1987
Tyr Glu Leu Lys Phe Val Ser Glu Leu Thr His Pro Met Phe Leu Gln
    615                 620                 625

ctc gca atg tat ttg gtc atg tct ggg atg aag gac ggt att ttg tgg   2035
Leu Ala Met Tyr Leu Val Met Ser Gly Met Lys Asp Gly Ile Leu Trp
630                 635                 640                 645
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aac acc cgg aca gat gag gcg tgg cag gtg cgt gtt cct gac ccg aag   2083
Asn Thr Arg Thr Asp Glu Ala Trp Gln Val Arg Val Pro Asp Pro Lys
                650                 655                 660

cgt ttt ctt aat gct gtg gtg ttg tgt gtc tcc aag cag gat tac cgg   2131
Arg Phe Leu Asn Ala Val Val Leu Cys Val Ser Lys Gln Asp Tyr Arg
            665                 670                 675

gtc ggt aac ttt gat ctg ccg agc act ggt gga ggt gcg cgc           2173
Val Gly Asn Phe Asp Leu Pro Ser Thr Gly Gly Gly Ala Arg
        680                 685                 690

taaatggtgt tgatgtgtgg ggt                                        2196
```

<210> 1624
<211> 691
<212> PRT
<213> Corynebacterium glutamicum

<400> 1624

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Met Ser Leu Gly Asn Pro Ala Ala Met Leu Ala Ala Tyr Asn Thr Ser
  1               5                  10                  15

Thr Gln Val Ala Pro Gln Pro Gln Leu Gly Pro Arg Ala Gly Glu Val
             20                  25                  30

Gln Leu Ser Ser Glu Gln Gln Ala Met Ile Asp Tyr Val Leu Ala Gly
         35                  40                  45

Lys Asp Val Ile Val Asp Ala Thr Val Gly Ser Gly Lys Thr Thr Ala
     50                  55                  60

Ile Gln Arg Leu Cys Ser Ile Met Gly Ala Asp His Asp Val Leu Tyr
 65                  70                  75                  80

Leu Thr Tyr Ser Lys Leu Leu Lys Val Asp Ala Gln Gln Arg Val Arg
                 85                  90                  95

Gly Ala Lys Val Gln Asn Tyr His Gly Ile Val Tyr Pro His Leu Leu
            100                 105                 110

Lys Ala Gly Ile Lys Cys Gly Ile Ser Glu Ser Ile Arg Glu Phe Asn
        115                 120                 125

Lys Asn Phe Lys His Ile Ser Arg Thr Phe Pro Ser Tyr Asp Leu Leu
    130                 135                 140

Val Ile Asp Glu Tyr Gln Asp Ile Asn Glu Asp Tyr Ala Glu Leu Leu
145                 150                 155                 160

Arg Asn Ile Lys Ser Val Asn Pro Leu Met Gln Ile Val Met Val Gly
                165                 170                 175

Asp Leu Glu Gln Lys Val Arg Ser Asp Thr Thr Leu Asp Pro Gln Glu
            180                 185                 190

Phe Ala Ala Gln Leu Cys Glu Asp Pro Val Phe Ala Pro Phe Thr Gln
        195                 200                 205

Ser Phe Arg Ile Gly Glu Ala Met Ala Ala Gly Leu Ala Asp Ala Trp
```

```
    210                 215                 220

Asn Lys Pro Ile Val Gly Ala Asn Thr Ala Gln Gln Ile Glu Tyr Arg
225                 230                 235                 240

Ser Phe Ala Glu Ala Val Val Leu Ile Gln Ser Thr Glu Pro Ser Lys
                245                 250                 255

Leu Leu Cys Leu Gly Ser Arg Asn Gly Gln Met Ser Asp Ala Leu Asn
            260                 265                 270

Val Val Glu Arg Lys Ser Pro Ala Lys Phe Asn Lys Lys Thr Val Phe
        275                 280                 285

Ala Ser Ile Arg Asp Gly Asp Ser Gln Ile Ala His Pro Asn Asp Ala
    290                 295                 300

Ala Val Phe Thr Thr Phe Asp Ser Ser Lys Gly Leu Glu Arg Asp Thr
305                 310                 315                 320

Cys Val Val Phe Asp Tyr Asp Glu Glu Phe Trp Asp Met Arg Leu Gly
                325                 330                 335

Tyr Pro Asn Val Asp Pro Val Val Met Arg Asn Val Phe Leu Val Ala
            340                 345                 350

Ala Ser Arg Gly Lys Asn Lys Val Val Phe Val Arg Ser Asp Ser Leu
        355                 360                 365

Gln Ala Ala Tyr Glu Ala Gly Ala Asp Trp Ala Ala Gly Leu Ala Val
    370                 375                 380

Gly Val Val Asp Asn Asn Thr Glu Val Ala Pro Glu Val Asp Ala His
385                 390                 395                 400

Thr Pro Ala Glu Glu Ser Lys Gly Asp Val Gly Glu Val Gln Ser Gln
                405                 410                 415

Ile Glu Arg Met Met Gly Phe Ile Pro Val Ser Val Phe Lys Glu Leu
            420                 425                 430

Pro Glu Leu Ala Pro Ser Glu Tyr Ala Arg Pro Ile Ser Val Thr Glu
        435                 440                 445

Ala Phe Asp Phe Lys Tyr Ala Glu Asn Val Glu Ala Cys Phe Asp Leu
    450                 455                 460

Leu Asp Val Lys Arg Leu Asp Asn Gly Lys Gly Ala Ala Ile Glu Val
465                 470                 475                 480

Asn Arg Ser Asp Gly Leu Ile Asp Leu Ser Pro Thr Val Gly Asn Phe
                485                 490                 495

Gln Glu Ala Val Phe Phe Lys Asp Tyr Asn Val His Thr Ala Leu Ser
            500                 505                 510

Ala Tyr Pro Ser Gln Phe Ala Lys Asn Leu Lys Arg Leu Val Lys Lys
        515                 520                 525

Asn Asn Ser Val Trp Arg Asn Cys Leu Ile Val Thr Ala Ala Ser Thr
    530                 535                 540
```

```
Glu Gln Met Arg Tyr Val Asp Gln Val Arg Ser Ser Ile Pro Val Ala
545                 550                 555                 560

Ala Glu Lys Ala Leu Val Ser Arg Leu Ser Thr Arg Leu Asn Ala Asp
                565                 570                 575

Ser Arg Asn Gln Ile Pro Leu Ile Leu Asp Gly Glu Ala Val Gln Ser
            580                 585                 590

Lys Val Val Arg Thr Pro Met Ser Phe Ala Gly Val Ala Asp Ala Val
        595                 600                 605

His Lys Gly Val Leu Tyr Glu Leu Lys Phe Val Ser Glu Leu Thr His
    610                 615                 620

Pro Met Phe Leu Gln Leu Ala Met Tyr Leu Val Met Ser Gly Met Lys
625                 630                 635                 640

Asp Gly Ile Leu Trp Asn Thr Arg Thr Asp Glu Ala Trp Gln Val Arg
                645                 650                 655

Val Pro Asp Pro Lys Arg Phe Leu Asn Ala Val Val Leu Cys Val Ser
            660                 665                 670

Lys Gln Asp Tyr Arg Val Gly Asn Phe Asp Leu Pro Ser Thr Gly Gly
        675                 680                 685

Gly Ala Arg
    690
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US20050153417A1

<210> 1625
<211> 1977
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1954)
<223> RXA00170

<400> 1625

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taactaattc tttacctatc ctcagtttgt acatattttc cgacaggtaa aggtttgata 60

taagcggttg gtacgaagac tagtgggtgt ttctgctgtc atg ttg ctg gcc atc   115
                                              Met Leu Leu Ala Ile
                                                1               5

ggg gtt gca tct ccg gta gct caa gca caa gtg gaa gat caa ttt gag   163
Gly Val Ala Ser Pro Val Ala Gln Ala Gln Val Glu Asp Gln Phe Glu
                10                  15                  20

ctt gta aaa gaa atc agt gat gag cag ttt gct gat gat ggt gtt gac   211
Leu Val Lys Glu Ile Ser Asp Glu Gln Phe Ala Asp Asp Gly Val Asp
            25                  30                  35

tat gtt ccc aat agg aat gct ccg act gtt aag gaa caa ctt gag gat   259
Tyr Val Pro Asn Arg Asn Ala Pro Thr Val Lys Glu Gln Leu Glu Asp
        40                  45                  50
```

```
ttc gaa tca gca cat cca gaa gta gtc att gag tat cac gag cac gtc   307
Phe Glu Ser Ala His Pro Glu Val Val Ile Glu Tyr His Glu His Val
     55                  60                  65

aac gat agt aaa gac aat gtt gag gaa ctt ccg cta cct aag cgg gac   355
Asn Asp Ser Lys Asp Asn Val Glu Glu Leu Pro Leu Pro Lys Arg Asp
 70                  75                  80                  85

atc gtt gca ggg gaa atg cgc tca gat gtc atc gag tta ccg gag ggg   403
Ile Val Ala Gly Glu Met Arg Ser Asp Val Ile Glu Leu Pro Glu Gly
                 90                  95                 100

gtg agc aag gac gaa gct gat cag gtg gag gtt gcg gaa gcg cga ctt   451
Val Ser Lys Asp Glu Ala Asp Gln Val Glu Val Ala Glu Ala Arg Leu
            105                 110                 115

aat gag ggc gca cga ttg atg gct gca act ggg tgt gag gct atg tgg   499
Asn Glu Gly Ala Arg Leu Met Ala Ala Thr Gly Cys Glu Ala Met Trp
        120                 125                 130

cca aca ggt ttc tca gtt tgt ggc cgg att ctt gac gct tat cgg cag   547
Pro Thr Gly Phe Ser Val Cys Gly Arg Ile Leu Asp Ala Tyr Arg Gln
    135                 140                 145

gtt gga ggt cag ttg tca tgg ctt ggg cca cca aag tca aac gag ttg   595
Val Gly Gly Gln Leu Ser Trp Leu Gly Pro Pro Lys Ser Asn Glu Leu
150                 155                 160                 165

acc aat ccc gac ggt gtt ggc aaa aga agt gaa ttt gtt ggg ggt gcc   643
Thr Asn Pro Asp Gly Val Gly Lys Arg Ser Glu Phe Val Gly Gly Ala
                170                 175                 180

atc tat tgg cat cca gac aca ggc gct tat gca gtg acc ctg gac ggt   691
Ile Tyr Trp His Pro Asp Thr Gly Ala Tyr Ala Val Thr Leu Asp Gly
            185                 190                 195

ttg agg cag tgg ggg acc ttg aac tgg gaa tca ggg cca ttg ggg tac   739
Leu Arg Gln Trp Gly Thr Leu Asn Trp Glu Ser Gly Pro Leu Gly Tyr
        200                 205                 210

cca acc tct ggt ccg atg gat aca aac tat ccc ctt act cag cga cag   787
Pro Thr Ser Gly Pro Met Asp Thr Asn Tyr Pro Leu Thr Gln Arg Gln
    215                 220                 225

act ttt caa ggt ggt gac aac tat tac aac cca ttg act ggc ggt gct   835
Thr Phe Gln Gly Gly Asp Asn Tyr Tyr Asn Pro Leu Thr Gly Gly Ala
230                 235                 240                 245

gtg tgg ggc gat att aaa cag cgc tac gaa gaa ctt ggc ggc tcg aat   883
Val Trp Gly Asp Ile Lys Gln Arg Tyr Glu Glu Leu Gly Gly Ser Asn
                250                 255                 260

cat gcc att ggc atc ccg atc act aat gag cta cct agc ggt act gag   931
His Ala Ile Gly Ile Pro Ile Thr Asn Glu Leu Pro Ser Gly Thr Glu
            265                 270                 275

tat ttt tac aat aat ttc ttc aat gga aca att tcg tgg cga aat gat   979
Tyr Phe Tyr Asn Asn Phe Phe Asn Gly Thr Ile Ser Trp Arg Asn Asp
        280                 285                 290

cgt cag aca cgg ttt atg tat ttg gct acg cag cgg gtg tgg gat gcg   1027
```

```
Arg Gln Thr Arg Phe Met Tyr Leu Ala Thr Gln Arg Val Trp Asp Ala
    295                 300                 305

ttg ggt cgg gag acg ggt cgt tta ggt ttt cct gaa gca gat gaa aca   1075
Leu Gly Arg Glu Thr Gly Arg Leu Gly Phe Pro Glu Ala Asp Glu Thr
310                 315                 320                 325

cct gag gtt tct ggt cta ttc cat gtg gtg aat ttt gcg gag cgc ggg   1123
Pro Glu Val Ser Gly Leu Phe His Val Val Asn Phe Ala Glu Arg Gly
                330                 335                 340

gtg att gcg tgg aat gga atc cta ggc gcc aga gag ctg tat ggt gat   1171
Val Ile Ala Trp Asn Gly Ile Leu Gly Ala Arg Glu Leu Tyr Gly Asp
            345                 350                 355

gtt tac tcc ctg tgg ctg caa tac caa aat acc gat act cct tta ggg   1219
Val Tyr Ser Leu Trp Leu Gln Tyr Gln Asn Thr Asp Thr Pro Leu Gly
        360                 365                 370

tgg ccg ata cca tca ttg aca tca tta aat gag tca ctc gaa caa gaa   1267
Trp Pro Ile Pro Ser Leu Thr Ser Leu Asn Glu Ser Leu Glu Gln Glu
    375                 380                 385

ttc acc aga ggt gtt gtt tta ggc tca ggt gat gca ctg aca tgg att   1315
Phe Thr Arg Gly Val Val Leu Gly Ser Gly Asp Ala Leu Thr Trp Ile
390                 395                 400                 405

cct gac gat gaa gaa aga agt ttg gag gat ttc ctc cca att gga agt   1363
Pro Asp Asp Glu Glu Arg Ser Leu Glu Asp Phe Leu Pro Ile Gly Ser
                410                 415                 420

agc ggc tca tcc tca tcg agc caa gag atg acc ctg ttt tcc cag cgt   1411
Ser Gly Ser Ser Ser Ser Ser Gln Glu Met Thr Leu Phe Ser Gln Arg
            425                 430                 435

gca caa tac gtg gat tgc aag aat ctt ccc gat tta gat gag cag aga   1459
Ala Gln Tyr Val Asp Cys Lys Asn Leu Pro Asp Leu Asp Glu Gln Arg
        440                 445                 450

aaa act gaa aac aac att gaa aag aat ggt ggc ccg atc aaa aaa gag   1507
Lys Thr Glu Asn Asn Ile Glu Lys Asn Gly Gly Pro Ile Lys Lys Glu
    455                 460                 465

tat agt tcg cga ggt ttc ccc acc gag ttc aga ttt gtc gtg aga aaa   1555
Tyr Ser Ser Arg Gly Phe Pro Thr Glu Phe Arg Phe Val Val Arg Lys
470                 475                 480                 485

ggg cat tat gac cgt tac agg aat gaa ggc tgg gga tat tta aaa aac   1603
Gly His Tyr Asp Arg Tyr Arg Asn Glu Gly Trp Gly Tyr Leu Lys Asn
                490                 495                 500

tat tgc aaa cac aac ttc gcc aac cac gct atg gct gag gcc gta gta   1651
Tyr Cys Lys His Asn Phe Ala Asn His Ala Met Ala Glu Ala Val Val
            505                 510                 515

gat aaa gcg gtg att gat tat ggc tca tcg cca gga acc agc tat tac   1699
Asp Lys Ala Val Ile Asp Tyr Gly Ser Ser Pro Gly Thr Ser Tyr Tyr
        520                 525                 530

aag ttc gag aaa acg gtg tac ttt cta gat tgc aga act tat aca ttc   1747
Lys Phe Glu Lys Thr Val Tyr Phe Leu Asp Cys Arg Thr Tyr Thr Phe
```

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    535                 540                 545

aat aag aac tca gga tgt aaa gaa atg cac gct ccg caa tgg gtg act   1795
Asn Lys Asn Ser Gly Cys Lys Glu Met His Ala Pro Gln Trp Val Thr
550                 555                 560                 565

att att tac aat cct cat act ttc act gga gca aat tcg aac aga ccc   1843
Ile Ile Tyr Asn Pro His Thr Phe Thr Gly Ala Asn Ser Asn Arg Pro
                570                 575                 580

aag ggg gta att tca gca tgg tgt aat tca acc cca cct ggt gga atc   1891
Lys Gly Val Ile Ser Ala Trp Cys Asn Ser Thr Pro Pro Gly Gly Ile
            585                 590                 595

gaa cac gag cct gaa att tcc caa tgt cct gat cat gtg aat ctt tat   1939
Glu His Glu Pro Glu Ile Ser Gln Cys Pro Asp His Val Asn Leu Tyr
        600                 605                 610

aat aag ctt cgc ata tgacagaacc ccatcaactg tgc                     1977
Asn Lys Leu Arg Ile
    615
```

09550210.090505

<210> 1626
<211> 618
<212> PRT
<213> Corynebacterium glutamicum

<400> 1626

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Met Leu Leu Ala Ile Gly Val Ala Ser Pro Val Ala Gln Ala Gln Val
  1               5                  10                  15

Glu Asp Gln Phe Glu Leu Val Lys Glu Ile Ser Asp Glu Gln Phe Ala
             20                  25                  30

Asp Asp Gly Val Asp Tyr Val Pro Asn Arg Asn Ala Pro Thr Val Lys
         35                  40                  45

Glu Gln Leu Glu Asp Phe Glu Ser Ala His Pro Glu Val Val Ile Glu
     50                  55                  60

Tyr His Glu His Val Asn Asp Ser Lys Asp Asn Val Glu Glu Leu Pro
 65                  70                  75                  80

Leu Pro Lys Arg Asp Ile Val Ala Gly Glu Met Arg Ser Asp Val Ile
                 85                  90                  95

Glu Leu Pro Glu Gly Val Ser Lys Asp Glu Ala Asp Gln Val Glu Val
            100                 105                 110

Ala Glu Ala Arg Leu Asn Glu Gly Ala Arg Leu Met Ala Ala Thr Gly
        115                 120                 125

Cys Glu Ala Met Trp Pro Thr Gly Phe Ser Val Cys Gly Arg Ile Leu
    130                 135                 140

Asp Ala Tyr Arg Gln Val Gly Gly Gln Leu Ser Trp Leu Gly Pro Pro
145                 150                 155                 160

Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly Val Gly Lys Arg Ser Glu
                165                 170                 175
```

```
Phe Val Gly Gly Ala Ile Tyr Trp His Pro Asp Thr Gly Ala Tyr Ala
            180                 185                 190

Val Thr Leu Asp Gly Leu Arg Gln Trp Gly Thr Leu Asn Trp Glu Ser
        195                 200                 205

Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro Met Asp Thr Asn Tyr Pro
    210                 215                 220

Leu Thr Gln Arg Gln Thr Phe Gln Gly Gly Asp Asn Tyr Tyr Asn Pro
225                 230                 235                 240

Leu Thr Gly Gly Ala Val Trp Gly Asp Ile Lys Gln Arg Tyr Glu Glu
                245                 250                 255

Leu Gly Gly Ser Asn His Ala Ile Gly Ile Pro Ile Thr Asn Glu Leu
            260                 265                 270

Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn Phe Phe Asn Gly Thr Ile
        275                 280                 285

Ser Trp Arg Asn Asp Arg Gln Thr Arg Phe Met Tyr Leu Ala Thr Gln
    290                 295                 300

Arg Val Trp Asp Ala Leu Gly Arg Glu Thr Gly Arg Leu Gly Phe Pro
305                 310                 315                 320

Glu Ala Asp Glu Thr Pro Glu Val Ser Gly Leu Phe His Val Val Asn
                325                 330                 335

Phe Ala Glu Arg Gly Val Ile Ala Trp Asn Gly Ile Leu Gly Ala Arg
            340                 345                 350

Glu Leu Tyr Gly Asp Val Tyr Ser Leu Trp Leu Gln Tyr Gln Asn Thr
        355                 360                 365

Asp Thr Pro Leu Gly Trp Pro Ile Pro Ser Leu Thr Ser Leu Asn Glu
    370                 375                 380

Ser Leu Glu Gln Glu Phe Thr Arg Gly Val Val Leu Gly Ser Gly Asp
385                 390                 395                 400

Ala Leu Thr Trp Ile Pro Asp Asp Glu Glu Arg Ser Leu Glu Asp Phe
                405                 410                 415

Leu Pro Ile Gly Ser Ser Gly Ser Ser Ser Ser Ser Gln Glu Met Thr
            420                 425                 430

Leu Phe Ser Gln Arg Ala Gln Tyr Val Asp Cys Lys Asn Leu Pro Asp
        435                 440                 445

Leu Asp Glu Gln Arg Lys Thr Glu Asn Asn Ile Glu Lys Asn Gly Gly
    450                 455                 460

Pro Ile Lys Lys Glu Tyr Ser Ser Arg Gly Phe Pro Thr Glu Phe Arg
465                 470                 475                 480

Phe Val Val Arg Lys Gly His Tyr Asp Arg Tyr Arg Asn Glu Gly Trp
                485                 490                 495
```

```
Gly Tyr Leu Lys Asn Tyr Cys Lys His Asn Phe Ala Asn His Ala Met
            500                 505                 510

Ala Glu Ala Val Val Asp Lys Ala Val Ile Asp Tyr Gly Ser Ser Pro
        515                 520                 525

Gly Thr Ser Tyr Tyr Lys Phe Glu Lys Thr Val Tyr Phe Leu Asp Cys
    530                 535                 540

Arg Thr Tyr Thr Phe Asn Lys Asn Ser Gly Cys Lys Glu Met His Ala
545                 550                 555                 560

Pro Gln Trp Val Thr Ile Ile Tyr Asn Pro His Thr Phe Thr Gly Ala
                565                 570                 575

Asn Ser Asn Arg Pro Lys Gly Val Ile Ser Ala Trp Cys Asn Ser Thr
            580                 585                 590

Pro Pro Gly Gly Ile Glu His Glu Pro Glu Ile Ser Gln Cys Pro Asp
        595                 600                 605

His Val Asn Leu Tyr Asn Lys Leu Arg Ile
    610                 615
```

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<210> 1627
<211> 456
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(433)
<223> RXA00173

<400> 1627

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tgccctgatc cacacacaac tgtgaagaaa gaagccgcaa tgtccaccac atccacctat 60

gagagccgta aggcagctat tcgcgacgct attctcgcct atg tca aca aca atc   115
                                              Met Ser Thr Thr Ile
                                                1               5

aag gct gct gca ccc tac agc ctt cat gcc cat gat ctc gaa cag ctt   163
Lys Ala Ala Ala Pro Tyr Ser Leu His Ala His Asp Leu Glu Gln Leu
                10                  15                  20

gct gta gat ctc act tta gtt acc acc ttt gat agc aat gct gca gtt   211
Ala Val Asp Leu Thr Leu Val Thr Thr Phe Asp Ser Asn Ala Ala Val
            25                  30                  35

gat gtc acg cca aca cat aca gaa gca cct ggt ttt acc ctg cat gag   259
Asp Val Thr Pro Thr His Thr Glu Ala Pro Gly Phe Thr Leu His Glu
        40                  45                  50

ggc acc gat act gcg cct atg gct cca acc ctg gtc gta cct att tcc   307
Gly Thr Asp Thr Ala Pro Met Ala Pro Thr Leu Val Val Pro Ile Ser
    55                  60                  65

agc gac atc tcc aca gcc gtt tcg gaa ata tct aca tta gtg cag cag   355
Ser Asp Ile Ser Thr Ala Val Ser Glu Ile Ser Thr Leu Val Gln Gln
70                  75                  80                  85
```

```
gct cgc acc gac gca gca agc gcc att cat gaa gca gaa gct gaa ttt   403
Ala Arg Thr Asp Ala Ala Ser Ala Ile His Glu Ala Glu Ala Glu Phe
                 90                  95                 100

tac aac caa ctt gct gcg gtc ctt gct cag tgatttaatg tggccgacac     453
Tyr Asn Gln Leu Ala Ala Val Leu Ala Gln
            105                 110

acc                                                               456
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<210> 1628
<211> 111
<212> PRT
<213> Corynebacterium glutamicum

<400> 1628

```
Met Ser Thr Thr Ile Lys Ala Ala Ala Pro Tyr Ser Leu His Ala His
  1               5                  10                  15

Asp Leu Glu Gln Leu Ala Val Asp Leu Thr Leu Val Thr Thr Phe Asp
             20                  25                  30

Ser Asn Ala Ala Val Asp Val Thr Pro Thr His Thr Glu Ala Pro Gly
         35                  40                  45

Phe Thr Leu His Glu Gly Thr Asp Thr Ala Pro Met Ala Pro Thr Leu
     50                  55                  60

Val Val Pro Ile Ser Ser Asp Ile Ser Thr Ala Val Ser Glu Ile Ser
 65                  70                  75                  80

Thr Leu Val Gln Gln Ala Arg Thr Asp Ala Ala Ser Ala Ile His Glu
                 85                  90                  95

Ala Glu Ala Glu Phe Tyr Asn Gln Leu Ala Ala Val Leu Ala Gln
            100                 105                 110
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<210> 1629
<211> 408
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> RXA00174

<400> 1629

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gcggtgtggc tgttaccaac aatcccgatg gcactgaaca aggtgatgca cgccgctggg 60

taagccactg ggaatcataa aaaagaaagt agcactagct atg cct aat cac cca   115
                                              Met Pro Asn His Pro
                                                1               5

cct att tcc acc ttc gat gac cgt cgc tct gct atg cgc gaa ggc att   163
Pro Ile Ser Thr Phe Asp Asp Arg Arg Ser Ala Met Arg Glu Gly Ile
                 10                  15                  20
```

```
act gat tac ctt gcc aat aca aat gca aat ggg tta ggc ggt tac agc   211
Thr Asp Tyr Leu Ala Asn Thr Asn Ala Asn Gly Leu Gly Gly Tyr Ser
             25                  30                  35

atc agc gac acc cac ctc gac aat ctt gct gag aaa ttc acc cgc aca   259
Ile Ser Asp Thr His Leu Asp Asn Leu Ala Glu Lys Phe Thr Arg Thr
         40                  45                  50

cat ggt gaa gca cag tac gat gcc ggc ttt gat ccc aat gat ctt gaa   307
His Gly Glu Ala Gln Tyr Asp Ala Gly Phe Asp Pro Asn Asp Leu Glu
     55                  60                  65

cca gag act ttt gtt cgt gac att gag atg agc tgg gat gag cgt gct   355
Pro Glu Thr Phe Val Arg Asp Ile Glu Met Ser Trp Asp Glu Arg Ala
 70                  75                  80                  85

att gat cgt gcc ctg atc cac aca caa ctg tgaagaaaga agccgcaatg     405
Ile Asp Arg Ala Leu Ile His Thr Gln Leu
                 90                  95

tcc                                                              408
```

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<210> 1630
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 1630

```
Met Pro Asn His Pro Pro Ile Ser Thr Phe Asp Asp Arg Arg Ser Ala
  1               5                  10                  15

Met Arg Glu Gly Ile Thr Asp Tyr Leu Ala Asn Thr Asn Ala Asn Gly
             20                  25                  30

Leu Gly Gly Tyr Ser Ile Ser Asp Thr His Leu Asp Asn Leu Ala Glu
         35                  40                  45

Lys Phe Thr Arg Thr His Gly Glu Ala Gln Tyr Asp Ala Gly Phe Asp
     50                  55                  60

Pro Asn Asp Leu Glu Pro Glu Thr Phe Val Arg Asp Ile Glu Met Ser
 65                  70                  75                  80

Trp Asp Glu Arg Ala Ile Asp Arg Ala Leu Ile His Thr Gln Leu
                 85                  90                  95
```

<210> 1631
<211> 753
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(730)
<223> RXA00175

<400> 1631

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agctcgacag ccgtaaagaa gttgtaggtc tttttcgctt gggatactga tgctctccca 60
```

```
agcgaacatg ggcgggagcc catgtcgggg tgttgtgcga atg gct gtg tgt caa   115
                                              Met Ala Val Cys Gln
                                                1               5

cta cct cag cct gag aaa aca aca ctt ata aag aaa gac ctt tta ctc   163
Leu Pro Gln Pro Glu Lys Thr Thr Leu Ile Lys Lys Asp Leu Leu Leu
                  10                  15                  20

atg act tct aca act aac tcc acc gcc atg ttc aac gac cac ctt atc   211
Met Thr Ser Thr Thr Asn Ser Thr Ala Met Phe Asn Asp His Leu Ile
            25                  30                  35

cct atg gca gag ctt gat gaa caa gct ctg cgc gac agc gtt ggt tct   259
Pro Met Ala Glu Leu Asp Glu Gln Ala Leu Arg Asp Ser Val Gly Ser
        40                  45                  50

tgg gca cag tac aag cac ccg ctt gac cag cgc aaa gaa cca gag ctc   307
Trp Ala Gln Tyr Lys His Pro Leu Asp Gln Arg Lys Glu Pro Glu Leu
    55                  60                  65

gtc ctt att cgt cgc gtc aac agc tca gag cgt gtg tgg gtc tta agt   355
Val Leu Ile Arg Arg Val Asn Ser Ser Glu Arg Val Trp Val Leu Ser
70                  75                  80                  85

ttc act gac ctg cgt gct gat gca ggt ctt gtg cct cgt agc aca ccg   403
Phe Thr Asp Leu Arg Ala Asp Ala Gly Leu Val Pro Arg Ser Thr Pro
                90                  95                 100

aat gct gac ccc tcc aat atc cgc aat acc att ttc tct gtc gct gtc   451
Asn Ala Asp Pro Ser Asn Ile Arg Asn Thr Ile Phe Ser Val Ala Val
            105                 110                 115

cgc gat ctt gtc ctt gat cgc tca ctt ccc cgg ctg ctt aac ctc aac   499
Arg Asp Leu Val Leu Asp Arg Ser Leu Pro Arg Leu Leu Asn Leu Asn
        120                 125                 130

ggg caa cca cca gca ggt gaa tgg gaa gaa ggc ttt gtc tac gtc gat   547
Gly Gln Pro Pro Ala Gly Glu Trp Glu Glu Gly Phe Val Tyr Val Asp
    135                 140                 145

tat gac cag agc gac acc gta gat ggc tac ctc att gag cac agc gaa   595
Tyr Asp Gln Ser Asp Thr Val Asp Gly Tyr Leu Ile Glu His Ser Glu
150                 155                 160                 165

cct gtc tcc att gaa agt caa acc acc ggt gaa atg cac tat ttc gat   643
Pro Val Ser Ile Glu Ser Gln Thr Thr Gly Glu Met His Tyr Phe Asp
                170                 175                 180

aag gtg cca ggc ggt gtg gct gtt acc aac aat ccc gat ggc act gaa   691
Lys Val Pro Gly Gly Val Ala Val Thr Asn Asn Pro Asp Gly Thr Glu
            185                 190                 195

caa ggt gat gca cgc cgc tgg gta agc cac tgg gaa tca taaaaaagaa    740
Gln Gly Asp Ala Arg Arg Trp Val Ser His Trp Glu Ser
        200                 205                 210

agtagcacta gct                                                   753
```

CONFIDENTIAL

<210> 1632
<211> 210

<212> PRT
<213> Corynebacterium glutamicum

<400> 1632
Met Ala Val Cys Gln Leu Pro Gln Pro Glu Lys Thr Thr Leu Ile Lys
1 5 10 15

Lys Asp Leu Leu Leu Met Thr Ser Thr Thr Asn Ser Thr Ala Met Phe
20 25 30

Asn Asp His Leu Ile Pro Met Ala Glu Leu Asp Glu Gln Ala Leu Arg
35 40 45

Asp Ser Val Gly Ser Trp Ala Gln Tyr Lys His Pro Leu Asp Gln Arg
50 55 60

Lys Glu Pro Glu Leu Val Leu Ile Arg Arg Val Asn Ser Ser Glu Arg
65 70 75 80

Val Trp Val Leu Ser Phe Thr Asp Leu Arg Ala Asp Ala Gly Leu Val
85 90 95

Pro Arg Ser Thr Pro Asn Ala Asp Pro Ser Asn Ile Arg Asn Thr Ile
100 105 110

Phe Ser Val Ala Val Arg Asp Leu Val Leu Asp Arg Ser Leu Pro Arg
115 120 125

Leu Leu Asn Leu Asn Gly Gln Pro Pro Ala Gly Glu Trp Glu Glu Gly
130 135 140

Phe Val Tyr Val Asp Tyr Asp Gln Ser Asp Thr Val Asp Gly Tyr Leu
145 150 155 160

Ile Glu His Ser Glu Pro Val Ser Ile Glu Ser Gln Thr Thr Gly Glu
165 170 175

Met His Tyr Phe Asp Lys Val Pro Gly Gly Val Ala Val Thr Asn Asn
180 185 190

Pro Asp Gly Thr Glu Gln Gly Asp Ala Arg Arg Trp Val Ser His Trp
195 200 205

Glu Ser
210

<210> 1633
<211> 582
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(559)
<223> RXA00179

<400> 1633
gcgggttcgc caaaccttgg tgatctcgtt agtgtatgta tcaagcattt tctttttgcc 60

caaccataat tgaaaggtcc accagcccgt gaccaccatc atg atc gct att cac 115

```
                                                    Met Ile Ala Ile His
                                                      1               5

gct att gca gca atc ctg ttc cta gga cca gca aca gta gct aac tct   163
Ala Ile Ala Ala Ile Leu Phe Leu Gly Pro Ala Thr Val Ala Asn Ser
                 10                  15                  20

cag ttc cac gtc cgc gcg tac gat gca cac aac ggc aac acc caa gcc   211
Gln Phe His Val Arg Ala Tyr Asp Ala His Asn Gly Asn Thr Gln Ala
             25                  30                  35

gct ggc tcc gca aaa acc ctt ttc aag att tcc cag tcc tac ggc atg   259
Ala Gly Ser Ala Lys Thr Leu Phe Lys Ile Ser Gln Ser Tyr Gly Met
         40                  45                  50

ctg tcc ctg ctc gtg cct ttg ctg ggt atc gcc atc atg ctt ctc gat   307
Leu Ser Leu Leu Val Pro Leu Leu Gly Ile Ala Ile Met Leu Leu Asp
     55                  60                  65

tgg tct ttc tac aag tct gaa ggc cag ttc cac gca gca atc gct ctc   355
Trp Ser Phe Tyr Lys Ser Glu Gly Gln Phe His Ala Ala Ile Ala Leu
 70                  75                  80                  85

agt gtt atc acc tgg gcg ctg ctt ctc ttc gtt atc ttc cca cgc cag   403
Ser Val Ile Thr Trp Ala Leu Leu Leu Phe Val Ile Phe Pro Arg Gln
                 90                  95                 100

aag aag atg atg ggt gct ctt gac ctt ctg gag gac gat gag cag gct   451
Lys Lys Met Met Gly Ala Leu Asp Leu Leu Glu Asp Asp Glu Gln Ala
             105                 110                 115

gca aag act tac gag atc gaa aac tgg gac aag gcg aag agc cag ctg   499
Ala Lys Thr Tyr Glu Ile Glu Asn Trp Asp Lys Ala Lys Ser Gln Leu
         120                 125                 130

tcc atg ttc ggc ggc atc tgg gct ctg ctg tgg gtc atc atc gct gtg   547
Ser Met Phe Gly Gly Ile Trp Ala Leu Leu Trp Val Ile Ile Ala Val
     135                 140                 145

ctg atg ttc atc taacacatct caaattgcca aaa                        582
Leu Met Phe Ile
150
```

<210> 1634
<211> 153
<212> PRT
<213> Corynebacterium glutamicum

<400> 1634

```
Met Ile Ala Ile His Ala Ile Ala Ala Ile Leu Phe Leu Gly Pro Ala
  1               5                  10                  15

Thr Val Ala Asn Ser Gln Phe His Val Arg Ala Tyr Asp Ala His Asn
             20                  25                  30

Gly Asn Thr Gln Ala Ala Gly Ser Ala Lys Thr Leu Phe Lys Ile Ser
         35                  40                  45

Gln Ser Tyr Gly Met Leu Ser Leu Leu Val Pro Leu Leu Gly Ile Ala
     50                  55                  60
```

```
Ile Met Leu Leu Asp Trp Ser Phe Tyr Lys Ser Glu Gly Gln Phe His
 65                  70                  75                  80

Ala Ala Ile Ala Leu Ser Val Ile Thr Trp Ala Leu Leu Leu Phe Val
                 85                  90                  95

Ile Phe Pro Arg Gln Lys Lys Met Met Gly Ala Leu Asp Leu Leu Glu
            100                 105                 110

Asp Asp Glu Gln Ala Ala Lys Thr Tyr Glu Ile Glu Asn Trp Asp Lys
        115                 120                 125

Ala Lys Ser Gln Leu Ser Met Phe Gly Gly Ile Trp Ala Leu Leu Trp
    130                 135                 140

Val Ile Ile Ala Val Leu Met Phe Ile
145                 150


<210> 1635
<211> 663
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(640)
<223> RXA00180

<400> 1635
aaacgaggat gttgatttcg ctgacgcagc tcagaagctt tcgaaagaaa gttaagcctt 60

agagggaacc aaacgccaag gcgatgagtc taacccgagt atg aag aac ttt att   115
                                              Met Lys Asn Phe Ile
                                                1               5

cgg gta ctc atc gcc ttt agt gtt ttc ctc tgt ata tat acc gtt gct   163
Arg Val Leu Ile Ala Phe Ser Val Phe Leu Cys Ile Tyr Thr Val Ala
                10                  15                  20

ccc cac att ggc cga ggt cct gga gac ctc gca cca gtt aca gca atc   211
Pro His Ile Gly Arg Gly Pro Gly Asp Leu Ala Pro Val Thr Ala Ile
            25                  30                  35

ccc caa cga gcc aca gtc cta ggc tat gac aga gcc tcc atg ttt ggc   259
Pro Gln Arg Ala Thr Val Leu Gly Tyr Asp Arg Ala Ser Met Phe Gly
        40                  45                  50

gga tgg ttg ggt ggc gtg cgg gaa ggc atc gtg gat gaa gcc ggc gac   307
Gly Trp Leu Gly Gly Val Arg Glu Gly Ile Val Asp Glu Ala Gly Asp
    55                  60                  65

act gat cca tac tcc ggg aat cga tta gac ctc tct agt gcc gag gtg   355
Thr Asp Pro Tyr Ser Gly Asn Arg Leu Asp Leu Ser Ser Ala Glu Val
70                  75                  80                  85

gat cat att ctc ccg ctc agc gcc gcc tgg gat cta ggc gca cac cgg   403
Asp His Ile Leu Pro Leu Ser Ala Ala Trp Asp Leu Gly Ala His Arg
                90                  95                 100
```

```
tgg agc gct ggc gag aga atc agc ttt gcc aac gac ccc ctc aac ctc   451
Trp Ser Ala Gly Glu Arg Ile Ser Phe Ala Asn Asp Pro Leu Asn Leu
            105                 110                 115

gtg ctc gtc tca aaa gct gag aac caa gaa aaa tcc gat caa ctt ccc   499
Val Leu Val Ser Lys Ala Glu Asn Gln Glu Lys Ser Asp Gln Leu Pro
        120                 125                 130

agc gag tgg ctc ccc tct gat cga agt gca cga tgt tgg tac gtg gaa   547
Ser Glu Trp Leu Pro Ser Asp Arg Ser Ala Arg Cys Trp Tyr Val Glu
    135                 140                 145

cgc ctt ttc gcc gtg gcc aac gca tac gaa ctt ccg tta cca gaa aac   595
Arg Leu Phe Ala Val Ala Asn Ala Tyr Glu Leu Pro Leu Pro Glu Asn
150                 155                 160                 165

gac att cgg gtt gga cga aaa cag tgc ggg ttc gcc aaa cct tgg       640
Asp Ile Arg Val Gly Arg Lys Gln Cys Gly Phe Ala Lys Pro Trp
                170                 175                 180

tgatctcgtt agtgtatgta tca                                        663
```

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<210> 1636
<211> 180
<212> PRT
<213> Corynebacterium glutamicum

<400> 1636

```
Met Lys Asn Phe Ile Arg Val Leu Ile Ala Phe Ser Val Phe Leu Cys
  1               5                  10                  15

Ile Tyr Thr Val Ala Pro His Ile Gly Arg Gly Pro Gly Asp Leu Ala
            20                  25                  30

Pro Val Thr Ala Ile Pro Gln Arg Ala Thr Val Leu Gly Tyr Asp Arg
         35                  40                  45

Ala Ser Met Phe Gly Gly Trp Leu Gly Gly Val Arg Glu Gly Ile Val
     50                  55                  60

Asp Glu Ala Gly Asp Thr Asp Pro Tyr Ser Gly Asn Arg Leu Asp Leu
 65                  70                  75                  80

Ser Ser Ala Glu Val Asp His Ile Leu Pro Leu Ser Ala Ala Trp Asp
                85                  90                  95

Leu Gly Ala His Arg Trp Ser Ala Gly Glu Arg Ile Ser Phe Ala Asn
            100                 105                 110

Asp Pro Leu Asn Leu Val Leu Val Ser Lys Ala Glu Asn Gln Glu Lys
        115                 120                 125

Ser Asp Gln Leu Pro Ser Glu Trp Leu Pro Ser Asp Arg Ser Ala Arg
    130                 135                 140

Cys Trp Tyr Val Glu Arg Leu Phe Ala Val Ala Asn Ala Tyr Glu Leu
145                 150                 155                 160

Pro Leu Pro Glu Asn Asp Ile Arg Val Gly Arg Lys Gln Cys Gly Phe
                165                 170                 175
```

```
Ala Lys Pro Trp
            180


<210> 1637
<211> 975
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(952)
<223> RXA00183

<400> 1637
ctggccagcg ccatcgtggg cgagggcgaa ggctggatca ccgaactcaa cccagaagaa 60

ttggctatgc tgatgagtta ccgcgaaaag gagggtgcag atg act gaa tca cgc   115
                                        Met Thr Glu Ser Arg
                                          1               5

cgc gtg aaa atg gat aac gtt att tac gcc aat ttt ggc agc aaa cag   163
Arg Val Lys Met Asp Asn Val Ile Tyr Ala Asn Phe Gly Ser Lys Gln
                 10                  15                  20

cgc gta tct act cct gat gac cgc acc cag gtg att aat aaa tca cga   211
Arg Val Ser Thr Pro Asp Asp Arg Thr Gln Val Ile Asn Lys Ser Arg
             25                  30                  35

cac aaa caa ttc agc cca gcg ggt act cgt acc gtg atg ttg acg gag   259
His Lys Gln Phe Ser Pro Ala Gly Thr Arg Thr Val Met Leu Thr Glu
         40                  45                  50

aaa aac gcc gac agc gga cga cgg tcc cgc ggt gag cag tac tac cga   307
Lys Asn Ala Asp Ser Gly Arg Arg Ser Arg Gly Glu Gln Tyr Tyr Arg
     55                  60                  65

aac ggc aat gtc acc ggc atg act gtg ctg gaa ggc cgc gtg gaa tgc   355
Asn Gly Asn Val Thr Gly Met Thr Val Leu Glu Gly Arg Val Glu Cys
 70                  75                  80                  85

act gtc gcg ggc tcc caa aac gag ccg ttt gtt acc aca gtg acc ttc   403
Thr Val Ala Gly Ser Gln Asn Glu Pro Phe Val Thr Thr Val Thr Phe
                 90                  95                 100

cca tac cga agc tcg gaa aaa ctc cgc gaa gcc tac gca gct att gcg   451
Pro Tyr Arg Ser Ser Glu Lys Leu Arg Glu Ala Tyr Ala Ala Ile Ala
            105                 110                 115

gat act ccc aat ggc ctg cgg ctt gtg cgt gat ggc cat ctg acc tcc   499
Asp Thr Pro Asn Gly Leu Arg Leu Val Arg Asp Gly His Leu Thr Ser
        120                 125                 130

tcc atg ctg gat cac ttg gtg gga agt cct gat gag tcg att tat ttt   547
Ser Met Leu Asp His Leu Val Gly Ser Pro Asp Glu Ser Ile Tyr Phe
    135                 140                 145

gac tgc acc tgc ccc gac cga tcg ctt gtg tgt aaa cat gcc gtt gcc   595
Asp Cys Thr Cys Pro Asp Arg Ser Leu Val Cys Lys His Ala Val Ala
150                 155                 160                 165
```

```
agc gcg tat cac gtt gcc gag aag atg acc gcg aac ccc ggt ctg atc   643
Ser Ala Tyr His Val Ala Glu Lys Met Thr Ala Asn Pro Gly Leu Ile
                170                 175                 180

ttg gat att cgt ggt caa ggg atg gct gga tta gaa gca ctg att cgg   691
Leu Asp Ile Arg Gly Gln Gly Met Ala Gly Leu Glu Ala Leu Ile Arg
            185                 190                 195

acc tat cac acc aag gtt gaa act gaa cct gaa gac aat gac agt ttt   739
Thr Tyr His Thr Lys Val Glu Thr Glu Pro Glu Asp Asn Asp Ser Phe
        200                 205                 210

tgg aac ggc agg gaa ctt cct gct ttg cct gat cca aag att gcc cct   787
Trp Asn Gly Arg Glu Leu Pro Ala Leu Pro Asp Pro Lys Ile Ala Pro
    215                 220                 225

gct atc gac gat tcc gat atc aac tac ctc cac aag gct tta agg atg   835
Ala Ile Asp Asp Ser Asp Ile Asn Tyr Leu His Lys Ala Leu Arg Met
230                 235                 240                 245

gtc tca tac acc tcc ctg gag cag ctt cgt gcg gtc agt gat att gaa   883
Val Ser Tyr Thr Ser Leu Glu Gln Leu Arg Ala Val Ser Asp Ile Glu
                250                 255                 260

gat atg tac gag att ttg gta gcc aac cac cct gat aac cag caa gtg   931
Asp Met Tyr Glu Ile Leu Val Ala Asn His Pro Asp Asn Gln Gln Val
            265                 270                 275

tat gag gaa gaa gac act gat taaccagggc ttatggttgt ggt            975
Tyr Glu Glu Glu Asp Thr Asp
        280
```

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<210> 1638
<211> 284
<212> PRT
<213> Corynebacterium glutamicum

<400> 1638

```
Met Thr Glu Ser Arg Arg Val Lys Met Asp Asn Val Ile Tyr Ala Asn
  1               5                  10                  15

Phe Gly Ser Lys Gln Arg Val Ser Thr Pro Asp Asp Arg Thr Gln Val
             20                  25                  30

Ile Asn Lys Ser Arg His Lys Gln Phe Ser Pro Ala Gly Thr Arg Thr
         35                  40                  45

Val Met Leu Thr Glu Lys Asn Ala Asp Ser Gly Arg Arg Ser Arg Gly
     50                  55                  60

Glu Gln Tyr Tyr Arg Asn Gly Asn Val Thr Gly Met Thr Val Leu Glu
 65                  70                  75                  80

Gly Arg Val Glu Cys Thr Val Ala Gly Ser Gln Asn Glu Pro Phe Val
                 85                  90                  95

Thr Thr Val Thr Phe Pro Tyr Arg Ser Ser Glu Lys Leu Arg Glu Ala
            100                 105                 110
```

```
Tyr Ala Ala Ile Ala Asp Thr Pro Asn Gly Leu Arg Leu Val Arg Asp
        115                 120                 125

Gly His Leu Thr Ser Ser Met Leu Asp His Leu Val Gly Ser Pro Asp
    130                 135                 140

Glu Ser Ile Tyr Phe Asp Cys Thr Cys Pro Asp Arg Ser Leu Val Cys
145                 150                 155                 160

Lys His Ala Val Ala Ser Ala Tyr His Val Ala Glu Lys Met Thr Ala
                165                 170                 175

Asn Pro Gly Leu Ile Leu Asp Ile Arg Gly Gln Gly Met Ala Gly Leu
            180                 185                 190

Glu Ala Leu Ile Arg Thr Tyr His Thr Lys Val Glu Thr Glu Pro Glu
        195                 200                 205

Asp Asn Asp Ser Phe Trp Asn Gly Arg Glu Leu Pro Ala Leu Pro Asp
    210                 215                 220

Pro Lys Ile Ala Pro Ala Ile Asp Asp Ser Asp Ile Asn Tyr Leu His
225                 230                 235                 240

Lys Ala Leu Arg Met Val Ser Tyr Thr Ser Leu Glu Gln Leu Arg Ala
                245                 250                 255

Val Ser Asp Ile Glu Asp Met Tyr Glu Ile Leu Val Ala Asn His Pro
            260                 265                 270

Asp Asn Gln Gln Val Tyr Glu Glu Glu Asp Thr Asp
        275                 280


<210> 1639
<211> 2751
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2728)
<223> RXA00185

<400> 1639
attgcgagag ctcgctgact ctgtggtcaa tggtgcagcg ccggaagaag accgcgatgc 60

gctcaaccta ttgttccgac taagccggga ggtctaagac atg cgt att cat gaa   115
                                                Met Arg Ile His Glu
                                                  1               5

atc atc att gac aat ttc cga gcc atc gaa cat cta gaa ctt cgt gac   163
Ile Ile Ile Asp Asn Phe Arg Ala Ile Glu His Leu Glu Leu Arg Asp
                 10                  15                  20

att cct gac cag ggc gtt atc gtg atc cac ggt gac aat gag caa ggc   211
Ile Pro Asp Gln Gly Val Ile Val Ile His Gly Asp Asn Glu Gln Gly
             25                  30                  35

aaa tct tca atc ctt gaa gcc ata aaa aca gtt ctg aat agt aaa cac   259
Lys Ser Ser Ile Leu Glu Ala Ile Lys Thr Val Leu Asn Ser Lys His
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         40                  45                  50

aga acc acc agc aag acg atc aag gcc att cag cct gtt gac cgt gat   307
Arg Thr Thr Ser Lys Thr Ile Lys Ala Ile Gln Pro Val Asp Arg Asp
     55                  60                  65

gtt ccc atc agc atc acc ctc gag gca acc gta ggc acg gtt cga ttc   355
Val Pro Ile Ser Ile Thr Leu Glu Ala Thr Val Gly Thr Val Arg Phe
 70                  75                  80                  85

cgc ata cac aaa cgc ttc cta aaa tcc aca gcc gca gaa ctg caa gtc   403
Arg Ile His Lys Arg Phe Leu Lys Ser Thr Ala Ala Glu Leu Gln Val
                 90                  95                 100

atc gag cca cgt cca tcc aac cac cgt gga cta gaa gcc gaa gct gca   451
Ile Glu Pro Arg Pro Ser Asn His Arg Gly Leu Glu Ala Glu Ala Ala
            105                 110                 115

ctg gca gaa ata ctg gaa agc cat ttg gac acc tct ttg ctt gac gca   499
Leu Ala Glu Ile Leu Glu Ser His Leu Asp Thr Ser Leu Leu Asp Ala
        120                 125                 130

ttg ttt atg aaa cag ggt gaa gta gaa gca ggt atc agc gct gta gga   547
Leu Phe Met Lys Gln Gly Glu Val Glu Ala Gly Ile Ser Ala Val Gly
    135                 140                 145

att cct acc ctg acc agc gct ttg aac gct caa aat ggc aat acc gaa   595
Ile Pro Thr Leu Thr Ser Ala Leu Asn Ala Gln Asn Gly Asn Thr Glu
150                 155                 160                 165

gat gcc acc gaa gac acc gca ctc atg gag gct gta gaa aag gaa tac   643
Asp Ala Thr Glu Asp Thr Ala Leu Met Glu Ala Val Glu Lys Glu Tyr
                170                 175                 180

cta aag ttc tac acc aac tcc gga aag gcg aat acg agg ttc cta cag   691
Leu Lys Phe Tyr Thr Asn Ser Gly Lys Ala Asn Thr Arg Phe Leu Gln
            185                 190                 195

ttt tcc aaa cag gtg gaa acc ctt cgt act gat ttg gat gag gct aac   739
Phe Ser Lys Gln Val Glu Thr Leu Arg Thr Asp Leu Asp Glu Ala Asn
        200                 205                 210

gct gaa gta gca aag ctc tcc tcc cat gtt gac cga gtt aaa cga ttg   787
Ala Glu Val Ala Lys Leu Ser Ser His Val Asp Arg Val Lys Arg Leu
    215                 220                 225

gaa att gat cgg gat cag gcc aca gca cag tta ccc aag gca gag gaa   835
Glu Ile Asp Arg Asp Gln Ala Thr Ala Gln Leu Pro Lys Ala Glu Glu
230                 235                 240                 245

gaa ctc gca ggg agg aaa gca gaa ctg gag gaa gcc caa aag gtt aag   883
Glu Leu Ala Gly Arg Lys Ala Glu Leu Glu Glu Ala Gln Lys Val Lys
                250                 255                 260

gct caa gcc acg gaa atc ctt gcg cag ttt tcc cgg gcg gaa gaa cag   931
Ala Gln Ala Thr Glu Ile Leu Ala Gln Phe Ser Arg Ala Glu Glu Gln
            265                 270                 275

tta gag cag gca aca gga gct cag aaa cga cgt aaa gaa ctc cgc aat   979
Leu Glu Gln Ala Thr Gly Ala Gln Lys Arg Arg Lys Glu Leu Arg Asn
        280                 285                 290
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```
aag ctg gaa tta gca cag aca gaa gtc gaa aag gct gaa gca ggg caa   1027
Lys Leu Glu Leu Ala Gln Thr Glu Val Glu Lys Ala Glu Ala Gly Gln
    295                 300                 305

gag aac ctg gcg caa gaa gct tcc cgt gaa gca gaa gaa ttc cta gcc   1075
Glu Asn Leu Ala Gln Glu Ala Ser Arg Glu Ala Glu Glu Phe Leu Ala
310                 315                 320                 325

tta agt gaa aag ttc gag gca gcg cgc gca gct gaa act ctg gcc gtt   1123
Leu Ser Glu Lys Phe Glu Ala Ala Arg Ala Ala Glu Thr Leu Ala Val
                330                 335                 340

gaa aag gtg aaa gca gca cgt caa tcg gtt gct gga atc aaa aac cgt   1171
Glu Lys Val Lys Ala Ala Arg Gln Ser Val Ala Gly Ile Lys Asn Arg
            345                 350                 355

gac cgt aaa gaa cac ctc acg gtt atg ctt ggt gaa ctt gat cga att   1219
Asp Arg Lys Glu His Leu Thr Val Met Leu Gly Glu Leu Asp Arg Ile
        360                 365                 370

ggg cag cgc ctc tac gaa ttg cgc agc gtc cag cac tca tcg gtg cgt   1267
Gly Gln Arg Leu Tyr Glu Leu Arg Ser Val Gln His Ser Ser Val Arg
    375                 380                 385

gtg agc cag cgt gat att gat gct ctg caa aag gcg atc acc gag gtc   1315
Val Ser Gln Arg Asp Ile Asp Ala Leu Gln Lys Ala Ile Thr Glu Val
390                 395                 400                 405

gat atc caa agg acg ctc gtt gaa gcg cag cag gga agt att acc ctc   1363
Asp Ile Gln Arg Thr Leu Val Glu Ala Gln Gln Gly Ser Ile Thr Leu
                410                 415                 420

agt gct tcc aca ccc acc gac att caa cta ggt gat gac acc gtt tca   1411
Ser Ala Ser Thr Pro Thr Asp Ile Gln Leu Gly Asp Asp Thr Val Ser
            425                 430                 435

gct acc gac gct gga acc aca gtt gcc ctc gac cga gaa ctc acc gtc   1459
Ala Thr Asp Ala Gly Thr Thr Val Ala Leu Asp Arg Glu Leu Thr Val
        440                 445                 450

gtg gtc ggc gat gtc acc ttg gtg att aac cca gga aaa aca gca gcg   1507
Val Val Gly Asp Val Thr Leu Val Ile Asn Pro Gly Lys Thr Ala Ala
    455                 460                 465

gaa agt cgc acc gat ttt gaa tcc gcc gag gca gca ttg gcg gag ctg   1555
Glu Ser Arg Thr Asp Phe Glu Ser Ala Glu Ala Ala Leu Ala Glu Leu
470                 475                 480                 485

ctt gat caa ctc gac gtc tca gac ttg gac cag ctc agg gaa cgt ttc   1603
Leu Asp Gln Leu Asp Val Ser Asp Leu Asp Gln Leu Arg Glu Arg Phe
                490                 495                 500

act gcc caa gag caa cga gac gcg gat att gca gaa ctg gtt cgc gaa   1651
Thr Ala Gln Glu Gln Arg Asp Ala Asp Ile Ala Glu Leu Val Arg Glu
            505                 510                 515

caa cag cgc atg agc ggt ggg aca gaa aca aca gtt tta cgt gcc gag   1699
Gln Gln Arg Met Ser Gly Gly Thr Glu Thr Thr Val Leu Arg Ala Glu
        520                 525                 530
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cta gaa ggc ctg cac gtc cca gag gat cta gac cca tca att tct gtg   1747
Leu Glu Gly Leu His Val Pro Glu Asp Leu Asp Pro Ser Ile Ser Val
    535                 540                 545

gat gat gcg caa act cag ttg aat gag gca gaa gag tcc aga gag ctc   1795
Asp Asp Ala Gln Thr Gln Leu Asn Glu Ala Glu Glu Ser Arg Glu Leu
550                 555                 560                 565

gct gcg gag gcg cat aaa cac gca aat gca gca ctt gat gga ttg cgt   1843
Ala Ala Glu Ala His Lys His Ala Asn Ala Ala Leu Asp Gly Leu Arg
                570                 575                 580

tcg cgt ccc gta gat aaa gct ctg aca gtt ttc aac gct cag ctc gca   1891
Ser Arg Pro Val Asp Lys Ala Leu Thr Val Phe Asn Ala Gln Leu Ala
            585                 590                 595

gca ctg cag aga aac ctc tct tcc gca caa gtt gaa tta gac cgt gca   1939
Ala Leu Gln Arg Asn Leu Ser Ser Ala Gln Val Glu Leu Asp Arg Ala
        600                 605                 610

gtg gca gaa acc tcg gat gac gaa gtt gat gct gct gta cag cgg tgc   1987
Val Ala Glu Thr Ser Asp Asp Glu Val Asp Ala Ala Val Gln Arg Cys
    615                 620                 625

gct gaa gct cta gct ggg gtg cgg gta cag aag cag gag att gaa cag   2035
Ala Glu Ala Leu Ala Gly Val Arg Val Gln Lys Gln Glu Ile Glu Gln
630                 635                 640                 645

gtc ttg gca aaa acc aac cca gac atg gct caa cgc tta tgt gat gct   2083
Val Leu Ala Lys Thr Asn Pro Asp Met Ala Gln Arg Leu Cys Asp Ala
                650                 655                 660

gct gaa gca aat gtg cga tcg tat aaa acg gca gtg tct gat gcc acc   2131
Ala Glu Ala Asn Val Arg Ser Tyr Lys Thr Ala Val Ser Asp Ala Thr
            665                 670                 675

aca gag ttg gtg cgc ctg gaa ggc ctc atc ggt gta gct gca ggt gcg   2179
Thr Glu Leu Val Arg Leu Glu Gly Leu Ile Gly Val Ala Ala Gly Ala
        680                 685                 690

aaa gaa cga cta gat aaa gtt aag tct gcg ctg aca gca gct gaa aac   2227
Lys Glu Arg Leu Asp Lys Val Lys Ser Ala Leu Thr Ala Ala Glu Asn
    695                 700                 705

cgg ttt gaa tca gaa caa cgt cgc gcc cac gct gca cgt cgc ctc tat   2275
Arg Phe Glu Ser Glu Gln Arg Arg Ala His Ala Ala Arg Arg Leu Tyr
710                 715                 720                 725

gcc ctc atg gtg ttc tac cgt gat gaa tcc cga aag cgc tac gca gca   2323
Ala Leu Met Val Phe Tyr Arg Asp Glu Ser Arg Lys Arg Tyr Ala Ala
                730                 735                 740

ccc ttc gcg gac aaa cta tcc agg ctg gca gca tcc gta ttt gga gaa   2371
Pro Phe Ala Asp Lys Leu Ser Arg Leu Ala Ala Ser Val Phe Gly Glu
            745                 750                 755

tca gca gac ttt gat ctt gat gat gag ctg aag atc tcc agt cgt tcc   2419
Ser Ala Asp Phe Asp Leu Asp Asp Glu Leu Lys Ile Ser Ser Arg Ser
        760                 765                 770

ata gga cca cga aca gtg gac ctt gcc aat ctt tct ggc ggc gca aag   2467
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Ile Gly Pro Arg Thr Val Asp Leu Ala Asn Leu Ser Gly Gly Ala Lys
    775                 780                 785

gaa cag ctg gca atc ctc acc cgc ttt gct atc gca gaa ttg gta gca   2515
Glu Gln Leu Ala Ile Leu Thr Arg Phe Ala Ile Ala Glu Leu Val Ala
790                 795                 800                 805

gaa tcc tcc gcg caa ggt gct gtg cct gtg ttt att gat gat gca ttg   2563
Glu Ser Ser Ala Gln Gly Ala Val Pro Val Phe Ile Asp Asp Ala Leu
                810                 815                 820

ggg agc aca gac cca gag cga ctg acc cgc ata tct act ctg ttt agt   2611
Gly Ser Thr Asp Pro Glu Arg Leu Thr Arg Ile Ser Thr Leu Phe Ser
            825                 830                 835

gat gca ggc aag gac tct cag gtg ttt gtt ctc acc tgt gtt cca gac   2659
Asp Ala Gly Lys Asp Ser Gln Val Phe Val Leu Thr Cys Val Pro Asp
        840                 845                 850

cgg tac aac tat gta gag gtc acc caa aag cac agc atc gag tca ttg   2707
Arg Tyr Asn Tyr Val Glu Val Thr Gln Lys His Ser Ile Glu Ser Leu
    855                 860                 865

aaa act gcc aac gct ctg ctg tagctgagca aaaagccaag caa             2751
Lys Thr Ala Asn Ala Leu Leu
870                 875


<210> 1640
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<213> Corynebacterium glutamicum

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Met Arg Ile His Glu Ile Ile Ile Asp Asn Phe Arg Ala Ile Glu His
  1               5                  10                  15

Leu Glu Leu Arg Asp Ile Pro Asp Gln Gly Val Ile Val Ile His Gly
            20                  25                  30

Asp Asn Glu Gln Gly Lys Ser Ser Ile Leu Glu Ala Ile Lys Thr Val
        35                  40                  45

Leu Asn Ser Lys His Arg Thr Thr Ser Lys Thr Ile Lys Ala Ile Gln
    50                  55                  60

Pro Val Asp Arg Asp Val Pro Ile Ser Ile Thr Leu Glu Ala Thr Val
65                  70                  75                  80

Gly Thr Val Arg Phe Arg Ile His Lys Arg Phe Leu Lys Ser Thr Ala
                85                  90                  95

Ala Glu Leu Gln Val Ile Glu Pro Arg Pro Ser Asn His Arg Gly Leu
            100                 105                 110

Glu Ala Glu Ala Ala Leu Ala Glu Ile Leu Glu Ser His Leu Asp Thr
        115                 120                 125

Ser Leu Leu Asp Ala Leu Phe Met Lys Gln Gly Glu Val Glu Ala Gly
    130                 135                 140
```

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Ile Ser Ala Val Gly Ile Pro Thr Leu Thr Ser Ala Leu Asn Ala Gln
145                 150                 155                 160

Asn Gly Asn Thr Glu Asp Ala Thr Glu Asp Thr Ala Leu Met Glu Ala
                165                 170                 175

Val Glu Lys Glu Tyr Leu Lys Phe Tyr Thr Asn Ser Gly Lys Ala Asn
            180                 185                 190

Thr Arg Phe Leu Gln Phe Ser Lys Gln Val Glu Thr Leu Arg Thr Asp
        195                 200                 205

Leu Asp Glu Ala Asn Ala Glu Val Ala Lys Leu Ser Ser His Val Asp
    210                 215                 220

Arg Val Lys Arg Leu Glu Ile Asp Arg Asp Gln Ala Thr Ala Gln Leu
225                 230                 235                 240

Pro Lys Ala Glu Glu Glu Leu Ala Gly Arg Lys Ala Glu Leu Glu Glu
                245                 250                 255

Ala Gln Lys Val Lys Ala Gln Ala Thr Glu Ile Leu Ala Gln Phe Ser
            260                 265                 270

Arg Ala Glu Glu Gln Leu Glu Gln Ala Thr Gly Ala Gln Lys Arg Arg
        275                 280                 285

Lys Glu Leu Arg Asn Lys Leu Glu Leu Ala Gln Thr Glu Val Glu Lys
    290                 295                 300

Ala Glu Ala Gly Gln Glu Asn Leu Ala Gln Glu Ala Ser Arg Glu Ala
305                 310                 315                 320

Glu Glu Phe Leu Ala Leu Ser Glu Lys Phe Glu Ala Ala Arg Ala Ala
                325                 330                 335

Glu Thr Leu Ala Val Glu Lys Val Lys Ala Ala Arg Gln Ser Val Ala
            340                 345                 350

Gly Ile Lys Asn Arg Asp Arg Lys Glu His Leu Thr Val Met Leu Gly
        355                 360                 365

Glu Leu Asp Arg Ile Gly Gln Arg Leu Tyr Glu Leu Arg Ser Val Gln
    370                 375                 380

His Ser Ser Val Arg Val Ser Gln Arg Asp Ile Asp Ala Leu Gln Lys
385                 390                 395                 400

Ala Ile Thr Glu Val Asp Ile Gln Arg Thr Leu Val Glu Ala Gln Gln
                405                 410                 415

Gly Ser Ile Thr Leu Ser Ala Ser Thr Pro Thr Asp Ile Gln Leu Gly
            420                 425                 430

Asp Asp Thr Val Ser Ala Thr Asp Ala Gly Thr Thr Val Ala Leu Asp
        435                 440                 445

Arg Glu Leu Thr Val Val Val Gly Asp Val Thr Leu Val Ile Asn Pro
    450                 455                 460

Gly Lys Thr Ala Ala Glu Ser Arg Thr Asp Phe Glu Ser Ala Glu Ala
```

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465                 470                 475                 480

Ala Leu Ala Glu Leu Leu Asp Gln Leu Asp Val Ser Asp Leu Asp Gln
                485                 490                 495

Leu Arg Glu Arg Phe Thr Ala Gln Glu Gln Arg Asp Ala Asp Ile Ala
            500                 505                 510

Glu Leu Val Arg Glu Gln Gln Arg Met Ser Gly Gly Thr Glu Thr Thr
        515                 520                 525

Val Leu Arg Ala Glu Leu Glu Gly Leu His Val Pro Glu Asp Leu Asp
    530                 535                 540

Pro Ser Ile Ser Val Asp Asp Ala Gln Thr Gln Leu Asn Glu Ala Glu
545                 550                 555                 560

Glu Ser Arg Glu Leu Ala Ala Glu Ala His Lys His Ala Asn Ala Ala
                565                 570                 575

Leu Asp Gly Leu Arg Ser Arg Pro Val Asp Lys Ala Leu Thr Val Phe
            580                 585                 590

Asn Ala Gln Leu Ala Ala Leu Gln Arg Asn Leu Ser Ser Ala Gln Val
        595                 600                 605

Glu Leu Asp Arg Ala Val Ala Glu Thr Ser Asp Asp Glu Val Asp Ala
    610                 615                 620

Ala Val Gln Arg Cys Ala Glu Ala Leu Ala Gly Val Arg Val Gln Lys
625                 630                 635                 640

Gln Glu Ile Glu Gln Val Leu Ala Lys Thr Asn Pro Asp Met Ala Gln
                645                 650                 655

Arg Leu Cys Asp Ala Ala Glu Ala Asn Val Arg Ser Tyr Lys Thr Ala
            660                 665                 670

Val Ser Asp Ala Thr Thr Glu Leu Val Arg Leu Glu Gly Leu Ile Gly
        675                 680                 685

Val Ala Ala Gly Ala Lys Glu Arg Leu Asp Lys Val Lys Ser Ala Leu
    690                 695                 700

Thr Ala Ala Glu Asn Arg Phe Glu Ser Glu Gln Arg Arg Ala His Ala
705                 710                 715                 720

Ala Arg Arg Leu Tyr Ala Leu Met Val Phe Tyr Arg Asp Glu Ser Arg
                725                 730                 735

Lys Arg Tyr Ala Ala Pro Phe Ala Asp Lys Leu Ser Arg Leu Ala Ala
            740                 745                 750

Ser Val Phe Gly Glu Ser Ala Asp Phe Asp Leu Asp Asp Glu Leu Lys
        755                 760                 765

Ile Ser Ser Arg Ser Ile Gly Pro Arg Thr Val Asp Leu Ala Asn Leu
    770                 775                 780

Ser Gly Gly Ala Lys Glu Gln Leu Ala Ile Leu Thr Arg Phe Ala Ile
785                 790                 795                 800
```

```
Ala Glu Leu Val Ala Glu Ser Ser Ala Gln Gly Ala Val Pro Val Phe
                805                 810                 815

Ile Asp Asp Ala Leu Gly Ser Thr Asp Pro Glu Arg Leu Thr Arg Ile
            820                 825                 830

Ser Thr Leu Phe Ser Asp Ala Gly Lys Asp Ser Gln Val Phe Val Leu
        835                 840                 845

Thr Cys Val Pro Asp Arg Tyr Asn Tyr Val Glu Val Thr Gln Lys His
    850                 855                 860

Ser Ile Glu Ser Leu Lys Thr Ala Asn Ala Leu Leu
865                 870                 875


<210> 1641
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<213> Corynebacterium glutamicum

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<221> CDS
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<223> RXA00199

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gtacactccg cagcagcgca cgcgttatcg ccagctgctc atg gaa gat ctt gag   115
                                          Met Glu Asp Leu Glu
                                            1               5

att ttt gat cgg cat ttg cag cat tcc gat ttt gag gat cag ggt tcc   163
Ile Phe Asp Arg His Leu Gln His Ser Asp Phe Glu Asp Gln Gly Ser
                10                  15                  20

atc ggc ctc gag ttg gaa ctc aac ctc gtg gat aag cat atg caa cct   211
Ile Gly Leu Glu Leu Glu Leu Asn Leu Val Asp Lys His Met Gln Pro
            25                  30                  35

gct ttg gca ggc cac gcg gtg ctt tcc cat tta gac gat gag tac cag   259
Ala Leu Ala Gly His Ala Val Leu Ser His Leu Asp Asp Glu Tyr Gln
        40                  45                  50

tcg gag atc ggt aac ttt aat gtt gaa atg aac cac ccg cca cta tcc   307
Ser Glu Ile Gly Asn Phe Asn Val Glu Met Asn His Pro Pro Leu Ser
    55                  60                  65

gtt aaa ggc gat gct tta cga cgc ctc gag caa ggc atc acc tcg cgt   355
Val Lys Gly Asp Ala Leu Arg Arg Leu Glu Gln Gly Ile Thr Ser Arg
70                  75                  80                  85

cta ggt cgc gtg cgc gcg gcc gcc aca tcg gag aac gtg aac gtg gcg   403
Leu Gly Arg Val Arg Ala Ala Ala Thr Ser Glu Asn Val Asn Val Ala
                90                  95                  100

atg atc ggc acg ctg ccc acc atc acc cca gaa ttc ctc gaa gat ccg   451
Met Ile Gly Thr Leu Pro Thr Ile Thr Pro Glu Phe Leu Glu Asp Pro
            105                 110                 115
```

```
gca tgg atg acc caa gaa aac cgc tac cgt gcg ctg agc aat gcg gtg   499
Ala Trp Met Thr Gln Glu Asn Arg Tyr Arg Ala Leu Ser Asn Ala Val
        120                 125                 130

atg gaa tcg cgt ggc gag tta gtg cac atc aac atc gcc gac cgt gaa   547
Met Glu Ser Arg Gly Glu Leu Val His Ile Asn Ile Ala Asp Arg Glu
    135                 140                 145

caa atc atc cac gat ttc act gat ctc gcc ccc gaa tca act tgc acg   595
Gln Ile Ile His Asp Phe Thr Asp Leu Ala Pro Glu Ser Thr Cys Thr
150                 155                 160                 165

tct att cag ttg cac ctg caa tta gca ccc aat aag ttt gct gca gcg   643
Ser Ile Gln Leu His Leu Gln Leu Ala Pro Asn Lys Phe Ala Ala Ala
                170                 175                 180

tgg aat gcg tcg caa gca ata gct ggt gtt caa gca gct ctt tcc gcc   691
Trp Asn Ala Ser Gln Ala Ile Ala Gly Val Gln Ala Ala Leu Ser Ala
            185                 190                 195

aac tcc cca ctt ttc cta ggc cgt cgg gtg tgg cat gaa agc cgc att   739
Asn Ser Pro Leu Phe Leu Gly Arg Arg Val Trp His Glu Ser Arg Ile
        200                 205                 210

cca gtg ttt caa caa gct atc gat acg cgt act cct gaa ctt gtg aat   787
Pro Val Phe Gln Gln Ala Ile Asp Thr Arg Thr Pro Glu Leu Val Asn
    215                 220                 225

caa gga gtc cgc ccc aga gta tgg ttc ggc gaa cga tgg atc acc agt   835
Gln Gly Val Arg Pro Arg Val Trp Phe Gly Glu Arg Trp Ile Thr Ser
230                 235                 240                 245

gtt ttt gat ctt ttc gaa gaa aac gta cgc tac ttc tcc cct ctc atc   883
Val Phe Asp Leu Phe Glu Glu Asn Val Arg Tyr Phe Ser Pro Leu Ile
                250                 255                 260

gca gaa tcc cgc gcc ctg tct ggc aca cca atg atg aag gga aaa tcc   931
Ala Glu Ser Arg Ala Leu Ser Gly Thr Pro Met Met Lys Gly Lys Ser
            265                 270                 275

ccc gca ctc cac tac ctc aat ctc cac aac gga acg gtg tgg cgc tgg   979
Pro Ala Leu His Tyr Leu Asn Leu His Asn Gly Thr Val Trp Arg Trp
        280                 285                 290

aac cga ccc att tac gca ccg ggg gaa gag cgc tct cat ctg cgt ttg   1027
Asn Arg Pro Ile Tyr Ala Pro Gly Glu Glu Arg Ser His Leu Arg Leu
    295                 300                 305

gaa aac cgt ctc cta cct gca ggt ccc acc ccc atc gac atc acc gcc   1075
Glu Asn Arg Leu Leu Pro Ala Gly Pro Thr Pro Ile Asp Ile Thr Ala
310                 315                 320                 325

gat gcc gct ttc tac tac ggt ttg gtt aaa tat ctg gcc gag gaa aac   1123
Asp Ala Ala Phe Tyr Tyr Gly Leu Val Lys Tyr Leu Ala Glu Glu Asn
                330                 335                 340

cgc cct gtc tgg tca cgt ctc cta ttc cct gat gcg gaa aag aac ttc   1171
Arg Pro Val Trp Ser Arg Leu Leu Phe Pro Asp Ala Glu Lys Asn Phe
            345                 350                 355
```

```
caa tcc ggt gca cgt tca ggg ctg ttc gcc cgc atg acc tgg cca acc   1219
Gln Ser Gly Ala Arg Ser Gly Leu Phe Ala Arg Met Thr Trp Pro Thr
        360                 365                 370

ctc gga caa gtc aac gtt gcg aat ctg gtc caa gag cac ctc atc cct   1267
Leu Gly Gln Val Asn Val Ala Asn Leu Val Gln Glu His Leu Ile Pro
    375                 380                 385

caa gcc aga atc gga ctg gaa cga ctc gaa gta aac aaa gac ctt atc   1315
Gln Ala Arg Ile Gly Leu Glu Arg Leu Glu Val Asn Lys Asp Leu Ile
390                 395                 400                 405

gac caa tac ctg ggc atc atc acc gaa cgc gcg aag tcc cgc caa aac   1363
Asp Gln Tyr Leu Gly Ile Ile Thr Glu Arg Ala Lys Ser Arg Gln Asn
                410                 415                 420

ggt gcc acc tgg cag ttg cgt agc ctc aac aag ctg gaa gca cac gga   1411
Gly Ala Thr Trp Gln Leu Arg Ser Leu Asn Lys Leu Glu Ala His Gly
            425                 430                 435

agc atg ccg ggt tcc gat gct cga aaa gca ggt ctt gca gca atg ttg   1459
Ser Met Pro Gly Ser Asp Ala Arg Lys Ala Gly Leu Ala Ala Met Leu
        440                 445                 450

caa cag tat tta cag aat caa gaa agc ggc caa cct gtc cac aca tgg   1507
Gln Gln Tyr Leu Gln Asn Gln Glu Ser Gly Gln Pro Val His Thr Trp
    455                 460                 465

gct att ggt tcg taaaacggca aggaaagata ata                        1542
Ala Ile Gly Ser
470
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<210> 1642
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<213> Corynebacterium glutamicum

<400> 1642

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Met Glu Asp Leu Glu Ile Phe Asp Arg His Leu Gln His Ser Asp Phe
  1               5                  10                  15

Glu Asp Gln Gly Ser Ile Gly Leu Glu Leu Glu Leu Asn Leu Val Asp
             20                  25                  30

Lys His Met Gln Pro Ala Leu Ala Gly His Ala Val Leu Ser His Leu
         35                  40                  45

Asp Asp Glu Tyr Gln Ser Glu Ile Gly Asn Phe Asn Val Glu Met Asn
     50                  55                  60

His Pro Pro Leu Ser Val Lys Gly Asp Ala Leu Arg Arg Leu Glu Gln
 65                  70                  75                  80

Gly Ile Thr Ser Arg Leu Gly Arg Val Arg Ala Ala Ala Thr Ser Glu
                 85                  90                  95

Asn Val Asn Val Ala Met Ile Gly Thr Leu Pro Thr Ile Thr Pro Glu
            100                 105                 110

Phe Leu Glu Asp Pro Ala Trp Met Thr Gln Glu Asn Arg Tyr Arg Ala
```

```
        115                 120                 125

Leu Ser Asn Ala Val Met Glu Ser Arg Gly Glu Leu Val His Ile Asn
    130                 135                 140

Ile Ala Asp Arg Glu Gln Ile Ile His Asp Phe Thr Asp Leu Ala Pro
145                 150                 155                 160

Glu Ser Thr Cys Thr Ser Ile Gln Leu His Leu Gln Leu Ala Pro Asn
                165                 170                 175

Lys Phe Ala Ala Ala Trp Asn Ala Ser Gln Ala Ile Ala Gly Val Gln
            180                 185                 190

Ala Ala Leu Ser Ala Asn Ser Pro Leu Phe Leu Gly Arg Arg Val Trp
        195                 200                 205

His Glu Ser Arg Ile Pro Val Phe Gln Gln Ala Ile Asp Thr Arg Thr
    210                 215                 220

Pro Glu Leu Val Asn Gln Gly Val Arg Pro Arg Val Trp Phe Gly Glu
225                 230                 235                 240

Arg Trp Ile Thr Ser Val Phe Asp Leu Phe Glu Glu Asn Val Arg Tyr
                245                 250                 255

Phe Ser Pro Leu Ile Ala Glu Ser Arg Ala Leu Ser Gly Thr Pro Met
            260                 265                 270

Met Lys Gly Lys Ser Pro Ala Leu His Tyr Leu Asn Leu His Asn Gly
        275                 280                 285

Thr Val Trp Arg Trp Asn Arg Pro Ile Tyr Ala Pro Gly Glu Glu Arg
    290                 295                 300

Ser His Leu Arg Leu Glu Asn Arg Leu Leu Pro Ala Gly Pro Thr Pro
305                 310                 315                 320

Ile Asp Ile Thr Ala Asp Ala Ala Phe Tyr Tyr Gly Leu Val Lys Tyr
                325                 330                 335

Leu Ala Glu Glu Asn Arg Pro Val Trp Ser Arg Leu Leu Phe Pro Asp
            340                 345                 350

Ala Glu Lys Asn Phe Gln Ser Gly Ala Arg Ser Gly Leu Phe Ala Arg
        355                 360                 365

Met Thr Trp Pro Thr Leu Gly Gln Val Asn Val Ala Asn Leu Val Gln
    370                 375                 380

Glu His Leu Ile Pro Gln Ala Arg Ile Gly Leu Glu Arg Leu Glu Val
385                 390                 395                 400

Asn Lys Asp Leu Ile Asp Gln Tyr Leu Gly Ile Ile Thr Glu Arg Ala
                405                 410                 415

Lys Ser Arg Gln Asn Gly Ala Thr Trp Gln Leu Arg Ser Leu Asn Lys
            420                 425                 430

Leu Glu Ala His Gly Ser Met Pro Gly Ser Asp Ala Arg Lys Ala Gly
        435                 440                 445
```

```
Leu Ala Ala Met Leu Gln Gln Tyr Leu Gln Asn Gln Glu Ser Gly Gln
    450                 455                 460

Pro Val His Thr Trp Ala Ile Gly Ser
465                 470


<210> 1643
<211> 326
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(303)
<223> RXA00200

<400> 1643
cac tac gcc gga gtc acc gag att cct gaa tac cga atc tcc cca gac   48
His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr Arg Ile Ser Pro Asp
  1               5                  10                  15

cac ggc gga aaa tcc acc ctc tcc cca ttc caa gac tgg gca ggc ggc   96
His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln Asp Trp Ala Gly Gly
             20                  25                  30

gga tcc atg ggc acg gcc gaa gca gta aac aac gcc tac gaa atc ccg   144
Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn Ala Tyr Glu Ile Pro
         35                  40                  45

tcc tac ctc cgc aac gac tgg ggc cgc gac tgg ggt tcc atc gaa cgc   192
Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp Gly Ser Ile Glu Arg
     50                  55                  60

tac tcg ctg cgc acc aac tcc aac ggc gat gca cct aag gtt gca gac   240
Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala Pro Lys Val Ala Asp
 65                  70                  75                  80

atc aac ctt gaa acc atc caa cgt tcc gga ctc tgg aat cca ggg cat   288
Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu Trp Asn Pro Gly His
                 85                  90                  95

atg aag gta gat gaa taagaccttc agtactggaa gtt                    326
Met Lys Val Asp Glu
            100


<210> 1644
<211> 101
<212> PRT
<213> Corynebacterium glutamicum

<400> 1644
His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr Arg Ile Ser Pro Asp
  1               5                  10                  15

His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln Asp Trp Ala Gly Gly
             20                  25                  30

Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn Ala Tyr Glu Ile Pro
```

```
         35                  40                  45

Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp Gly Ser Ile Glu Arg
     50                  55                  60

Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala Pro Lys Val Ala Asp
 65                  70                  75                  80

Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu Trp Asn Pro Gly His
                 85                  90                  95

Met Lys Val Asp Glu
            100


<210> 1645
<211> 441
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(418)
<223> RXA00207

<400> 1645
ctgcacaatt tttggtcgga cacatttttg cccccattgg gttgtcggat cagatcaaga 60

aaacccccgc ggaaaaattt tgtctctaga ctggctcacc atg gaa atg aaa ttg   115
                                              Met Glu Met Lys Leu
                                                1               5

aaa aag gca tcc cag gtc agc act gcc acc gtc gtc gca gca ggt ttg   163
Lys Lys Ala Ser Gln Val Ser Thr Ala Thr Val Val Ala Ala Gly Leu
                10                  15                  20

atc ggc ggt tgg ttg act gcc cgt gaa tcc ggc att cgc cca ctg ggc   211
Ile Gly Gly Trp Leu Thr Ala Arg Glu Ser Gly Ile Arg Pro Leu Gly
            25                  30                  35

acc att cca ttg gca gca tcc gga gcg ctt gct gca cga agc tgg aat   259
Thr Ile Pro Leu Ala Ala Ser Gly Ala Leu Ala Ala Arg Ser Trp Asn
        40                  45                  50

gaa aag aag ggt cct gca gta gct act ggc ctg ctg gca acc tac gtt   307
Glu Lys Lys Gly Pro Ala Val Ala Thr Gly Leu Leu Ala Thr Tyr Val
    55                  60                  65

ggt gca ttt ggc ctg tcc cac cca ctt gcc aag aag att ggc gcg tgg   355
Gly Ala Phe Gly Leu Ser His Pro Leu Ala Lys Lys Ile Gly Ala Trp
70                  75                  80                  85

cct gca gtt ctt act gtg acc gct ggc gct gct gcg att gct tac gca   403
Pro Ala Val Leu Thr Val Thr Ala Gly Ala Ala Ala Ile Ala Tyr Ala
                90                  95                  100

gta tct gac tcc cag taataattac ggtaaaaaaa ctt                    441
Val Ser Asp Ser Gln
            105
```

<210> 1646
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 1646
Met Glu Met Lys Leu Lys Lys Ala Ser Gln Val Ser Thr Ala Thr Val
1 5 10 15

Val Ala Ala Gly Leu Ile Gly Gly Trp Leu Thr Ala Arg Glu Ser Gly
20 25 30

Ile Arg Pro Leu Gly Thr Ile Pro Leu Ala Ala Ser Gly Ala Leu Ala
35 40 45

Ala Arg Ser Trp Asn Glu Lys Lys Gly Pro Ala Val Ala Thr Gly Leu
50 55 60

Leu Ala Thr Tyr Val Gly Ala Phe Gly Leu Ser His Pro Leu Ala Lys
65 70 75 80

Lys Ile Gly Ala Trp Pro Ala Val Leu Thr Val Thr Ala Gly Ala Ala
85 90 95

Ala Ile Ala Tyr Ala Val Ser Asp Ser Gln
100 105

<210> 1647
<211> 786
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(763)
<223> RXA00211

<400> 1647
tgagccaaaa tcaataaggt gtttttcagc ctgaggtaaa aatacggtgg tactgtcgaa 60

accaatcatc ccctagtttt gaaaagaagg aagcgagcca atg tca ttc ctg atc 115
Met Ser Phe Leu Ile
1 5

cgc gtc ctg ttg tcc gac acc cca ggc agc ctc gcg tta ctc gct gaa 163
Arg Val Leu Leu Ser Asp Thr Pro Gly Ser Leu Ala Leu Leu Ala Glu
10 15 20

gcc ctt ggg att gta gag gcc aat att caa tcc gtg gac gtg gtg gaa 211
Ala Leu Gly Ile Val Glu Ala Asn Ile Gln Ser Val Asp Val Val Glu
25 30 35

cgc ttc ccc aat ggc acg gtc atg gac gat ctg gtg atc tcc atc cct 259
Arg Phe Pro Asn Gly Thr Val Met Asp Asp Leu Val Ile Ser Ile Pro
40 45 50

cgc gat gtc atg gca gac acc atc atc acc gca gct gaa gaa gtc gac 307
Arg Asp Val Met Ala Asp Thr Ile Ile Thr Ala Ala Glu Glu Val Asp
55 60 65

```
ggc gtg gag att gat tcc atc cgc cca ttc tcc ggg act gtt gac cgc   355
Gly Val Glu Ile Asp Ser Ile Arg Pro Phe Ser Gly Thr Val Asp Arg
 70                  75                  80                  85

cgc gga cag atc caa atg ctg gct gct gtt gct cac caa cgc cgc gat   403
Arg Gly Gln Ile Gln Met Leu Ala Ala Val Ala His Gln Arg Arg Asp
                 90                  95                 100

atc acc gca gcg atg gaa gaa atg gtc gat gtc atc ccc cgc acc atg   451
Ile Thr Ala Ala Met Glu Glu Met Val Asp Val Ile Pro Arg Thr Met
            105                 110                 115

acc tct ggt tgg gct ttg gtc att gat cta aaa gga ccc atc act cgc   499
Thr Ser Gly Trp Ala Leu Val Ile Asp Leu Lys Gly Pro Ile Thr Arg
        120                 125                 130

atc gct ggt tcc cta gca gcg ccc gaa gat gac ggc acc gtt ccg gag   547
Ile Ala Gly Ser Leu Ala Ala Pro Glu Asp Asp Gly Thr Val Pro Glu
    135                 140                 145

aac atc gtt ctc aaa gaa gct cgc atg ctc aac ccg gaa aac gat ccg   595
Asn Ile Val Leu Lys Glu Ala Arg Met Leu Asn Pro Glu Asn Asp Pro
150                 155                 160                 165

tgg att cca gag tcc tgg aca ctg ctt gat tct tcc ctt gcc atc gct   643
Trp Ile Pro Glu Ser Trp Thr Leu Leu Asp Ser Ser Leu Ala Ile Ala
                170                 175                 180

ccg atc ggc aag cac ggc ctg gct ctg att atc ggt cgc cct ggt ggc   691
Pro Ile Gly Lys His Gly Leu Ala Leu Ile Ile Gly Arg Pro Gly Gly
            185                 190                 195

cct gat ttc ttg gcc agc gaa gtg gag cac tta ggc caa gtc ggt gac   739
Pro Asp Phe Leu Ala Ser Glu Val Glu His Leu Gly Gln Val Gly Asp
        200                 205                 210

att atc gga gca atg ctt caa aaa taatctgagc tgtttaaaaa atg         786
Ile Ile Gly Ala Met Leu Gln Lys
    215                 220
```

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<210> 1648
<211> 221
<212> PRT
<213> Corynebacterium glutamicum

<400> 1648

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Met Ser Phe Leu Ile Arg Val Leu Leu Ser Asp Thr Pro Gly Ser Leu
  1               5                  10                  15

Ala Leu Leu Ala Glu Ala Leu Gly Ile Val Glu Ala Asn Ile Gln Ser
             20                  25                  30

Val Asp Val Val Glu Arg Phe Pro Asn Gly Thr Val Met Asp Asp Leu
         35                  40                  45

Val Ile Ser Ile Pro Arg Asp Val Met Ala Asp Thr Ile Ile Thr Ala
     50                  55                  60

Ala Glu Glu Val Asp Gly Val Glu Ile Asp Ser Ile Arg Pro Phe Ser
 65                  70                  75                  80
```

```
Gly Thr Val Asp Arg Arg Gly Gln Ile Gln Met Leu Ala Ala Val Ala
                 85                  90                  95

His Gln Arg Arg Asp Ile Thr Ala Ala Met Glu Glu Met Val Asp Val
            100                 105                 110

Ile Pro Arg Thr Met Thr Ser Gly Trp Ala Leu Val Ile Asp Leu Lys
        115                 120                 125

Gly Pro Ile Thr Arg Ile Ala Gly Ser Leu Ala Ala Pro Glu Asp Asp
    130                 135                 140

Gly Thr Val Pro Glu Asn Ile Val Leu Lys Glu Ala Arg Met Leu Asn
145                 150                 155                 160

Pro Glu Asn Asp Pro Trp Ile Pro Glu Ser Trp Thr Leu Leu Asp Ser
                165                 170                 175

Ser Leu Ala Ile Ala Pro Ile Gly Lys His Gly Leu Ala Leu Ile Ile
            180                 185                 190

Gly Arg Pro Gly Gly Pro Asp Phe Leu Ala Ser Glu Val Glu His Leu
        195                 200                 205

Gly Gln Val Gly Asp Ile Ile Gly Ala Met Leu Gln Lys
    210                 215                 220


<210> 1649
<211> 1263
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1240)
<223> RXA00218

<400> 1649
tctaaactca cgctagactt ctaaaagatc taaagttcag ttccaacaca agccagcact 60

gcattccgca aacccgacta gaccatccaa ggtgtcttct atg tca gct cgc aat   115
                                              Met Ser Ala Arg Asn
                                                1               5

ccg ttc cgc ccc act ttc gga gtt tcc ccc acc gta ctt gca ggc cga   163
Pro Phe Arg Pro Thr Phe Gly Val Ser Pro Thr Val Leu Ala Gly Arg
                10                  15                  20

gac tca ctt cta cag tct ttc aaa ctt ggt ctc gcg gaa ggc ccc gga   211
Asp Ser Leu Leu Gln Ser Phe Lys Leu Gly Leu Ala Glu Gly Pro Gly
            25                  30                  35

agc ccc ttt aga gca ttg ctg att tcg gga tct cgt ggc atg ggt aaa   259
Ser Pro Phe Arg Ala Leu Leu Ile Ser Gly Ser Arg Gly Met Gly Lys
        40                  45                  50

act gtg ttg ctc aat gaa ttt gaa gat gca gct gcg tct caa ggg tgg   307
Thr Val Leu Leu Asn Glu Phe Glu Asp Ala Ala Ala Ser Gln Gly Trp
    55                  60                  65
```

```
atc acg ctg cgc gcc tat ccg gat aat tcc atg gtg gat ggc tta gtt   355
Ile Thr Leu Arg Ala Tyr Pro Asp Asn Ser Met Val Asp Gly Leu Val
 70                  75                  80                  85

aat tcc gcc atc ccg gag gcg cta cag aat ctt gac gga ccg cag tcc   403
Asn Ser Ala Ile Pro Glu Ala Leu Gln Asn Leu Asp Gly Pro Gln Ser
                 90                  95                 100

aaa aga atg ctc agt ggt gtg gcc att cct ggt atc gct acg gtg acg   451
Lys Arg Met Leu Ser Gly Val Ala Ile Pro Gly Ile Ala Thr Val Thr
            105                 110                 115

gcc att gct gat cca acc aag aag gat ccc act ccc acg ctg att tcc   499
Ala Ile Ala Asp Pro Thr Lys Lys Asp Pro Thr Pro Thr Leu Ile Ser
        120                 125                 130

agg ctc cgc gag ttg gct act cgt ttg caa aag cac ggc tcc gga att   547
Arg Leu Arg Glu Leu Ala Thr Arg Leu Gln Lys His Gly Ser Gly Ile
    135                 140                 145

ttg atc acc ctt gat gaa ctc caa agc gcc aat gtg gat ctt ttg cat   595
Leu Ile Thr Leu Asp Glu Leu Gln Ser Ala Asn Val Asp Leu Leu His
150                 155                 160                 165

gtg ttg gcc act gcg gtc cag gat ctc cta cgg gat gat ttc gat atc   643
Val Leu Ala Thr Ala Val Gln Asp Leu Leu Arg Asp Asp Phe Asp Ile
                170                 175                 180

gca ttg gta gca gcg ggt ctg cca gag gga atc gat cgt ctt ctc cag   691
Ala Leu Val Ala Ala Gly Leu Pro Glu Gly Ile Asp Arg Leu Leu Gln
            185                 190                 195

cat gag ggc aca acc ttt atc cgc cga gcc gaa aga atc ctg ctc aat   739
His Glu Gly Thr Thr Phe Ile Arg Arg Ala Glu Arg Ile Leu Leu Asn
        200                 205                 210

cct gtc aac cat gaa gat tcg gtg gag atg ttc ctg gat acc gct gcg   787
Pro Val Asn His Glu Asp Ser Val Glu Met Phe Leu Asp Thr Ala Ala
    215                 220                 225

gaa ggc caa cgc cac atg act tcc gag gcc gcc gaa ctc gcg gcg cag   835
Glu Gly Gln Arg His Met Thr Ser Glu Ala Ala Glu Leu Ala Ala Gln
230                 235                 240                 245

atc agc aag ggc tac ccc tac tcc atg cag ctg act ggt tct ctg gca   883
Ile Ser Lys Gly Tyr Pro Tyr Ser Met Gln Leu Thr Gly Ser Leu Ala
                250                 255                 260

tgg gcg cga agt act ctt gac aac tcc gat acc atc cag gcc gaa caa   931
Trp Ala Arg Ser Thr Leu Asp Asn Ser Asp Thr Ile Gln Ala Glu Gln
            265                 270                 275

gta gat gct gtc cgc gac gag gtt gtg cgc cgc atg ggc atg caa gtc   979
Val Asp Ala Val Arg Asp Glu Val Val Arg Arg Met Gly Met Gln Val
        280                 285                 290

cac gag cca agc ctg cac cag gtc cct gat ggt gag ctg acc att ttg   1027
His Glu Pro Ser Leu His Gln Val Pro Asp Gly Glu Leu Thr Ile Leu
    295                 300                 305
```

```
tac gcg att gcc caa ctg tca aaa aac ggc gag atg gtg tct act gga   1075
Tyr Ala Ile Ala Gln Leu Ser Lys Asn Gly Glu Met Val Ser Thr Gly
310                 315                 320                 325

gat atc gca cac ctc atg ggc gtc aag ccc aac gcc ttg tcg atg cag   1123
Asp Ile Ala His Leu Met Gly Val Lys Pro Asn Ala Leu Ser Met Gln
                330                 335                 340

aga aag caa ctt ctc agc aga ggt ctc gta gag gtt ccc aag tac ggt   1171
Arg Lys Gln Leu Leu Ser Arg Gly Leu Val Glu Val Pro Lys Tyr Gly
            345                 350                 355

ttc ctc aat ttc act ttg ccg tac atg cgc gag cac ctc ctc aac agc   1219
Phe Leu Asn Phe Thr Leu Pro Tyr Met Arg Glu His Leu Leu Asn Ser
        360                 365                 370

ccg cac cac cga cca atc aca taagacacaa gcactaaaac agc             1263
Pro His His Arg Pro Ile Thr
    375                 380
```

<210> 1650
<211> 380
<212> PRT
<213> Corynebacterium glutamicum

<400> 1650

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Met Ser Ala Arg Asn Pro Phe Arg Pro Thr Phe Gly Val Ser Pro Thr
  1               5                  10                  15

Val Leu Ala Gly Arg Asp Ser Leu Leu Gln Ser Phe Lys Leu Gly Leu
             20                  25                  30

Ala Glu Gly Pro Gly Ser Pro Phe Arg Ala Leu Leu Ile Ser Gly Ser
         35                  40                  45

Arg Gly Met Gly Lys Thr Val Leu Leu Asn Glu Phe Glu Asp Ala Ala
     50                  55                  60

Ala Ser Gln Gly Trp Ile Thr Leu Arg Ala Tyr Pro Asp Asn Ser Met
 65                  70                  75                  80

Val Asp Gly Leu Val Asn Ser Ala Ile Pro Glu Ala Leu Gln Asn Leu
                 85                  90                  95

Asp Gly Pro Gln Ser Lys Arg Met Leu Ser Gly Val Ala Ile Pro Gly
            100                 105                 110

Ile Ala Thr Val Thr Ala Ile Ala Asp Pro Thr Lys Lys Asp Pro Thr
        115                 120                 125

Pro Thr Leu Ile Ser Arg Leu Arg Glu Leu Ala Thr Arg Leu Gln Lys
    130                 135                 140

His Gly Ser Gly Ile Leu Ile Thr Leu Asp Glu Leu Gln Ser Ala Asn
145                 150                 155                 160

Val Asp Leu Leu His Val Leu Ala Thr Ala Val Gln Asp Leu Leu Arg
                165                 170                 175

Asp Asp Phe Asp Ile Ala Leu Val Ala Ala Gly Leu Pro Glu Gly Ile
```

```
            180                 185                 190

Asp Arg Leu Leu Gln His Glu Gly Thr Thr Phe Ile Arg Arg Ala Glu
        195                 200                 205

Arg Ile Leu Leu Asn Pro Val Asn His Glu Asp Ser Val Glu Met Phe
    210                 215                 220

Leu Asp Thr Ala Ala Glu Gly Gln Arg His Met Thr Ser Glu Ala Ala
225                 230                 235                 240

Glu Leu Ala Ala Gln Ile Ser Lys Gly Tyr Pro Tyr Ser Met Gln Leu
                245                 250                 255

Thr Gly Ser Leu Ala Trp Ala Arg Ser Thr Leu Asp Asn Ser Asp Thr
            260                 265                 270

Ile Gln Ala Glu Gln Val Asp Ala Val Arg Asp Glu Val Val Arg Arg
        275                 280                 285

Met Gly Met Gln Val His Glu Pro Ser Leu His Gln Val Pro Asp Gly
    290                 295                 300

Glu Leu Thr Ile Leu Tyr Ala Ile Ala Gln Leu Ser Lys Asn Gly Glu
305                 310                 315                 320

Met Val Ser Thr Gly Asp Ile Ala His Leu Met Gly Val Lys Pro Asn
                325                 330                 335

Ala Leu Ser Met Gln Arg Lys Gln Leu Leu Ser Arg Gly Leu Val Glu
            340                 345                 350

Val Pro Lys Tyr Gly Phe Leu Asn Phe Thr Leu Pro Tyr Met Arg Glu
        355                 360                 365

His Leu Leu Asn Ser Pro His His Arg Pro Ile Thr
    370                 375                 380
```

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<210> 1651
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> RXA00220

<400> 1651
agatcgtgcc gagtttccgg tttggatggg gtttgggatg ttaatgggag aggatcggcg 60

tgatcgtgcc ggttttcctt gcgttggtag tcttggggct atg agc gca ttc cac 115
Met Ser Ala Phe His
1 5

atc cga gcg gaa caa tcg cac gat atc agc gcg att cat gat gtt act 163
Ile Arg Ala Glu Gln Ser His Asp Ile Ser Ala Ile His Asp Val Thr
10 15 20

gaa gcg gcc ttt aca gga att gag cat tca gat gga aca gag caa gat 211

```
Glu Ala Ala Phe Thr Gly Ile Glu His Ser Asp Gly Thr Glu Gln Asp
            25                  30                  35

ctc gtc gat aag ctt cgt gct gca aag gcg ctg agc ctt tcg ctc gtc   259
Leu Val Asp Lys Leu Arg Ala Ala Lys Ala Leu Ser Leu Ser Leu Val
         40                  45                  50

gct gag gcg gat ggc gag gtc att ggg cat att gct gcc tct gag gtg   307
Ala Glu Ala Asp Gly Glu Val Ile Gly His Ile Ala Ala Ser Glu Val
     55                  60                  65

ctg att ggc ggt ggg gtg cag ggc tgg ttt ggc att ggg cct gtc agt   355
Leu Ile Gly Gly Gly Val Gln Gly Trp Phe Gly Ile Gly Pro Val Ser
 70                  75                  80                  85

gtt cgg ccc gat aag cag cag caa ggc gtg ggt att gcg ctg atg ggc   403
Val Arg Pro Asp Lys Gln Gln Gln Gly Val Gly Ile Ala Leu Met Gly
                 90                  95                 100

agc gcg ctt gat cag ttg cgt gcg gag ggt gct ggc ggc atc gtg ttg   451
Ser Ala Leu Asp Gln Leu Arg Ala Glu Gly Ala Gly Gly Ile Val Leu
            105                 110                 115

ctg ggg gat ccg ggc tat tat cga cgc ttc ggt ttt gag gtc gtg ccc   499
Leu Gly Asp Pro Gly Tyr Tyr Arg Arg Phe Gly Phe Glu Val Val Pro
        120                 125                 130

ggg ctg gtc tat ccg gac gcg cca gcg gaa ttt ttt atg gct gtg tgt   547
Gly Leu Val Tyr Pro Asp Ala Pro Ala Glu Phe Phe Met Ala Val Cys
    135                 140                 145

ttg aat gct ccg gcg ttt ccg cag ggt gtt gtg gag tat cac tcg gca   595
Leu Asn Ala Pro Ala Phe Pro Gln Gly Val Val Glu Tyr His Ser Ala
150                 155                 160                 165

ttt gga ggg tagagacccc atcgtggcgg gcc                            627
Phe Gly Gly
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<210> 1652
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 1652

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Met Ser Ala Phe His Ile Arg Ala Glu Gln Ser His Asp Ile Ser Ala
  1               5                  10                  15

Ile His Asp Val Thr Glu Ala Ala Phe Thr Gly Ile Glu His Ser Asp
            20                  25                  30

Gly Thr Glu Gln Asp Leu Val Asp Lys Leu Arg Ala Ala Lys Ala Leu
        35                  40                  45

Ser Leu Ser Leu Val Ala Glu Ala Asp Gly Glu Val Ile Gly His Ile
    50                  55                  60

Ala Ala Ser Glu Val Leu Ile Gly Gly Gly Val Gln Gly Trp Phe Gly
65                  70                  75                  80
```

```
Ile Gly Pro Val Ser Val Arg Pro Asp Lys Gln Gln Gln Gly Val Gly
                 85                  90                  95

Ile Ala Leu Met Gly Ser Ala Leu Asp Gln Leu Arg Ala Glu Gly Ala
            100                 105                 110

Gly Gly Ile Val Leu Leu Gly Asp Pro Gly Tyr Tyr Arg Arg Phe Gly
        115                 120                 125

Phe Glu Val Val Pro Gly Leu Val Tyr Pro Asp Ala Pro Ala Glu Phe
    130                 135                 140

Phe Met Ala Val Cys Leu Asn Ala Pro Ala Phe Pro Gln Gly Val Val
145                 150                 155                 160

Glu Tyr His Ser Ala Phe Gly Gly
                165
```

<210> 1653
<211> 843
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(820)
<223> RXA00230

<400> 1653

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aggtcttacc gcccctcaaa tcctgcagat tttccgtcgt caatcaggga cgaaagtaca 60

tcctatctat ctagctccac tagcacagat aggaactccg ttg att cat gag caa   115
                                        Leu Ile His Glu Gln
                                          1               5

gac gtt cag aag ctg tta aac tac atc act tca cac ttt ggt gtt gac   163
Asp Val Gln Lys Leu Leu Asn Tyr Ile Thr Ser His Phe Gly Val Asp
                  10                  15                  20

cct gaa aga tgg ttt cat cct gaa ggc tac caa agc att gcc cta gcg   211
Pro Glu Arg Trp Phe His Pro Glu Gly Tyr Gln Ser Ile Ala Leu Ala
              25                  30                  35

att ctt gac tcc att tac tcg act ggt aat cgc tat aca ggt gta ctc   259
Ile Leu Asp Ser Ile Tyr Ser Thr Gly Asn Arg Tyr Thr Gly Val Leu
          40                  45                  50

aac ctt gtc aat cga tac tgc ggg ctg cgc gca aat gaa gga tca cac   307
Asn Leu Val Asn Arg Tyr Cys Gly Leu Arg Ala Asn Glu Gly Ser His
      55                  60                  65

cct gaa gcc gat act gcc act gat ctc atc gag aca ttc tac cgg tgg   355
Pro Glu Ala Asp Thr Ala Thr Asp Leu Ile Glu Thr Phe Tyr Arg Trp
  70                  75                  80                  85

gga ggg gtc gac gaa ttt gtt ctc aaa acg aat aat cgg tgg aga act   403
Gly Gly Val Asp Glu Phe Val Leu Lys Thr Asn Asn Arg Trp Arg Thr
                  90                  95                 100

tcc tcc aag att cac gca ccc tat aag gca tac gca gct ttg gaa gca   451
```

```
Ser Ser Lys Ile His Ala Pro Tyr Lys Ala Tyr Ala Ala Leu Glu Ala
            105                 110                 115

gca aag gta ctt gcg ggt cat tcc atc gaa tcc atc agc gat gtt gtc   499
Ala Lys Val Leu Ala Gly His Ser Ile Glu Ser Ile Ser Asp Val Val
        120                 125                 130

ggc agg ttc gat tcg cgc gaa agc cgt gaa cac tca gat atc gcg aga   547
Gly Arg Phe Asp Ser Arg Glu Ser Arg Glu His Ser Asp Ile Ala Arg
    135                 140                 145

gaa tgg ttg atg ata acc ggc caa agt agt gcg ttg acc tgg agt tac   595
Glu Trp Leu Met Ile Thr Gly Gln Ser Ser Ala Leu Thr Trp Ser Tyr
150                 155                 160                 165

ttc ctt atg ctc gta ggt gtc cca gga gtg aaa gca gac cga atg atc   643
Phe Leu Met Leu Val Gly Val Pro Gly Val Lys Ala Asp Arg Met Ile
                170                 175                 180

gtc cgt ttc gtc act cac gtg ctc gag cgt ccg aaa gag att tcc agg   691
Val Arg Phe Val Thr His Val Leu Glu Arg Pro Lys Glu Ile Ser Arg
            185                 190                 195

cac gaa gct tca cgg ttg att gag gaa gtt gcg gac att atg tgc gtc   739
His Glu Ala Ser Arg Leu Ile Glu Glu Val Ala Asp Ile Met Cys Val
        200                 205                 210

aac tac atc tac ctc gac cac acc atc tgg cgg ttc caa tca ggg cgc   787
Asn Tyr Ile Tyr Leu Asp His Thr Ile Trp Arg Phe Gln Ser Gly Arg
    215                 220                 225

ccc tac ctc caa gaa gac tcc tcc cct ttc gaa taaatccatc acatttcaca 840
Pro Tyr Leu Gln Glu Asp Ser Ser Pro Phe Glu
230                 235                 240

gtc                                                               843


<210> 1654
<211> 240
<212> PRT
<213> Corynebacterium glutamicum

<400> 1654
Leu Ile His Glu Gln Asp Val Gln Lys Leu Leu Asn Tyr Ile Thr Ser
  1               5                  10                  15

His Phe Gly Val Asp Pro Glu Arg Trp Phe His Pro Glu Gly Tyr Gln
             20                  25                  30

Ser Ile Ala Leu Ala Ile Leu Asp Ser Ile Tyr Ser Thr Gly Asn Arg
         35                  40                  45

Tyr Thr Gly Val Leu Asn Leu Val Asn Arg Tyr Cys Gly Leu Arg Ala
     50                  55                  60

Asn Glu Gly Ser His Pro Glu Ala Asp Thr Ala Thr Asp Leu Ile Glu
 65                  70                  75                  80

Thr Phe Tyr Arg Trp Gly Gly Val Asp Glu Phe Val Leu Lys Thr Asn
                 85                  90                  95
```

```
Asn Arg Trp Arg Thr Ser Ser Lys Ile His Ala Pro Tyr Lys Ala Tyr
            100                 105                 110

Ala Ala Leu Glu Ala Ala Lys Val Leu Ala Gly His Ser Ile Glu Ser
        115                 120                 125

Ile Ser Asp Val Val Gly Arg Phe Asp Ser Arg Glu Ser Arg Glu His
    130                 135                 140

Ser Asp Ile Ala Arg Glu Trp Leu Met Ile Thr Gly Gln Ser Ser Ala
145                 150                 155                 160

Leu Thr Trp Ser Tyr Phe Leu Met Leu Val Gly Val Pro Gly Val Lys
                165                 170                 175

Ala Asp Arg Met Ile Val Arg Phe Val Thr His Val Leu Glu Arg Pro
            180                 185                 190

Lys Glu Ile Ser Arg His Glu Ala Ser Arg Leu Ile Glu Glu Val Ala
        195                 200                 205

Asp Ile Met Cys Val Asn Tyr Ile Tyr Leu Asp His Thr Ile Trp Arg
    210                 215                 220

Phe Gln Ser Gly Arg Pro Tyr Leu Gln Glu Asp Ser Ser Pro Phe Glu
225                 230                 235                 240
```

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<210> 1655
<211> 517
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(517)
<223> RXA00233

<400> 1655

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cgcctccagc agttgaggga gaagttccaa cacttgcacc aactgaggaa gcaactgtgc 60

aatagcgctt tagacacaga ctcatgacag aatagaagac atg agt gtg aat gaa   115
                                            Met Ser Val Asn Glu
                                              1               5

gca gat ctg aac gct gtc gaa gag caa ttg gga agg gcc cca cga ggt   163
Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly Arg Ala Pro Arg Gly
                 10                  15                  20

gtc ctc gat att tct tac cgc agc cct gat gga gta ccc ggt gtg gtg   211
Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly Val Pro Gly Val Val
             25                  30                  35

atg acc gca cca aaa ctg gat gac gga acc cca ttc cca acc ctg tac   259
Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro Phe Pro Thr Leu Tyr
         40                  45                  50
```

```
tac ttg aca gat cca cgc ctg acc acc gag gca tcc cgc ctc gag gtc   307
Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala Ser Arg Leu Glu Val
     55                  60                  65

gca ttg gta atg aag tgg atg act gat cgc ctt tcc acc gac gaa gag   355
Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu Ser Thr Asp Glu Glu
 70                  75                  80                  85

ctt cgt gcc gac tac cag cgc gcc cac gag cac ttc ctg gca aag cgc   403
Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His Phe Leu Ala Lys Arg
                 90                  95                 100

aac gca att gaa gat ctc ggc acg gat ttt tcc ggc ggt ggc atg cct   451
Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser Gly Gly Gly Met Pro
            105                 110                 115

gac cga gtg aag tgc ctt cac gtc ctc att gac tat gca ctg gca gaa   499
Asp Arg Val Lys Cys Leu His Val Leu Ile Asp Tyr Ala Leu Ala Glu
        120                 125                 130

ggc cca cac cat ttc ctt                                          517
Gly Pro His His Phe Leu
    135
```

20050208030

<210> 1656
<211> 139
<212> PRT
<213> Corynebacterium glutamicum

<400> 1656

```
Met Ser Val Asn Glu Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly
  1               5                  10                  15

Arg Ala Pro Arg Gly Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly
             20                  25                  30

Val Pro Gly Val Val Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro
         35                  40                  45

Phe Pro Thr Leu Tyr Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala
     50                  55                  60

Ser Arg Leu Glu Val Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu
 65                  70                  75                  80

Ser Thr Asp Glu Glu Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His
                 85                  90                  95

Phe Leu Ala Lys Arg Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser
            100                 105                 110

Gly Gly Gly Met Pro Asp Arg Val Lys Cys Leu His Val Leu Ile Asp
        115                 120                 125

Tyr Ala Leu Ala Glu Gly Pro His His Phe Leu
    130                 135
```

<210> 1657
<211> 663

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(640)
<223> RXA00234

<400> 1657
ttcagggcta aataaaagcg cttttcgacg cccggtaacc tcaaggttgc cgggcgtcgt 60

tgccttacta ctgttactgg tgtgactatg atcgaggatt atg gca aag cag aag 115
Met Ala Lys Gln Lys
1 5

aaa act cat aaa ggc ctt gtt cct gtc tca agc agg gaa cgt gct tca 163
Lys Thr His Lys Gly Leu Val Pro Val Ser Ser Arg Glu Arg Ala Ser
10 15 20

gag tca gtt tct gct acc cgc gcc cca ttt aga ttg ggt gcc gtc ggc 211
Glu Ser Val Ser Ala Thr Arg Ala Pro Phe Arg Leu Gly Ala Val Gly
25 30 35

atc ggt gca atc gca ctc gta gtt ctt ctc atc ctg ttt gtc atc gcg 259
Ile Gly Ala Ile Ala Leu Val Val Leu Leu Ile Leu Phe Val Ile Ala
40 45 50

att cct gtg cgt aac tat ttt cag ctg cgc tcc gac atc gcc caa aca 307
Ile Pro Val Arg Asn Tyr Phe Gln Leu Arg Ser Asp Ile Ala Gln Thr
55 60 65

gag gct tcc att gaa gcc aaa gaa caa cag atc aaa caa ctg gaa tct 355
Glu Ala Ser Ile Glu Ala Lys Glu Gln Gln Ile Lys Gln Leu Glu Ser
70 75 80 85

gac ctc aac agg tac caa tca gag gcg tac atc cgc gaa caa gca cgc 403
Asp Leu Asn Arg Tyr Gln Ser Glu Ala Tyr Ile Arg Glu Gln Ala Arg
90 95 100

ctg cgc cta ggc gtc att gaa cct gga gaa acc gcg ttc aga atc gtg 451
Leu Arg Leu Gly Val Ile Glu Pro Gly Glu Thr Ala Phe Arg Ile Val
105 110 115

gac cca gca cta gat acc gac acc tca gtc acc tct gac ggc aac gaa 499
Asp Pro Ala Leu Asp Thr Asp Thr Ser Val Thr Ser Asp Gly Asn Glu
120 125 130

gag aaa cca ctg gga gct tgg tat gaa aac ctc tgg gac tca gtc acc 547
Glu Lys Pro Leu Gly Ala Trp Tyr Glu Asn Leu Trp Asp Ser Val Thr
135 140 145

aag cca gaa gca ctc ggc gaa gag gaa att gcg cct cca gca gtt gag 595
Lys Pro Glu Ala Leu Gly Glu Glu Glu Ile Ala Pro Pro Ala Val Glu
150 155 160 165

gga gaa gtt cca aca ctt gca cca act gag gaa gca act gtg caa 640
Gly Glu Val Pro Thr Leu Ala Pro Thr Glu Glu Ala Thr Val Gln
170 175 180

tagcgcttta gacacagact cat 663

<210> 1658
<211> 180
<212> PRT
<213> Corynebacterium glutamicum

<400> 1658
Met Ala Lys Gln Lys Lys Thr His Lys Gly Leu Val Pro Val Ser Ser
1 5 10 15

Arg Glu Arg Ala Ser Glu Ser Val Ser Ala Thr Arg Ala Pro Phe Arg
20 25 30

Leu Gly Ala Val Gly Ile Gly Ala Ile Ala Leu Val Val Leu Leu Ile
35 40 45

Leu Phe Val Ile Ala Ile Pro Val Arg Asn Tyr Phe Gln Leu Arg Ser
50 55 60

Asp Ile Ala Gln Thr Glu Ala Ser Ile Glu Ala Lys Glu Gln Gln Ile
65 70 75 80

Lys Gln Leu Glu Ser Asp Leu Asn Arg Tyr Gln Ser Glu Ala Tyr Ile
85 90 95

Arg Glu Gln Ala Arg Leu Arg Leu Gly Val Ile Glu Pro Gly Glu Thr
100 105 110

Ala Phe Arg Ile Val Asp Pro Ala Leu Asp Thr Asp Thr Ser Val Thr
115 120 125

Ser Asp Gly Asn Glu Glu Lys Pro Leu Gly Ala Trp Tyr Glu Asn Leu
130 135 140

Trp Asp Ser Val Thr Lys Pro Glu Ala Leu Gly Glu Glu Glu Ile Ala
145 150 155 160

Pro Pro Ala Val Glu Gly Glu Val Pro Thr Leu Ala Pro Thr Glu Glu
165 170 175

Ala Thr Val Gln
180

<210> 1659
<211> 501
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(478)
<223> RXA00237

<400> 1659
actggtagaa gctttgatga tctacatcac aaatttacaa tgtgtggtga gttattcata 60

ttacccaagg acttaaacct taaaaggagc cctaaaaatc atg aag ctt tca cac 115
Met Lys Leu Ser His
1 5

```
cgc atc gca gca atg gca gca acc gca ggc atc aca gtg gca gca ttc   163
Arg Ile Ala Ala Met Ala Ala Thr Ala Gly Ile Thr Val Ala Ala Phe
                 10                  15                  20

gca gca cct gct tcc gca tcc gac ttc gca aac cta tcc tcc acc aac   211
Ala Ala Pro Ala Ser Ala Ser Asp Phe Ala Asn Leu Ser Ser Thr Asn
             25                  30                  35

aaa gaa ctg tcc cct cag tac aac tgg gtt gct tgc ggc atc ctt gag   259
Lys Glu Leu Ser Pro Gln Tyr Asn Trp Val Ala Cys Gly Ile Leu Glu
         40                  45                  50

ggt ggc ctc aaa gca gct ggc gtc ctt gaa gaa ggc cag tac aac cgc   307
Gly Gly Leu Lys Ala Ala Gly Val Leu Glu Glu Gly Gln Tyr Asn Arg
     55                  60                  65

gag ctc gca gaa gca atc gcc gca aag ggt gaa ggc ttc tgg acc act   355
Glu Leu Ala Glu Ala Ile Ala Ala Lys Gly Glu Gly Phe Trp Thr Thr
 70                  75                  80                  85

cag ttc cca caa atc ggt gat tgg aac gaa gat cag gca gca gca ctt   403
Gln Phe Pro Gln Ile Gly Asp Trp Asn Glu Asp Gln Ala Ala Ala Leu
                 90                  95                 100

gcc gac cgc gca caa acc tgt ggc cta gtt aag gct gac acc tac ctt   451
Ala Asp Arg Ala Gln Thr Cys Gly Leu Val Lys Ala Asp Thr Tyr Leu
             105                 110                 115

tct gag ctg tcc tcc aac ttc tct tcc taaaaggttc gggggtaacc        498
Ser Glu Leu Ser Ser Asn Phe Ser Ser
         120                 125

cca                                                              501
```

<210> 1660
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 1660

```
Met Lys Leu Ser His Arg Ile Ala Ala Met Ala Ala Thr Ala Gly Ile
  1               5                  10                  15

Thr Val Ala Ala Phe Ala Ala Pro Ala Ser Ala Ser Asp Phe Ala Asn
             20                  25                  30

Leu Ser Ser Thr Asn Lys Glu Leu Ser Pro Gln Tyr Asn Trp Val Ala
         35                  40                  45

Cys Gly Ile Leu Glu Gly Gly Leu Lys Ala Ala Gly Val Leu Glu Glu
     50                  55                  60

Gly Gln Tyr Asn Arg Glu Leu Ala Glu Ala Ile Ala Ala Lys Gly Glu
 65                  70                  75                  80

Gly Phe Trp Thr Thr Gln Phe Pro Gln Ile Gly Asp Trp Asn Glu Asp
                 85                  90                  95

Gln Ala Ala Ala Leu Ala Asp Arg Ala Gln Thr Cys Gly Leu Val Lys
             100                 105                 110
```

```
Ala Asp Thr Tyr Leu Ser Glu Leu Ser Ser Asn Phe Ser Ser
        115                 120                 125


<210> 1661
<211> 492
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(469)
<223> RXA00238

<400> 1661
aacagtcaca taaatcactt cagtaacgta tgattttgga ctgttgtggc ttttgccata 60

tttatttcat ttccatctca gtgatctctt aaggaaaccc atg aag aaa cta cgt   115
                                          Met Lys Lys Leu Arg
                                            1               5

ttc gcc acc atc gct gcc gct acc gtt gcc ctg act gcg agc ctt acc   163
Phe Ala Thr Ile Ala Ala Ala Thr Val Ala Leu Thr Ala Ser Leu Thr
                  10                  15                  20

ccc tca gct tcc gca cag gat ttc aac caa atc atc gac aac ttt gat   211
Pro Ser Ala Ser Ala Gln Asp Phe Asn Gln Ile Ile Asp Asn Phe Asp
              25                  30                  35

tgc ggc atc ctt cag acc gct atc tac acc acc ggc ctg gct cac gag   259
Cys Gly Ile Leu Gln Thr Ala Ile Tyr Thr Thr Gly Leu Ala His Glu
          40                  45                  50

aac tcc act cgc tca gag ctc gcc gct aat ctg cgc aac tcc gca gct   307
Asn Ser Thr Arg Ser Glu Leu Ala Ala Asn Leu Arg Asn Ser Ala Ala
      55                  60                  65

gtc ggc caa cta gac ttc cca ttg aat atc gcg gct acc ggc tac tcc   355
Val Gly Gln Leu Asp Phe Pro Leu Asn Ile Ala Ala Thr Gly Tyr Ser
  70                  75                  80                  85

gag cgc atc gct aac cgc gca ctg acc tgc gga atc gtg aag gaa gat   403
Glu Arg Ile Ala Asn Arg Ala Leu Thr Cys Gly Ile Val Lys Glu Asp
                  90                  95                 100

cca cag gac ttc ctc tcc cag ctg cag ctt ctg tcc tct aac cta tct   451
Pro Gln Asp Phe Leu Ser Gln Leu Gln Leu Leu Ser Ser Asn Leu Ser
              105                 110                 115

tct tcc ttc ttc act gct tagtttctct tgggcttttc ctt                 492
Ser Ser Phe Phe Thr Ala
        120


<210> 1662
<211> 123
<212> PRT
<213> Corynebacterium glutamicum

<400> 1662
```

```
Met Lys Lys Leu Arg Phe Ala Thr Ile Ala Ala Ala Thr Val Ala Leu
  1               5                  10                  15

Thr Ala Ser Leu Thr Pro Ser Ala Ser Ala Gln Asp Phe Asn Gln Ile
             20                  25                  30

Ile Asp Asn Phe Asp Cys Gly Ile Leu Gln Thr Ala Ile Tyr Thr Thr
         35                  40                  45

Gly Leu Ala His Glu Asn Ser Thr Arg Ser Glu Leu Ala Ala Asn Leu
     50                  55                  60

Arg Asn Ser Ala Ala Val Gly Gln Leu Asp Phe Pro Leu Asn Ile Ala
 65                  70                  75                  80

Ala Thr Gly Tyr Ser Glu Arg Ile Ala Asn Arg Ala Leu Thr Cys Gly
                 85                  90                  95

Ile Val Lys Glu Asp Pro Gln Asp Phe Leu Ser Gln Leu Gln Leu Leu
            100                 105                 110

Ser Ser Asn Leu Ser Ser Ser Phe Phe Thr Ala
        115                 120
```

<210> 1663
<211> 708
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(685)
<223> RXA00239

<400> 1663

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acaaagcgga tcagattaac aaggtccgtg acgctgtcga tgagcgcatt ggcaaaaaca 60

acggcggcga agagaatcca gccaactagt attaggcgtc atg cgc gtc gta gtt   115
                                            Met Arg Val Val Val
                                              1               5

gtt gat cct aaa cac ccc gtc ctt cca gtc tct ttc ctc gag gct gtt   163
Val Asp Pro Lys His Pro Val Leu Pro Val Ser Phe Leu Glu Ala Val
                 10                  15                  20

ctt ggg cgg ggt gaa cct gtt tct atc gat ccc gat ttt cca ttt gat   211
Leu Gly Arg Gly Glu Pro Val Ser Ile Asp Pro Asp Phe Pro Phe Asp
             25                  30                  35

att gaa aaa tgg ggg atc aag acg tcg aca agc gcc tcc tgg ttt atc   259
Ile Glu Lys Trp Gly Ile Lys Thr Ser Thr Ser Ala Ser Trp Phe Ile
         40                  45                  50

atc gca aaa ccg caa agc acg ctg ctt atc gac gcg ccc ctc aac cct   307
Ile Ala Lys Pro Gln Ser Thr Leu Leu Ile Asp Ala Pro Leu Asn Pro
     55                  60                  65

ttg cat gag gcc gtc ggc gtc atg cgg gcg gcc gtg ggc cgc ggc gag   355
Leu His Glu Ala Val Gly Val Met Arg Ala Ala Val Gly Arg Gly Glu
 70                  75                  80                  85
```

```
tgg gaa cgc acg caa acc cat gag agt ttg att ccg tat ctg gaa gaa   403
Trp Glu Arg Thr Gln Thr His Glu Ser Leu Ile Pro Tyr Leu Glu Glu
                 90                  95                 100

gaa tcg cag gag ttt att gaa gcg att cat ggt ggc gat gat gag cac   451
Glu Ser Gln Glu Phe Ile Glu Ala Ile His Gly Gly Asp Asp Glu His
            105                 110                 115

atg aaa agc gaa ctg ggg gat gtt ttg ctg cag gtg ctt ttt cat gca   499
Met Lys Ser Glu Leu Gly Asp Val Leu Leu Gln Val Leu Phe His Ala
        120                 125                 130

gaa atc gcc gcc cgt cag ggt cga ttc gac att ttt gac gtg gcg gcg   547
Glu Ile Ala Ala Arg Gln Gly Arg Phe Asp Ile Phe Asp Val Ala Ala
    135                 140                 145

agt ttc gta gcc aag atg caa tct cgt tcg ccg tac ctg ttc gac ggc   595
Ser Phe Val Ala Lys Met Gln Ser Arg Ser Pro Tyr Leu Phe Asp Gly
150                 155                 160                 165

tct acc gga att gtg gac acc gac gag cag cag cgg ctg tgg gct caa   643
Ser Thr Gly Ile Val Asp Thr Asp Glu Gln Gln Arg Leu Trp Ala Gln
                170                 175                 180

gga aaa gcc caa gag aaa cta agc agt gaa gaa gga aga aga           685
Gly Lys Ala Gln Glu Lys Leu Ser Ser Glu Glu Gly Arg Arg
            185                 190                 195

taggttagag gacagaagct gca                                        708


<210> 1664
<211> 195
<212> PRT
<213> Corynebacterium glutamicum

<400> 1664
Met Arg Val Val Val Val Asp Pro Lys His Pro Val Leu Pro Val Ser
  1               5                  10                  15

Phe Leu Glu Ala Val Leu Gly Arg Gly Glu Pro Val Ser Ile Asp Pro
             20                  25                  30

Asp Phe Pro Phe Asp Ile Glu Lys Trp Gly Ile Lys Thr Ser Thr Ser
         35                  40                  45

Ala Ser Trp Phe Ile Ile Ala Lys Pro Gln Ser Thr Leu Leu Ile Asp
     50                  55                  60

Ala Pro Leu Asn Pro Leu His Glu Ala Val Gly Val Met Arg Ala Ala
 65                  70                  75                  80

Val Gly Arg Gly Glu Trp Glu Arg Thr Gln Thr His Glu Ser Leu Ile
                 85                  90                  95

Pro Tyr Leu Glu Glu Glu Ser Gln Glu Phe Ile Glu Ala Ile His Gly
            100                 105                 110

Gly Asp Asp Glu His Met Lys Ser Glu Leu Gly Asp Val Leu Leu Gln
        115                 120                 125
```

```
Val Leu Phe His Ala Glu Ile Ala Ala Arg Gln Gly Arg Phe Asp Ile
    130                 135                 140

Phe Asp Val Ala Ala Ser Phe Val Ala Lys Met Gln Ser Arg Ser Pro
145                 150                 155                 160

Tyr Leu Phe Asp Gly Ser Thr Gly Ile Val Asp Thr Asp Glu Gln Gln
                165                 170                 175

Arg Leu Trp Ala Gln Gly Lys Ala Gln Glu Lys Leu Ser Ser Glu Glu
            180                 185                 190

Gly Arg Arg
        195
```

<210> 1665
<211> 333
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(310)
<223> RXA00240

<400> 1665
tcatttaacg tagttgacgt acggcgaagt cgctaaactt cgcgtaatct tggggccaat 60

taatcaagtg cagatgaatt gtttagaaag gctggagacc atg ggt att ttt gac 115
                                            Met Gly Ile Phe Asp
                                              1   5

gaa gct aag aag aag gca acc gaa ttc ctc gac tct gat tca ggc gag 163
Glu Ala Lys Lys Lys Ala Thr Glu Phe Leu Asp Ser Asp Ser Gly Glu
                 10   15   20

cag aag tcc gat gga ctg ctg gat aag gcc gca gac aaa gct aag ggt 211
Gln Lys Ser Asp Gly Leu Leu Asp Lys Ala Ala Asp Lys Ala Lys Gly
            25   30   35

ctc ctc ggt gaa gac aaa gcg gat cag att aac aag gtc cgt gac gct 259
Leu Leu Gly Glu Asp Lys Ala Asp Gln Ile Asn Lys Val Arg Asp Ala
        40   45   50

gtc gat gag cgc att ggc aaa aac aac ggc ggc gaa gag aat cca gcc 307
Val Asp Glu Arg Ile Gly Lys Asn Asn Gly Gly Glu Glu Asn Pro Ala
    55   60   65

aac tagtattagg cgtcatgcgc gtc   333
Asn
 70

<210> 1666
<211> 70
<212> PRT
<213> Corynebacterium glutamicum

<400> 1666
```
```

```
Met Gly Ile Phe Asp Glu Ala Lys Lys Lys Ala Thr Glu Phe Leu Asp
  1               5                  10                  15

Ser Asp Ser Gly Glu Gln Lys Ser Asp Gly Leu Leu Asp Lys Ala Ala
             20                  25                  30

Asp Lys Ala Lys Gly Leu Leu Gly Glu Asp Lys Ala Asp Gln Ile Asn
         35                  40                  45

Lys Val Arg Asp Ala Val Asp Glu Arg Ile Gly Lys Asn Asn Gly Gly
     50                  55                  60

Glu Glu Asn Pro Ala Asn
 65                  70
```

<210> 1667
<211> 759
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(736)
<223> RXA00244

<400> 1667

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agtgggaaag tgatgatgcc acacaccgcc ggcggattac aggatggcag ttcatcaggg 60

gtttaaacag tgaagatttg gcagaaagcg agatggataa atg aat gat cag ctg   115
                                            Met Asn Asp Gln Leu
                                              1               5

tgg gaa ggc gac act gga acg ctg act ttt ggg tcc agg aaa gct ctg   163
Trp Glu Gly Asp Thr Gly Thr Leu Thr Phe Gly Ser Arg Lys Ala Leu
                 10                  15                  20

gtg caa tta ctc aaa ggt ccc atg gtg aat gct ttg cag cat gtt gaa   211
Val Gln Leu Leu Lys Gly Pro Met Val Asn Ala Leu Gln His Val Glu
             25                  30                  35

gtg tgg cgg gct atc acc aca gat caa gat gcg ctc aat gct gtg ctt   259
Val Trp Arg Ala Ile Thr Thr Asp Gln Asp Ala Leu Asn Ala Val Leu
         40                  45                  50

aac aat ttg ttc ctc gag ttg gtt ctt gat gag gat gcg ggt gtt gca   307
Asn Asn Leu Phe Leu Glu Leu Val Leu Asp Glu Asp Ala Gly Val Ala
     55                  60                  65

ttt act cgg cct gcc aat ggt aga caa gaa gta ttg gtt gga aat aac   355
Phe Thr Arg Pro Ala Asn Gly Arg Gln Glu Val Leu Val Gly Asn Asn
 70                  75                  80                  85

aaa act gaa gcg atg ccc aaa gtg ctg cgc acg gag acg ctg tcg cat   403
Lys Thr Glu Ala Met Pro Lys Val Leu Arg Thr Glu Thr Leu Ser His
                 90                  95                 100

ttt gat acg ttg atc att ttg att ctg cgc caa gaa ctc acc atg gcg   451
Phe Asp Thr Leu Ile Ile Leu Ile Leu Arg Gln Glu Leu Thr Met Ala
            105                 110                 115
```

```
cca ccg ggg gaa cga gtc att gtg gat cgt gaa gaa atc cgc gaa caa   499
Pro Pro Gly Glu Arg Val Ile Val Asp Arg Glu Glu Ile Arg Glu Gln
        120                 125                 130

gtg ttg ctc tac cgc gtt gat gaa gag cga gat gaa gcc aaa cta gct   547
Val Leu Leu Tyr Arg Val Asp Glu Glu Arg Asp Glu Ala Lys Leu Ala
    135                 140                 145

aag cga ttc gac gct gca ttt agg cgc atc gtg gat tat tca tta gct   595
Lys Arg Phe Asp Ala Ala Phe Arg Arg Ile Val Asp Tyr Ser Leu Ala
150                 155                 160                 165

aaa aag aca gag aca cct gaa cgt ttt gag gtc tca cca gca ctg cgc   643
Lys Lys Thr Glu Thr Pro Glu Arg Phe Glu Val Ser Pro Ala Leu Arg
                170                 175                 180

cag att ttt gat gcc gac act gtg gca ggt gtg cgc gct gag tac gaa   691
Gln Ile Phe Asp Ala Asp Thr Val Ala Gly Val Arg Ala Glu Tyr Glu
            185                 190                 195

aaa ttt aac aaa gca gcc cat gat gga aat gaa gag gaa cag aag       736
Lys Phe Asn Lys Ala Ala His Asp Gly Asn Glu Glu Glu Gln Lys
        200                 205                 210

tgaccagcga acaagcttta gat                                        759


<210> 1668
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 1668
Met Asn Asp Gln Leu Trp Glu Gly Asp Thr Gly Thr Leu Thr Phe Gly
  1               5                  10                  15

Ser Arg Lys Ala Leu Val Gln Leu Leu Lys Gly Pro Met Val Asn Ala
             20                  25                  30

Leu Gln His Val Glu Val Trp Arg Ala Ile Thr Thr Asp Gln Asp Ala
         35                  40                  45

Leu Asn Ala Val Leu Asn Asn Leu Phe Leu Glu Leu Val Leu Asp Glu
     50                  55                  60

Asp Ala Gly Val Ala Phe Thr Arg Pro Ala Asn Gly Arg Gln Glu Val
 65                  70                  75                  80

Leu Val Gly Asn Asn Lys Thr Glu Ala Met Pro Lys Val Leu Arg Thr
                 85                  90                  95

Glu Thr Leu Ser His Phe Asp Thr Leu Ile Ile Leu Ile Leu Arg Gln
            100                 105                 110

Glu Leu Thr Met Ala Pro Pro Gly Glu Arg Val Ile Val Asp Arg Glu
        115                 120                 125

Glu Ile Arg Glu Gln Val Leu Leu Tyr Arg Val Asp Glu Glu Arg Asp
    130                 135                 140

Glu Ala Lys Leu Ala Lys Arg Phe Asp Ala Ala Phe Arg Arg Ile Val
```

```
145                 150                 155                 160

Asp Tyr Ser Leu Ala Lys Lys Thr Glu Thr Pro Glu Arg Phe Glu Val
                165                 170                 175

Ser Pro Ala Leu Arg Gln Ile Phe Asp Ala Asp Thr Val Ala Gly Val
            180                 185                 190

Arg Ala Glu Tyr Glu Lys Phe Asn Lys Ala Ala His Asp Gly Asn Glu
        195                 200                 205

Glu Glu Gln Lys
    210


<210> 1669
<211> 1608
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1585)
<223> RXA00245

<400> 1669
atgacctttg tttgaagttg gtgcggtgat gggggagtgt gaccggattc gaacaggaat 60

gtacgacacg tgtccacccc ttctggaata gtcaattggc atg acc gtt gta tcg   115
                                        Met Thr Val Val Ser
                                          1               5

cac gcg ctt ggg ttt aag cga ttt agg cag gaa tcc ctg gag ctg tct   163
His Ala Leu Gly Phe Lys Arg Phe Arg Gln Glu Ser Leu Glu Leu Ser
                10                  15                  20

ttg ttg cgc agt gac aac ttt ccg gtg gtg ctc gcc gtg gta gcg cag   211
Leu Leu Arg Ser Asp Asn Phe Pro Val Val Leu Ala Val Val Ala Gln
            25                  30                  35

tat ttt ccg cag ggg gct atc gct aag ccg gcc tca gag ctg tat cag   259
Tyr Phe Pro Gln Gly Ala Ile Ala Lys Pro Ala Ser Glu Leu Tyr Gln
        40                  45                  50

ctg ctc agc gat gat ttt cgg gtg ctg cgt gaa gaa gga ttt gag ctg   307
Leu Leu Ser Asp Asp Phe Arg Val Leu Arg Glu Glu Gly Phe Glu Leu
    55                  60                  65

ccg aaa agc ccg tcg gat tat gtg agt gat tgg gtg aag tcc cgg tgg   355
Pro Lys Ser Pro Ser Asp Tyr Val Ser Asp Trp Val Lys Ser Arg Trp
70                  75                  80                  85

ttt gtg cgt cgt ccg ggt agt tcg cag act ggt gag acc gtg gaa ccg   403
Phe Val Arg Arg Pro Gly Ser Ser Gln Thr Gly Glu Thr Val Glu Pro
                90                  95                  100

agt gaa gag ctg ttg gcg gtg ctg gat tcg gtg cag cgg tgg gat aac   451
Ser Glu Glu Leu Leu Ala Val Leu Asp Ser Val Gln Arg Trp Asp Asn
            105                 110                 115

ccg cat cga agc att tcg gcg tct cga att gaa tcg ttg acg cag gcg   499
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Pro His Arg Ser Ile Ser Ala Ser Arg Ile Glu Ser Leu Thr Gln Ala
        120                 125                 130

ttg cag act ttg gcg ttg gaa tcg gac ccc agc aca gcg aaa cgt tta   547
Leu Gln Thr Leu Ala Leu Glu Ser Asp Pro Ser Thr Ala Lys Arg Leu
    135                 140                 145

gct gag tta gag cgt gaa cgc gac agg att gaa cgc cag att gaa gcg   595
Ala Glu Leu Glu Arg Glu Arg Asp Arg Ile Glu Arg Gln Ile Glu Ala
150                 155                 160                 165

gtc cac gct ggt gaa ttt gaa gtc ctc acc acc gtg cag att ggt gat   643
Val His Ala Gly Glu Phe Glu Val Leu Thr Thr Val Gln Ile Gly Asp
                170                 175                 180

cgg gta gca gat att ttg gat cta gca gca tct att cct gca gat ttc   691
Arg Val Ala Asp Ile Leu Asp Leu Ala Ala Ser Ile Pro Ala Asp Phe
            185                 190                 195

gcc agg gta agg cat gag ctg agc gat ctg aac cgg aag ctg cgc agg   739
Ala Arg Val Arg His Glu Leu Ser Asp Leu Asn Arg Lys Leu Arg Arg
        200                 205                 210

cag ttg ctt gat cct gaa gat tcc cgt ggt gat gtt ttg gaa gag atc   787
Gln Leu Leu Asp Pro Glu Asp Ser Arg Gly Asp Val Leu Glu Glu Ile
    215                 220                 225

ttc agg gga gtt gat ctg att ggg gat tcc gat gcg ggg cgc agc ttc   835
Phe Arg Gly Val Asp Leu Ile Gly Asp Ser Asp Ala Gly Arg Ser Phe
230                 235                 240                 245

aat agt ttc ttt gat gtt ttg ctc gat cgg gaa cgc tca agt ctg att   883
Asn Ser Phe Phe Asp Val Leu Leu Asp Arg Glu Arg Ser Ser Leu Ile
                250                 255                 260

gat cga tgg atc aga gaa gtt ctg gga cgc gat gag gct att gat ctg   931
Asp Arg Trp Ile Arg Glu Val Leu Gly Arg Asp Glu Ala Ile Asp Leu
            265                 270                 275

gat tca aaa tta agg aca ggg ctg tac cga att ttc cgg gat atg gag   979
Asp Ser Lys Leu Arg Thr Gly Leu Tyr Arg Ile Phe Arg Asp Met Glu
        280                 285                 290

gat gcc agc ttc gag gtc aac ggg gaa atg aca ggg ctg gct cga agt   1027
Asp Ala Ser Phe Glu Val Asn Gly Glu Met Thr Gly Leu Ala Arg Ser
    295                 300                 305

ttg cgt cac tat gtc act acc gag gag ttc gca gag agc cga cgc atg   1075
Leu Arg His Tyr Val Thr Thr Glu Glu Phe Ala Glu Ser Arg Arg Met
310                 315                 320                 325

att cag ttg ctt cgc gat acc cgc agt gcc gct gct aag gcc gcc gag   1123
Ile Gln Leu Leu Arg Asp Thr Arg Ser Ala Ala Ala Lys Ala Ala Glu
                330                 335                 340

gct ggt gaa gtg acc tca ctc aat cac atg gac aca cca ctc gtg cgc   1171
Ala Gly Glu Val Thr Ser Leu Asn His Met Asp Thr Pro Leu Val Arg
            345                 350                 355

att ggt atg gat gtt cgc tcg att gcg ggg ttg aaa ctg aag aac cca   1219
Ile Gly Met Asp Val Arg Ser Ile Ala Gly Leu Lys Leu Lys Asn Pro
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        360                 365                 370

ggt gaa gaa cgc gtc gaa gat ttg cct gag cca gtt gaa gaa caa gaa   1267
Gly Glu Glu Arg Val Glu Asp Leu Pro Glu Pro Val Glu Glu Gln Glu
    375                 380                 385

cta gac act gaa gtc ttg atg gaa caa att cgg gca agc gag att gat   1315
Leu Asp Thr Glu Val Leu Met Glu Gln Ile Arg Ala Ser Glu Ile Asp
390                 395                 400                 405

ttt gag gaa ttg gaa gag gct gtt tct tta gtt ctt gcc gag caa tcg   1363
Phe Glu Glu Leu Glu Glu Ala Val Ser Leu Val Leu Ala Glu Gln Ser
            410                 415                 420

cac gcc acg atc acc gag gta cta gaa cat ttc ccg gca acg caa ggt   1411
His Ala Thr Ile Thr Glu Val Leu Glu His Phe Pro Ala Thr Gln Gly
        425                 430                 435

ctc gcc agc att gtt gga ttg tta tac ctg gcg atg cgt gat ggt gtt   1459
Leu Ala Ser Ile Val Gly Leu Leu Tyr Leu Ala Met Arg Asp Gly Val
        440                 445                 450

ccc aca ggt cgc gcg caa ata gtg gag tgg gaa agt gat gat gcc aca   1507
Pro Thr Gly Arg Ala Gln Ile Val Glu Trp Glu Ser Asp Asp Ala Thr
    455                 460                 465

cac cgc cgg cgg att aca gga tgg cag ttc atc agg ggt tta aac agt   1555
His Arg Arg Arg Ile Thr Gly Trp Gln Phe Ile Arg Gly Leu Asn Ser
470                 475                 480                 485

gaa gat ttg gca gaa agc gag atg gat aaa tgaatgatca gctgtgggaa     1605
Glu Asp Leu Ala Glu Ser Glu Met Asp Lys
                490                 495

ggc                                                              1608


<210> 1670
<211> 495
<212> PRT
<213> Corynebacterium glutamicum

<400> 1670
Met Thr Val Val Ser His Ala Leu Gly Phe Lys Arg Phe Arg Gln Glu
  1               5                  10                  15

Ser Leu Glu Leu Ser Leu Leu Arg Ser Asp Asn Phe Pro Val Val Leu
            20                  25                  30

Ala Val Val Ala Gln Tyr Phe Pro Gln Gly Ala Ile Ala Lys Pro Ala
        35                  40                  45

Ser Glu Leu Tyr Gln Leu Leu Ser Asp Asp Phe Arg Val Leu Arg Glu
    50                  55                  60

Glu Gly Phe Glu Leu Pro Lys Ser Pro Ser Asp Tyr Val Ser Asp Trp
65                  70                  75                  80

Val Lys Ser Arg Trp Phe Val Arg Arg Pro Gly Ser Ser Gln Thr Gly
                85                  90                  95
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Glu Thr Val Glu Pro Ser Glu Glu Leu Leu Ala Val Leu Asp Ser Val
            100                 105                 110

Gln Arg Trp Asp Asn Pro His Arg Ser Ile Ser Ala Ser Arg Ile Glu
        115                 120                 125

Ser Leu Thr Gln Ala Leu Gln Thr Leu Ala Leu Glu Ser Asp Pro Ser
    130                 135                 140

Thr Ala Lys Arg Leu Ala Glu Leu Glu Arg Glu Arg Asp Arg Ile Glu
145                 150                 155                 160

Arg Gln Ile Glu Ala Val His Ala Gly Glu Phe Glu Val Leu Thr Thr
                165                 170                 175

Val Gln Ile Gly Asp Arg Val Ala Asp Ile Leu Asp Leu Ala Ala Ser
            180                 185                 190

Ile Pro Ala Asp Phe Ala Arg Val Arg His Glu Leu Ser Asp Leu Asn
        195                 200                 205

Arg Lys Leu Arg Arg Gln Leu Leu Asp Pro Glu Asp Ser Arg Gly Asp
    210                 215                 220

Val Leu Glu Glu Ile Phe Arg Gly Val Asp Leu Ile Gly Asp Ser Asp
225                 230                 235                 240

Ala Gly Arg Ser Phe Asn Ser Phe Phe Asp Val Leu Leu Asp Arg Glu
                245                 250                 255

Arg Ser Ser Leu Ile Asp Arg Trp Ile Arg Glu Val Leu Gly Arg Asp
            260                 265                 270

Glu Ala Ile Asp Leu Asp Ser Lys Leu Arg Thr Gly Leu Tyr Arg Ile
        275                 280                 285

Phe Arg Asp Met Glu Asp Ala Ser Phe Glu Val Asn Gly Glu Met Thr
    290                 295                 300

Gly Leu Ala Arg Ser Leu Arg His Tyr Val Thr Thr Glu Glu Phe Ala
305                 310                 315                 320

Glu Ser Arg Arg Met Ile Gln Leu Leu Arg Asp Thr Arg Ser Ala Ala
                325                 330                 335

Ala Lys Ala Ala Glu Ala Gly Glu Val Thr Ser Leu Asn His Met Asp
            340                 345                 350

Thr Pro Leu Val Arg Ile Gly Met Asp Val Arg Ser Ile Ala Gly Leu
        355                 360                 365

Lys Leu Lys Asn Pro Gly Glu Glu Arg Val Glu Asp Leu Pro Glu Pro
    370                 375                 380

Val Glu Glu Gln Glu Leu Asp Thr Glu Val Leu Met Glu Gln Ile Arg
385                 390                 395                 400

Ala Ser Glu Ile Asp Phe Glu Glu Leu Glu Glu Ala Val Ser Leu Val
                405                 410                 415

Leu Ala Glu Gln Ser His Ala Thr Ile Thr Glu Val Leu Glu His Phe
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            420                 425                 430

Pro Ala Thr Gln Gly Leu Ala Ser Ile Val Gly Leu Leu Tyr Leu Ala
        435                 440                 445

Met Arg Asp Gly Val Pro Thr Gly Arg Ala Gln Ile Val Glu Trp Glu
    450                 455                 460

Ser Asp Asp Ala Thr His Arg Arg Arg Ile Thr Gly Trp Gln Phe Ile
465                 470                 475                 480

Arg Gly Leu Asn Ser Glu Asp Leu Ala Glu Ser Glu Met Asp Lys
                485                 490                 495


<210> 1671
<211> 846
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(823)
<223> RXA00248

<400> 1671
tccggcgata ccctcgcagc tggcttggtt ggccaccgcc tacgcaataa ctggtcgatc 60

tagaccagtg tcttaggcaa gaccccattt aggacacctc atg att ccc ctg att   115
                                           Met Ile Pro Leu Ile
                                             1               5

acg ctt tcc cac ggt tcc cgc aaa aag tcc gca gct gca ggc att act   163
Thr Leu Ser His Gly Ser Arg Lys Lys Ser Ala Ala Ala Gly Ile Thr
                 10                  15                  20

gcg ctg act cat gag gcc gga cga atg ctg gaa aca cca gcc gtg gaa   211
Ala Leu Thr His Glu Ala Gly Arg Met Leu Glu Thr Pro Ala Val Glu
             25                  30                  35

gcg cat tta gag ctt gct gaa cct tcc ctt gat cag gtt gtg gca acg   259
Ala His Leu Glu Leu Ala Glu Pro Ser Leu Asp Gln Val Val Ala Thr
         40                  45                  50

ctc agt gcg gaa ggt gta acc agg gca gcg ttg gtt cct ttg ctg ttt   307
Leu Ser Ala Glu Gly Val Thr Arg Ala Ala Leu Val Pro Leu Leu Phe
     55                  60                  65

agc aat gcg tat cac gca aag att gac gtt cct gag gca gta aaa gat   355
Ser Asn Ala Tyr His Ala Lys Ile Asp Val Pro Glu Ala Val Lys Asp
 70                  75                  80                  85

gct tca gaa aag tat ggt gtg gaa ctt ctc gtg ggt ccg cat ttg ggc   403
Ala Ser Glu Lys Tyr Gly Val Glu Leu Leu Val Gly Pro His Leu Gly
                 90                  95                 100

act ggc tcc gat gta gcc agc gtg ctt gcg cag cgg ttg agt gcg gac   451
Thr Gly Ser Asp Val Ala Ser Val Leu Ala Gln Arg Leu Ser Ala Asp
            105                 110                 115

gcc ccc aca gat gcc cat gtg att ttg tat tcc gtt ggc agc tca cac   499
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Ala Pro Thr Asp Ala His Val Ile Leu Tyr Ser Val Gly Ser Ser His
        120                 125                 130

gtg tcc gcc aat gaa tca gtc atc gat ctt gcc cac acc att gct ctc   547
Val Ser Ala Asn Glu Ser Val Ile Asp Leu Ala His Thr Ile Ala Leu
    135                 140                 145

ctc act ggc ttt tcg gtt gag gtg gtg ccc gct acc ggt ggg cca ggt   595
Leu Thr Gly Phe Ser Val Glu Val Val Pro Ala Thr Gly Gly Pro Gly
150                 155                 160                 165

gcc ggc ggc gcc gga gta ata gag gtg gcc tcg aaa cac aag gcc gtc   643
Ala Gly Gly Ala Gly Val Ile Glu Val Ala Ser Lys His Lys Ala Val
                170                 175                 180

cac atc ctg ccg ctg ttt gtt acg gaa ggt ttg ctg ctg gat cgg gct   691
His Ile Leu Pro Leu Phe Val Thr Glu Gly Leu Leu Leu Asp Arg Ala
            185                 190                 195

att gat caa tcc gcc aac atc gca gct gcc acc ggc aca aac ttc acc   739
Ile Asp Gln Ser Ala Asn Ile Ala Ala Ala Thr Gly Thr Asn Phe Thr
        200                 205                 210

tat tcc gaa ccc cta act act gac ctc gca cca ctt gtt gca gcc cgt   787
Tyr Ser Glu Pro Leu Thr Thr Asp Leu Ala Pro Leu Val Ala Ala Arg
    215                 220                 225

tac cac gct gca ttg agc gca ctg ctg gca cat atc taagaccgct        833
Tyr His Ala Ala Leu Ser Ala Leu Leu Ala His Ile
230                 235                 240

aaggaaatca gct                                                   846


<210> 1672
<211> 241
<212> PRT
<213> Corynebacterium glutamicum

<400> 1672
Met Ile Pro Leu Ile Thr Leu Ser His Gly Ser Arg Lys Lys Ser Ala
  1               5                  10                  15

Ala Ala Gly Ile Thr Ala Leu Thr His Glu Ala Gly Arg Met Leu Glu
            20                  25                  30

Thr Pro Ala Val Glu Ala His Leu Glu Leu Ala Glu Pro Ser Leu Asp
        35                  40                  45

Gln Val Val Ala Thr Leu Ser Ala Glu Gly Val Thr Arg Ala Ala Leu
    50                  55                  60

Val Pro Leu Leu Phe Ser Asn Ala Tyr His Ala Lys Ile Asp Val Pro
65                  70                  75                  80

Glu Ala Val Lys Asp Ala Ser Glu Lys Tyr Gly Val Glu Leu Leu Val
                85                  90                  95

Gly Pro His Leu Gly Thr Gly Ser Asp Val Ala Ser Val Leu Ala Gln
            100                 105                 110
```

```
Arg Leu Ser Ala Asp Ala Pro Thr Asp Ala His Val Ile Leu Tyr Ser
        115                 120                 125

Val Gly Ser Ser His Val Ser Ala Asn Glu Ser Val Ile Asp Leu Ala
    130                 135                 140

His Thr Ile Ala Leu Leu Thr Gly Phe Ser Val Glu Val Val Pro Ala
145                 150                 155                 160

Thr Gly Gly Pro Gly Ala Gly Gly Ala Gly Val Ile Glu Val Ala Ser
                165                 170                 175

Lys His Lys Ala Val His Ile Leu Pro Leu Phe Val Thr Glu Gly Leu
            180                 185                 190

Leu Leu Asp Arg Ala Ile Asp Gln Ser Ala Asn Ile Ala Ala Ala Thr
        195                 200                 205

Gly Thr Asn Phe Thr Tyr Ser Glu Pro Leu Thr Thr Asp Leu Ala Pro
    210                 215                 220

Leu Val Ala Ala Arg Tyr His Ala Ala Leu Ser Ala Leu Leu Ala His
225                 230                 235                 240

Ile
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5000000000000000

<210> 1673
<211> 239
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(216)
<223> RXA00250

<400> 1673

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gct ttg ggt gct gcg ttg ggt cag ttc gat ttc gtc cgc aac aat att   48
Ala Leu Gly Ala Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Asn Ile
  1               5                  10                  15

gat ctg att ttc ttg ctg atc gtg ttc att tcg gtg gtt cct ggt ttg   96
Asp Leu Ile Phe Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly Leu
             20                  25                  30

gtc ggc atg gcc cgc aag ctg gct gac ggc cac aag caa gcc aac acc   144
Val Gly Met Ala Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn Thr
         35                  40                  45

gag cca caa gaa aac ccc gca gtc cag aca gcc cca gta aaa acc cag   192
Glu Pro Gln Glu Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr Gln
     50                  55                  60

gaa gcc cag gaa gcc ccc cag aac taatctttcc ggtccgccag ttc        239
Glu Ala Gln Glu Ala Pro Gln Asn
 65                  70
```

<210> 1674

<211> 72
<212> PRT
<213> Corynebacterium glutamicum

<400> 1674
Ala Leu Gly Ala Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Asn Ile
1 5 10 15

Asp Leu Ile Phe Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly Leu
20 25 30

Val Gly Met Ala Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn Thr
35 40 45

Glu Pro Gln Glu Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr Gln
50 55 60

Glu Ala Gln Glu Ala Pro Gln Asn
65 70

<210> 1675
<211> 366
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(343)
<223> RXA00252

<400> 1675
gcagcatggg ggtgttggtg gggccggggc tgacagtgct gacgcggatg ccgttgttgg 60

cttcttcttt gcggaaggcg tcggcgagtc cgcggagggc gtg ttt gct ggc ggc 115
Val Phe Ala Gly Gly
1 5

gta gat ggt gtt gcc ggg gtg tgg tcc gtt gcc ggc gcc gga gtt gat 163
Val Asp Gly Val Ala Gly Val Trp Ser Val Ala Gly Ala Gly Val Asp
10 15 20

gta gat gac gca gcc gga tgc cgc gcg gag ggc ggg caa gag ttg gcg 211
Val Asp Asp Ala Ala Gly Cys Arg Ala Glu Gly Gly Gln Glu Leu Ala
25 30 35

act caa ctc ggc cgg gac aat gac gtt gag atc aag gtg tgc gtg cca 259
Thr Gln Leu Gly Arg Asp Asn Asp Val Glu Ile Lys Val Cys Val Pro
40 45 50

ttc ggc cac act gcc ggc ttc gat ggt cgt gtc acg cgc cac cgc cgc 307
Phe Gly His Thr Ala Gly Phe Asp Gly Arg Val Thr Arg His Arg Arg
55 60 65

ggc gtg cac cag cgt atc cac gtg gtc gag gtt ttt tagcttgtcg 353
Gly Val His Gln Arg Ile His Val Val Glu Val Phe
70 75 80

acgcctccct ctt 366

<210> 1676
<211> 81
<212> PRT
<213> Corynebacterium glutamicum

<400> 1676
Val Phe Ala Gly Gly Val Asp Gly Val Ala Gly Val Trp Ser Val Ala
1 5 10 15

Gly Ala Gly Val Asp Val Asp Asp Ala Ala Gly Cys Arg Ala Glu Gly
20 25 30

Gly Gln Glu Leu Ala Thr Gln Leu Gly Arg Asp Asn Asp Val Glu Ile
35 40 45

Lys Val Cys Val Pro Phe Gly His Thr Ala Gly Phe Asp Gly Arg Val
50 55 60

Thr Arg His Arg Arg Gly Val His Gln Arg Ile His Val Val Glu Val
65 70 75 80

Phe

<210> 1677
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXA00257

<400> 1677
catcatcaat ggcgatgaaa cgggtgcgct cagtacttgt gtatccatgg ctaatatcgg 60

gctacttcat actctgttgt aaacaaagga agtttctatc atg aaa atc aag aaa 115
Met Lys Ile Lys Lys
1 5

ttc agc atc aca gcg cta gcc tca gtt cta atg ctc acg ggt tgc gcg 163
Phe Ser Ile Thr Ala Leu Ala Ser Val Leu Met Leu Thr Gly Cys Ala
10 15 20

acc aat cac agc tca cct ctg tac agt tat ctg aat gcg tca aca tca 211
Thr Asn His Ser Ser Pro Leu Tyr Ser Tyr Leu Asn Ala Ser Thr Ser
25 30 35

acc act gtt gaa caa gta cgt ctc agc gat ctt tac ggt gag cag tgg 259
Thr Thr Val Glu Gln Val Arg Leu Ser Asp Leu Tyr Gly Glu Gln Trp
40 45 50

acc gag ttc gct ctt gtc tgc ccc tac acc aca aaa gac gag gta aaa 307
Thr Glu Phe Ala Leu Val Cys Pro Tyr Thr Thr Lys Asp Glu Val Lys
55 60 65

gaa gag ctt ggt ata aaa ata aac acc tac ctc acc gat tcg acc gat 355
Glu Glu Leu Gly Ile Lys Ile Asn Thr Tyr Leu Thr Asp Ser Thr Asp
70 75 80 85

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gac agt agt aac gat att gtg ctc agg gat aaa gac ggt tca tat gat   403
Asp Ser Ser Asn Asp Ile Val Leu Arg Asp Lys Asp Gly Ser Tyr Asp
                 90                  95                 100

tgg atc tat ttc aac aga ttc gac att gtg tac ctc tgc aac ggc tca   451
Trp Ile Tyr Phe Asn Arg Phe Asp Ile Val Tyr Leu Cys Asn Gly Ser
            105                 110                 115

gcg gaa aat cta aaa atc tac ccc att gat tca gtt cta gaa ttt gag   499
Ala Glu Asn Leu Lys Ile Tyr Pro Ile Asp Ser Val Leu Glu Phe Glu
        120                 125                 130

cat aga gac gac tac ggt acc tgg aaa ctg agc gct atc aca gag ccg   547
His Arg Asp Asp Tyr Gly Thr Trp Lys Leu Ser Ala Ile Thr Glu Pro
    135                 140                 145

ggt aat caa taataacgcg gacacttaag tac                            579
Gly Asn Gln
150
```

<210> 1678
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 1678

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Met Lys Ile Lys Lys Phe Ser Ile Thr Ala Leu Ala Ser Val Leu Met
  1               5                  10                  15

Leu Thr Gly Cys Ala Thr Asn His Ser Ser Pro Leu Tyr Ser Tyr Leu
            20                  25                  30

Asn Ala Ser Thr Ser Thr Thr Val Glu Gln Val Arg Leu Ser Asp Leu
        35                  40                  45

Tyr Gly Glu Gln Trp Thr Glu Phe Ala Leu Val Cys Pro Tyr Thr Thr
    50                  55                  60

Lys Asp Glu Val Lys Glu Glu Leu Gly Ile Lys Ile Asn Thr Tyr Leu
65                  70                  75                  80

Thr Asp Ser Thr Asp Asp Ser Ser Asn Asp Ile Val Leu Arg Asp Lys
                85                  90                  95

Asp Gly Ser Tyr Asp Trp Ile Tyr Phe Asn Arg Phe Asp Ile Val Tyr
            100                 105                 110

Leu Cys Asn Gly Ser Ala Glu Asn Leu Lys Ile Tyr Pro Ile Asp Ser
        115                 120                 125

Val Leu Glu Phe Glu His Arg Asp Asp Tyr Gly Thr Trp Lys Leu Ser
    130                 135                 140

Ala Ile Thr Glu Pro Gly Asn Gln
145                 150
```

<210> 1679
<211> 795

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(772)
<223> RXA00258

<400> 1679
taattaatat aattaatgta gtttattaac ctattatgca atgacatttt ttaataatta 60

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accacgtcac aacattctct cagatcacag aggttcgctc atg cgc cac acc acg   115
                                            Met Arg His Thr Thr
                                              1               5

tca gcc aca tca act aca tct att att aag cgt gct atg acc att agt   163
Ser Ala Thr Ser Thr Thr Ser Ile Ile Lys Arg Ala Met Thr Ile Ser
                 10                  15                  20

gcc gct gtt ctt att gcc agc gct gtt ggt ctc aca acc agc gca agt   211
Ala Ala Val Leu Ile Ala Ser Ala Val Gly Leu Thr Thr Ser Ala Ser
             25                  30                  35

tcg ctc aat act ctc agc gct aca tca cct gaa tca ccc gat cag gca   259
Ser Leu Asn Thr Leu Ser Ala Thr Ser Pro Glu Ser Pro Asp Gln Ala
         40                  45                  50

gcc act gtg tca cag gct gaa tca gat agt gaa tta gat gac ggc atg   307
Ala Thr Val Ser Gln Ala Glu Ser Asp Ser Glu Leu Asp Asp Gly Met
     55                  60                  65

aaa aag ctt gca acc aag atc ctt aat cgc gct gac aac gct gaa aat   355
Lys Lys Leu Ala Thr Lys Ile Leu Asn Arg Ala Asp Asn Ala Glu Asn
 70                  75                  80                  85

aat gat gac acc ggc aaa aac ctc aac aat gat gat aag aag ctc aac   403
Asn Asp Asp Thr Gly Lys Asn Leu Asn Asn Asp Asp Lys Lys Leu Asn
                 90                  95                 100

acg aag cag ccg cag cgc cct gct gaa aaa gtt gcc cag gcg atc gag   451
Thr Lys Gln Pro Gln Arg Pro Ala Glu Lys Val Ala Gln Ala Ile Glu
            105                 110                 115

cta agc ctt gat acc acc acg aat gca gaa aag cct gat aaa agt ttt   499
Leu Ser Leu Asp Thr Thr Thr Asn Ala Glu Lys Pro Asp Lys Ser Phe
        120                 125                 130

cac cat gaa aaa ccc gta aac gcc tat gtc aca agt gtc agc tac aac   547
His His Glu Lys Pro Val Asn Ala Tyr Val Thr Ser Val Ser Tyr Asn
    135                 140                 145

aaa agc aat gac acc tgg act atc aaa cca tca gac agc gcg gtg aat   595
Lys Ser Asn Asp Thr Trp Thr Ile Lys Pro Ser Asp Ser Ala Val Asn
150                 155                 160                 165

aca ccg acc aat gat gct gag cgc atc agc aat atc atc caa gaa gct   643
Thr Pro Thr Asn Asp Ala Glu Arg Ile Ser Asn Ile Ile Gln Glu Ala
                170                 175                 180

cgc gac ctc ggt ctc agc gac gat gaa tcc ttg acg caa cag atc gca   691
Arg Asp Leu Gly Leu Ser Asp Asp Glu Ser Leu Thr Gln Gln Ile Ala
```

```
            185                 190                 195

ttt cac gct cat gct gct aat tat tta gtc acc gaa tgg gta ctt cgc   739
Phe His Ala His Ala Ala Asn Tyr Leu Val Thr Glu Trp Val Leu Arg
        200                 205                 210

ggc tat cag ctt gct aac ccg aag gtg ctt cca tgagaaaaca acgacgcatg 792
Gly Tyr Gln Leu Ala Asn Pro Lys Val Leu Pro
    215                 220

atg                                                               795


<210> 1680
<211> 224
<212> PRT
<213> Corynebacterium glutamicum

<400> 1680
Met Arg His Thr Thr Ser Ala Thr Ser Thr Thr Ser Ile Ile Lys Arg
  1               5                  10                  15

Ala Met Thr Ile Ser Ala Ala Val Leu Ile Ala Ser Ala Val Gly Leu
             20                  25                  30

Thr Thr Ser Ala Ser Ser Leu Asn Thr Leu Ser Ala Thr Ser Pro Glu
         35                  40                  45

Ser Pro Asp Gln Ala Ala Thr Val Ser Gln Ala Glu Ser Asp Ser Glu
     50                  55                  60

Leu Asp Asp Gly Met Lys Lys Leu Ala Thr Lys Ile Leu Asn Arg Ala
 65                  70                  75                  80

Asp Asn Ala Glu Asn Asn Asp Asp Thr Gly Lys Asn Leu Asn Asn Asp
                 85                  90                  95

Asp Lys Lys Leu Asn Thr Lys Gln Pro Gln Arg Pro Ala Glu Lys Val
            100                 105                 110

Ala Gln Ala Ile Glu Leu Ser Leu Asp Thr Thr Thr Asn Ala Glu Lys
        115                 120                 125

Pro Asp Lys Ser Phe His His Glu Lys Pro Val Asn Ala Tyr Val Thr
    130                 135                 140

Ser Val Ser Tyr Asn Lys Ser Asn Asp Thr Trp Thr Ile Lys Pro Ser
145                 150                 155                 160

Asp Ser Ala Val Asn Thr Pro Thr Asn Asp Ala Glu Arg Ile Ser Asn
                165                 170                 175

Ile Ile Gln Glu Ala Arg Asp Leu Gly Leu Ser Asp Asp Glu Ser Leu
            180                 185                 190

Thr Gln Gln Ile Ala Phe His Ala His Ala Ala Asn Tyr Leu Val Thr
        195                 200                 205

Glu Trp Val Leu Arg Gly Tyr Gln Leu Ala Asn Pro Lys Val Leu Pro
    210                 215                 220
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<210> 1681
<211> 1299
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1276)
<223> RXA00260

<400> 1681
gcaacagcgg cttgcagatc agaaggcgcg agaggcgcga cagctgctag atattgaacg 60

tcagcaggtg attgcagatc gctatgggcc gttggtgaat atg cat agc gac gct 115
Met His Ser Asp Ala
1 5

gtg cta gcg ggt gct tca ata aga gca aaa ata ggt gct ctc gca act 163
Val Leu Ala Gly Ala Ser Ile Arg Ala Lys Ile Gly Ala Leu Ala Thr
10 15 20

att tac ggt gct caa aac tta gag aat gtc att cac tca gtt agt ttt 211
Ile Tyr Gly Ala Gln Asn Leu Glu Asn Val Ile His Ser Val Ser Phe
25 30 35

act gac aga cgt att tct ccc gat gga caa ctg tcg aaa gaa tta ttt 259
Thr Asp Arg Arg Ile Ser Pro Asp Gly Gln Leu Ser Lys Glu Leu Phe
40 45 50

cgc gaa gct tgg agc gca aac ctt ctt atc cct gat cca tct tct gat 307
Arg Glu Ala Trp Ser Ala Asn Leu Leu Ile Pro Asp Pro Ser Ser Asp
55 60 65

gtg gaa gcg ttt gcg tgg agc gaa aag aat tcc act gag cta gcg gga 355
Val Glu Ala Phe Ala Trp Ser Glu Lys Asn Ser Thr Glu Leu Ala Gly
70 75 80 85

ggc ata ttc gtt gag aaa atg cta ttt act gtc ccg gac aca ggc cgc 403
Gly Ile Phe Val Glu Lys Met Leu Phe Thr Val Pro Asp Thr Gly Arg
90 95 100

tcc aat aac cgt gtc cag agc ttc tca gaa gaa ctt cgt aac cac att 451
Ser Asn Asn Arg Val Gln Ser Phe Ser Glu Glu Leu Arg Asn His Ile
105 110 115

tct ttg aaa gat atg tat tct aca caa cgt gaa gag cta tta gac ctt 499
Ser Leu Lys Asp Met Tyr Ser Thr Gln Arg Glu Glu Leu Leu Asp Leu
120 125 130

gcc tac gag ctc atg gtg ggg gaa gca gta cgt ttt gct aac ttc cgc 547
Ala Tyr Glu Leu Met Val Gly Glu Ala Val Arg Phe Ala Asn Phe Arg
135 140 145

ctt tat gat cag aat ctc cca cca ctt act gaa gca aat ata gac aaa 595
Leu Tyr Asp Gln Asn Leu Pro Pro Leu Thr Glu Ala Asn Ile Asp Lys
150 155 160 165

```
ttg aga gcc cat cta cgt gag gcc gca gct agt gcg tca cta gga gtg   643
Leu Arg Ala His Leu Arg Glu Ala Ala Ala Ser Ala Ser Leu Gly Val
                170                 175                 180

tta tat cta atg gtg tgg cga tct gta aaa gac gca gct gca gcg cac   691
Leu Tyr Leu Met Val Trp Arg Ser Val Lys Asp Ala Ala Ala Ala His
            185                 190                 195

act aaa cat aca aga atg agc aaa gaa aat gcg aca acg cat agt gtt   739
Thr Lys His Thr Arg Met Ser Lys Glu Asn Ala Thr Thr His Ser Val
        200                 205                 210

aca aaa gtt tct atc ttt gtt gac caa tta tta agc gga aca ttc cct   787
Thr Lys Val Ser Ile Phe Val Asp Gln Leu Leu Ser Gly Thr Phe Pro
    215                 220                 225

tgt tca aag cct ttt cac gaa tct tca caa gtc cca ctg agt gaa gcc   835
Cys Ser Lys Pro Phe His Glu Ser Ser Gln Val Pro Leu Ser Glu Ala
230                 235                 240                 245

acc aag ata gtt ttt aat ttg att atg gag tca ccg ccg atg gaa act   883
Thr Lys Ile Val Phe Asn Leu Ile Met Glu Ser Pro Pro Met Glu Thr
                250                 255                 260

gag ccg agt gtg ctg cga aat tcc ctc caa gaa cac tcg gat tgg gag   931
Glu Pro Ser Val Leu Arg Asn Ser Leu Gln Glu His Ser Asp Trp Glu
            265                 270                 275

cta ttg caa cag tgt gat gag aag att cct gat cgg gag ttt ctg atg   979
Leu Leu Gln Gln Cys Asp Glu Lys Ile Pro Asp Arg Glu Phe Leu Met
        280                 285                 290

gag tgg tta tat caa gaa cag acg tgg act gca gag caa ttt ttt gat  1027
Glu Trp Leu Tyr Gln Glu Gln Thr Trp Thr Ala Glu Gln Phe Phe Asp
    295                 300                 305

gct cta gct atg gtt tct tct agc gag ttt cgt ata tgt gca cct gga  1075
Ala Leu Ala Met Val Ser Ser Ser Glu Phe Arg Ile Cys Ala Pro Gly
310                 315                 320                 325

tgt gcg cat caa gta agt gca gac atc gct aca caa gtc tta gaa ttc  1123
Cys Ala His Gln Val Ser Ala Asp Ile Ala Thr Gln Val Leu Glu Phe
                330                 335                 340

cac gat cga gtg tct ttc cat gac gat cgt aaa agc gcc atg ctt gct  1171
His Asp Arg Val Ser Phe His Asp Asp Arg Lys Ser Ala Met Leu Ala
            345                 350                 355

gct gaa gca act att att ggt aac aaa att ggt tca caa gca cgg gcc  1219
Ala Glu Ala Thr Ile Ile Gly Asn Lys Ile Gly Ser Gln Ala Arg Ala
        360                 365                 370

gga gac ttt gtt tta ggt gaa gta atc acc aag ctg cag aac ata cct  1267
Gly Asp Phe Val Leu Gly Glu Val Ile Thr Lys Leu Gln Asn Ile Pro
    375                 380                 385

ggt gag gta taacttctgc gtcgtccaat tag                           1299
Gly Glu Val
390
```

<210> 1682
<211> 392
<212> PRT
<213> Corynebacterium glutamicum

<400> 1682

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Met His Ser Asp Ala Val Leu Ala Gly Ala Ser Ile Arg Ala Lys Ile
  1               5                  10                  15

Gly Ala Leu Ala Thr Ile Tyr Gly Ala Gln Asn Leu Glu Asn Val Ile
             20                  25                  30

His Ser Val Ser Phe Thr Asp Arg Arg Ile Ser Pro Asp Gly Gln Leu
         35                  40                  45

Ser Lys Glu Leu Phe Arg Glu Ala Trp Ser Ala Asn Leu Leu Ile Pro
     50                  55                  60

Asp Pro Ser Ser Asp Val Glu Ala Phe Ala Trp Ser Glu Lys Asn Ser
 65                  70                  75                  80

Thr Glu Leu Ala Gly Gly Ile Phe Val Glu Lys Met Leu Phe Thr Val
                 85                  90                  95

Pro Asp Thr Gly Arg Ser Asn Asn Arg Val Gln Ser Phe Ser Glu Glu
            100                 105                 110

Leu Arg Asn His Ile Ser Leu Lys Asp Met Tyr Ser Thr Gln Arg Glu
        115                 120                 125

Glu Leu Leu Asp Leu Ala Tyr Glu Leu Met Val Gly Glu Ala Val Arg
    130                 135                 140

Phe Ala Asn Phe Arg Leu Tyr Asp Gln Asn Leu Pro Pro Leu Thr Glu
145                 150                 155                 160

Ala Asn Ile Asp Lys Leu Arg Ala His Leu Arg Glu Ala Ala Ala Ser
                165                 170                 175

Ala Ser Leu Gly Val Leu Tyr Leu Met Val Trp Arg Ser Val Lys Asp
            180                 185                 190

Ala Ala Ala Ala His Thr Lys His Thr Arg Met Ser Lys Glu Asn Ala
        195                 200                 205

Thr Thr His Ser Val Thr Lys Val Ser Ile Phe Val Asp Gln Leu Leu
    210                 215                 220

Ser Gly Thr Phe Pro Cys Ser Lys Pro Phe His Glu Ser Ser Gln Val
225                 230                 235                 240

Pro Leu Ser Glu Ala Thr Lys Ile Val Phe Asn Leu Ile Met Glu Ser
                245                 250                 255

Pro Pro Met Glu Thr Glu Pro Ser Val Leu Arg Asn Ser Leu Gln Glu
            260                 265                 270

His Ser Asp Trp Glu Leu Leu Gln Gln Cys Asp Glu Lys Ile Pro Asp
        275                 280                 285

Arg Glu Phe Leu Met Glu Trp Leu Tyr Gln Glu Gln Thr Trp Thr Ala
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    290                 295                 300

Glu Gln Phe Phe Asp Ala Leu Ala Met Val Ser Ser Ser Glu Phe Arg
305                 310                 315                 320

Ile Cys Ala Pro Gly Cys Ala His Gln Val Ser Ala Asp Ile Ala Thr
                325                 330                 335

Gln Val Leu Glu Phe His Asp Arg Val Ser Phe His Asp Asp Arg Lys
            340                 345                 350

Ser Ala Met Leu Ala Ala Glu Ala Thr Ile Ile Gly Asn Lys Ile Gly
        355                 360                 365

Ser Gln Ala Arg Ala Gly Asp Phe Val Leu Gly Glu Val Ile Thr Lys
    370                 375                 380

Leu Gln Asn Ile Pro Gly Glu Val
385                 390


<210> 1683
<211> 1236
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1213)
<223> RXA00273

<400> 1683
tcggtcttgg tggcggctcc gtcattagtt ccagtaagta gttttttcac tccctgtttt 60

gagtttttt ctcaccttta tatagataag gaatattcac atg tct ttg aag ctt   115
                                        Met Ser Leu Lys Leu
                                          1               5

aat tct cgt cgt ctt gca tcc att gct gtc gct gtt gca gtc ggt gtc   163
Asn Ser Arg Arg Leu Ala Ser Ile Ala Val Ala Val Ala Val Gly Val
                 10                  15                  20

tct ggt gtt gct gct gtt ggt gcg gca cca gct acg gct cag cag gta   211
Ser Gly Val Ala Ala Val Gly Ala Ala Pro Ala Thr Ala Gln Gln Val
             25                  30                  35

ggt gct ggt acc ccg att cac gtt gtc aac ctt gat cgc acc gtt gtt   259
Gly Ala Gly Thr Pro Ile His Val Val Asn Leu Asp Arg Thr Val Val
         40                  45                  50

gat cca gtg act ggt gac atc acc ttc cac ttc acc gac ggc act ttt   307
Asp Pro Val Thr Gly Asp Ile Thr Phe His Phe Thr Asp Gly Thr Phe
     55                  60                  65

gtc acc ctc aag gcg ggt gtt gat ggc aag gat ggt acc gat ggc caa   355
Val Thr Leu Lys Ala Gly Val Asp Gly Lys Asp Gly Thr Asp Gly Gln
 70                  75                  80                  85

gat ggt gtg atc ggc aag gac gca acc att gtt gat gtc gct acg gag   403
Asp Gly Val Ile Gly Lys Asp Ala Thr Ile Val Asp Val Ala Thr Glu
                 90                  95                 100
```

```
tcc aat ggt gat gtc aag ctc acc ttc tct gat ggc acc gtc gtc acc   451
Ser Asn Gly Asp Val Lys Leu Thr Phe Ser Asp Gly Thr Val Val Thr
            105                 110                 115

att cct gca gct aag gac ggt gtg gat ggt gaa gat ggc aag gat ggc   499
Ile Pro Ala Ala Lys Asp Gly Val Asp Gly Glu Asp Gly Lys Asp Gly
        120                 125                 130

gag gac gct act gtg gtg tct act gcg act gac gcc aac ggc aat atc   547
Glu Asp Ala Thr Val Val Ser Thr Ala Thr Asp Ala Asn Gly Asn Ile
    135                 140                 145

gtc att acg ttc tct gat ggc tct gtg ctt gtt gtt gct aac ggt aag   595
Val Ile Thr Phe Ser Asp Gly Ser Val Leu Val Val Ala Asn Gly Lys
150                 155                 160                 165

gac ggc aac gat ggc tca gac ggc cag gat ggt gct gat ggt gaa aat   643
Asp Gly Asn Asp Gly Ser Asp Gly Gln Asp Gly Ala Asp Gly Glu Asn
                170                 175                 180

ggc aag gat ggt gag aac ggc gct aac gcg acc att gtc gat cag att   691
Gly Lys Asp Gly Glu Asn Gly Ala Asn Ala Thr Ile Val Asp Gln Ile
            185                 190                 195

gcc aat gac gat ggt tcc att acc att gtg ttc tcc gat ggt tct gag   739
Ala Asn Asp Asp Gly Ser Ile Thr Ile Val Phe Ser Asp Gly Ser Glu
        200                 205                 210

gtc act atc cca gcg cca gct aag ggt gcc acc gat gag ctg gca cag   787
Val Thr Ile Pro Ala Pro Ala Lys Gly Ala Thr Asp Glu Leu Ala Gln
    215                 220                 225

tgt ctg ctg aac ccg aag atg ttg ctg ctg gca gca att cct gct gca   835
Cys Leu Leu Asn Pro Lys Met Leu Leu Leu Ala Ala Ile Pro Ala Ala
230                 235                 240                 245

ggt gct att gct aac gct gtg gca ccg gcg atc cca cgt gtt gtt gaa   883
Gly Ala Ile Ala Asn Ala Val Ala Pro Ala Ile Pro Arg Val Val Glu
                250                 255                 260

gat gtg cgt gca cag ttc aat ctt cca agc ctc aac ccc cag ttt gat   931
Asp Val Arg Ala Gln Phe Asn Leu Pro Ser Leu Asn Pro Gln Phe Asp
            265                 270                 275

cag tgg ctc tac aac gcg acc aag gat att gat gca ggg ttg ttg atc   979
Gln Trp Leu Tyr Asn Ala Thr Lys Asp Ile Asp Ala Gly Leu Leu Ile
        280                 285                 290

tct ggt gct acc ggc ctt gct gtg ctg tcg gtg ctc gct gat gat ttc  1027
Ser Gly Ala Thr Gly Leu Ala Val Leu Ser Val Leu Ala Asp Asp Phe
    295                 300                 305

tgt ggc gac att gat gcc gat gac aac gca gat ggt gac gtg gcg gca  1075
Cys Gly Asp Ile Asp Ala Asp Asp Asn Ala Asp Gly Asp Val Ala Ala
310                 315                 320                 325

gaa aag cca act ggc tct tct ggg ctt gga tca tct gaa cag agt gaa  1123
Glu Lys Pro Thr Gly Ser Ser Gly Leu Gly Ser Ser Glu Gln Ser Glu
                330                 335                 340
```

```
aag gtt gat ggt gac gac gat agt gtg atc gac act gaa act gat gca   1171
Lys Val Asp Gly Asp Asp Asp Ser Val Ile Asp Thr Glu Thr Asp Ala
            345                 350                 355

gat ctc gaa gta gaa gaa gac cct gag ctt gtt aac gca ggt           1213
Asp Leu Glu Val Glu Glu Asp Pro Glu Leu Val Asn Ala Gly
        360                 365                 370

taacgccagt gtaatgctgg att                                        1236
```

<210> 1684
<211> 371
<212> PRT
<213> Corynebacterium glutamicum

<400> 1684

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Met Ser Leu Lys Leu Asn Ser Arg Arg Leu Ala Ser Ile Ala Val Ala
  1               5                  10                  15

Val Ala Val Gly Val Ser Gly Val Ala Ala Val Gly Ala Ala Pro Ala
             20                  25                  30

Thr Ala Gln Gln Val Gly Ala Gly Thr Pro Ile His Val Val Asn Leu
         35                  40                  45

Asp Arg Thr Val Val Asp Pro Val Thr Gly Asp Ile Thr Phe His Phe
     50                  55                  60

Thr Asp Gly Thr Phe Val Thr Leu Lys Ala Gly Val Asp Gly Lys Asp
 65                  70                  75                  80

Gly Thr Asp Gly Gln Asp Gly Val Ile Gly Lys Asp Ala Thr Ile Val
                 85                  90                  95

Asp Val Ala Thr Glu Ser Asn Gly Asp Val Lys Leu Thr Phe Ser Asp
            100                 105                 110

Gly Thr Val Val Thr Ile Pro Ala Ala Lys Asp Gly Val Asp Gly Glu
        115                 120                 125

Asp Gly Lys Asp Gly Glu Asp Ala Thr Val Val Ser Thr Ala Thr Asp
    130                 135                 140

Ala Asn Gly Asn Ile Val Ile Thr Phe Ser Asp Gly Ser Val Leu Val
145                 150                 155                 160

Val Ala Asn Gly Lys Asp Gly Asn Asp Gly Ser Asp Gly Gln Asp Gly
                165                 170                 175

Ala Asp Gly Glu Asn Gly Lys Asp Gly Glu Asn Gly Ala Asn Ala Thr
            180                 185                 190

Ile Val Asp Gln Ile Ala Asn Asp Asp Gly Ser Ile Thr Ile Val Phe
        195                 200                 205

Ser Asp Gly Ser Glu Val Thr Ile Pro Ala Pro Ala Lys Gly Ala Thr
    210                 215                 220

Asp Glu Leu Ala Gln Cys Leu Leu Asn Pro Lys Met Leu Leu Leu Ala
225                 230                 235                 240
```

```
Ala Ile Pro Ala Ala Gly Ala Ile Ala Asn Ala Val Ala Pro Ala Ile
                245                 250                 255

Pro Arg Val Val Glu Asp Val Arg Ala Gln Phe Asn Leu Pro Ser Leu
            260                 265                 270

Asn Pro Gln Phe Asp Gln Trp Leu Tyr Asn Ala Thr Lys Asp Ile Asp
        275                 280                 285

Ala Gly Leu Leu Ile Ser Gly Ala Thr Gly Leu Ala Val Leu Ser Val
    290                 295                 300

Leu Ala Asp Asp Phe Cys Gly Asp Ile Asp Ala Asp Asp Asn Ala Asp
305                 310                 315                 320

Gly Asp Val Ala Ala Glu Lys Pro Thr Gly Ser Ser Gly Leu Gly Ser
                325                 330                 335

Ser Glu Gln Ser Glu Lys Val Asp Gly Asp Asp Asp Ser Val Ile Asp
            340                 345                 350

Thr Glu Thr Asp Ala Asp Leu Glu Val Glu Glu Asp Pro Glu Leu Val
        355                 360                 365

Asn Ala Gly
    370
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09.06.2005 15:55:55

<210> 1685
<211> 2733
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2710)
<223> RXA00274

<400> 1685

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agtttaaaag tcattaatta ctttatggga ataataattt aagttttcat cttttaacta 60

gttacagcat gttattacct tttatgaaag gcgtttcacc ttg tct ctt aat ttg   115
                                            Leu Ser Leu Asn Leu
                                              1               5

aag aag aat tct gcg cgt tct att acc gcg ctg act gtt gct ggt ctg   163
Lys Lys Asn Ser Ala Arg Ser Ile Thr Ala Leu Thr Val Ala Gly Leu
                 10                  15                  20

ggt ctg tct att gtt cct gcg gca tct gca cag gat gtt gcg gat gac   211
Gly Leu Ser Ile Val Pro Ala Ala Ser Ala Gln Asp Val Ala Asp Asp
             25                  30                  35

act acc aac tcc gat tcc acc cgt gat gcc att tgt gct gct gca ccg   259
Thr Thr Asn Ser Asp Ser Thr Arg Asp Ala Ile Cys Ala Ala Ala Pro
         40                  45                  50

ctt gtt gca ggc gca gca gtg ggt gtt ggt ctg ctg tct cag cag cca   307
Leu Val Ala Gly Ala Ala Val Gly Val Gly Leu Leu Ser Gln Gln Pro
     55                  60                  65
```

```
gaa ttc cag cat atg gtg tcc cag att cag tct gac gca cag cgc att   355
Glu Phe Gln His Met Val Ser Gln Ile Gln Ser Asp Ala Gln Arg Ile
 70                  75                  80                  85

ggg cag gat ctc agc aat cag ttc aac aac tct ctt gaa tcg ctc aac   403
Gly Gln Asp Leu Ser Asn Gln Phe Asn Asn Ser Leu Glu Ser Leu Asn
                 90                  95                 100

att ggc ctc ggt aac ggc gtg cac ggc cca cag cag aac gct gtg cag   451
Ile Gly Leu Gly Asn Gly Val His Gly Pro Gln Gln Asn Ala Val Gln
            105                 110                 115

ggt att gat ctc act gaa gca gca cga acc atg gct gga tgg aat gac   499
Gly Ile Asp Leu Thr Glu Ala Ala Arg Thr Met Ala Gly Trp Asn Asp
        120                 125                 130

ctg gcg gca cag gtg ggc cag act gca ggc cct gct atc ggc gct gtt   547
Leu Ala Ala Gln Val Gly Gln Thr Ala Gly Pro Ala Ile Gly Ala Val
    135                 140                 145

gct ggt act gcc ggc ctg atc gca ctg gtt gac tac tgc tgg ctg gaa   595
Ala Gly Thr Ala Gly Leu Ile Ala Leu Val Asp Tyr Cys Trp Leu Glu
150                 155                 160                 165

ggc ttc gac ttc gcg ggt ggc tcc agt ggc act gat ggt gaa aat ggt   643
Gly Phe Asp Phe Ala Gly Gly Ser Ser Gly Thr Asp Gly Glu Asn Gly
                170                 175                 180

gtt gat ggt caa gat ggt acc tcg atc acc att act gag att aag act   691
Val Asp Gly Gln Asp Gly Thr Ser Ile Thr Ile Thr Glu Ile Lys Thr
            185                 190                 195

gat gat gac ggc aat acc att gtt gtc ttt tcc gat ggt tct gaa atc   739
Asp Asp Asp Gly Asn Thr Ile Val Val Phe Ser Asp Gly Ser Glu Ile
        200                 205                 210

acc atc acc aat ggt aaa gac ggc gct gct atc acc att gtt aat act   787
Thr Ile Thr Asn Gly Lys Asp Gly Ala Ala Ile Thr Ile Val Asn Thr
    215                 220                 225

tac cgc gac gat gaa ggt aat act gtt gtt gag ttc tct gac ggt tcc   835
Tyr Arg Asp Asp Glu Gly Asn Thr Val Val Glu Phe Ser Asp Gly Ser
230                 235                 240                 245

acc att gtt atc gac aag ggt gaa gac ggt aaa gat gga gaa gac ggc   883
Thr Ile Val Ile Asp Lys Gly Glu Asp Gly Lys Asp Gly Glu Asp Gly
                250                 255                 260

aag gac ggc gaa gac ggt aag gac ctt acc gta act gat acc tac atc   931
Lys Asp Gly Glu Asp Gly Lys Asp Leu Thr Val Thr Asp Thr Tyr Ile
            265                 270                 275

aac gat gat gga gac acc gtt gtt gag ctt tcc gat ggt tcc acg atc   979
Asn Asp Asp Gly Asp Thr Val Val Glu Leu Ser Asp Gly Ser Thr Ile
        280                 285                 290

att gta aag aag ggt acc gat ggt aag gac ggt gct gac ggc tct gac  1027
Ile Val Lys Lys Gly Thr Asp Gly Lys Asp Gly Ala Asp Gly Ser Asp
    295                 300                 305
```

```
ggt gct gat gga gtc agc atc act gtg gag aac tct tat gtt gat gcg   1075
Gly Ala Asp Gly Val Ser Ile Thr Val Glu Asn Ser Tyr Val Asp Ala
310                 315                 320                 325

gac ggc aac act gtt gtc gaa ttc tcc gat ggc tcc aat gtg acc atc   1123
Asp Gly Asn Thr Val Val Glu Phe Ser Asp Gly Ser Asn Val Thr Ile
                330                 335                 340

aac aag ggt gag aag ggc gac aag ggt gac gct ggc gcc gat ggc gaa   1171
Asn Lys Gly Glu Lys Gly Asp Lys Gly Asp Ala Gly Ala Asp Gly Glu
            345                 350                 355

gac ggc gca gat ggt gaa tca att act gtt gtt aac acc agc aac gat   1219
Asp Gly Ala Asp Gly Glu Ser Ile Thr Val Val Asn Thr Ser Asn Asp
        360                 365                 370

gct gaa ggc aac act ctt gtt gag ctc tcc gat ggc act gtt att acc   1267
Ala Glu Gly Asn Thr Leu Val Glu Leu Ser Asp Gly Thr Val Ile Thr
    375                 380                 385

att aat aag ggt gat aag ggt gac gct ggc gcc gat ggt gaa gat gga   1315
Ile Asn Lys Gly Asp Lys Gly Asp Ala Gly Ala Asp Gly Glu Asp Gly
390                 395                 400                 405

agt aat ggc gca gat ggc gag tcc att acg gtc atc gaa acc cgt ttc   1363
Ser Asn Gly Ala Asp Gly Glu Ser Ile Thr Val Ile Glu Thr Arg Phe
                410                 415                 420

gat gcg gac ggc aac act gtt gtg gtg ttc tcg aac ggc act gaa atc   1411
Asp Ala Asp Gly Asn Thr Val Val Val Phe Ser Asn Gly Thr Glu Ile
            425                 430                 435

acc atc aac aag ggt gag aag ggc gac aag gga gat acc ggc gaa gac   1459
Thr Ile Asn Lys Gly Glu Lys Gly Asp Lys Gly Asp Thr Gly Glu Asp
        440                 445                 450

ggt aag gac gga ctg acc ccg tac atc ggc cca gat ggt aac tgg tgg   1507
Gly Lys Asp Gly Leu Thr Pro Tyr Ile Gly Pro Asp Gly Asn Trp Trp
    455                 460                 465

atc ggt gag aac aac acc tgt act gct gca cgt ggc aat gac ggt aaa   1555
Ile Gly Glu Asn Asn Thr Cys Thr Ala Ala Arg Gly Asn Asp Gly Lys
470                 475                 480                 485

gac ggt gac acc cca cgc atc ggt gat aat ggt aat tgg tgg atc ggc   1603
Asp Gly Asp Thr Pro Arg Ile Gly Asp Asn Gly Asn Trp Trp Ile Gly
                490                 495                 500

atc gtt gat acc ggc gtt cct gct cgt ggt cag gat ggc gcc aac gga   1651
Ile Val Asp Thr Gly Val Pro Ala Arg Gly Gln Asp Gly Ala Asn Gly
            505                 510                 515

gcc gat ggt gct aac acc gtt gag atc att aat ggc tac tgg tac atc   1699
Ala Asp Gly Ala Asn Thr Val Glu Ile Ile Asn Gly Tyr Trp Tyr Ile
        520                 525                 530

aat ggt gaa aat acc ggt gtc aag gca gtt ggt gaa aat ggc acc aac   1747
Asn Gly Glu Asn Thr Gly Val Lys Ala Val Gly Glu Asn Gly Thr Asn
    535                 540                 545

gga gcc gat gga caa gac ggt gaa aat gga acc aac ggt gct aac acc   1795
```

```
Gly Ala Asp Gly Gln Asp Gly Glu Asn Gly Thr Asn Gly Ala Asn Thr
550                 555                 560                 565

gtt gag atc att aat ggc tac tgg tac atc aat ggt gaa aat acc ggt   1843
Val Glu Ile Ile Asn Gly Tyr Trp Tyr Ile Asn Gly Glu Asn Thr Gly
                570                 575                 580

gtc aag gcg cag ggt cca aag ggc gat aag ggt gac act ggt gac acg   1891
Val Lys Ala Gln Gly Pro Lys Gly Asp Lys Gly Asp Thr Gly Asp Thr
            585                 590                 595

ggc gct ccg ggc gag ggt tcc ggt aat gtg gac att gag atc cga gaa   1939
Gly Ala Pro Gly Glu Gly Ser Gly Asn Val Asp Ile Glu Ile Arg Glu
        600                 605                 610

tcg agt tat cca ggt ggt ggc cag gcc acc atc atc att ctt gat caa   1987
Ser Ser Tyr Pro Gly Gly Gly Gln Ala Thr Ile Ile Ile Leu Asp Gln
    615                 620                 625

ttt gaa tat gaa atc ccg cac act gtt att ggt gac aac ggt aac tgg   2035
Phe Glu Tyr Glu Ile Pro His Thr Val Ile Gly Asp Asn Gly Asn Trp
630                 635                 640                 645

tac atc ggt gaa aag gat act ggt atc cca gct cag ggt ggc act gga   2083
Tyr Ile Gly Glu Lys Asp Thr Gly Ile Pro Ala Gln Gly Gly Thr Gly
                650                 655                 660

aca cct ggt gag gat ggc ctc aca cca cac att ggc gac aac ggt aac   2131
Thr Pro Gly Glu Asp Gly Leu Thr Pro His Ile Gly Asp Asn Gly Asn
            665                 670                 675

tgg tgg atc ggt gat acc gat aca ggt gtc tct gca agc ccg acc ccc   2179
Trp Trp Ile Gly Asp Thr Asp Thr Gly Val Ser Ala Ser Pro Thr Pro
        680                 685                 690

gtt ggt gag gcg gta gcg ggt gtc act gat gtg gtc ttc aac act agt   2227
Val Gly Glu Ala Val Ala Gly Val Thr Asp Val Val Phe Asn Thr Ser
    695                 700                 705

gat gaa ccc aag acc att act gca acg atc aat ggt gaa gaa tat gat   2275
Asp Glu Pro Lys Thr Ile Thr Ala Thr Ile Asn Gly Glu Glu Tyr Asp
710                 715                 720                 725

tac acc ctt cca cca cat agt gct gtt gtg ttc tac gct aca ggt tca   2323
Tyr Thr Leu Pro Pro His Ser Ala Val Val Phe Tyr Ala Thr Gly Ser
                730                 735                 740

cca atg gca tat tct cta ccg aat gca tcg ggc ctc act gtt ata ggt   2371
Pro Met Ala Tyr Ser Leu Pro Asn Ala Ser Gly Leu Thr Val Ile Gly
            745                 750                 755

act gaa gag act cct ggt ttc acc act att cga ttc agt gac cat tcc   2419
Thr Glu Glu Thr Pro Gly Phe Thr Thr Ile Arg Phe Ser Asp His Ser
        760                 765                 770

act gtg acc att cca cat gga cga gat ggc acc aac ggt act aac gaa   2467
Thr Val Thr Ile Pro His Gly Arg Asp Gly Thr Asn Gly Thr Asn Glu
    775                 780                 785

ctg acg gta agg atg gtc tca ccc cgc aca tcg gtg aga acg gaa act   2515
Leu Thr Val Arg Met Val Ser Pro Arg Thr Ser Val Arg Thr Glu Thr
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790                 795                 800                 805

ggt gga tcg gcg aaa agg aca ctg gta ttt cga caa cct ttg gcg gtg   2563
Gly Gly Ser Ala Lys Arg Thr Leu Val Phe Arg Gln Pro Leu Ala Val
                 810                 815                 820

gcg gca acc ctg gta ccg gca atg act gca tca cgg tcc cag gtg atg   2611
Ala Ala Thr Leu Val Pro Ala Met Thr Ala Ser Arg Ser Gln Val Met
            825                 830                 835

atc ttg gat tcc cag atg atg ctg agg ccg gtg cag aga ccg gtg cag   2659
Ile Leu Asp Ser Gln Met Met Leu Arg Pro Val Gln Arg Pro Val Gln
        840                 845                 850

atg ccg aag gta cta ttg act aaa ggt cat aga gca acg acc atg act   2707
Met Pro Lys Val Leu Leu Thr Lys Gly His Arg Ala Thr Thr Met Thr
    855                 860                 865

gat taaagtcgga acacaacccc tag                                    2733
Asp
870
```

<210> 1686
<211> 870
<212> PRT
<213> Corynebacterium glutamicum

<400> 1686

```
Leu Ser Leu Asn Leu Lys Lys Asn Ser Ala Arg Ser Ile Thr Ala Leu
  1               5                  10                  15

Thr Val Ala Gly Leu Gly Leu Ser Ile Val Pro Ala Ala Ser Ala Gln
             20                  25                  30

Asp Val Ala Asp Asp Thr Thr Asn Ser Asp Ser Thr Arg Asp Ala Ile
         35                  40                  45

Cys Ala Ala Ala Pro Leu Val Ala Gly Ala Ala Val Gly Val Gly Leu
     50                  55                  60

Leu Ser Gln Gln Pro Glu Phe Gln His Met Val Ser Gln Ile Gln Ser
 65                  70                  75                  80

Asp Ala Gln Arg Ile Gly Gln Asp Leu Ser Asn Gln Phe Asn Asn Ser
                 85                  90                  95

Leu Glu Ser Leu Asn Ile Gly Leu Gly Asn Gly Val His Gly Pro Gln
            100                 105                 110

Gln Asn Ala Val Gln Gly Ile Asp Leu Thr Glu Ala Ala Arg Thr Met
        115                 120                 125

Ala Gly Trp Asn Asp Leu Ala Ala Gln Val Gly Gln Thr Ala Gly Pro
    130                 135                 140

Ala Ile Gly Ala Val Ala Gly Thr Ala Gly Leu Ile Ala Leu Val Asp
145                 150                 155                 160

Tyr Cys Trp Leu Glu Gly Phe Asp Phe Ala Gly Gly Ser Ser Gly Thr
                165                 170                 175
```

```
Asp Gly Glu Asn Gly Val Asp Gly Gln Asp Gly Thr Ser Ile Thr Ile
            180                 185                 190

Thr Glu Ile Lys Thr Asp Asp Asp Gly Asn Thr Ile Val Val Phe Ser
        195                 200                 205

Asp Gly Ser Glu Ile Thr Ile Thr Asn Gly Lys Asp Gly Ala Ala Ile
    210                 215                 220

Thr Ile Val Asn Thr Tyr Arg Asp Asp Glu Gly Asn Thr Val Val Glu
225                 230                 235                 240

Phe Ser Asp Gly Ser Thr Ile Val Ile Asp Lys Gly Glu Asp Gly Lys
                245                 250                 255

Asp Gly Glu Asp Gly Lys Asp Gly Glu Asp Gly Lys Asp Leu Thr Val
            260                 265                 270

Thr Asp Thr Tyr Ile Asn Asp Asp Gly Asp Thr Val Val Glu Leu Ser
        275                 280                 285

Asp Gly Ser Thr Ile Ile Val Lys Lys Gly Thr Asp Gly Lys Asp Gly
    290                 295                 300

Ala Asp Gly Ser Asp Gly Ala Asp Gly Val Ser Ile Thr Val Glu Asn
305                 310                 315                 320

Ser Tyr Val Asp Ala Asp Gly Asn Thr Val Val Glu Phe Ser Asp Gly
                325                 330                 335

Ser Asn Val Thr Ile Asn Lys Gly Glu Lys Gly Asp Lys Gly Asp Ala
            340                 345                 350

Gly Ala Asp Gly Glu Asp Gly Ala Asp Gly Glu Ser Ile Thr Val Val
        355                 360                 365

Asn Thr Ser Asn Asp Ala Glu Gly Asn Thr Leu Val Glu Leu Ser Asp
    370                 375                 380

Gly Thr Val Ile Thr Ile Asn Lys Gly Asp Lys Gly Asp Ala Gly Ala
385                 390                 395                 400

Asp Gly Glu Asp Gly Ser Asn Gly Ala Asp Gly Glu Ser Ile Thr Val
                405                 410                 415

Ile Glu Thr Arg Phe Asp Ala Asp Gly Asn Thr Val Val Val Phe Ser
            420                 425                 430

Asn Gly Thr Glu Ile Thr Ile Asn Lys Gly Glu Lys Gly Asp Lys Gly
        435                 440                 445

Asp Thr Gly Glu Asp Gly Lys Asp Gly Leu Thr Pro Tyr Ile Gly Pro
    450                 455                 460

Asp Gly Asn Trp Trp Ile Gly Glu Asn Asn Thr Cys Thr Ala Ala Arg
465                 470                 475                 480

Gly Asn Asp Gly Lys Asp Gly Asp Thr Pro Arg Ile Gly Asp Asn Gly
                485                 490                 495
```

```
Asn Trp Trp Ile Gly Ile Val Asp Thr Gly Val Pro Ala Arg Gly Gln
            500                 505                 510

Asp Gly Ala Asn Gly Ala Asp Gly Ala Asn Thr Val Glu Ile Ile Asn
        515                 520                 525

Gly Tyr Trp Tyr Ile Asn Gly Glu Asn Thr Gly Val Lys Ala Val Gly
    530                 535                 540

Glu Asn Gly Thr Asn Gly Ala Asp Gly Gln Asp Gly Glu Asn Gly Thr
545                 550                 555                 560

Asn Gly Ala Asn Thr Val Glu Ile Ile Asn Gly Tyr Trp Tyr Ile Asn
                565                 570                 575

Gly Glu Asn Thr Gly Val Lys Ala Gln Gly Pro Lys Gly Asp Lys Gly
            580                 585                 590

Asp Thr Gly Asp Thr Gly Ala Pro Gly Glu Gly Ser Gly Asn Val Asp
        595                 600                 605

Ile Glu Ile Arg Glu Ser Ser Tyr Pro Gly Gly Gly Gln Ala Thr Ile
    610                 615                 620

Ile Ile Leu Asp Gln Phe Glu Tyr Glu Ile Pro His Thr Val Ile Gly
625                 630                 635                 640

Asp Asn Gly Asn Trp Tyr Ile Gly Glu Lys Asp Thr Gly Ile Pro Ala
                645                 650                 655

Gln Gly Gly Thr Gly Thr Pro Gly Glu Asp Gly Leu Thr Pro His Ile
            660                 665                 670

Gly Asp Asn Gly Asn Trp Trp Ile Gly Asp Thr Asp Thr Gly Val Ser
        675                 680                 685

Ala Ser Pro Thr Pro Val Gly Glu Ala Val Ala Gly Val Thr Asp Val
    690                 695                 700

Val Phe Asn Thr Ser Asp Glu Pro Lys Thr Ile Thr Ala Thr Ile Asn
705                 710                 715                 720

Gly Glu Glu Tyr Asp Tyr Thr Leu Pro Pro His Ser Ala Val Val Phe
                725                 730                 735

Tyr Ala Thr Gly Ser Pro Met Ala Tyr Ser Leu Pro Asn Ala Ser Gly
            740                 745                 750

Leu Thr Val Ile Gly Thr Glu Glu Thr Pro Gly Phe Thr Thr Ile Arg
        755                 760                 765

Phe Ser Asp His Ser Thr Val Thr Ile Pro His Gly Arg Asp Gly Thr
    770                 775                 780

Asn Gly Thr Asn Glu Leu Thr Val Arg Met Val Ser Pro Arg Thr Ser
785                 790                 795                 800

Val Arg Thr Glu Thr Gly Gly Ser Ala Lys Arg Thr Leu Val Phe Arg
                805                 810                 815

Gln Pro Leu Ala Val Ala Ala Thr Leu Val Pro Ala Met Thr Ala Ser
```

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            820                 825                 830

Arg Ser Gln Val Met Ile Leu Asp Ser Gln Met Met Leu Arg Pro Val
        835                 840                 845

Gln Arg Pro Val Gln Met Pro Lys Val Leu Leu Thr Lys Gly His Arg
    850                 855                 860

Ala Thr Thr Met Thr Asp
865                 870


<210> 1687
<211> 582
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(559)
<223> RXA00275

<400> 1687
ctgacgcaga cgttgcacag ctcgcaaccg ctattgacga acagaaccgc cccacaaaga 60

gctgttccct acggcagatc gcaaggaact attcgcctgg ttg gat aag cgt cgc   115
                                              Leu Asp Lys Arg Arg
                                                1               5

cca gaa tta agc gac gat ttc atc aaa gct ttt gat gat ttc ctt cat   163
Pro Glu Leu Ser Asp Asp Phe Ile Lys Ala Phe Asp Asp Phe Leu His
                10                  15                  20

tct ttt gcg tgc ctg gac aaa aca acg atc acc cta ttg gcg caa tca   211
Ser Phe Ala Cys Leu Asp Lys Thr Thr Ile Thr Leu Leu Ala Gln Ser
            25                  30                  35

ccg gtg cgc aca tcc act ggc tat aca ggt act ttt atc ggc atc ccc   259
Pro Val Arg Thr Ser Thr Gly Tyr Thr Gly Thr Phe Ile Gly Ile Pro
        40                  45                  50

aat aat gaa cca ctg tcc gaa gag ccc acc ccc acc att tac att gtg   307
Asn Asn Glu Pro Leu Ser Glu Glu Pro Thr Pro Thr Ile Tyr Ile Val
    55                  60                  65

cac gat aat cac aca ggg ata atc cac agt tac ccc gca cga atg att   355
His Asp Asn His Thr Gly Ile Ile His Ser Tyr Pro Ala Arg Met Ile
70                  75                  80                  85

aat ctt aaa tct gag ctc ggt tcc gct gag atg att cac gag gca atc   403
Asn Leu Lys Ser Glu Leu Gly Ser Ala Glu Met Ile His Glu Ala Ile
                90                  95                  100

tgg ggg tca ccc cat caa cag cag tta atc tca tgg tat gag act tac   451
Trp Gly Ser Pro His Gln Gln Gln Leu Ile Ser Trp Tyr Glu Thr Tyr
            105                 110                 115

tac acc aac atc tac tat ggt ttt aac cca ccc act gaa cca cat aag   499
Tyr Thr Asn Ile Tyr Tyr Gly Phe Asn Pro Pro Thr Glu Pro His Lys
        120                 125                 130
```

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agt ctt gag att ttt gct caa gac ttc tgt ctg acc cca cca gag aaa   547
Ser Leu Glu Ile Phe Ala Gln Asp Phe Cys Leu Thr Pro Pro Glu Lys
    135                 140                 145

cct cct ttt ttc taaggcaagg cccgtggcac aca                         582
Pro Pro Phe Phe
150


<210> 1688
<211> 153
<212> PRT
<213> Corynebacterium glutamicum

<400> 1688
Leu Asp Lys Arg Arg Pro Glu Leu Ser Asp Asp Phe Ile Lys Ala Phe
  1               5                  10                  15

Asp Asp Phe Leu His Ser Phe Ala Cys Leu Asp Lys Thr Thr Ile Thr
             20                  25                  30

Leu Leu Ala Gln Ser Pro Val Arg Thr Ser Thr Gly Tyr Thr Gly Thr
         35                  40                  45

Phe Ile Gly Ile Pro Asn Asn Glu Pro Leu Ser Glu Glu Pro Thr Pro
     50                  55                  60

Thr Ile Tyr Ile Val His Asp Asn His Thr Gly Ile Ile His Ser Tyr
 65                  70                  75                  80

Pro Ala Arg Met Ile Asn Leu Lys Ser Glu Leu Gly Ser Ala Glu Met
                 85                  90                  95

Ile His Glu Ala Ile Trp Gly Ser Pro His Gln Gln Gln Leu Ile Ser
            100                 105                 110

Trp Tyr Glu Thr Tyr Tyr Thr Asn Ile Tyr Tyr Gly Phe Asn Pro Pro
        115                 120                 125

Thr Glu Pro His Lys Ser Leu Glu Ile Phe Ala Gln Asp Phe Cys Leu
    130                 135                 140

Thr Pro Pro Glu Lys Pro Pro Phe Phe
145                 150


<210> 1689
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXA00276

<400> 1689
ggcacactac cctatgacta caccgcaacc cagcaaacct gcgccatggt cgcttgccta 60

taagtatcaa gccatcagca atgatgattt tgacaaccat atg gat gac ctc agc   115
                                            Met Asp Asp Leu Ser
```

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                                                    1               5

agt cgc caa gac cat gaa gcc tac ggc acg tac aac ccc gat aac ggt   163
Ser Arg Gln Asp His Glu Ala Tyr Gly Thr Tyr Asn Pro Asp Asn Gly
                 10                  15                  20

gtc atg ccc gat cat gtc atc gtg cct tca ccc tat gaa cca tat gat   211
Val Met Pro Asp His Val Ile Val Pro Ser Pro Tyr Glu Pro Tyr Asp
             25                  30                  35

gat gct gcg ccg att gat cct ttc gac tac gac gaa gat ctt ctc gat   259
Asp Ala Ala Pro Ile Asp Pro Phe Asp Tyr Asp Glu Asp Leu Leu Asp
         40                  45                  50

gag att aaa gaa gag cgc gct gca cat gcg gtt gac gca caa gta aca   307
Glu Ile Lys Glu Glu Arg Ala Ala His Ala Val Asp Ala Gln Val Thr
     55                  60                  65

gaa aca act aaa gct gac gca gac gtt gca cag ctc gca acc gct att   355
Glu Thr Thr Lys Ala Asp Ala Asp Val Ala Gln Leu Ala Thr Ala Ile
 70                  75                  80                  85

gac gaa cag aac cgc ccc aca aag agc tgt tcc cta cgg cag atc gca   403
Asp Glu Gln Asn Arg Pro Thr Lys Ser Cys Ser Leu Arg Gln Ile Ala
                 90                  95                 100

agg aac tat tcg cct ggt tgg ata agc gtc gcc cag aat taagcgacga    452
Arg Asn Tyr Ser Pro Gly Trp Ile Ser Val Ala Gln Asn
            105                 110

tttcatcaaa gct                                                   465


<210> 1690
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 1690
Met Asp Asp Leu Ser Ser Arg Gln Asp His Glu Ala Tyr Gly Thr Tyr
  1               5                  10                  15

Asn Pro Asp Asn Gly Val Met Pro Asp His Val Ile Val Pro Ser Pro
             20                  25                  30

Tyr Glu Pro Tyr Asp Asp Ala Ala Pro Ile Asp Pro Phe Asp Tyr Asp
         35                  40                  45

Glu Asp Leu Leu Asp Glu Ile Lys Glu Glu Arg Ala Ala His Ala Val
     50                  55                  60

Asp Ala Gln Val Thr Glu Thr Thr Lys Ala Asp Ala Asp Val Ala Gln
 65                  70                  75                  80

Leu Ala Thr Ala Ile Asp Glu Gln Asn Arg Pro Thr Lys Ser Cys Ser
                 85                  90                  95

Leu Arg Gln Ile Ala Arg Asn Tyr Ser Pro Gly Trp Ile Ser Val Ala
            100                 105                 110

Gln Asn
```

<210> 1691
<211> 1509
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1486)
<223> RXA00279

<400> 1691
tggggagcat tcagaggtgc ctaatcctct ggatgattct gcggtgcaaa attcagcccc 60

```
acattcagcc ccacattcag ctcggacccg gttggagttt ttg gat acc gat gac   115
                                            Leu Asp Thr Asp Asp
                                              1               5

tcg cct gat cat tgg ctt gat ccg tta acg gag aag gat act tct aag   163
Ser Pro Asp His Trp Leu Asp Pro Leu Thr Glu Lys Asp Thr Ser Lys
                  10                  15                  20

cgc act ctc gtt aat tcg att gtt cag gaa act ttc ggc cag cct att   211
Arg Thr Leu Val Asn Ser Ile Val Gln Glu Thr Phe Gly Gln Pro Ile
             25                  30                  35

ttt gtt gcc cgc aag att tgg gct ttc gtc aat acg tcg ccg ggc cgg   259
Phe Val Ala Arg Lys Ile Trp Ala Phe Val Asn Thr Ser Pro Gly Arg
         40                  45                  50

atg acg ttg atg acg att atc att tcg atc gcc att ttt gct gct ggt   307
Met Thr Leu Met Thr Ile Ile Ile Ser Ile Ala Ile Phe Ala Ala Gly
     55                  60                  65

tac gcc atg tcg gtg tct tcg gat act agg cag tcc aat ttg gat gat   355
Tyr Ala Met Ser Val Ser Ser Asp Thr Arg Gln Ser Asn Leu Asp Asp
 70                  75                  80                  85

ttg atc act aat gcg gag cct gtt tcc tat aac gcg cat gtg ctg tat   403
Leu Ile Thr Asn Ala Glu Pro Val Ser Tyr Asn Ala His Val Leu Tyr
                 90                  95                 100

aca tca ttg tcg gtt gct gat acc act gct acc act ggt ttt gtt cag   451
Thr Ser Leu Ser Val Ala Asp Thr Thr Ala Thr Thr Gly Phe Val Gln
            105                 110                 115

gct ggt gtg gag ggc ccg gtg aat cgg gtg aag tat cac act gct att   499
Ala Gly Val Glu Gly Pro Val Asn Arg Val Lys Tyr His Thr Ala Ile
        120                 125                 130

gat cgt gct gcg gtt gct gct act cat act gcg gcg tct gcg gat agt   547
Asp Arg Ala Ala Val Ala Ala Thr His Thr Ala Ala Ser Ala Asp Ser
    135                 140                 145

agt aat gag cat ttg atg gag ttg gtg ctg gag att cag cgt cag ttg   595
Ser Asn Glu His Leu Met Glu Leu Val Leu Glu Ile Gln Arg Gln Leu
150                 155                 160                 165

ccg gtg tat acg ggg ttg gtg gaa act gct cgg act aat aac cgt gcg   643
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```
Pro Val Tyr Thr Gly Leu Val Glu Thr Ala Arg Thr Asn Asn Arg Ala
                170                 175                 180

ggt aat ccc gtg ggt gtg gcc tat atg tct gag gcc agc gcg atg atg   691
Gly Asn Pro Val Gly Val Ala Tyr Met Ser Glu Ala Ser Ala Met Met
            185                 190                 195

cgt aat gaa att ttg ccg atg gcg tct gag ctt tac aac ctg acg agt   739
Arg Asn Glu Ile Leu Pro Met Ala Ser Glu Leu Tyr Asn Leu Thr Ser
        200                 205                 210

cgt gcg gtg tct gat cag cag cgt tcg gtg acg ggt ccg cag tgg ttt   787
Arg Ala Val Ser Asp Gln Gln Arg Ser Val Thr Gly Pro Gln Trp Phe
    215                 220                 225

ccg ctg tct gga ttg ctt gcg gct ctt gcc atg ttg att gtt gcg cag   835
Pro Leu Ser Gly Leu Leu Ala Ala Leu Ala Met Leu Ile Val Ala Gln
230                 235                 240                 245

tgg tgg ttg atg cgg att acg cgc agg cgc atc aac aag ggg ttt gcc   883
Trp Trp Leu Met Arg Ile Thr Arg Arg Arg Ile Asn Lys Gly Phe Ala
                250                 255                 260

ctg gcc acg gtg atg atg atg acg gca acg tta tgg gtg tca gct gca   931
Leu Ala Thr Val Met Met Met Thr Ala Thr Leu Trp Val Ser Ala Ala
            265                 270                 275

aac tgg gcg acg tgg cag gct ggc acg aag ggt ttt gag gaa gcg tcg   979
Asn Trp Ala Thr Trp Gln Ala Gly Thr Lys Gly Phe Glu Glu Ala Ser
        280                 285                 290

ggg ccg ttg aat tcc atg act acg gct cgt att tat gcg cag cag acc   1027
Gly Pro Leu Asn Ser Met Thr Thr Ala Arg Ile Tyr Ala Gln Gln Thr
    295                 300                 305

cgc acg acg gag acg ttg tcg ttg gtg cgt agg cag tcg att cag ggc   1075
Arg Thr Thr Glu Thr Leu Ser Leu Val Arg Arg Gln Ser Ile Gln Gly
310                 315                 320                 325

agt ggc act ggt ttt acc gca acg att aat cag att aag cgt gcg ctg   1123
Ser Gly Thr Gly Phe Thr Ala Thr Ile Asn Gln Ile Lys Arg Ala Leu
                330                 335                 340

gat gag tat gaa acc act gcg cag tca cag act ccg gag cat cag cag   1171
Asp Glu Tyr Glu Thr Thr Ala Gln Ser Gln Thr Pro Glu His Gln Gln
            345                 350                 355

ttg att acg gcg att cgt aat gcg att gct gca tgg act gcc gat cac   1219
Leu Ile Thr Ala Ile Arg Asn Ala Ile Ala Ala Trp Thr Ala Asp His
        360                 365                 370

gat gag ttc acg gtg ttg ttg gcg tct ggt gat tac aac ggt gcg gtc   1267
Asp Glu Phe Thr Val Leu Leu Ala Ser Gly Asp Tyr Asn Gly Ala Val
    375                 380                 385

aat gcg gtg ctc aac aaa gat gag gag ggc cag acc agc ttt gat gag   1315
Asn Ala Val Leu Asn Lys Asp Glu Glu Gly Gln Thr Ser Phe Asp Glu
390                 395                 400                 405

ctc gat act gcg ctg gct gag ctg atc gcg gat tct cgc agc tcc atg   1363
Leu Asp Thr Ala Leu Ala Glu Leu Ile Ala Asp Ser Arg Ser Ser Met
```

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                410                 415                 420

cgt tcc tat atc cag tcg ggc ctg cag gcc acg gag ttg gtg tcc gtc   1411
Arg Ser Tyr Ile Gln Ser Gly Leu Gln Ala Thr Glu Leu Val Ser Val
            425                 430                 435

atg gtg atg att ctg tct gtc gtt tct gtg ttg gct ttg tgg gtc ggc   1459
Met Val Met Ile Leu Ser Val Val Ser Val Leu Ala Leu Trp Val Gly
        440                 445                 450

atc cgc ccc cgt ttg cag gag tac tta taaatgcacg cttttcgacg         1506
Ile Arg Pro Arg Leu Gln Glu Tyr Leu
    455                 460

ccc                                                               1509


<210> 1692
<211> 462
<212> PRT
<213> Corynebacterium glutamicum

<400> 1692
Leu Asp Thr Asp Asp Ser Pro Asp His Trp Leu Asp Pro Leu Thr Glu
  1               5                  10                  15

Lys Asp Thr Ser Lys Arg Thr Leu Val Asn Ser Ile Val Gln Glu Thr
             20                  25                  30

Phe Gly Gln Pro Ile Phe Val Ala Arg Lys Ile Trp Ala Phe Val Asn
         35                  40                  45

Thr Ser Pro Gly Arg Met Thr Leu Met Thr Ile Ile Ile Ser Ile Ala
     50                  55                  60

Ile Phe Ala Ala Gly Tyr Ala Met Ser Val Ser Ser Asp Thr Arg Gln
 65                  70                  75                  80

Ser Asn Leu Asp Asp Leu Ile Thr Asn Ala Glu Pro Val Ser Tyr Asn
                 85                  90                  95

Ala His Val Leu Tyr Thr Ser Leu Ser Val Ala Asp Thr Thr Ala Thr
            100                 105                 110

Thr Gly Phe Val Gln Ala Gly Val Glu Gly Pro Val Asn Arg Val Lys
        115                 120                 125

Tyr His Thr Ala Ile Asp Arg Ala Ala Val Ala Ala Thr His Thr Ala
    130                 135                 140

Ala Ser Ala Asp Ser Ser Asn Glu His Leu Met Glu Leu Val Leu Glu
145                 150                 155                 160

Ile Gln Arg Gln Leu Pro Val Tyr Thr Gly Leu Val Glu Thr Ala Arg
                165                 170                 175

Thr Asn Asn Arg Ala Gly Asn Pro Val Gly Val Ala Tyr Met Ser Glu
            180                 185                 190

Ala Ser Ala Met Met Arg Asn Glu Ile Leu Pro Met Ala Ser Glu Leu
        195                 200                 205
```

```
Tyr Asn Leu Thr Ser Arg Ala Val Ser Asp Gln Gln Arg Ser Val Thr
    210                 215                 220

Gly Pro Gln Trp Phe Pro Leu Ser Gly Leu Leu Ala Ala Leu Ala Met
225                 230                 235                 240

Leu Ile Val Ala Gln Trp Trp Leu Met Arg Ile Thr Arg Arg Arg Ile
                245                 250                 255

Asn Lys Gly Phe Ala Leu Ala Thr Val Met Met Met Thr Ala Thr Leu
            260                 265                 270

Trp Val Ser Ala Ala Asn Trp Ala Thr Trp Gln Ala Gly Thr Lys Gly
        275                 280                 285

Phe Glu Glu Ala Ser Gly Pro Leu Asn Ser Met Thr Thr Ala Arg Ile
    290                 295                 300

Tyr Ala Gln Gln Thr Arg Thr Thr Glu Thr Leu Ser Leu Val Arg Arg
305                 310                 315                 320

Gln Ser Ile Gln Gly Ser Gly Thr Gly Phe Thr Ala Thr Ile Asn Gln
                325                 330                 335

Ile Lys Arg Ala Leu Asp Glu Tyr Glu Thr Thr Ala Gln Ser Gln Thr
            340                 345                 350

Pro Glu His Gln Gln Leu Ile Thr Ala Ile Arg Asn Ala Ile Ala Ala
        355                 360                 365

Trp Thr Ala Asp His Asp Glu Phe Thr Val Leu Leu Ala Ser Gly Asp
    370                 375                 380

Tyr Asn Gly Ala Val Asn Ala Val Leu Asn Lys Asp Glu Glu Gly Gln
385                 390                 395                 400

Thr Ser Phe Asp Glu Leu Asp Thr Ala Leu Ala Glu Leu Ile Ala Asp
                405                 410                 415

Ser Arg Ser Ser Met Arg Ser Tyr Ile Gln Ser Gly Leu Gln Ala Thr
            420                 425                 430

Glu Leu Val Ser Val Met Val Met Ile Leu Ser Val Val Ser Val Leu
        435                 440                 445

Ala Leu Trp Val Gly Ile Arg Pro Arg Leu Gln Glu Tyr Leu
    450                 455                 460
```

<210> 1693
<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(789)
<223> RXA00282

<400> 1693

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atg agc cgc gac gac cag acg aac aac aac ggt gag ggc gac gac aca   48
Met Ser Arg Asp Asp Gln Thr Asn Asn Asn Gly Glu Gly Asp Asp Thr
  1               5                  10                  15

tcg cgc gag cag tcc tgg gat caa tcc tgg cag aac cta aat aag gat   96
Ser Arg Glu Gln Ser Trp Asp Gln Ser Trp Gln Asn Leu Asn Lys Asp
             20                  25                  30

tcc cag tac ggt ccg acc tcg cat ccg gag gac gcg ccg gga gga ttc  144
Ser Gln Tyr Gly Pro Thr Ser His Pro Glu Asp Ala Pro Gly Gly Phe
         35                  40                  45

cag gga aac ggc cag ggt aac agc cgg ggc aac gct cag ggc aat ggt  192
Gln Gly Asn Gly Gln Gly Asn Ser Arg Gly Asn Ala Gln Gly Asn Gly
     50                  55                  60

cag ggc aat ggt cag ggc ttt ggc ccg ggt aat gct tcg gga tat gga  240
Gln Gly Asn Gly Gln Gly Phe Gly Pro Gly Asn Ala Ser Gly Tyr Gly
 65                  70                  75                  80

ggc tac ggt cag cca tac ccg cag act ccg tac cag aat tcc tac caa  288
Gly Tyr Gly Gln Pro Tyr Pro Gln Thr Pro Tyr Gln Asn Ser Tyr Gln
                 85                  90                  95

ggt tat ggc gct act tca ccg cag aac gac gtg gcg ctg gaa gcg agc  336
Gly Tyr Gly Ala Thr Ser Pro Gln Asn Asp Val Ala Leu Glu Ala Ser
            100                 105                 110

aac ggc aaa gtc gac atc atg cgg gcg att cgc ttc gga ttc aaa gcc  384
Asn Gly Lys Val Asp Ile Met Arg Ala Ile Arg Phe Gly Phe Lys Ala
        115                 120                 125

acg ttt gcc aat cca gca gtg tgg att ttg ggc acc gtc ggt ctt ggc  432
Thr Phe Ala Asn Pro Ala Val Trp Ile Leu Gly Thr Val Gly Leu Gly
    130                 135                 140

ctt gcg ttc atg att gtg agt ggg ttg ctt ggc tac tta tca ttt ttg  480
Leu Ala Phe Met Ile Val Ser Gly Leu Leu Gly Tyr Leu Ser Phe Leu
145                 150                 155                 160

atc gac cct aat gcg ggc acg acg act tct ggt ttt tcg gtt tcc gag  528
Ile Asp Pro Asn Ala Gly Thr Thr Thr Ser Gly Phe Ser Val Ser Glu
                165                 170                 175

acc ctg ttg aac gta gct atc gga atc atc acc ttc gca ata acc att  576
Thr Leu Leu Asn Val Ala Ile Gly Ile Ile Thr Phe Ala Ile Thr Ile
            180                 185                 190

tgc gtc atg cgc ggt gca ctg ctt tct gtt gat gga cac aaa gtt cgc  624
Cys Val Met Arg Gly Ala Leu Leu Ser Val Asp Gly His Lys Val Arg
        195                 200                 205

ttc ggt gat ttc ttt aaa ccc atc aat gtt ggt caa aca gtg att ctg  672
Phe Gly Asp Phe Phe Lys Pro Ile Asn Val Gly Gln Thr Val Ile Leu
    210                 215                 220

atg gtg ggg ctg ggt atc ttc ggc atc atc ctg ggc acc ttc acc act  720
Met Val Gly Leu Gly Ile Phe Gly Ile Ile Leu Gly Thr Phe Thr Thr
225                 230                 235                 240

ttt ctc act caa aat ctg gtg tcg ttt aat gac gct gcc ggt acc gtt  768
```

```
Phe Leu Thr Gln Asn Leu Val Ser Phe Asn Asp Ala Ala Gly Thr Val
                245                 250                 255

gag gtc aat aac agc ggt tta                                     789
Glu Val Asn Asn Ser Gly Leu
            260
```

<210> 1694
<211> 263
<212> PRT
<213> Corynebacterium glutamicum

<400> 1694

```
Met Ser Arg Asp Asp Gln Thr Asn Asn Asn Gly Glu Gly Asp Asp Thr
  1               5                  10                  15

Ser Arg Glu Gln Ser Trp Asp Gln Ser Trp Gln Asn Leu Asn Lys Asp
             20                  25                  30

Ser Gln Tyr Gly Pro Thr Ser His Pro Glu Asp Ala Pro Gly Gly Phe
         35                  40                  45

Gln Gly Asn Gly Gln Gly Asn Ser Arg Gly Asn Ala Gln Gly Asn Gly
     50                  55                  60

Gln Gly Asn Gly Gln Gly Phe Gly Pro Gly Asn Ala Ser Gly Tyr Gly
 65                  70                  75                  80

Gly Tyr Gly Gln Pro Tyr Pro Gln Thr Pro Tyr Gln Asn Ser Tyr Gln
                85                  90                  95

Gly Tyr Gly Ala Thr Ser Pro Gln Asn Asp Val Ala Leu Glu Ala Ser
            100                 105                 110

Asn Gly Lys Val Asp Ile Met Arg Ala Ile Arg Phe Gly Phe Lys Ala
        115                 120                 125

Thr Phe Ala Asn Pro Ala Val Trp Ile Leu Gly Thr Val Gly Leu Gly
    130                 135                 140

Leu Ala Phe Met Ile Val Ser Gly Leu Leu Gly Tyr Leu Ser Phe Leu
145                 150                 155                 160

Ile Asp Pro Asn Ala Gly Thr Thr Thr Ser Gly Phe Ser Val Ser Glu
                165                 170                 175

Thr Leu Leu Asn Val Ala Ile Gly Ile Ile Thr Phe Ala Ile Thr Ile
            180                 185                 190

Cys Val Met Arg Gly Ala Leu Leu Ser Val Asp Gly His Lys Val Arg
        195                 200                 205

Phe Gly Asp Phe Phe Lys Pro Ile Asn Val Gly Gln Thr Val Ile Leu
    210                 215                 220

Met Val Gly Leu Gly Ile Phe Gly Ile Ile Leu Gly Thr Phe Thr Thr
225                 230                 235                 240

Phe Leu Thr Gln Asn Leu Val Ser Phe Asn Asp Ala Ala Gly Thr Val
                245                 250                 255
```

```
Glu Val Asn Asn Ser Gly Leu
            260


<210> 1695
<211> 536
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(513)
<223> RXA00285

<400> 1695
gga act gaa ttg ggc gca ttg tta ctg cgt gtc ctc aac agg gaa gaa   48
Gly Thr Glu Leu Gly Ala Leu Leu Leu Arg Val Leu Asn Arg Glu Glu
  1               5                  10                  15

atg atg gac aga ttc gca cgg gag ctg ggt ttt ttc gtc gac aag cag   96
Met Met Asp Arg Phe Ala Arg Glu Leu Gly Phe Phe Val Asp Lys Gln
             20                  25                  30

ctt gaa gag gtc gag cgc atc aac tgt cac cat aac tac acg gtc cag   144
Leu Glu Glu Val Glu Arg Ile Asn Cys His His Asn Tyr Thr Val Gln
         35                  40                  45

gag gag cac tac ggc gag acc att tgg ctc acc cgt aag ggt gcc gtg   192
Glu Glu His Tyr Gly Glu Thr Ile Trp Leu Thr Arg Lys Gly Ala Val
     50                  55                  60

ttg gcg gac gaa ggc acg ccg gcg ttg att ccg ggg tcg atg ggc acc   240
Leu Ala Asp Glu Gly Thr Pro Ala Leu Ile Pro Gly Ser Met Gly Thr
 65                  70                  75                  80

gcg tcg tac gtg ggc agt ggc aag ggc aac gcc gag gca ctg cgg tcg   288
Ala Ser Tyr Val Gly Ser Gly Lys Gly Asn Ala Glu Ala Leu Arg Ser
                 85                  90                  95

gcg ccg cat ggg gcg ggc cgg agg atg tac cgc aac cag gct aaa aag   336
Ala Pro His Gly Ala Gly Arg Arg Met Tyr Arg Asn Gln Ala Lys Lys
            100                 105                 110

cgc ttc tcg acg gcc gac ctg gat tct cgg atg gcg ggc atc gtc tac   384
Arg Phe Ser Thr Ala Asp Leu Asp Ser Arg Met Ala Gly Ile Val Tyr
        115                 120                 125

cgg ccc ggc aag gag tgg atc gat gaa att ccc gac gct tac aaa gac   432
Arg Pro Gly Lys Glu Trp Ile Asp Glu Ile Pro Asp Ala Tyr Lys Asp
    130                 135                 140

atc gat cag gtg atg gcc gat gct gcc gat ttg gtg aca att cgc cat   480
Ile Asp Gln Val Met Ala Asp Ala Ala Asp Leu Val Thr Ile Arg His
145                 150                 155                 160

aaa ttg cgc cag atc gtc aac gtg aaa ggc acc taaagcgcat tacggtaaag 533
Lys Leu Arg Gln Ile Val Asn Val Lys Gly Thr
                165                 170

tgc                                                               536
```

<210> 1696
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 1696
Gly Thr Glu Leu Gly Ala Leu Leu Leu Arg Val Leu Asn Arg Glu Glu
1 5 10 15

Met Met Asp Arg Phe Ala Arg Glu Leu Gly Phe Phe Val Asp Lys Gln
20 25 30

Leu Glu Glu Val Glu Arg Ile Asn Cys His His Asn Tyr Thr Val Gln
35 40 45

Glu Glu His Tyr Gly Glu Thr Ile Trp Leu Thr Arg Lys Gly Ala Val
50 55 60

Leu Ala Asp Glu Gly Thr Pro Ala Leu Ile Pro Gly Ser Met Gly Thr
65 70 75 80

Ala Ser Tyr Val Gly Ser Gly Lys Gly Asn Ala Glu Ala Leu Arg Ser
85 90 95

Ala Pro His Gly Ala Gly Arg Arg Met Tyr Arg Asn Gln Ala Lys Lys
100 105 110

Arg Phe Ser Thr Ala Asp Leu Asp Ser Arg Met Ala Gly Ile Val Tyr
115 120 125

Arg Pro Gly Lys Glu Trp Ile Asp Glu Ile Pro Asp Ala Tyr Lys Asp
130 135 140

Ile Asp Gln Val Met Ala Asp Ala Ala Asp Leu Val Thr Ile Arg His
145 150 155 160

Lys Leu Arg Gln Ile Val Asn Val Lys Gly Thr
165 170

<210> 1697
<211> 687
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(664)
<223> RXA00286

<400> 1697
ccataaattg cgccagatcg tcaacgtgaa aggcacctaa agcgcattac ggtaaagtgc 60

gagaggtatt ttgacgggtt tagattgagg gatgtggata gtg ctg aaa atc cca 115
Val Leu Lys Ile Pro
1 5

cgg ctg ctt cta cgc cgt gtg ctt ccg gta ctc atc acc ttg gcg ctc 163
Arg Leu Leu Leu Arg Arg Val Leu Pro Val Leu Ile Thr Leu Ala Leu

```
                10                  15                  20

ctg tgc gga ctg gtg ctt gcg tgg ttt atc tat cct gcg aag gct gag   211
Leu Cys Gly Leu Val Leu Ala Trp Phe Ile Tyr Pro Ala Lys Ala Glu
            25                  30                  35

ccc aaa aaa gat gat gta gtt ctg gtg ctg gcc ggt tcc agc gat ggt   259
Pro Lys Lys Asp Asp Val Val Leu Val Leu Ala Gly Ser Ser Asp Gly
        40                  45                  50

cga cac gaa tat ggt gcc gag ctt gtt gaa gaa ggc tac gcc agc aat   307
Arg His Glu Tyr Gly Ala Glu Leu Val Glu Glu Gly Tyr Ala Ser Asn
    55                  60                  65

tac gtc gtc tcc aac ccg agt ggc tcc aaa gac aaa gtg gga tat gcc   355
Tyr Val Val Ser Asn Pro Ser Gly Ser Lys Asp Lys Val Gly Tyr Ala
70                  75                  80                  85

cac tgc gca gga aag tca cgg cca aaa aat gcg gaa agt ttc tgc atg   403
His Cys Ala Gly Lys Ser Arg Pro Lys Asn Ala Glu Ser Phe Cys Met
                90                  95                  100

gat cct tac ccc gtg atc acc tcc ggc gaa gcc cgc acg ttt aac gag   451
Asp Pro Tyr Pro Val Ile Thr Ser Gly Glu Ala Arg Thr Phe Asn Glu
            105                 110                 115

ctt gcc aaa aag gaa ggc tgg gaa agc gta ttg gta gtg acc agc cgc   499
Leu Ala Lys Lys Glu Gly Trp Glu Ser Val Leu Val Val Thr Ser Arg
        120                 125                 130

acg cac acc caa cgc gtt cgc acc atg ttt gac cag tgc tat acc ggt   547
Thr His Thr Gln Arg Val Arg Thr Met Phe Asp Gln Cys Tyr Thr Gly
    135                 140                 145

gat tcc aca gtg ctc aac gtc aac agc cta gga cgt acc ggg ctt cac   595
Asp Ser Thr Val Leu Asn Val Asn Ser Leu Gly Arg Thr Gly Leu His
150                 155                 160                 165

aat gca gta ctc cac gag att ggc ggc ttc att aaa ttt tgg att acc   643
Asn Ala Val Leu His Glu Ile Gly Gly Phe Ile Lys Phe Trp Ile Thr
                170                 175                 180

gct ccg tgc gcg gac aca aac taaggacgtt ccagctccaa cag            687
Ala Pro Cys Ala Asp Thr Asn
            185
```

<210> 1698
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 1698

```
Val Leu Lys Ile Pro Arg Leu Leu Leu Arg Arg Val Leu Pro Val Leu
  1               5                  10                  15

Ile Thr Leu Ala Leu Leu Cys Gly Leu Val Leu Ala Trp Phe Ile Tyr
            20                  25                  30

Pro Ala Lys Ala Glu Pro Lys Lys Asp Asp Val Val Leu Val Leu Ala
        35                  40                  45
```

```
Gly Ser Ser Asp Gly Arg His Glu Tyr Gly Ala Glu Leu Val Glu Glu
     50                  55                  60

Gly Tyr Ala Ser Asn Tyr Val Val Ser Asn Pro Ser Gly Ser Lys Asp
 65                  70                  75                  80

Lys Val Gly Tyr Ala His Cys Ala Gly Lys Ser Arg Pro Lys Asn Ala
                 85                  90                  95

Glu Ser Phe Cys Met Asp Pro Tyr Pro Val Ile Thr Ser Gly Glu Ala
            100                 105                 110

Arg Thr Phe Asn Glu Leu Ala Lys Lys Glu Gly Trp Glu Ser Val Leu
        115                 120                 125

Val Val Thr Ser Arg Thr His Thr Gln Arg Val Arg Thr Met Phe Asp
    130                 135                 140

Gln Cys Tyr Thr Gly Asp Ser Thr Val Leu Asn Val Asn Ser Leu Gly
145                 150                 155                 160

Arg Thr Gly Leu His Asn Ala Val Leu His Glu Ile Gly Gly Phe Ile
                165                 170                 175

Lys Phe Trp Ile Thr Ala Pro Cys Ala Asp Thr Asn
            180                 185
```

<210> 1699
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> RXA00294

<400> 1699

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ttgttggtgt gaggttgggt tttgtcatcc tgaatgcttc atttctaccc tcgtgggtaa 60

agttggtgcc gaatcaacaa tctcttttgg aggaacttta atg agc att tcc aac   115
                                              Met Ser Ile Ser Asn
                                                1               5

gca atc ctg cgt ggt gtg tct ggc gct tat att ctg cag tcc ggc tac   163
Ala Ile Leu Arg Gly Val Ser Gly Ala Tyr Ile Leu Gln Ser Gly Tyr
                10                  15                  20

gga aaa ctt gga ttg cct aat gag gcc gct gct ggc att cag ggt cta   211
Gly Lys Leu Gly Leu Pro Asn Glu Ala Ala Ala Gly Ile Gln Gly Leu
            25                  30                  35

gct gca acg ggt atc cca gcg gtg gct gat atg gat tca gat act ttc   259
Ala Ala Thr Gly Ile Pro Ala Val Ala Asp Met Asp Ser Asp Thr Phe
        40                  45                  50

ggt aag ttt gtt gcc tac tcg gag ttg ggt atc ggt gga gct ttg ctt   307
Gly Lys Phe Val Ala Tyr Ser Glu Leu Gly Ile Gly Gly Ala Leu Leu
    55                  60                  65
```

```
gct cca ttt atc cct agc cgt ctt gca ggt ttg ggt ctt ggt gct ttc   355
Ala Pro Phe Ile Pro Ser Arg Leu Ala Gly Leu Gly Leu Gly Ala Phe
 70                  75                  80                  85

tct aca ggt ttg ttg gcc att tac ttc cgt aac cca gcg atg act caa   403
Ser Thr Gly Leu Leu Ala Ile Tyr Phe Arg Asn Pro Ala Met Thr Gln
                 90                  95                 100

gac gac gga atc cgc cct tcc cag gat gga acc gga ttg tct aag gat   451
Asp Asp Gly Ile Arg Pro Ser Gln Asp Gly Thr Gly Leu Ser Lys Asp
            105                 110                 115

ctt ttc ctt gct gct att gcg ggt gct ttg gtg ttc gca cct gct aag   499
Leu Phe Leu Ala Ala Ile Ala Gly Ala Leu Val Phe Ala Pro Ala Lys
        120                 125                 130

aag cgt aag aag gcg aag aac aag tct aag taagcttgct tgaacggcgc     549
Lys Arg Lys Lys Ala Lys Asn Lys Ser Lys
    135                 140

ttg                                                               552
```

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<210> 1700
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 1700

```
Met Ser Ile Ser Asn Ala Ile Leu Arg Gly Val Ser Gly Ala Tyr Ile
  1               5                  10                  15

Leu Gln Ser Gly Tyr Gly Lys Leu Gly Leu Pro Asn Glu Ala Ala Ala
             20                  25                  30

Gly Ile Gln Gly Leu Ala Ala Thr Gly Ile Pro Ala Val Ala Asp Met
         35                  40                  45

Asp Ser Asp Thr Phe Gly Lys Phe Val Ala Tyr Ser Glu Leu Gly Ile
     50                  55                  60

Gly Gly Ala Leu Leu Ala Pro Phe Ile Pro Ser Arg Leu Ala Gly Leu
 65                  70                  75                  80

Gly Leu Gly Ala Phe Ser Thr Gly Leu Leu Ala Ile Tyr Phe Arg Asn
                 85                  90                  95

Pro Ala Met Thr Gln Asp Asp Gly Ile Arg Pro Ser Gln Asp Gly Thr
            100                 105                 110

Gly Leu Ser Lys Asp Leu Phe Leu Ala Ala Ile Ala Gly Ala Leu Val
        115                 120                 125

Phe Ala Pro Ala Lys Lys Arg Lys Lys Ala Lys Asn Lys Ser Lys
    130                 135                 140
```

<210> 1701
<211> 1035
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> RXA00297

<400> 1701
aacaaggcac cggaaaacaa gcaacgcacc ttgcagaggt ggtcttaagc atcttggagc 60

aaaacaacat ggcacaataa cgatcatgca acaggtgctc atg ggt ttc acg gtg 115
Met Gly Phe Thr Val
1 5

gtg ttc atc gtc atc gga ata ggt tgg att ctc ggt aga aga gac acc 163
Val Phe Ile Val Ile Gly Ile Gly Trp Ile Leu Gly Arg Arg Asp Thr
10 15 20

ttg ggc aca cat gcc cag aaa cct ttg agc ctg ttt gtc tat tac gtg 211
Leu Gly Thr His Ala Gln Lys Pro Leu Ser Leu Phe Val Tyr Tyr Val
25 30 35

gcc acc cca gcg ttg ttg ttt gat cgg gtc acc aag tca gat acc tcg 259
Ala Thr Pro Ala Leu Leu Phe Asp Arg Val Thr Lys Ser Asp Thr Ser
40 45 50

acg att ttc tct ctg aac ttc gtg gtc att gca ctc tct gcg ttg atc 307
Thr Ile Phe Ser Leu Asn Phe Val Val Ile Ala Leu Ser Ala Leu Ile
55 60 65

gta ggt ttc ctg ttt ttc cta ctc atg cgg ttc gtg atc aaa aga act 355
Val Gly Phe Leu Phe Phe Leu Leu Met Arg Phe Val Ile Lys Arg Thr
70 75 80 85

gcc gca gta tcg gtg atc ggc atg cta gct gcg tcc tac gcc aac gcc 403
Ala Ala Val Ser Val Ile Gly Met Leu Ala Ala Ser Tyr Ala Asn Ala
90 95 100

ggt aac ctg ggt atc cct ttg gca gcc tat att ttg gat gat ttc acc 451
Gly Asn Leu Gly Ile Pro Leu Ala Ala Tyr Ile Leu Asp Asp Phe Thr
105 110 115

gtg gtg att ccc gtg att ttg ttc cag gtg gcg ttc tac gca ccg atc 499
Val Val Ile Pro Val Ile Leu Phe Gln Val Ala Phe Tyr Ala Pro Ile
120 125 130

acc atg acc atc atg gag atg ctg acc aac aag aaa tcc acc aac ttg 547
Thr Met Thr Ile Met Glu Met Leu Thr Asn Lys Lys Ser Thr Asn Leu
135 140 145

gtg cgc aac ctc ctg gtc acg cca cta acc aac acc atg gtg ctc gca 595
Val Arg Asn Leu Leu Val Thr Pro Leu Thr Asn Thr Met Val Leu Ala
150 155 160 165

gcg att gcc ggt att gct gtg tct ttg act tcg atg agc gtg ccc gtg 643
Ala Ile Ala Gly Ile Ala Val Ser Leu Thr Ser Met Ser Val Pro Val
170 175 180

gtg att gct cag cca gtg gaa atg ttg gcg aat gct tca gtg cca ctg 691
Val Ile Ala Gln Pro Val Glu Met Leu Ala Asn Ala Ser Val Pro Leu
185 190 195

```
gct ttg gtg gtg ttc gga ctg tcc ttg tcc aag agc aag atc ctg gaa   739
Ala Leu Val Val Phe Gly Leu Ser Leu Ser Lys Ser Lys Ile Leu Glu
        200                 205                 210

aag ggg cag gta tcc agg cgc gat gtg ttt acg gcg gca ctg ttc aag   787
Lys Gly Gln Val Ser Arg Arg Asp Val Phe Thr Ala Ala Leu Phe Lys
    215                 220                 225

aat gtt ctg cac cca att gtt gcg gga ctt tta gcc tta gcc ttt ggt   835
Asn Val Leu His Pro Ile Val Ala Gly Leu Leu Ala Leu Ala Phe Gly
230                 235                 240                 245

atg gaa ggt act gcc ttg ttg tcg gcg gtg att ctc ggt gca ctg cca   883
Met Glu Gly Thr Ala Leu Leu Ser Ala Val Ile Leu Gly Ala Leu Pro
                250                 255                 260

aca gcg cag aat gtc tac acc tac gcg ttg cga ttt aga aca gct gaa   931
Thr Ala Gln Asn Val Tyr Thr Tyr Ala Leu Arg Phe Arg Thr Ala Glu
            265                 270                 275

tcg atg gcg aga gac aca ggg gtg gtc acc aca ctc att tcc ttc ccc   979
Ser Met Ala Arg Asp Thr Gly Val Val Thr Thr Leu Ile Ser Phe Pro
        280                 285                 290

gta ttg gtg gcg gtc tcc att atc ttt gga tct tagggttagc attagtggtc 1032
Val Leu Val Ala Val Ser Ile Ile Phe Gly Ser
    295                 300

atg                                                               1035


<210> 1702
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 1702
Met Gly Phe Thr Val Val Phe Ile Val Ile Gly Ile Gly Trp Ile Leu
  1               5                  10                  15

Gly Arg Arg Asp Thr Leu Gly Thr His Ala Gln Lys Pro Leu Ser Leu
             20                  25                  30

Phe Val Tyr Tyr Val Ala Thr Pro Ala Leu Leu Phe Asp Arg Val Thr
         35                  40                  45

Lys Ser Asp Thr Ser Thr Ile Phe Ser Leu Asn Phe Val Val Ile Ala
     50                  55                  60

Leu Ser Ala Leu Ile Val Gly Phe Leu Phe Phe Leu Leu Met Arg Phe
 65                  70                  75                  80

Val Ile Lys Arg Thr Ala Ala Val Ser Val Ile Gly Met Leu Ala Ala
                 85                  90                  95

Ser Tyr Ala Asn Ala Gly Asn Leu Gly Ile Pro Leu Ala Ala Tyr Ile
            100                 105                 110

Leu Asp Asp Phe Thr Val Val Ile Pro Val Ile Leu Phe Gln Val Ala
        115                 120                 125
```

```
Phe Tyr Ala Pro Ile Thr Met Thr Ile Met Glu Met Leu Thr Asn Lys
    130                 135                 140

Lys Ser Thr Asn Leu Val Arg Asn Leu Leu Val Thr Pro Leu Thr Asn
145                 150                 155                 160

Thr Met Val Leu Ala Ala Ile Ala Gly Ile Ala Val Ser Leu Thr Ser
                165                 170                 175

Met Ser Val Pro Val Val Ile Ala Gln Pro Val Glu Met Leu Ala Asn
            180                 185                 190

Ala Ser Val Pro Leu Ala Leu Val Val Phe Gly Leu Ser Leu Ser Lys
        195                 200                 205

Ser Lys Ile Leu Glu Lys Gly Gln Val Ser Arg Arg Asp Val Phe Thr
    210                 215                 220

Ala Ala Leu Phe Lys Asn Val Leu His Pro Ile Val Ala Gly Leu Leu
225                 230                 235                 240

Ala Leu Ala Phe Gly Met Glu Gly Thr Ala Leu Leu Ser Ala Val Ile
                245                 250                 255

Leu Gly Ala Leu Pro Thr Ala Gln Asn Val Tyr Thr Tyr Ala Leu Arg
            260                 265                 270

Phe Arg Thr Ala Glu Ser Met Ala Arg Asp Thr Gly Val Val Thr Thr
        275                 280                 285

Leu Ile Ser Phe Pro Val Leu Val Ala Val Ser Ile Ile Phe Gly Ser
    290                 295                 300
```

CONFIDENTIAL

<210> 1703
<211> 303
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(280)
<223> RXA00320

<400> 1703
aacagaccca ctctagccgt tgcgggttct tattgaggtc tatagtgggg tgctacacac 60

tacaaaccgt gatttgtttc gtgattggag ctgagcccac atg gct aaa gaa gat 115
                                                Met Ala Lys Glu Asp
                                                  1   5

ttg aag tgg ttc tac gat ctg gca acc ggc aag gtt ttt caa ggc aag 163
Leu Lys Trp Phe Tyr Asp Leu Ala Thr Gly Lys Val Phe Gln Gly Lys
                 10   15   20

gtt tcc ggc ttt gaa acc cgc atg ggc cca tat gac act gaa gag gaa 211
Val Ser Gly Phe Glu Thr Arg Met Gly Pro Tyr Asp Thr Glu Glu Glu

```
            25                  30                  35

gcc cat cac gcc atc tcc att gcg gca gcc cga acc aag gca gcc gaa   259
Ala His His Ala Ile Ser Ile Ala Ala Ala Arg Thr Lys Ala Ala Glu
         40                  45                  50

att tgg gac gac aag gaa gac taaaaaaaac tggggtcaca ctt             303
Ile Trp Asp Asp Lys Glu Asp
     55                  60


<210> 1704
<211> 60
<212> PRT
<213> Corynebacterium glutamicum

<400> 1704
Met Ala Lys Glu Asp Leu Lys Trp Phe Tyr Asp Leu Ala Thr Gly Lys
  1               5                  10                  15

Val Phe Gln Gly Lys Val Ser Gly Phe Glu Thr Arg Met Gly Pro Tyr
             20                  25                  30

Asp Thr Glu Glu Glu Ala His His Ala Ile Ser Ile Ala Ala Ala Arg
         35                  40                  45

Thr Lys Ala Ala Glu Ile Trp Asp Asp Lys Glu Asp
     50                  55                  60


<210> 1705
<211> 1938
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1915)
<223> RXA00321

<400> 1705
caaagacaac acaggttccc tatgaaaacg gggaacctgt ttcacctact ttttaatcac 60

gcttcacaat cacataagtc tttaaaggat ggatacaaca atg ggc cag cat cta   115
                                              Met Gly Gln His Leu
                                                1               5

gaa gtg gaa act aag ttt tcc gtc agt gaa tca act cag att cca caa   163
Glu Val Glu Thr Lys Phe Ser Val Ser Glu Ser Thr Gln Ile Pro Gln
                10                  15                  20

ctt gag gct atc gca gaa gtc gac cac att gat cgc acc gaa atc cac   211
Leu Glu Ala Ile Ala Glu Val Asp His Ile Asp Arg Thr Glu Ile His
            25                  30                  35

caa cta agc gct gtt tac ttt gac acc gta gat ttg cgc ctc acc cgc   259
Gln Leu Ser Ala Val Tyr Phe Asp Thr Val Asp Leu Arg Leu Thr Arg
         40                  45                  50

gca aaa att acc ctc cgt cgc cgc acc ggt gga aac gat gcc ggc tgg   307
Ala Lys Ile Thr Leu Arg Arg Arg Thr Gly Gly Asn Asp Ala Gly Trp
```

```
     55                  60                  65

cac att aag ttc ccc gga acc atc ggt cgc cgt gaa gtc caa gcc cca   355
His Ile Lys Phe Pro Gly Thr Ile Gly Arg Arg Glu Val Gln Ala Pro
 70                  75                  80                  85

ctt gat ggc gaa ggc gca aca gaa acc ctc cct cca cgt gag ctc ttg   403
Leu Asp Gly Glu Gly Ala Thr Glu Thr Leu Pro Pro Arg Glu Leu Leu
                 90                  95                 100

gga cac atc cga gcg ctg atc caa ggc cgt gag ctg acc cct atc gcc   451
Gly His Ile Arg Ala Leu Ile Gln Gly Arg Glu Leu Thr Pro Ile Ala
            105                 110                 115

cag gtg gat aat gaa cgc cac atg tct tac ctc gcg gat gag gac ggc   499
Gln Val Asp Asn Glu Arg His Met Ser Tyr Leu Ala Asp Glu Asp Gly
        120                 125                 130

gca gtc atc gca gaa ttc tgc gac gat cat gta tcc acc gtg tcc cac   547
Ala Val Ile Ala Glu Phe Cys Asp Asp His Val Ser Thr Val Ser His
    135                 140                 145

ctt cca ggt ggc gtg cgc aag cag tgg cgt gag tgg gaa ttc gaa ctc   595
Leu Pro Gly Gly Val Arg Lys Gln Trp Arg Glu Trp Glu Phe Glu Leu
150                 155                 160                 165

gct gat ggc acc ctc gcc gaa gaa gcc atc tca gta ctg ctg caa tct   643
Ala Asp Gly Thr Leu Ala Glu Glu Ala Ile Ser Val Leu Leu Gln Ser
                170                 175                 180

gca cag tca gtc ctg acc gca gct gga gct ttt gtc tcc aac agc cca   691
Ala Gln Ser Val Leu Thr Ala Ala Gly Ala Phe Val Ser Asn Ser Pro
            185                 190                 195

tcc aaa ctt gtt tcg gcg ctg gac gaa tca gtc aac cac gcg cca aag   739
Ser Lys Leu Val Ser Ala Leu Asp Glu Ser Val Asn His Ala Pro Lys
        200                 205                 210

cct cca cag atg gcg cag ctg gac aag aat gac cca gca cgt ggt gtt   787
Pro Pro Gln Met Ala Gln Leu Asp Lys Asn Asp Pro Ala Arg Gly Val
    215                 220                 225

ctt gca gca atc gca gcc aac gcc tca aag atc gcc gaa tac gat cct   835
Leu Ala Ala Ile Ala Ala Asn Ala Ser Lys Ile Ala Glu Tyr Asp Pro
230                 235                 240                 245

cga gta cgc gcc gat gaa tat gat tca gtc cac cag atg cgc gta gct   883
Arg Val Arg Ala Asp Glu Tyr Asp Ser Val His Gln Met Arg Val Ala
                250                 255                 260

acc cga gaa cta cgc agc cac ctc caa acc ttt gag ggc atc ctc ggc   931
Thr Arg Glu Leu Arg Ser His Leu Gln Thr Phe Glu Gly Ile Leu Gly
            265                 270                 275

ggc gaa gac tac ctc aac ctg gaa aag gaa ctg aag gtt ctc gcc aac   979
Gly Glu Asp Tyr Leu Asn Leu Glu Lys Glu Leu Lys Val Leu Ala Asn
        280                 285                 290

atc ttg ggt cgc gca cgc gat gct gaa gtt gtg gaa gag cgc ctc agc   1027
Ile Leu Gly Arg Ala Arg Asp Ala Glu Val Val Glu Glu Arg Leu Ser
    295                 300                 305
```

```
aac ctg att aac act gag gtt ggc gac tcc atc gag gag gag act aag   1075
Asn Leu Ile Asn Thr Glu Val Gly Asp Ser Ile Glu Glu Glu Thr Lys
310                 315                 320                 325

aag gaa ctg ctt gaa gat ctt ggt gca gaa tac cgt cgt gag cat gag   1123
Lys Glu Leu Leu Glu Asp Leu Gly Ala Glu Tyr Arg Arg Glu His Glu
                330                 335                 340

cga gta gtt cgt gcg ctg gat aat gat cgc tac act gat ctt ctt cag   1171
Arg Val Val Arg Ala Leu Asp Asn Asp Arg Tyr Thr Asp Leu Leu Gln
            345                 350                 355

gca ctg gaa aac ctc ctt gtt gat cca ccg ctg atc aca gaa gtc gaa   1219
Ala Leu Glu Asn Leu Leu Val Asp Pro Pro Leu Ile Thr Glu Val Glu
        360                 365                 370

gaa ccc gaa gct acc gaa gcc cct gag tcc gct gag act acc gag tcc   1267
Glu Pro Glu Ala Thr Glu Ala Pro Glu Ser Ala Glu Thr Thr Glu Ser
    375                 380                 385

act gac gtc tct gaa gca acc gaa gaa gca gac gca gaa gct gag tct   1315
Thr Asp Val Ser Glu Ala Thr Glu Glu Ala Asp Ala Glu Ala Glu Ser
390                 395                 400                 405

gtc gaa gaa gct act gag cag gaa gaa tca gca gac gcg cct gaa tct   1363
Val Glu Glu Ala Thr Glu Gln Glu Glu Ser Ala Asp Ala Pro Glu Ser
                410                 415                 420

gca gat ctg gac gct ctc gat gag gag tac tcc cct ggt tcc caa gcg   1411
Ala Asp Leu Asp Ala Leu Asp Glu Glu Tyr Ser Pro Gly Ser Gln Ala
            425                 430                 435

ccg gtg gag gag ccg aag gaa ccg aag aag gtt gat gct gct ctc gta   1459
Pro Val Glu Glu Pro Lys Glu Pro Lys Lys Val Asp Ala Ala Leu Val
        440                 445                 450

ctt cta gag cac ctt gat aag gcg cac gtg aag ctc gtc aag ctg gaa   1507
Leu Leu Glu His Leu Asp Lys Ala His Val Lys Leu Val Lys Leu Glu
    455                 460                 465

aag aag gct cgc tca cag tgg gat gat ctc agc att ccg atg ctg gag   1555
Lys Lys Ala Arg Ser Gln Trp Asp Asp Leu Ser Ile Pro Met Leu Glu
470                 475                 480                 485

cgg gaa gaa aac ttc cac aac ctg cgc aag gct gcc aag aag ctt cgc   1603
Arg Glu Glu Asn Phe His Asn Leu Arg Lys Ala Ala Lys Lys Leu Arg
                490                 495                 500

tac agt gca gag gca gtg ggc aaa gca acc acc gtt gag acg aag aaa   1651
Tyr Ser Ala Glu Ala Val Gly Lys Ala Thr Thr Val Glu Thr Lys Lys
            505                 510                 515

ctg tac aag gcg tgc agt ggt ttg cag tca gtt ctt ggc gat tac caa   1699
Leu Tyr Lys Ala Cys Ser Gly Leu Gln Ser Val Leu Gly Asp Tyr Gln
        520                 525                 530

gat gcc att act tcc cgt aat gag ctg ttg cgc cga gct cag gtt gcc   1747
Asp Ala Ile Thr Ser Arg Asn Glu Leu Leu Arg Arg Ala Gln Val Ala
    535                 540                 545
```

```
cgc cgc caa ggc cgg gat acc ttc gca tac gga atc ctc tac cag cac   1795
Arg Arg Gln Gly Arg Asp Thr Phe Ala Tyr Gly Ile Leu Tyr Gln His
550                 555                 560                 565

gaa caa acc ctg tcg agg gaa tac ctg act ggt tat tcc gat gcg ttc   1843
Glu Gln Thr Leu Ser Arg Glu Tyr Leu Thr Gly Tyr Ser Asp Ala Phe
                570                 575                 580

aag agc gta gaa aaa gcc tat gca aag ctg gct gaa gat acc gcc aag   1891
Lys Ser Val Glu Lys Ala Tyr Ala Lys Leu Ala Glu Asp Thr Ala Lys
            585                 590                 595

cgt tca aag aag aac aag cgt aag taaacgcagg caataaaaaa ctg         1938
Arg Ser Lys Lys Asn Lys Arg Lys
        600                 605
```

<210> 1706
<211> 605
<212> PRT
<213> Corynebacterium glutamicum

<400> 1706

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Met Gly Gln His Leu Glu Val Glu Thr Lys Phe Ser Val Ser Glu Ser
  1               5                  10                  15

Thr Gln Ile Pro Gln Leu Glu Ala Ile Ala Glu Val Asp His Ile Asp
             20                  25                  30

Arg Thr Glu Ile His Gln Leu Ser Ala Val Tyr Phe Asp Thr Val Asp
         35                  40                  45

Leu Arg Leu Thr Arg Ala Lys Ile Thr Leu Arg Arg Arg Thr Gly Gly
     50                  55                  60

Asn Asp Ala Gly Trp His Ile Lys Phe Pro Gly Thr Ile Gly Arg Arg
 65                  70                  75                  80

Glu Val Gln Ala Pro Leu Asp Gly Glu Gly Ala Thr Glu Thr Leu Pro
                 85                  90                  95

Pro Arg Glu Leu Leu Gly His Ile Arg Ala Leu Ile Gln Gly Arg Glu
            100                 105                 110

Leu Thr Pro Ile Ala Gln Val Asp Asn Glu Arg His Met Ser Tyr Leu
        115                 120                 125

Ala Asp Glu Asp Gly Ala Val Ile Ala Glu Phe Cys Asp Asp His Val
    130                 135                 140

Ser Thr Val Ser His Leu Pro Gly Gly Val Arg Lys Gln Trp Arg Glu
145                 150                 155                 160

Trp Glu Phe Glu Leu Ala Asp Gly Thr Leu Ala Glu Glu Ala Ile Ser
                165                 170                 175

Val Leu Leu Gln Ser Ala Gln Ser Val Leu Thr Ala Ala Gly Ala Phe
            180                 185                 190

Val Ser Asn Ser Pro Ser Lys Leu Val Ser Ala Leu Asp Glu Ser Val
        195                 200                 205
```

```
Asn His Ala Pro Lys Pro Pro Gln Met Ala Gln Leu Asp Lys Asn Asp
.   210                 215                 220

Pro Ala Arg Gly Val Leu Ala Ala Ile Ala Ala Asn Ala Ser Lys Ile
225                 230                 235                 240

Ala Glu Tyr Asp Pro Arg Val Arg Ala Asp Glu Tyr Asp Ser Val His
                245                 250                 255

Gln Met Arg Val Ala Thr Arg Glu Leu Arg Ser His Leu Gln Thr Phe
            260                 265                 270

Glu Gly Ile Leu Gly Gly Glu Asp Tyr Leu Asn Leu Glu Lys Glu Leu
        275                 280                 285

Lys Val Leu Ala Asn Ile Leu Gly Arg Ala Arg Asp Ala Glu Val Val
    290                 295                 300

Glu Glu Arg Leu Ser Asn Leu Ile Asn Thr Glu Val Gly Asp Ser Ile
305                 310                 315                 320

Glu Glu Glu Thr Lys Lys Glu Leu Leu Glu Asp Leu Gly Ala Glu Tyr
                325                 330                 335

Arg Arg Glu His Glu Arg Val Val Arg Ala Leu Asp Asn Asp Arg Tyr
            340                 345                 350

Thr Asp Leu Leu Gln Ala Leu Glu Asn Leu Leu Val Asp Pro Pro Leu
        355                 360                 365

Ile Thr Glu Val Glu Glu Pro Glu Ala Thr Glu Ala Pro Glu Ser Ala
    370                 375                 380

Glu Thr Thr Glu Ser Thr Asp Val Ser Glu Ala Thr Glu Glu Ala Asp
385                 390                 395                 400

Ala Glu Ala Glu Ser Val Glu Glu Ala Thr Glu Gln Glu Glu Ser Ala
                405                 410                 415

Asp Ala Pro Glu Ser Ala Asp Leu Asp Ala Leu Asp Glu Glu Tyr Ser
            420                 425                 430

Pro Gly Ser Gln Ala Pro Val Glu Glu Pro Lys Glu Pro Lys Lys Val
        435                 440                 445

Asp Ala Ala Leu Val Leu Leu Glu His Leu Asp Lys Ala His Val Lys
    450                 455                 460

Leu Val Lys Leu Glu Lys Lys Ala Arg Ser Gln Trp Asp Asp Leu Ser
465                 470                 475                 480

Ile Pro Met Leu Glu Arg Glu Glu Asn Phe His Asn Leu Arg Lys Ala
                485                 490                 495

Ala Lys Lys Leu Arg Tyr Ser Ala Glu Ala Val Gly Lys Ala Thr Thr
            500                 505                 510

Val Glu Thr Lys Lys Leu Tyr Lys Ala Cys Ser Gly Leu Gln Ser Val
        515                 520                 525
```

```
Leu Gly Asp Tyr Gln Asp Ala Ile Thr Ser Arg Asn Glu Leu Leu Arg
    530                 535                 540

Arg Ala Gln Val Ala Arg Arg Gln Gly Arg Asp Thr Phe Ala Tyr Gly
545                 550                 555                 560

Ile Leu Tyr Gln His Glu Gln Thr Leu Ser Arg Glu Tyr Leu Thr Gly
                565                 570                 575

Tyr Ser Asp Ala Phe Lys Ser Val Glu Lys Ala Tyr Ala Lys Leu Ala
            580                 585                 590

Glu Asp Thr Ala Lys Arg Ser Lys Lys Asn Lys Arg Lys
        595                 600                 605


<210> 1707
<211> 1227
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1204)
<223> RXA00322

<400> 1707
cgcggttttt tgatgacacg ggggtgggag gtgtccagct tgggtggttc actgagaacc 60

gcaccgaaat tagaacactc ctacgaataa ggaaaccgca atg act ctc tcc cac   115
                                              Met Thr Leu Ser His
                                                1               5

ttc tcc gac aac gtc acc gac gca caa gac tct tac cgt cag att tta   163
Phe Ser Asp Asn Val Thr Asp Ala Gln Asp Ser Tyr Arg Gln Ile Leu
                10                  15                  20

gaa gaa agc atc atc agc cac cta ggt ttc tgt gcg ctt cgt ggg tgg   211
Glu Glu Ser Ile Ile Ser His Leu Gly Phe Cys Ala Leu Arg Gly Trp
            25                  30                  35

act ccc gcc gat ctc cgc cat gag ttt tcc gcc gat att gat cca ctc   259
Thr Pro Ala Asp Leu Arg His Glu Phe Ser Ala Asp Ile Asp Pro Leu
        40                  45                  50

ctg ttt cac gcg cta cct gag att gct tac tcc tgc tcc gat gag atg   307
Leu Phe His Ala Leu Pro Glu Ile Ala Tyr Ser Cys Ser Asp Glu Met
    55                  60                  65

tac aca ctg tgg gtg aac gga acg cgt gcc gcc gaa act agc cac ttg   355
Tyr Thr Leu Trp Val Asn Gly Thr Arg Ala Ala Glu Thr Ser His Leu
70                  75                  80                  85

ccg gtg atg acc ctg gag aag att ctc acc gag cta ccg aag cta agt   403
Pro Val Met Thr Leu Glu Lys Ile Leu Thr Glu Leu Pro Lys Leu Ser
                90                  95                  100

acc ttg cct gac tgg gca atg ctc gca gag ctc cac gcc tta gac aat   451
Thr Leu Pro Asp Trp Ala Met Leu Ala Glu Leu His Ala Leu Asp Asn
            105                 110                 115
```

```
caa gac acc agc cca atg acc ccg gca cag gcc aaa gcg cat cat cgt   499
Gln Asp Thr Ser Pro Met Thr Pro Ala Gln Ala Lys Ala His His Arg
        120                 125                 130

atc acc gca ctt ttg aaa aag gca gag tcc acc aac ttc gaa gaa gaa   547
Ile Thr Ala Leu Leu Lys Lys Ala Glu Ser Thr Asn Phe Glu Glu Glu
    135                 140                 145

gcc gaa gca ttg atc ctt aaa gca gag aca ctt cga cag cag tac cgg   595
Ala Glu Ala Leu Ile Leu Lys Ala Glu Thr Leu Arg Gln Gln Tyr Arg
150                 155                 160                 165

att gaa tca ctg ctg att aat tcc tat gac caa gat gtc caa gct cga   643
Ile Glu Ser Leu Leu Ile Asn Ser Tyr Asp Gln Asp Val Gln Ala Arg
                170                 175                 180

tct tct acg att cgt gca tct cgg gtg tat ctg gaa gct cca tgg atc   691
Ser Ser Thr Ile Arg Ala Ser Arg Val Tyr Leu Glu Ala Pro Trp Ile
            185                 190                 195

cga cac caa tac aaa ctg ctc aat gcc att gct cgg gtg cat tcc agc   739
Arg His Gln Tyr Lys Leu Leu Asn Ala Ile Ala Arg Val His Ser Ser
        200                 205                 210

gaa gcg ctg ctg atc acc aaa tct ggc atc tgc acc ctc ttc ggc gag   787
Glu Ala Leu Leu Ile Thr Lys Ser Gly Ile Cys Thr Leu Phe Gly Glu
    215                 220                 225

caa gat gac gta gcc cac att att gat ctg ttc aac agt ctt aat cga   835
Gln Asp Asp Val Ala His Ile Ile Asp Leu Phe Asn Ser Leu Asn Arg
230                 235                 240                 245

caa cgt gcc cac ttc atg aaa acg tca gca ggt gcc cga att gcc caa   883
Gln Arg Ala His Phe Met Lys Thr Ser Ala Gly Ala Arg Ile Ala Gln
                250                 255                 260

tta aat ggc gaa aca agc tca tat cgc cgt agt ttt atg atc tcc tac   931
Leu Asn Gly Glu Thr Ser Ser Tyr Arg Arg Ser Phe Met Ile Ser Tyr
            265                 270                 275

gcc agc caa atc tct aga ctt ctc atc tca gca aaa gag gat gca ttc   979
Ala Ser Gln Ile Ser Arg Leu Leu Ile Ser Ala Lys Glu Asp Ala Phe
        280                 285                 290

aac gaa cta gct ggt cag gca cca cta gct cac agc gcc atc gtt cct   1027
Asn Glu Leu Ala Gly Gln Ala Pro Leu Ala His Ser Ala Ile Val Pro
    295                 300                 305

gtc cta gag aac aga agt gtg agg tca aag gaa gca ctg aag gaa acc   1075
Val Leu Glu Asn Arg Ser Val Arg Ser Lys Glu Ala Leu Lys Glu Thr
310                 315                 320                 325

ttc ccg aat atg cgg aca atg acc ttc aaa tcg acc aac cga cga ggc   1123
Phe Pro Asn Met Arg Thr Met Thr Phe Lys Ser Thr Asn Arg Arg Gly
                330                 335                 340

att att gac gga ttt aat gct gcc aat gaa tcc cac ctt ggc ggg gaa   1171
Ile Ile Asp Gly Phe Asn Ala Ala Asn Glu Ser His Leu Gly Gly Glu
            345                 350                 355

tct gcc agc ttg gaa gac tca aca ttc atg ttc tagagcgggt gaaagcccca 1224
```

```
Ser Ala Ser Leu Glu Asp Ser Thr Phe Met Phe
        360                 365

ttt                                                                    1227


<210> 1708
<211> 368
<212> PRT
<213> Corynebacterium glutamicum

<400> 1708
Met Thr Leu Ser His Phe Ser Asp Asn Val Thr Asp Ala Gln Asp Ser
  1               5                  10                  15

Tyr Arg Gln Ile Leu Glu Glu Ser Ile Ile Ser His Leu Gly Phe Cys
             20                  25                  30

Ala Leu Arg Gly Trp Thr Pro Ala Asp Leu Arg His Glu Phe Ser Ala
         35                  40                  45

Asp Ile Asp Pro Leu Leu Phe His Ala Leu Pro Glu Ile Ala Tyr Ser
     50                  55                  60

Cys Ser Asp Glu Met Tyr Thr Leu Trp Val Asn Gly Thr Arg Ala Ala
 65                  70                  75                  80

Glu Thr Ser His Leu Pro Val Met Thr Leu Glu Lys Ile Leu Thr Glu
                 85                  90                  95

Leu Pro Lys Leu Ser Thr Leu Pro Asp Trp Ala Met Leu Ala Glu Leu
            100                 105                 110

His Ala Leu Asp Asn Gln Asp Thr Ser Pro Met Thr Pro Ala Gln Ala
        115                 120                 125

Lys Ala His His Arg Ile Thr Ala Leu Leu Lys Lys Ala Glu Ser Thr
    130                 135                 140

Asn Phe Glu Glu Glu Ala Glu Ala Leu Ile Leu Lys Ala Glu Thr Leu
145                 150                 155                 160

Arg Gln Gln Tyr Arg Ile Glu Ser Leu Leu Ile Asn Ser Tyr Asp Gln
                165                 170                 175

Asp Val Gln Ala Arg Ser Ser Thr Ile Arg Ala Ser Arg Val Tyr Leu
            180                 185                 190

Glu Ala Pro Trp Ile Arg His Gln Tyr Lys Leu Leu Asn Ala Ile Ala
        195                 200                 205

Arg Val His Ser Ser Glu Ala Leu Leu Ile Thr Lys Ser Gly Ile Cys
    210                 215                 220

Thr Leu Phe Gly Glu Gln Asp Asp Val Ala His Ile Ile Asp Leu Phe
225                 230                 235                 240

Asn Ser Leu Asn Arg Gln Arg Ala His Phe Met Lys Thr Ser Ala Gly
                245                 250                 255

Ala Arg Ile Ala Gln Leu Asn Gly Glu Thr Ser Ser Tyr Arg Arg Ser
```

```
            260                 265                 270

Phe Met Ile Ser Tyr Ala Ser Gln Ile Ser Arg Leu Leu Ile Ser Ala
        275                 280                 285

Lys Glu Asp Ala Phe Asn Glu Leu Ala Gly Gln Ala Pro Leu Ala His
    290                 295                 300

Ser Ala Ile Val Pro Val Leu Glu Asn Arg Ser Val Arg Ser Lys Glu
305                 310                 315                 320

Ala Leu Lys Glu Thr Phe Pro Asn Met Arg Thr Met Thr Phe Lys Ser
                325                 330                 335

Thr Asn Arg Arg Gly Ile Ile Asp Gly Phe Asn Ala Ala Asn Glu Ser
            340                 345                 350

His Leu Gly Gly Glu Ser Ala Ser Leu Glu Asp Ser Thr Phe Met Phe
        355                 360                 365
```

5 5 5

```
ttg gaa gct gat ctg gat aag ctg cac gaa aac acc acc tgg cgt gac   403
Leu Glu Ala Asp Leu Asp Lys Leu His Glu Asn Thr Thr Trp Arg Asp
                 90                  95                 100

aac gtc acg gcc act gca gcg aca gcg tct tat gtg gaa cgt ctt gaa   451
Asn Val Thr Ala Thr Ala Ala Thr Ala Ser Tyr Val Glu Arg Leu Glu
            105                 110                 115

agc atc gaa gcg gcc aag gat ttc cct cgt ttg gtt gct cat cac tat   499
Ser Ile Glu Ala Ala Lys Asp Phe Pro Arg Leu Val Ala His His Tyr
        120                 125                 130

gtc cgc tac ctg ggt gat ttg tcc ggt ggg cag gtt att gca cgt ctg   547
Val Arg Tyr Leu Gly Asp Leu Ser Gly Gly Gln Val Ile Ala Arg Leu
    135                 140                 145

gtg aac agg gaa tat gga gtt tcg gaa gag gcg ttg agc ttc tac tgc   595
Val Asn Arg Glu Tyr Gly Val Ser Glu Glu Ala Leu Ser Phe Tyr Cys
150                 155                 160                 165

ttt gaa gat ctt ggc aag ctc aaa ccg tac aag gat aat tac cgt gca   643
Phe Glu Asp Leu Gly Lys Leu Lys Pro Tyr Lys Asp Asn Tyr Arg Ala
                170                 175                 180

gag ctt gat gct ttg gaa tta aca gca gag gag cgt gct gcg ttg ctg   691
Glu Leu Asp Ala Leu Glu Leu Thr Ala Glu Glu Arg Ala Ala Leu Leu
            185                 190                 195

gat gaa gca tct gat gcg ttc agg ttt aat cag caa gtt ttt cag gct   739
Asp Glu Ala Ser Asp Ala Phe Arg Phe Asn Gln Gln Val Phe Gln Ala
        200                 205                 210

ctt gct taaccgaagg tgaagtcttg gcg                                768
Leu Ala
    215
```

09542769.090502

<210> 1710
<211> 215
<212> PRT
<213> Corynebacterium glutamicum

<400> 1710

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Met Thr Ser Ile Ile Ala Ser Asn Ser Asp Leu Ser Glu Ala Leu Arg
  1               5                  10                  15

Thr His Thr Ala Gln Ala His Glu Glu Ala Glu His Ser Thr Phe Met
             20                  25                  30

Asn Asp Leu Leu Thr Gly Lys Leu Asp Ala Gln Ala Phe Ile Lys Leu
         35                  40                  45

Gln Glu Gln Ser Trp Leu Phe Tyr Thr Ala Leu Glu Ala Ala Ala Arg
     50                  55                  60

Ala Cys Ala Glu Asp Ser Arg Ala Ala Gly Leu Leu Asp Pro Arg Leu
 65                  70                  75                  80

Glu Arg Lys Glu Thr Leu Glu Ala Asp Leu Asp Lys Leu His Glu Asn
                 85                  90                  95
```

```
Thr Thr Trp Arg Asp Asn Val Thr Ala Thr Ala Ala Thr Ala Ser Tyr
            100                 105                 110

Val Glu Arg Leu Glu Ser Ile Glu Ala Ala Lys Asp Phe Pro Arg Leu
        115                 120                 125

Val Ala His His Tyr Val Arg Tyr Leu Gly Asp Leu Ser Gly Gly Gln
    130                 135                 140

Val Ile Ala Arg Leu Val Asn Arg Glu Tyr Gly Val Ser Glu Glu Ala
145                 150                 155                 160

Leu Ser Phe Tyr Cys Phe Glu Asp Leu Gly Lys Leu Lys Pro Tyr Lys
                165                 170                 175

Asp Asn Tyr Arg Ala Glu Leu Asp Ala Leu Glu Leu Thr Ala Glu Glu
            180                 185                 190

Arg Ala Ala Leu Leu Asp Glu Ala Ser Asp Ala Phe Arg Phe Asn Gln
        195                 200                 205

Gln Val Phe Gln Ala Leu Ala
    210                 215


<210> 1711
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> RXA00326

<400> 1711
cctgatcttt gcccctaagt ggtttacggg ctggaaaatg gtacgtagtc tcgggtgtaa 60

agcacacttc ggtactcgac aggaagttag gaattccacc atg gca atc aag ctg   115
                                              Met Ala Ile Lys Leu
                                                1               5

tcc att gac cta tca gat gca aca ttc gca gaa ctt tcg gca gtc atc   163
Ser Ile Asp Leu Ser Asp Ala Thr Phe Ala Glu Leu Ser Ala Val Ile
                10                  15                  20

ggt tac gca cat cag ttg ggt gtt gat gcg gat gag aag ctc acc ttt   211
Gly Tyr Ala His Gln Leu Gly Val Asp Ala Asp Glu Lys Leu Thr Phe
            25                  30                  35

gaa ggt aca gtc ctt aac att gaa ttc gac ggc gac ctt cag ttt gat   259
Glu Gly Thr Val Leu Asn Ile Glu Phe Asp Gly Asp Leu Gln Phe Asp
        40                  45                  50

gat gtt ttt gat gcc ttt gat gag gcg gaa att gag ctc gac aac cct   307
Asp Val Phe Asp Ala Phe Asp Glu Ala Glu Ile Glu Leu Asp Asn Pro
    55                  60                  65

cgc gaa gac ggc ccc atc tac gca gat gat ctg atc gat gag gat gag   355
Arg Glu Asp Gly Pro Ile Tyr Ala Asp Asp Leu Ile Asp Glu Asp Glu
70                  75                  80                  85
```

```
gac tac cgc gca cag acc aag agc cag atc aac gac gag gtt atc aac   403
Asp Tyr Arg Ala Gln Thr Lys Ser Gln Ile Asn Asp Glu Val Ile Asn
                 90                  95                 100

gag atc cgc gat ggt att tca agc ttc gtt gat ggc atc gta aat ggc   451
Glu Ile Arg Asp Gly Ile Ser Ser Phe Val Asp Gly Ile Val Asn Gly
            105                 110                 115

ctt ggc cag ggt cgc cgc ggt gga cgt tac ggt gat ttc ggt ggg cca   499
Leu Gly Gln Gly Arg Arg Gly Gly Arg Tyr Gly Asp Phe Gly Gly Pro
        120                 125                 130

cgc ggc cct cgc ggt cca cgc aat gac ggt cca ttc ggc cca ttt gga   547
Arg Gly Pro Arg Gly Pro Arg Asn Asp Gly Pro Phe Gly Pro Phe Gly
    135                 140                 145

cca ttc ggt ccg gga tac cgc ggt ccg cgt ttc tagcggttac ggtcgggttt 600
Pro Phe Gly Pro Gly Tyr Arg Gly Pro Arg Phe
150                 155                 160

tag                                                               603
```

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<210> 1712
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 1712

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Met Ala Ile Lys Leu Ser Ile Asp Leu Ser Asp Ala Thr Phe Ala Glu
  1               5                  10                  15

Leu Ser Ala Val Ile Gly Tyr Ala His Gln Leu Gly Val Asp Ala Asp
             20                  25                  30

Glu Lys Leu Thr Phe Glu Gly Thr Val Leu Asn Ile Glu Phe Asp Gly
         35                  40                  45

Asp Leu Gln Phe Asp Asp Val Phe Asp Ala Phe Asp Glu Ala Glu Ile
     50                  55                  60

Glu Leu Asp Asn Pro Arg Glu Asp Gly Pro Ile Tyr Ala Asp Asp Leu
 65                  70                  75                  80

Ile Asp Glu Asp Glu Asp Tyr Arg Ala Gln Thr Lys Ser Gln Ile Asn
                 85                  90                  95

Asp Glu Val Ile Asn Glu Ile Arg Asp Gly Ile Ser Ser Phe Val Asp
            100                 105                 110

Gly Ile Val Asn Gly Leu Gly Gln Gly Arg Arg Gly Gly Arg Tyr Gly
        115                 120                 125

Asp Phe Gly Gly Pro Arg Gly Pro Arg Gly Pro Arg Asn Asp Gly Pro
    130                 135                 140

Phe Gly Pro Phe Gly Pro Phe Gly Pro Gly Tyr Arg Gly Pro Arg Phe
145                 150                 155                 160
```

<210> 1713
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXA00336

<400> 1713
ttaggatctt aaaggtagga aattgcgctt tgcgacgtcg aaaagcaacg ccttttgact 60

gcagtatccg ccctctacat gtttggattt gattgtaaca atg gca aag ccg aag 115
Met Ala Lys Pro Lys
1 5

aga agt tgg ctt gac gga ccc gaa att cca gct gat ttt gac gat cct 163
Arg Ser Trp Leu Asp Gly Pro Glu Ile Pro Ala Asp Phe Asp Asp Pro
10 15 20

gat gca ccc ggc agg tgg cct ggc gaa aag ttg ggg ctt cct caa gaa 211
Asp Ala Pro Gly Arg Trp Pro Gly Glu Lys Leu Gly Leu Pro Gln Glu
25 30 35

ggg gcc ggc tct ctg tcc tca gtg gct cgt cgt atc ggc ggg gtc tgc 259
Gly Ala Gly Ser Leu Ser Ser Val Ala Arg Arg Ile Gly Gly Val Cys
40 45 50

gtg gac tgg ggt gtt tcc tgg gtt att gct att gtg ctg tcc aat ttc 307
Val Asp Trp Gly Val Ser Trp Val Ile Ala Ile Val Leu Ser Asn Phe
55 60 65

acg gat gtg ctg ggc gat gta gcg aca tcc acg ctc att att ttc gtg 355
Thr Asp Val Leu Gly Asp Val Ala Thr Ser Thr Leu Ile Ile Phe Val
70 75 80 85

atc ctg ggt tgg ctt acc ggt tgg atc ttt gct cgc acc cca ggt cat 403
Ile Leu Gly Trp Leu Thr Gly Trp Ile Phe Ala Arg Thr Pro Gly His
90 95 100

gcc gtg ttt ggc atg ggc ctt gcg cgt gtg gat gca gag gaa cgt gtg 451
Ala Val Phe Gly Met Gly Leu Ala Arg Val Asp Ala Glu Glu Arg Val
105 110 115

ggc tgg tgg cgt gcg ctg gtt cgc cca ctg ctg acg atc ttg att ctg 499
Gly Trp Trp Arg Ala Leu Val Arg Pro Leu Leu Thr Ile Leu Ile Leu
120 125 130

cct gcc gtg atg gtg gat gct gac ggc cgt ggg ctc cac gac aag gca 547
Pro Ala Val Met Val Asp Ala Asp Gly Arg Gly Leu His Asp Lys Ala
135 140 145

acg gga act gca gtt atc cgc ggg taatttgtct tgagtgaaat tta 594
Thr Gly Thr Ala Val Ile Arg Gly
150 155

<210> 1714
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 1714
Met Ala Lys Pro Lys Arg Ser Trp Leu Asp Gly Pro Glu Ile Pro Ala
1 5 10 15

Asp Phe Asp Asp Pro Asp Ala Pro Gly Arg Trp Pro Gly Glu Lys Leu
20 25 30

Gly Leu Pro Gln Glu Gly Ala Gly Ser Leu Ser Ser Val Ala Arg Arg
35 40 45

Ile Gly Gly Val Cys Val Asp Trp Gly Val Ser Trp Val Ile Ala Ile
50 55 60

Val Leu Ser Asn Phe Thr Asp Val Leu Gly Asp Val Ala Thr Ser Thr
65 70 75 80

Leu Ile Ile Phe Val Ile Leu Gly Trp Leu Thr Gly Trp Ile Phe Ala
85 90 95

Arg Thr Pro Gly His Ala Val Phe Gly Met Gly Leu Ala Arg Val Asp
100 105 110

Ala Glu Glu Arg Val Gly Trp Trp Arg Ala Leu Val Arg Pro Leu Leu
115 120 125

Thr Ile Leu Ile Leu Pro Ala Val Met Val Asp Ala Asp Gly Arg Gly
130 135 140

Leu His Asp Lys Ala Thr Gly Thr Ala Val Ile Arg Gly
145 150 155

<210> 1715
<211> 525
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(525)
<223> RXA00337

<400> 1715
gat gtg gag gga ggc gtc gaa aag cat tct tta agc act gcg gac att 48
Asp Val Glu Gly Gly Val Glu Lys His Ser Leu Ser Thr Ala Asp Ile
1 5 10 15

gca gct cgc gca cac gcc cat atg aaa tcc cat gat gtt ttg ggg cgg 96
Ala Ala Arg Ala His Ala His Met Lys Ser His Asp Val Leu Gly Arg
20 25 30

cag act acg ccg cct cag ccg gag ggc ggc gtt gct gcc cgg ttg ggc 144
Gln Thr Thr Pro Pro Gln Pro Glu Gly Gly Val Ala Ala Arg Leu Gly
35 40 45

ggg att gcg tgg aca atg atc cat aag caa atg ctt tcg cgt gac aca 192

```
Gly Ile Ala Trp Thr Met Ile His Lys Gln Met Leu Ser Arg Asp Thr
     50                  55                  60

aaa ggc ctg gat atc acc gtg ttg agc acc att cct gag ggg gtg ggg   240
Lys Gly Leu Asp Ile Thr Val Leu Ser Thr Ile Pro Glu Gly Val Gly
 65                  70                  75                  80

ctg ggt gaa aat tcc gcc atg gat gtg gcg ctc gca ttg gcg ctg tat   288
Leu Gly Glu Asn Ser Ala Met Asp Val Ala Leu Ala Leu Ala Leu Tyr
                 85                  90                  95

cgg gaa aat att gag gaa gcc ccc acg aag gcg cgc att gcg gac att   336
Arg Glu Asn Ile Glu Glu Ala Pro Thr Lys Ala Arg Ile Ala Asp Ile
            100                 105                 110

tgt tcg cag tcc gca ttc atg ttc agt gag act tca gtg ttg cgt gcg   384
Cys Ser Gln Ser Ala Phe Met Phe Ser Glu Thr Ser Val Leu Arg Ala
        115                 120                 125

cgg cac acc gag gcg ttg cgg ggt gaa act gga cac att tcg gtg gtt   432
Arg His Thr Glu Ala Leu Arg Gly Glu Thr Gly His Ile Ser Val Val
    130                 135                 140

gat tac gcc gat ggt tcg gtc act cag gcg cca cat ccg gtg agt cgt   480
Asp Tyr Ala Asp Gly Ser Val Thr Gln Ala Pro His Pro Val Ser Arg
145                 150                 155                 160

tcc gct ggt ttg tcg gca ttt gtt gct gct gcg caa act gaa act       525
Ser Ala Gly Leu Ser Ala Phe Val Ala Ala Ala Gln Thr Glu Thr
                165                 170                 175
```

<210> 1716
<211> 175
<212> PRT
<213> Corynebacterium glutamicum

<400> 1716

```
Asp Val Glu Gly Gly Val Glu Lys His Ser Leu Ser Thr Ala Asp Ile
  1               5                  10                  15

Ala Ala Arg Ala His Ala His Met Lys Ser His Asp Val Leu Gly Arg
            20                  25                  30

Gln Thr Thr Pro Pro Gln Pro Glu Gly Gly Val Ala Ala Arg Leu Gly
        35                  40                  45

Gly Ile Ala Trp Thr Met Ile His Lys Gln Met Leu Ser Arg Asp Thr
     50                  55                  60

Lys Gly Leu Asp Ile Thr Val Leu Ser Thr Ile Pro Glu Gly Val Gly
 65                  70                  75                  80

Leu Gly Glu Asn Ser Ala Met Asp Val Ala Leu Ala Leu Ala Leu Tyr
                 85                  90                  95

Arg Glu Asn Ile Glu Glu Ala Pro Thr Lys Ala Arg Ile Ala Asp Ile
            100                 105                 110

Cys Ser Gln Ser Ala Phe Met Phe Ser Glu Thr Ser Val Leu Arg Ala
        115                 120                 125
```

```
Arg His Thr Glu Ala Leu Arg Gly Glu Thr Gly His Ile Ser Val Val
    130                 135                 140

Asp Tyr Ala Asp Gly Ser Val Thr Gln Ala Pro His Pro Val Ser Arg
145                 150                 155                 160

Ser Ala Gly Leu Ser Ala Phe Val Ala Ala Ala Gln Thr Glu Thr
                165                 170                 175


<210> 1717
<211> 840
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(817)
<223> RXA00339

<400> 1717
acaggttgaa gttgatgtga tttcgatccg cacagacccc tggaccatgt ctgcgcgagc 60

agtgaactaa attcttgaga actaaaaaag gagaacttca atg aag ctg gac cca   115
                                            Met Lys Leu Asp Pro
                                              1               5

tct ctg cac aaa acc ctg ctg cag ctc gcc acc acc ctg cgc acc caa   163
Ser Leu His Lys Thr Leu Leu Gln Leu Ala Thr Thr Leu Arg Thr Gln
                 10                  15                  20

aac gcc aac tcc gca ccg aag acc acc ccg gag cag gaa gct gta gac   211
Asn Ala Asn Ser Ala Pro Lys Thr Thr Pro Glu Gln Glu Ala Val Asp
             25                  30                  35

aag gct gtc gct gaa ctt tcc cgc aac cgc gac gct gca tcc gct gga   259
Lys Ala Val Ala Glu Leu Ser Arg Asn Arg Asp Ala Ala Ser Ala Gly
         40                  45                  50

caa atg gct gtc gat gac atg gaa aac gaa atc ctg cgc att cag tcc   307
Gln Met Ala Val Asp Asp Met Glu Asn Glu Ile Leu Arg Ile Gln Ser
     55                  60                  65

gac gaa cgc aaa ctg cgc cgc cgc aag aaa gac ggc cag gac gca ctc   355
Asp Glu Arg Lys Leu Arg Arg Arg Lys Lys Asp Gly Gln Asp Ala Leu
 70                  75                  80                  85

ggt gca gaa act gac gaa gag cgt cgc cgc gac ctc aac cac gac gtc   403
Gly Ala Glu Thr Asp Glu Glu Arg Arg Arg Asp Leu Asn His Asp Val
                 90                  95                 100

tac act gcg aag tcc cgc atc gct gac ctc atg agc gaa ctg caa gaa   451
Tyr Thr Ala Lys Ser Arg Ile Ala Asp Leu Met Ser Glu Leu Gln Glu
            105                 110                 115

gct cac aat gaa atc cat gcg ctg cgc aac aac cgc gac ctc gca cag   499
Ala His Asn Glu Ile His Ala Leu Arg Asn Asn Arg Asp Leu Ala Gln
        120                 125                 130

tct cgc gtc aaa gac acc gaa cgc aaa gtt gcc gac gcc cgc gca gcc   547
```

```
Ser Arg Val Lys Asp Thr Glu Arg Lys Val Ala Asp Ala Arg Ala Ala
    135                 140                 145

gca gaa gcc gcc gca gca gca acc cca gaa ggt gaa gac cca gca gta   595
Ala Glu Ala Ala Ala Ala Ala Thr Pro Glu Gly Glu Asp Pro Ala Val
150                 155                 160                 165

gtc atc gca cac ctg gaa gag aaa ctt ccc tcc gaa gca ctg gca gaa   643
Val Ile Ala His Leu Glu Glu Lys Leu Pro Ser Glu Ala Leu Ala Glu
                170                 175                 180

ttc cat gca caa cgc ctc gaa aac ggc gta ggc gca gca ctc ttc aac   691
Phe His Ala Gln Arg Leu Glu Asn Gly Val Gly Ala Ala Leu Phe Asn
            185                 190                 195

ggc cgc tcc tgc agc gga tgc gcc atg gtt ctc cct gca acc ggt atc   739
Gly Arg Ser Cys Ser Gly Cys Ala Met Val Leu Pro Ala Thr Gly Ile
        200                 205                 210

tcc gac atc cgc aac acc ccc aaa gat gag gtt cca cag tgc cca gaa   787
Ser Asp Ile Arg Asn Thr Pro Lys Asp Glu Val Pro Gln Cys Pro Glu
    215                 220                 225

tgt ggc tct tac ctc atc act gac atc tct tagaaagacc acccagtgaa     837
Cys Gly Ser Tyr Leu Ile Thr Asp Ile Ser
230                 235

att                                                               840
```

EP 2 036 976 A2

<210> 1718
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 1718

```
Met Lys Leu Asp Pro Ser Leu His Lys Thr Leu Leu Gln Leu Ala Thr
  1               5                  10                  15

Thr Leu Arg Thr Gln Asn Ala Asn Ser Ala Pro Lys Thr Thr Pro Glu
             20                  25                  30

Gln Glu Ala Val Asp Lys Ala Val Ala Glu Leu Ser Arg Asn Arg Asp
         35                  40                  45

Ala Ala Ser Ala Gly Gln Met Ala Val Asp Asp Met Glu Asn Glu Ile
     50                  55                  60

Leu Arg Ile Gln Ser Asp Glu Arg Lys Leu Arg Arg Arg Lys Lys Asp
 65                  70                  75                  80

Gly Gln Asp Ala Leu Gly Ala Glu Thr Asp Glu Glu Arg Arg Arg Asp
                 85                  90                  95

Leu Asn His Asp Val Tyr Thr Ala Lys Ser Arg Ile Ala Asp Leu Met
            100                 105                 110

Ser Glu Leu Gln Glu Ala His Asn Glu Ile His Ala Leu Arg Asn Asn
        115                 120                 125

Arg Asp Leu Ala Gln Ser Arg Val Lys Asp Thr Glu Arg Lys Val Ala
```

```
    130                 135                 140

Asp Ala Arg Ala Ala Ala Glu Ala Ala Ala Ala Ala Thr Pro Glu Gly
145                 150                 155                 160

Glu Asp Pro Ala Val Val Ile Ala His Leu Glu Glu Lys Leu Pro Ser
                165                 170                 175

Glu Ala Leu Ala Glu Phe His Ala Gln Arg Leu Glu Asn Gly Val Gly
            180                 185                 190

Ala Ala Leu Phe Asn Gly Arg Ser Cys Ser Gly Cys Ala Met Val Leu
        195                 200                 205

Pro Ala Thr Gly Ile Ser Asp Ile Arg Asn Thr Pro Lys Asp Glu Val
    210                 215                 220

Pro Gln Cys Pro Glu Cys Gly Ser Tyr Leu Ile Thr Asp Ile Ser
225                 230                 235


<210> 1719
<211> 1082
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1059)
<223> RXA00349

<400> 1719
gag aaa atc ctg gac gag ttg gag caa tcc cct gcg tct tat ggt ttc   48
Glu Lys Ile Leu Asp Glu Leu Glu Gln Ser Pro Ala Ser Tyr Gly Phe
  1               5                  10                  15

cct gtt gcg ttg ctt ggc tgg cca atg atg ggt ggt gct gtt gct gtg   96
Pro Val Ala Leu Leu Gly Trp Pro Met Met Gly Gly Ala Val Ala Val
             20                  25                  30

ctg ttg ggt ggt gga tgc cag gtt tcc cta att gct ttt att acc gcg   144
Leu Leu Gly Gly Gly Cys Gln Val Ser Leu Ile Ala Phe Ile Thr Ala
         35                  40                  45

ttc acg atc att gcc acg acg tca ttt ttg gga aag aag ggt ttg cct   192
Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys Gly Leu Pro
     50                  55                  60

act ttc ttc caa aat gtt gtt ggt ggt ttt att gcc acg ctg cct gca   240
Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr Leu Pro Ala
 65                  70                  75                  80

tcg att gct tat tct ttg gcg ttg caa ttt ggt ctt gag atc aaa ccg   288
Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu Ile Lys Pro
                 85                  90                  95

agc cag atc atc gca tct gga att gtt gtg ctg ttg gca ggt ttg aca   336
Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala Gly Leu Thr
            100                 105                 110

ctc gtg caa tct ctg cag gac ggc atc acg ggc gct ccg gtg aca gca   384
```

```
Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro Val Thr Ala
        115                 120                 125

agt gca cga ttt ttc gaa aca ctc ctg ttt acc ggc ggc att gtt gct   432
Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly Ile Val Ala
    130                 135                 140

ggc gtg ggt ttg ggc att cag ctt tct gaa atc ttg cat gtc atg ttg   480
Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His Val Met Leu
145                 150                 155                 160

cct gcc atg gag tcc gct gca gca cct aat tat tcg tct aca ttc gcc   528
Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser Thr Phe Ala
                165                 170                 175

cgc att atc gct ggt ggc gtc acc gca gcg gcc ttc gca gtg ggt tgt   576
Arg Ile Ile Ala Gly Gly Val Thr Ala Ala Ala Phe Ala Val Gly Cys
            180                 185                 190

tac gcg gag tgg tcc tcg gtg att att gcg ggg ctt act gcg ctg atg   624
Tyr Ala Glu Trp Ser Ser Val Ile Ile Ala Gly Leu Thr Ala Leu Met
        195                 200                 205

ggt tct gcg ttt tat tac ctc ttc gtt gtt tat tta ggc ccc gtc tct   672
Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly Pro Val Ser
    210                 215                 220

gcc gct gcg att gct gca aca gca gtt ggt ttc act ggt ggt ttg ctt   720
Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly Gly Leu Leu
225                 230                 235                 240

gcc cgt cga ttc ttg att cca ccg ttg att gtg gcg att gcc ggc atc   768
Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile Ala Gly Ile
                245                 250                 255

aca cca atg ctt cca ggt cta gca att tac cgc gga atg tac gcc acc   816
Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met Tyr Ala Thr
            260                 265                 270

ctg aat gat caa aca ctc atg ggt ttc acc aac att gcg gtt gct tta   864
Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala Val Ala Leu
        275                 280                 285

gcc act gct tca tca ctt gcc gct ggc gtg gtt ttg ggt gag tgg att   912
Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly Glu Trp Ile
    290                 295                 300

gcc cgc agg cta cgt cgt cca cca cgc ttc aac cca tac cgt gca ttt   960
Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr Arg Ala Phe
305                 310                 315                 320

acc aag gcg aat gag ttc tcc ttc cag gag gaa gct gag cag aat cag  1008
Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu Gln Asn Gln
                325                 330                 335

cgc cgg cag aga aaa cgt cca aag act aat cag aga ttc ggt aat aaa  1056
Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe Gly Asn Lys
            340                 345                 350

agg taaaaatcaa cctgcttagg cgt                                   1082
Arg
```

<210> 1720
<211> 353
<212> PRT
<213> Corynebacterium glutamicum

<400> 1720

```
Glu Lys Ile Leu Asp Glu Leu Glu Gln Ser Pro Ala Ser Tyr Gly Phe
  1               5                  10                  15

Pro Val Ala Leu Leu Gly Trp Pro Met Met Gly Gly Ala Val Ala Val
             20                  25                  30

Leu Leu Gly Gly Gly Cys Gln Val Ser Leu Ile Ala Phe Ile Thr Ala
         35                  40                  45

Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys Gly Leu Pro
     50                  55                  60

Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr Leu Pro Ala
 65                  70                  75                  80

Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu Ile Lys Pro
                 85                  90                  95

Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala Gly Leu Thr
            100                 105                 110

Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro Val Thr Ala
        115                 120                 125

Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly Ile Val Ala
    130                 135                 140

Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His Val Met Leu
145                 150                 155                 160

Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser Thr Phe Ala
                165                 170                 175

Arg Ile Ile Ala Gly Gly Val Thr Ala Ala Ala Phe Ala Val Gly Cys
            180                 185                 190

Tyr Ala Glu Trp Ser Ser Val Ile Ile Ala Gly Leu Thr Ala Leu Met
        195                 200                 205

Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly Pro Val Ser
    210                 215                 220

Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly Gly Leu Leu
225                 230                 235                 240

Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile Ala Gly Ile
                245                 250                 255

Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met Tyr Ala Thr
            260                 265                 270

Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala Val Ala Leu
```

```
        275                 280                 285

Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly Glu Trp Ile
    290                 295                 300

Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr Arg Ala Phe
305                 310                 315                 320

Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu Gln Asn Gln
                325                 330                 335

Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe Gly Asn Lys
            340                 345                 350

Arg
```

<210> 1721
<211> 149
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(126)
<223> RXA00355

<400> 1721

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atc gct ttc ggt cgc gca gct cac cgc atg aag cag cag ggc caa agc   48
Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys Gln Gln Gly Gln Ser
  1               5                  10                  15

gga gct ttc acc gtc ctc gaa gtt gct cca tac ctg ctc tcc cca gag   96
Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu
             20                  25                  30

aac ttg gac gat ctg atc gca cgc gac gtc taatttagct cgaggggcaa     146
Asn Leu Asp Asp Leu Ile Ala Arg Asp Val
         35                  40

gga                                                               149
```

<210> 1722
<211> 42
<212> PRT
<213> Corynebacterium glutamicum

<400> 1722

```
Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys Gln Gln Gly Gln Ser
  1               5                  10                  15

Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu
             20                  25                  30

Asn Leu Asp Asp Leu Ile Ala Arg Asp Val
         35                  40
```

<210> 1723

<211> 624
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(601)
<223> RXA00375

<400> 1723
cagcctgtca aaatgctcac cgactacgca ccagaagacg ctaaacggta agtactgaag 60

```
aatttttaaa gacgacggag atttcaccac aatgccaagc atg ttc cca tca ccc   115
                                            Met Phe Pro Ser Pro
                                              1               5

gca act ggc gga gat gac atc aac cga cgc ccc ctg aat gaa cca aac   163
Ala Thr Gly Gly Asp Asp Ile Asn Arg Arg Pro Leu Asn Glu Pro Asn
                 10                  15                  20

gca gat gca acc acc atc ccc act gca cta aaa gtg gtg ttc tgg atg   211
Ala Asp Ala Thr Thr Ile Pro Thr Ala Leu Lys Val Val Phe Trp Met
            25                  30                  35

ctg ttt gcc act gca gcg ttc atg att ttt aca ggc ctg gtg atg tac   259
Leu Phe Ala Thr Ala Ala Phe Met Ile Phe Thr Gly Leu Val Met Tyr
        40                  45                  50

acc gcc gga tac acg gga cct gat gat gtg gat gag agc tac aaa gcc   307
Thr Ala Gly Tyr Thr Gly Pro Asp Asp Val Asp Glu Ser Tyr Lys Ala
    55                  60                  65

gtt gtg gtg aac aac cag gag ttc atc ggt ggc atc aat gcc ttt gct   355
Val Val Val Asn Asn Gln Glu Phe Ile Gly Gly Ile Asn Ala Phe Ala
70                  75                  80                  85

ggc gtc gtg att gct gca ctt act tca caa ctg cca aag ggc ggc aag   403
Gly Val Val Ile Ala Ala Leu Thr Ser Gln Leu Pro Lys Gly Gly Lys
                90                  95                 100

aat ccg cgc cgt ctt ttg ttg gcc atc atg ttg ttg gta ttg ctg aca   451
Asn Pro Arg Arg Leu Leu Leu Ala Ile Met Leu Leu Val Leu Leu Thr
            105                 110                 115

gat ctg ttg tct ttt gcc acc cgc gct gga ggc ttc gca ctc gca atc   499
Asp Leu Leu Ser Phe Ala Thr Arg Ala Gly Gly Phe Ala Leu Ala Ile
        120                 125                 130

atc gca gtc ttg ttg gct ttg gaa gca ctc ttg atg ttc cgc cca gca   547
Ile Ala Val Leu Leu Ala Leu Glu Ala Leu Leu Met Phe Arg Pro Ala
    135                 140                 145

gtc aat gat cac att gac cga aat cat atg gct cgt gta atg aat cgc   595
Val Asn Asp His Ile Asp Arg Asn His Met Ala Arg Val Met Asn Arg
150                 155                 160                 165

gag aag tagaacggtt cgaccgtact ttt                                624
Glu Lys
```

<210> 1724
<211> 167
<212> PRT
<213> Corynebacterium glutamicum

<400> 1724

```
Met Phe Pro Ser Pro Ala Thr Gly Gly Asp Asp Ile Asn Arg Arg Pro
  1               5                  10                  15

Leu Asn Glu Pro Asn Ala Asp Ala Thr Thr Ile Pro Thr Ala Leu Lys
             20                  25                  30

Val Val Phe Trp Met Leu Phe Ala Thr Ala Ala Phe Met Ile Phe Thr
         35                  40                  45

Gly Leu Val Met Tyr Thr Ala Gly Tyr Thr Gly Pro Asp Asp Val Asp
     50                  55                  60

Glu Ser Tyr Lys Ala Val Val Val Asn Asn Gln Glu Phe Ile Gly Gly
 65                  70                  75                  80

Ile Asn Ala Phe Ala Gly Val Val Ile Ala Ala Leu Thr Ser Gln Leu
                 85                  90                  95

Pro Lys Gly Gly Lys Asn Pro Arg Arg Leu Leu Leu Ala Ile Met Leu
            100                 105                 110

Leu Val Leu Leu Thr Asp Leu Leu Ser Phe Ala Thr Arg Ala Gly Gly
        115                 120                 125

Phe Ala Leu Ala Ile Ile Ala Val Leu Leu Ala Leu Glu Ala Leu Leu
    130                 135                 140

Met Phe Arg Pro Ala Val Asn Asp His Ile Asp Arg Asn His Met Ala
145                 150                 155                 160

Arg Val Met Asn Arg Glu Lys
                165
```

<210> 1725
<211> 744
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(721)
<223> RXA00380

<400> 1725

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caggcaatgc gacctcgcct cagtgacatc cttggtgttc caagacgatc aaattgtcgg 60

cgtgcattac aacgaaccag ctcaggagat ttgatcactc gtg cgt ttg acc aaa   115
                                              Val Arg Leu Thr Lys
                                                1               5

cta gca gca aca atc ggc tgc gtg aca ctc agc gga ctt gcg cta gta   163
Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser Gly Leu Ala Leu Val
                10                  15                  20
```

```
gcc tgc agc agt gac agt acc gct ggt act gac gct gtt gct gtc ggc   211
Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp Ala Val Ala Val Gly
             25                  30                  35

gga acc ttc caa ttc cac tcc ccg gat gga aag atg gaa att ttc tac   259
Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys Met Glu Ile Phe Tyr
         40                  45                  50

gac gag gct gac cgt caa caa ctc ccc gac att ggt gga gat tcc ctc   307
Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile Gly Gly Asp Ser Leu
     55                  60                  65

atg gaa gag ggc aca cag atc aac ctg tct gat ttc gaa aac caa gtt   355
Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp Phe Glu Asn Gln Val
 70                  75                  80                  85

gtc atc ctc aat gcg tgg ggg cag tgg tgt gca ccg tgc cgc tcc gaa   403
Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala Pro Cys Arg Ser Glu
                 90                  95                 100

tcc gat gat ctc cag att atc cat gag gaa ctc caa gct gcc gga aac   451
Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu Gln Ala Ala Gly Asn
            105                 110                 115

ggc gac acc cct ggt ggc acc gtg ttg ggt atc aat gtg cgt gat tac   499
Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile Asn Val Arg Asp Tyr
        120                 125                 130

tcc cgc gac atc gcc caa gac ttt gtc acc gac aac ggc ctt gat tac   547
Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp Asn Gly Leu Asp Tyr
    135                 140                 145

cca agc att tac gat cca cca ttt atg aca gca gca tcc ctc ggt ggt   595
Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala Ala Ser Leu Gly Gly
150                 155                 160                 165

gtt ccc gca tcg gtg atc cca acc acc atc gtg ctg gat aaa cag cac   643
Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val Leu Asp Lys Gln His
                170                 175                 180

cgc ccc gca gca gtg ttc ttg cgc gaa gtc acc tcc aaa gat gtg ttg   691
Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr Ser Lys Asp Val Leu
            185                 190                 195

gat gtt gcg ttg cca ttg gta gat gag gcc taaatgtctg agattgtggt     741
Asp Val Ala Leu Pro Leu Val Asp Glu Ala
        200                 205

agc                                                               744
```

CONFIDENTIAL

<210> 1726
<211> 207
<212> PRT
<213> Corynebacterium glutamicum

<400> 1726

```
Val Arg Leu Thr Lys Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser
  1               5                  10                  15

Gly Leu Ala Leu Val Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp
```

```
            20                  25                  30

Ala Val Ala Val Gly Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys
         35                  40                  45

Met Glu Ile Phe Tyr Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile
     50                  55                  60

Gly Gly Asp Ser Leu Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp
 65                  70                  75                  80

Phe Glu Asn Gln Val Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala
                 85                  90                  95

Pro Cys Arg Ser Glu Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu
            100                 105                 110

Gln Ala Ala Gly Asn Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile
        115                 120                 125

Asn Val Arg Asp Tyr Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp
    130                 135                 140

Asn Gly Leu Asp Tyr Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala
145                 150                 155                 160

Ala Ser Leu Gly Gly Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val
                165                 170                 175

Leu Asp Lys Gln His Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr
            180                 185                 190

Ser Lys Asp Val Leu Asp Val Ala Leu Pro Leu Val Asp Glu Ala
        195                 200                 205


<210> 1727
<211> 836
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(813)
<223> RXA00387

<400> 1727
caa aac gac cca gaa acc tgg gaa gac tac gaa ctt cgc gtc aac cac   48
Gln Asn Asp Pro Glu Thr Trp Glu Asp Tyr Glu Leu Arg Val Asn His
  1               5                  10                  15

cca ctg cgc atc gaa ggc gac cgc gtc tac ctt cag ggc cac ggc ttc   96
Pro Leu Arg Ile Glu Gly Asp Arg Val Tyr Leu Gln Gly His Gly Phe
             20                  25                  30

gcc cca aca ttc acc gtg acc tgg cca aat ggc gag acc cgc acc cag   144
Ala Pro Thr Phe Thr Val Thr Trp Pro Asn Gly Glu Thr Arg Thr Gln
         35                  40                  45

acc gtg cag tgg cgc cca gac gac ccg acc ttc ttc ctg tcc tca ggc   192
Thr Val Gln Trp Arg Pro Asp Asp Pro Thr Phe Phe Leu Ser Ser Gly
```

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     50                  55                  60

gtg gtc cgt ttc gat cca ccc gcc ggc atg tac cca gac ctt tac gag   240
Val Val Arg Phe Asp Pro Pro Ala Gly Met Tyr Pro Asp Leu Tyr Glu
 65                  70                  75                  80

cgc cgc caa aac cag ttg gcc atc cag gga ctt ttc gca ccg acc gcg   288
Arg Arg Gln Asn Gln Leu Ala Ile Gln Gly Leu Phe Ala Pro Thr Ala
                 85                  90                  95

gaa tgg gaa ggc gac aac aac gaa ctg ctg acc tcc tcc tac ccg gcg   336
Glu Trp Glu Gly Asp Asn Asn Glu Leu Leu Thr Ser Ser Tyr Pro Ala
            100                 105                 110

atg cgt gac cca gcc gtg gcg atc gat att tac cgc ggc gac aat ggc   384
Met Arg Asp Pro Ala Val Ala Ile Asp Ile Tyr Arg Gly Asp Asn Gly
        115                 120                 125

ctc gat acc ggc atc gga cag tca ttg ttc agc ctg gac tct agt ctc   432
Leu Asp Thr Gly Ile Gly Gln Ser Leu Phe Ser Leu Asp Ser Ser Leu
    130                 135                 140

atg cac agc ggc gtg ctg caa aaa att gag cgc gtc aac ctc caa atc   480
Met His Ser Gly Val Leu Gln Lys Ile Glu Arg Val Asn Leu Gln Ile
145                 150                 155                 160

ggc gac acc gtc acc ctg gat gat ggc acc acc gtc tcc ttc gac ggc   528
Gly Asp Thr Val Thr Leu Asp Asp Gly Thr Thr Val Ser Phe Asp Gly
                165                 170                 175

gcg tca gaa ttt gcc aac tac cag atc agc cgc gac ccc aca caa aac   576
Ala Ser Glu Phe Ala Asn Tyr Gln Ile Ser Arg Asp Pro Thr Gln Asn
            180                 185                 190

tgg gtg ctg gtc acc acc gtg att tcg ctg gtc tcc ctg gtt gga tcc   624
Trp Val Leu Val Thr Thr Val Ile Ser Leu Val Ser Leu Val Gly Ser
        195                 200                 205

ctg atg atc cga cgc cgc cgc att tgg gtg cgt ttc tat cca caa gaa   672
Leu Met Ile Arg Arg Arg Arg Ile Trp Val Arg Phe Tyr Pro Gln Glu
    210                 215                 220

aac gga acc acc cgc gtg gaa acc ggc gga ctt gcc cgc acc gac cgc   720
Asn Gly Thr Thr Arg Val Glu Thr Gly Gly Leu Ala Arg Thr Asp Arg
225                 230                 235                 240

gca ggc tgg ggt ggc gaa tac gag aaa ttc cac cgc gaa ctg ctg ggt   768
Ala Gly Trp Gly Gly Glu Tyr Glu Lys Phe His Arg Glu Leu Leu Gly
                245                 250                 255

ctg aag gag gaa gat gaa gac gaa gag tac ttc gac cac gac gac       813
Leu Lys Glu Glu Asp Glu Asp Glu Glu Tyr Phe Asp His Asp Asp
            260                 265                 270

taacaccgca atttaaaggc ttt                                        836
```

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<210> 1728
<211> 271
<212> PRT
<213> Corynebacterium glutamicum

<400> 1728

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Gln Asn Asp Pro Glu Thr Trp Glu Asp Tyr Glu Leu Arg Val Asn His
  1               5                  10                  15

Pro Leu Arg Ile Glu Gly Asp Arg Val Tyr Leu Gln Gly His Gly Phe
             20                  25                  30

Ala Pro Thr Phe Thr Val Thr Trp Pro Asn Gly Glu Thr Arg Thr Gln
         35                  40                  45

Thr Val Gln Trp Arg Pro Asp Asp Pro Thr Phe Phe Leu Ser Ser Gly
     50                  55                  60

Val Val Arg Phe Asp Pro Pro Ala Gly Met Tyr Pro Asp Leu Tyr Glu
 65                  70                  75                  80

Arg Arg Gln Asn Gln Leu Ala Ile Gln Gly Leu Phe Ala Pro Thr Ala
                 85                  90                  95

Glu Trp Glu Gly Asp Asn Asn Glu Leu Leu Thr Ser Ser Tyr Pro Ala
            100                 105                 110

Met Arg Asp Pro Ala Val Ala Ile Asp Ile Tyr Arg Gly Asp Asn Gly
        115                 120                 125

Leu Asp Thr Gly Ile Gly Gln Ser Leu Phe Ser Leu Asp Ser Ser Leu
    130                 135                 140

Met His Ser Gly Val Leu Gln Lys Ile Glu Arg Val Asn Leu Gln Ile
145                 150                 155                 160

Gly Asp Thr Val Thr Leu Asp Asp Gly Thr Thr Val Ser Phe Asp Gly
                165                 170                 175

Ala Ser Glu Phe Ala Asn Tyr Gln Ile Ser Arg Asp Pro Thr Gln Asn
            180                 185                 190

Trp Val Leu Val Thr Thr Val Ile Ser Leu Val Ser Leu Val Gly Ser
        195                 200                 205

Leu Met Ile Arg Arg Arg Arg Ile Trp Val Arg Phe Tyr Pro Gln Glu
    210                 215                 220

Asn Gly Thr Thr Arg Val Glu Thr Gly Gly Leu Ala Arg Thr Asp Arg
225                 230                 235                 240

Ala Gly Trp Gly Gly Glu Tyr Glu Lys Phe His Arg Glu Leu Leu Gly
                245                 250                 255

Leu Lys Glu Glu Asp Glu Asp Glu Glu Tyr Phe Asp His Asp Asp
            260                 265                 270
```

<210> 1729
<211> 987
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(964)
<223> RXA00392

<400> 1729
tgcttgaaat acgttcggca ggctatgggg gagtgtgaaa cgctattgtg aaatgaatag 60

ataggttcca tagtcgatcg aggaggagtc gcagaagttt atg tgg gtt ggt tat 115
Met Trp Val Gly Tyr
1 5

gcg gtt cga cag atc gcc agt gtt ttt ctt act ctt ttg cgc atg ctg 163
Ala Val Arg Gln Ile Ala Ser Val Phe Leu Thr Leu Leu Arg Met Leu
10 15 20

cca cta gca gcg cga aat cga gtt gcc agg gga cgc atc ccg gaa acc 211
Pro Leu Ala Ala Arg Asn Arg Val Ala Arg Gly Arg Ile Pro Glu Thr
25 30 35

ggc gat gtg gtg atc tca ttg acc acc cat ggg aag cga att aac tac 259
Gly Asp Val Val Ile Ser Leu Thr Thr His Gly Lys Arg Ile Asn Tyr
40 45 50

gtt cac ttc acc atc gaa tcg atc gca cgc ggc cat gtg aaa gca cca 307
Val His Phe Thr Ile Glu Ser Ile Ala Arg Gly His Val Lys Ala Pro
55 60 65

att gtg ctg tgg ttg gac aaa cca gac ttt gat gcg ccg tgg cct gcc 355
Ile Val Leu Trp Leu Asp Lys Pro Asp Phe Asp Ala Pro Trp Pro Ala
70 75 80 85

acc att aag cga ctt gtc gcc cgc ggt ctg caa gta cgg tgc agc gac 403
Thr Ile Lys Arg Leu Val Ala Arg Gly Leu Gln Val Arg Cys Ser Asp
90 95 100

ggc ttc tac ggc ccc cac acc aaa tac tgg aac caa ttc cga gaa atc 451
Gly Phe Tyr Gly Pro His Thr Lys Tyr Trp Asn Gln Phe Arg Glu Ile
105 110 115

cac ggc acc ggc gtg cgt gtc gcc acc gtc gac gat gac atg atc tac 499
His Gly Thr Gly Val Arg Val Ala Thr Val Asp Asp Asp Met Ile Tyr
120 125 130

ccc gag tgg ttc ctg cag cgc ttg ctt ttt att ggc gac ctg cgc atg 547
Pro Glu Trp Phe Leu Gln Arg Leu Leu Phe Ile Gly Asp Leu Arg Met
135 140 145

gat gcg gtt gtc gcc tac cgg gcg cac aga att gag ctt cgc gac gac 595
Asp Ala Val Val Ala Tyr Arg Ala His Arg Ile Glu Leu Arg Asp Asp
150 155 160 165

cga atg ctc ccg tac gtt aaa tgg agt gcc gca gac acc tca aaa gcg 643
Arg Met Leu Pro Tyr Val Lys Trp Ser Ala Ala Asp Thr Ser Lys Ala
170 175 180

tca ttc ctg cac ttt gcc acg gga gtg tca ggc gtt ttg tac ccc gtg 691
Ser Phe Leu His Phe Ala Thr Gly Val Ser Gly Val Leu Tyr Pro Val
185 190 195

acc ttc att gat tat gtg gtc tcc cag ggc gat gta ttc ctt gag aac 739
Thr Phe Ile Asp Tyr Val Val Ser Gln Gly Asp Val Phe Leu Glu Asn
200 205 210

```
tgc aag cgc gcc gat gac gta tgg ctg cat gcc tgc gca ctg cgc tct   787
Cys Lys Arg Ala Asp Asp Val Trp Leu His Ala Cys Ala Leu Arg Ser
    215                 220                 225

gat cac cct att cgc cag gtc tac gct cag ccc cga cac ttc gct gtc   835
Asp His Pro Ile Arg Gln Val Tyr Ala Gln Pro Arg His Phe Ala Val
230                 235                 240                 245

gtg ccc acc acc caa gtg gga gca cta gtt gtt ggc aac acc ctc atg   883
Val Pro Thr Thr Gln Val Gly Ala Leu Val Val Gly Asn Thr Leu Met
                250                 255                 260

ggt gga aat gat gag cag atc gcc aaa gtg tac acc gat gaa gat gtg   931
Gly Gly Asn Asp Glu Gln Ile Ala Lys Val Tyr Thr Asp Glu Asp Val
            265                 270                 275

gca aaa cta gtt gca gcc agc aag aat gaa gac taaaacagct tcgcgatagc 984
Ala Lys Leu Val Ala Ala Ser Lys Asn Glu Asp
        280                 285

acg                                                               987
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<210> 1730
<211> 288
<212> PRT
<213> Corynebacterium glutamicum

<400> 1730

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Met Trp Val Gly Tyr Ala Val Arg Gln Ile Ala Ser Val Phe Leu Thr
  1               5                  10                  15

Leu Leu Arg Met Leu Pro Leu Ala Ala Arg Asn Arg Val Ala Arg Gly
             20                  25                  30

Arg Ile Pro Glu Thr Gly Asp Val Val Ile Ser Leu Thr Thr His Gly
         35                  40                  45

Lys Arg Ile Asn Tyr Val His Phe Thr Ile Glu Ser Ile Ala Arg Gly
     50                  55                  60

His Val Lys Ala Pro Ile Val Leu Trp Leu Asp Lys Pro Asp Phe Asp
 65                  70                  75                  80

Ala Pro Trp Pro Ala Thr Ile Lys Arg Leu Val Ala Arg Gly Leu Gln
                 85                  90                  95

Val Arg Cys Ser Asp Gly Phe Tyr Gly Pro His Thr Lys Tyr Trp Asn
            100                 105                 110

Gln Phe Arg Glu Ile His Gly Thr Gly Val Arg Val Ala Thr Val Asp
        115                 120                 125

Asp Asp Met Ile Tyr Pro Glu Trp Phe Leu Gln Arg Leu Leu Phe Ile
    130                 135                 140

Gly Asp Leu Arg Met Asp Ala Val Val Ala Tyr Arg Ala His Arg Ile
145                 150                 155                 160

Glu Leu Arg Asp Asp Arg Met Leu Pro Tyr Val Lys Trp Ser Ala Ala
```

```
                165                 170                 175

Asp Thr Ser Lys Ala Ser Phe Leu His Phe Ala Thr Gly Val Ser Gly
            180                 185                 190

Val Leu Tyr Pro Val Thr Phe Ile Asp Tyr Val Val Ser Gln Gly Asp
        195                 200                 205

Val Phe Leu Glu Asn Cys Lys Arg Ala Asp Asp Val Trp Leu His Ala
    210                 215                 220

Cys Ala Leu Arg Ser Asp His Pro Ile Arg Gln Val Tyr Ala Gln Pro
225                 230                 235                 240

Arg His Phe Ala Val Val Pro Thr Thr Gln Val Gly Ala Leu Val Val
                245                 250                 255

Gly Asn Thr Leu Met Gly Gly Asn Asp Glu Gln Ile Ala Lys Val Tyr
            260                 265                 270

Thr Asp Glu Asp Val Ala Lys Leu Val Ala Ala Ser Lys Asn Glu Asp
        275                 280                 285
```

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<210> 1731
<211> 456
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(433)
<223> RXA00394

<400> 1731

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acccacttga acctctcctt aaatatttgc ttcaacctcc cacaatacgg aactttgagg 60

cattcttggg tatcggtatg tattgagtag ggttgaatat gtg agt gag tcc aat   115
                                            Val Ser Glu Ser Asn
                                              1               5

acc ccc aat ctc cag aca cac caa gcg ccg gaa tta aac ccg gaa cta   163
Thr Pro Asn Leu Gln Thr His Gln Ala Pro Glu Leu Asn Pro Glu Leu
                  10                  15                  20

caa aaa gct gcc cgg aaa aac gtg ctg att tac ggt ctg gca cgt ttg   211
Gln Lys Ala Ala Arg Lys Asn Val Leu Ile Tyr Gly Leu Ala Arg Leu
             25                  30                  35

ctt ctg ttc gtc gtg ctg acc ttg att att cat agc ctg gct ctg ctg   259
Leu Leu Phe Val Val Leu Thr Leu Ile Ile His Ser Leu Ala Leu Leu
         40                  45                  50

att agt gcg cct gtg cca ctc gtt atg tct gcg atg ctg gct ctg att   307
Ile Ser Ala Pro Val Pro Leu Val Met Ser Ala Met Leu Ala Leu Ile
     55                  60                  65

gtg gcg ttc cca ttg tcc atg ctg gtg ttc agc aaa ctg cgc atg aat   355
```

```
Val Ala Phe Pro Leu Ser Met Leu Val Phe Ser Lys Leu Arg Met Asn
 70                  75                  80                  85

gcc acc cag gct gtt tcc cag tgg gat gca cag cgc aag gcc cac aag   403
Ala Thr Gln Ala Val Ser Gln Trp Asp Ala Gln Arg Lys Ala His Lys
                 90                  95                 100

gaa tgg gtt cga agc gag ctg gcg gac cgc taaaaaattc ccctcgttct     453
Glu Trp Val Arg Ser Glu Leu Ala Asp Arg
            105                 110

ttg                                                               456


<210> 1732
<211> 111
<212> PRT
<213> Corynebacterium glutamicum

<400> 1732
Val Ser Glu Ser Asn Thr Pro Asn Leu Gln Thr His Gln Ala Pro Glu
  1               5                  10                  15

Leu Asn Pro Glu Leu Gln Lys Ala Ala Arg Lys Asn Val Leu Ile Tyr
             20                  25                  30

Gly Leu Ala Arg Leu Leu Leu Phe Val Val Leu Thr Leu Ile Ile His
         35                  40                  45

Ser Leu Ala Leu Leu Ile Ser Ala Pro Val Pro Leu Val Met Ser Ala
     50                  55                  60

Met Leu Ala Leu Ile Val Ala Phe Pro Leu Ser Met Leu Val Phe Ser
 65                  70                  75                  80

Lys Leu Arg Met Asn Ala Thr Gln Ala Val Ser Gln Trp Asp Ala Gln
                 85                  90                  95

Arg Lys Ala His Lys Glu Trp Val Arg Ser Glu Leu Ala Asp Arg
            100                 105                 110


<210> 1733
<211> 423
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(400)
<223> RXA00395

<400> 1733
actcacatat tcaaccctac tcaatacata ccgataccca agaatgcctc aaagttccgt 60

attgtgggag gttgaagcaa atatttaagg agaggttcaa gtg ggt agg ctt ttg   115
                                               Val Gly Arg Leu Leu
                                                 1               5

ctg att att ttg gtt atc gtc gca atc gtc ttg ctg tgg aag gcc ttc   163
Leu Ile Ile Leu Val Ile Val Ala Ile Val Leu Leu Trp Lys Ala Phe
```

```
                10                  15                  20

aag cca tct aca tgg aag cgt aac gcg gag atc aat cag ggc cag gca   211
Lys Pro Ser Thr Trp Lys Arg Asn Ala Glu Ile Asn Gln Gly Gln Ala
            25                  30                  35

cct cgt gca gtg aaa ggc ccc gac gat gat gaa gaa ttc ttg tgg aat   259
Pro Arg Ala Val Lys Gly Pro Asp Asp Asp Glu Glu Phe Leu Trp Asn
        40                  45                  50

att gaa aag aat cgc ttc aaa cag cgt cgc gcc gac gag gct gcc caa   307
Ile Glu Lys Asn Arg Phe Lys Gln Arg Arg Ala Asp Glu Ala Ala Gln
    55                  60                  65

tta gaa gag gaa gaa cgt ctc aaa cgg gcc agg gaa cgc tac gca aag   355
Leu Glu Glu Glu Glu Arg Leu Lys Arg Ala Arg Glu Arg Tyr Ala Lys
70                  75                  80                  85

cct gaa agc tca gaa gaa ggt cca gag aag ccc act gag gat tct       400
Pro Glu Ser Ser Glu Glu Gly Pro Glu Lys Pro Thr Glu Asp Ser
                90                  95                  100

taaaagggct tctttaaaaa gat                                        423


<210> 1734
<211> 100
<212> PRT
<213> Corynebacterium glutamicum

<400> 1734
Val Gly Arg Leu Leu Leu Ile Ile Leu Val Ile Val Ala Ile Val Leu
  1               5                  10                  15

Leu Trp Lys Ala Phe Lys Pro Ser Thr Trp Lys Arg Asn Ala Glu Ile
            20                  25                  30

Asn Gln Gly Gln Ala Pro Arg Ala Val Lys Gly Pro Asp Asp Asp Glu
        35                  40                  45

Glu Phe Leu Trp Asn Ile Glu Lys Asn Arg Phe Lys Gln Arg Arg Ala
    50                  55                  60

Asp Glu Ala Ala Gln Leu Glu Glu Glu Glu Arg Leu Lys Arg Ala Arg
65                  70                  75                  80

Glu Arg Tyr Ala Lys Pro Glu Ser Ser Glu Glu Gly Pro Glu Lys Pro
                85                  90                  95

Thr Glu Asp Ser
            100


<210> 1735
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
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<223> RXA00396

<400> 1735

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atcccttggc gctacaacgg tgtagccatt ggtaccgagg atctgtggta catcggcgca 60

gacaagacct acattttgag ccagcgctaa ggagaaccca gtg aca gaa att gca   115
                                             Val Thr Glu Ile Ala
                                               1               5

gaa aac ctt cag cgc ttg ggt att gaa tta cct gat cta cca gca ccg   163
Glu Asn Leu Gln Arg Leu Gly Ile Glu Leu Pro Asp Leu Pro Ala Pro
                 10                  15                  20

cag tat tcc tac gta ccg ttc aac cgc caa gga aac acc ctc tat gta   211
Gln Tyr Ser Tyr Val Pro Phe Asn Arg Gln Gly Asn Thr Leu Tyr Val
             25                  30                  35

tcg ggg cag att tca cga acc gca gcg gga gac atc ctc gcc gga cga   259
Ser Gly Gln Ile Ser Arg Thr Ala Ala Gly Asp Ile Leu Ala Gly Arg
         40                  45                  50

gtt ggc gaa gac gca aca tta gaa gaa gga atc cac gcc gca gag gta   307
Val Gly Glu Asp Ala Thr Leu Glu Glu Gly Ile His Ala Ala Glu Val
     55                  60                  65

gcc acc atc aat ctg ctg gcc aga atc cac caa tcc atc ggt tta gac   355
Ala Thr Ile Asn Leu Leu Ala Arg Ile His Gln Ser Ile Gly Leu Asp
 70                  75                  80                  85

aat gtg gcc caa att ctg aaa ctg aat gtg tgg gtc aat agc tcc gat   403
Asn Val Ala Gln Ile Leu Lys Leu Asn Val Trp Val Asn Ser Ser Asp
                 90                  95                 100

gac ttt att cag cag cct caa gtg gcc gac ggt gca tcc cag ctc ctt   451
Asp Phe Ile Gln Gln Pro Gln Val Ala Asp Gly Ala Ser Gln Leu Leu
            105                 110                 115

gag gca gtg ttg ggt gag gcc gga aaa cat gca cgc aca gca cta ccc   499
Glu Ala Val Leu Gly Glu Ala Gly Lys His Ala Arg Thr Ala Leu Pro
        120                 125                 130

aca aat act ctc ccc cag gga gca cta gtg gaa ttg gat gct gtc gtt   547
Thr Asn Thr Leu Pro Gln Gly Ala Leu Val Glu Leu Asp Ala Val Val
    135                 140                 145

gcg gtc acc gag gcc gcc gaa gtt taggacgcgt gggcgaaaat ttc         594
Ala Val Thr Glu Ala Ala Glu Val
150                 155
```

<210> 1736
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 1736

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Val Thr Glu Ile Ala Glu Asn Leu Gln Arg Leu Gly Ile Glu Leu Pro
  1               5                  10                  15

Asp Leu Pro Ala Pro Gln Tyr Ser Tyr Val Pro Phe Asn Arg Gln Gly
             20                  25                  30
```

```
Asn Thr Leu Tyr Val Ser Gly Gln Ile Ser Arg Thr Ala Ala Gly Asp
          35                  40                  45

Ile Leu Ala Gly Arg Val Gly Glu Asp Ala Thr Leu Glu Glu Gly Ile
      50                  55                  60

His Ala Ala Glu Val Ala Thr Ile Asn Leu Leu Ala Arg Ile His Gln
 65                  70                  75                  80

Ser Ile Gly Leu Asp Asn Val Ala Gln Ile Leu Lys Leu Asn Val Trp
                 85                  90                  95

Val Asn Ser Ser Asp Asp Phe Ile Gln Gln Pro Gln Val Ala Asp Gly
            100                 105                 110

Ala Ser Gln Leu Leu Glu Ala Val Leu Gly Glu Ala Gly Lys His Ala
        115                 120                 125

Arg Thr Ala Leu Pro Thr Asn Thr Leu Pro Gln Gly Ala Leu Val Glu
    130                 135                 140

Leu Asp Ala Val Val Ala Val Thr Glu Ala Ala Glu Val
145                 150                 155


<210> 1737
<211> 563
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(540)
<223> RXA00397

<400> 1737
aac ctg cac tcc tcc aac aga atg ctc ttc cct gga cct cct gtg gat   48
Asn Leu His Ser Ser Asn Arg Met Leu Phe Pro Gly Pro Pro Val Asp
  1               5                  10                  15

ttc ccg atc aac gca gaa acc cga tgc att cag ctc gac gcc ggt gtt   96
Phe Pro Ile Asn Ala Glu Thr Arg Cys Ile Gln Leu Asp Ala Gly Val
             20                  25                  30

gca gta aag aag gac ggc gtg gtg ctg ggt acc tca gat atg gcg agg   144
Ala Val Lys Lys Asp Gly Val Val Leu Gly Thr Ser Asp Met Ala Arg
         35                  40                  45

tcc ctg cct cga acc gcc gct ggc caa gaa gcc tat gag tac ttc ttc   192
Ser Leu Pro Arg Thr Ala Ala Gly Gln Glu Ala Tyr Glu Tyr Phe Phe
     50                  55                  60

aag gtg gtt cgt gaa ggc atc atc ggg cag ctg cgc ccg ggc gtg atc   240
Lys Val Val Arg Glu Gly Ile Ile Gly Gln Leu Arg Pro Gly Val Ile
 65                  70                  75                  80

tgc gct gac gtg cac gaa gca acc ctt gat tac cta agc ccg cag cta   288
Cys Ala Asp Val His Glu Ala Thr Leu Asp Tyr Leu Ser Pro Gln Leu
                 85                  90                  95
```

```
cct cgc atg att gac atc gga atg ctg ggt gcc gac acc gat ttc aac   336
Pro Arg Met Ile Asp Ile Gly Met Leu Gly Ala Asp Thr Asp Phe Asn
            100                 105                 110

acc atc tac cgc aag cgc aat gtt ggc cac ctc atg ggc aag cag gaa   384
Thr Ile Tyr Arg Lys Arg Asn Val Gly His Leu Met Gly Lys Gln Glu
        115                 120                 125

tcc ttt gcc aat gag ctt cgc cct gga tac aag cac att ctt cac cac   432
Ser Phe Ala Asn Glu Leu Arg Pro Gly Tyr Lys His Ile Leu His His
    130                 135                 140

ggc tcc tat ggt gcc gcg gag atc cct tgg cgc tac aac ggt gta gcc   480
Gly Ser Tyr Gly Ala Ala Glu Ile Pro Trp Arg Tyr Asn Gly Val Ala
145                 150                 155                 160

att ggt acc gag gat ctg tgg tac atc ggc gca gac aag acc tac att   528
Ile Gly Thr Glu Asp Leu Trp Tyr Ile Gly Ala Asp Lys Thr Tyr Ile
                165                 170                 175

ttg agc cag cgc taaggagaac ccagtgacag aaa                        563
Leu Ser Gln Arg
            180
```

<210> 1738
<211> 180
<212> PRT
<213> Corynebacterium glutamicum

<400> 1738

```
Asn Leu His Ser Ser Asn Arg Met Leu Phe Pro Gly Pro Pro Val Asp
  1               5                  10                  15

Phe Pro Ile Asn Ala Glu Thr Arg Cys Ile Gln Leu Asp Ala Gly Val
             20                  25                  30

Ala Val Lys Lys Asp Gly Val Val Leu Gly Thr Ser Asp Met Ala Arg
         35                  40                  45

Ser Leu Pro Arg Thr Ala Ala Gly Gln Glu Ala Tyr Glu Tyr Phe Phe
     50                  55                  60

Lys Val Val Arg Glu Gly Ile Ile Gly Gln Leu Arg Pro Gly Val Ile
 65                  70                  75                  80

Cys Ala Asp Val His Glu Ala Thr Leu Asp Tyr Leu Ser Pro Gln Leu
                 85                  90                  95

Pro Arg Met Ile Asp Ile Gly Met Leu Gly Ala Asp Thr Asp Phe Asn
            100                 105                 110

Thr Ile Tyr Arg Lys Arg Asn Val Gly His Leu Met Gly Lys Gln Glu
        115                 120                 125

Ser Phe Ala Asn Glu Leu Arg Pro Gly Tyr Lys His Ile Leu His His
    130                 135                 140

Gly Ser Tyr Gly Ala Ala Glu Ile Pro Trp Arg Tyr Asn Gly Val Ala
145                 150                 155                 160
```

```
Ile Gly Thr Glu Asp Leu Trp Tyr Ile Gly Ala Asp Lys Thr Tyr Ile
                165                 170                 175

Leu Ser Gln Arg
            180
```

<210> 1739
<211> 704
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(681)
<223> RXA00398

<400> 1739

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tac ctc ccc gag cct ttc acc gtg gag gat tac act gcg cgt gtt gaa   48
Tyr Leu Pro Glu Pro Phe Thr Val Glu Asp Tyr Thr Ala Arg Val Glu
  1               5                  10                  15

ggc ctc gaa gtt gct ggc gga gcg att gtt tcc ggt tct ttc cag gct   96
Gly Leu Glu Val Ala Gly Gly Ala Ile Val Ser Gly Ser Phe Gln Ala
            20                  25                  30

ttc gac cag ggc tac ctc aaa gat gct ctc gca gtg ctt ggc cca ggc   144
Phe Asp Gln Gly Tyr Leu Lys Asp Ala Leu Ala Val Leu Gly Pro Gly
        35                  40                  45

tat gtc ggt gtc act cag atc ccc gca gat acc tct gat cag gag att   192
Tyr Val Gly Val Thr Gln Ile Pro Ala Asp Thr Ser Asp Gln Glu Ile
    50                  55                  60

ctt gat ctg gac aaa gct ggc gtg aag gct gtg cgt tta aac ttg aag   240
Leu Asp Leu Asp Lys Ala Gly Val Lys Ala Val Arg Leu Asn Leu Lys
65                  70                  75                  80

cgc ggt ggt tcg gca ggt ctt gac gat ctc gag acc ttg gca cgc cga   288
Arg Gly Gly Ser Ala Gly Leu Asp Asp Leu Glu Thr Leu Ala Arg Arg
                85                  90                  95

gtc cac gac cta gcc ggt tgg cac acc gaa ctc tat gtg gat gct cgc   336
Val His Asp Leu Ala Gly Trp His Thr Glu Leu Tyr Val Asp Ala Arg
            100                 105                 110

gaa cta gac gag ttg gaa tca acc ttg gcc tcc ctc cct gct gtc agc   384
Glu Leu Asp Glu Leu Glu Ser Thr Leu Ala Ser Leu Pro Ala Val Ser
        115                 120                 125

att gat cac tta ggg ctc cac cgc gat gga ctt ccc gca ctt ctt cgc   432
Ile Asp His Leu Gly Leu His Arg Asp Gly Leu Pro Ala Leu Leu Arg
    130                 135                 140

ttg gta gaa aat ggc att aaa gtc aaa gca acc gga ttc gga cgg gta   480
Leu Val Glu Asn Gly Ile Lys Val Lys Ala Thr Gly Phe Gly Arg Val
145                 150                 155                 160

gaa cta gat cca act gaa gtc atc cag gca atc atg gct gtc gat ccc   528
Glu Leu Asp Pro Thr Glu Val Ile Gln Ala Ile Met Ala Val Asp Pro
                165                 170                 175
```

```
act gct ttg atg atc gga act gat ctt cca tcc acc cgc act aag cga   576
Thr Ala Leu Met Ile Gly Thr Asp Leu Pro Ser Thr Arg Thr Lys Arg
            180                 185                 190

cct ttc gaa gac gct gac cta gat ttg atc gct gaa acg gtt ggc gaa   624
Pro Phe Glu Asp Ala Asp Leu Asp Leu Ile Ala Glu Thr Val Gly Glu
        195                 200                 205

gat cat gtc gac aac gtc ttc tgg aac aac gct gca gcg ttc tac ctc   672
Asp His Val Asp Asn Val Phe Trp Asn Asn Ala Ala Ala Phe Tyr Leu
    210                 215                 220

gga gac cag tagttttaag acccgaaatg tct                            704
Gly Asp Gln
225
```

<210> 1740
<211> 227
<212> PRT
<213> Corynebacterium glutamicum

<400> 1740

```
Tyr Leu Pro Glu Pro Phe Thr Val Glu Asp Tyr Thr Ala Arg Val Glu
  1               5                  10                  15

Gly Leu Glu Val Ala Gly Gly Ala Ile Val Ser Gly Ser Phe Gln Ala
            20                  25                  30

Phe Asp Gln Gly Tyr Leu Lys Asp Ala Leu Ala Val Leu Gly Pro Gly
        35                  40                  45

Tyr Val Gly Val Thr Gln Ile Pro Ala Asp Thr Ser Asp Gln Glu Ile
    50                  55                  60

Leu Asp Leu Asp Lys Ala Gly Val Lys Ala Val Arg Leu Asn Leu Lys
65                  70                  75                  80

Arg Gly Gly Ser Ala Gly Leu Asp Asp Leu Glu Thr Leu Ala Arg Arg
                85                  90                  95

Val His Asp Leu Ala Gly Trp His Thr Glu Leu Tyr Val Asp Ala Arg
            100                 105                 110

Glu Leu Asp Glu Leu Glu Ser Thr Leu Ala Ser Leu Pro Ala Val Ser
        115                 120                 125

Ile Asp His Leu Gly Leu His Arg Asp Gly Leu Pro Ala Leu Leu Arg
    130                 135                 140

Leu Val Glu Asn Gly Ile Lys Val Lys Ala Thr Gly Phe Gly Arg Val
145                 150                 155                 160

Glu Leu Asp Pro Thr Glu Val Ile Gln Ala Ile Met Ala Val Asp Pro
                165                 170                 175

Thr Ala Leu Met Ile Gly Thr Asp Leu Pro Ser Thr Arg Thr Lys Arg
            180                 185                 190

Pro Phe Glu Asp Ala Asp Leu Asp Leu Ile Ala Glu Thr Val Gly Glu
```

```
        195                 200                 205

Asp His Val Asp Asn Val Phe Trp Asn Asn Ala Ala Ala Phe Tyr Leu
    210                 215                 220

Gly Asp Gln
225
```

<210> 1741
<211> 570
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(547)
<223> RXA00408

<400> 1741

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ggggggagttt ctcagccgtg gctcacgaga ttttcgataa tttggcaaag tggacattat 60

gacaaatacg cacaggcgaa ccccagaacc acatgagggc atg aat cca gtg tca   115
                                          Met Asn Pro Val Ser
                                            1               5

cca aaa ctg acc acg gcc agg tac ctc acc cgc att cca tgg ctg ctg   163
Pro Lys Leu Thr Thr Ala Arg Tyr Leu Thr Arg Ile Pro Trp Leu Leu
                10                  15                  20

atc agc gcg att gtg ttt ggg gtg ctt gga gtt ttt gtg tct tcg tgg   211
Ile Ser Ala Ile Val Phe Gly Val Leu Gly Val Phe Val Ser Ser Trp
            25                  30                  35

ttt tac gcc ggt gtg atc gta gtt gcc gtc att ctt atc tgg cag ctg   259
Phe Tyr Ala Gly Val Ile Val Val Ala Val Ile Leu Ile Trp Gln Leu
        40                  45                  50

tgg ctg atc ccg cag cag gtc aag cga ctg gga tgg ctg gaa acc tcc   307
Trp Leu Ile Pro Gln Gln Val Lys Arg Leu Gly Trp Leu Glu Thr Ser
    55                  60                  65

gat gag ctg ctg atc acc aag gga aaa ctg tgg cac acc ttc acg gtt   355
Asp Glu Leu Leu Ile Thr Lys Gly Lys Leu Trp His Thr Phe Thr Val
70                  75                  80                  85

gtt ccc tat ggc cgc atc cag ttt gtt gat gtc acc gca ggt ccc ctc   403
Val Pro Tyr Gly Arg Ile Gln Phe Val Asp Val Thr Ala Gly Pro Leu
                90                  95                  100

gag cgc gcg ttt ggc atg aaa caa gtg caa ttg cat acc gcg tcg gcg   451
Glu Arg Ala Phe Gly Met Lys Gln Val Gln Leu His Thr Ala Ser Ala
            105                 110                 115

tcc tct gac tcc acc att caa ggc ctg cct gtc gcg gaa gcc gat gcc   499
Ser Ser Asp Ser Thr Ile Gln Gly Leu Pro Val Ala Glu Ala Asp Ala
        120                 125                 130

tta cgt gag cga ctg gct att aag gcc cgg gag agg atg agc gga cta   547
Leu Arg Glu Arg Leu Ala Ile Lys Ala Arg Glu Arg Met Ser Gly Leu
    135                 140                 145
```

tgagcagcct tgaagggttt cga 570

<210> 1742
<211> 149
<212> PRT
<213> Corynebacterium glutamicum

<400> 1742
Met Asn Pro Val Ser Pro Lys Leu Thr Thr Ala Arg Tyr Leu Thr Arg
1 5 10 15

Ile Pro Trp Leu Leu Ile Ser Ala Ile Val Phe Gly Val Leu Gly Val
20 25 30

Phe Val Ser Ser Trp Phe Tyr Ala Gly Val Ile Val Val Ala Val Ile
35 40 45

Leu Ile Trp Gln Leu Trp Leu Ile Pro Gln Gln Val Lys Arg Leu Gly
50 55 60

Trp Leu Glu Thr Ser Asp Glu Leu Leu Ile Thr Lys Gly Lys Leu Trp
65 70 75 80

His Thr Phe Thr Val Val Pro Tyr Gly Arg Ile Gln Phe Val Asp Val
85 90 95

Thr Ala Gly Pro Leu Glu Arg Ala Phe Gly Met Lys Gln Val Gln Leu
100 105 110

His Thr Ala Ser Ala Ser Ser Asp Ser Thr Ile Gln Gly Leu Pro Val
115 120 125

Ala Glu Ala Asp Ala Leu Arg Glu Arg Leu Ala Ile Lys Ala Arg Glu
130 135 140

Arg Met Ser Gly Leu
145

<210> 1743
<211> 1536
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1513)
<223> RXA00409

<400> 1743
cggcgtcctc tgactccacc attcaaggcc tgcctgtcgc ggaagccgat gccttacgtg 60

agcgactggc tattaaggcc cgggagagga tgagcggact atg agc agc ctt gaa 115
Met Ser Ser Leu Glu
1 5

ggg ttt cga aaa gtc cac cgc gcc acc cca ttc ctt cgc atc tgg acc 163
Gly Phe Arg Lys Val His Arg Ala Thr Pro Phe Leu Arg Ile Trp Thr
10 15 20

```
atc atc gtc gca gtt ctc gcg gca ttc gca ttc aat tcc ggc gca tcc   211
Ile Ile Val Ala Val Leu Ala Ala Phe Ala Phe Asn Ser Gly Ala Ser
          25                  30                  35

gtt tta agt ttc atc tgg ggt gtc gtc acc ggc gaa tac gga ttc gca   259
Val Leu Ser Phe Ile Trp Gly Val Val Thr Gly Glu Tyr Gly Phe Ala
        40                  45                  50

gtg ctg ccg att cta ttg acc gtc ggt ggc gcc gtc att gtg gtg gca   307
Val Leu Pro Ile Leu Leu Thr Val Gly Gly Ala Val Ile Val Val Ala
    55                  60                  65

ctg gcc tgg att atc acc gga att tgg tgg aaa gcc gtc gga ttc cgc   355
Leu Ala Trp Ile Ile Thr Gly Ile Trp Trp Lys Ala Val Gly Phe Arg
70                  75                  80                  85

atc acc aat gaa gag gtg cag ctg caa cgc gga gtg atc agc aaa gac   403
Ile Thr Asn Glu Glu Val Gln Leu Gln Arg Gly Val Ile Ser Lys Asp
                90                  95                 100

ctc cgc acc gcc cga ttt gac cgt atc caa gcc gtt gac ctg gtg gaa   451
Leu Arg Thr Ala Arg Phe Asp Arg Ile Gln Ala Val Asp Leu Val Glu
            105                 110                 115

tca ttc atc gcc cgt atc ttc cga ctg gca gaa gtc cgc atc gaa acc   499
Ser Phe Ile Ala Arg Ile Phe Arg Leu Ala Glu Val Arg Ile Glu Thr
        120                 125                 130

gcc ggc ggc agc gac tcc gcc atc agc att ggc ttt tta aga aaa agc   547
Ala Gly Gly Ser Asp Ser Ala Ile Ser Ile Gly Phe Leu Arg Lys Ser
    135                 140                 145

gag gcc gag gcc cta aaa agg gag ctt ctc gac gcc tcc cag cac tca   595
Glu Ala Glu Ala Leu Lys Arg Glu Leu Leu Asp Ala Ser Gln His Ser
150                 155                 160                 165

gtc gcc acc acc cca gcc gga gtt ccg gct gag cct ggg gta ggg gag   643
Val Ala Thr Thr Pro Ala Gly Val Pro Ala Glu Pro Gly Val Gly Glu
                170                 175                 180

acc gtt gta gtt gag agc gcg ggc gat gtt ctg gtt cca caa atc ccc   691
Thr Val Val Val Glu Ser Ala Gly Asp Val Leu Val Pro Gln Ile Pro
            185                 190                 195

gtg caa cgc acc ctc gcc agc acc gcc tta tca cta gca acc atc atc   739
Val Gln Arg Thr Leu Ala Ser Thr Ala Leu Ser Leu Ala Thr Ile Ile
        200                 205                 210

acc gcg atc ggt att gtg att ttg ctc ttc gtt cct ttc gga gtg agc   787
Thr Ala Ile Gly Ile Val Ile Leu Leu Phe Val Pro Phe Gly Val Ser
    215                 220                 225

att gcc gtg ccg ttc ttt gta ggc atg gtg cca gcg gtc tgg aac ttg   835
Ile Ala Val Pro Phe Phe Val Gly Met Val Pro Ala Val Trp Asn Leu
230                 235                 240                 245

atc gat aag tcg tgg caa ttc acc gca aca cag cgc aac gat gtc ctg   883
Ile Asp Lys Ser Trp Gln Phe Thr Ala Thr Gln Arg Asn Asp Val Leu
                250                 255                 260
```

```
cat gtc agc tat gga ctt gcc aac cgc cgc aaa caa tca atc cca ctg   931
His Val Ser Tyr Gly Leu Ala Asn Arg Arg Lys Gln Ser Ile Pro Leu
            265                 270                 275

gga cgc atc cac gca gtg aaa cta aaa cag cca ttg ctg tgg cga ctg   979
Gly Arg Ile His Ala Val Lys Leu Lys Gln Pro Leu Leu Trp Arg Leu
        280                 285                 290

gtt ggc tgg tgg acc gtg acc gtg cct gta gtt ggc tac ggc gac acc   1027
Val Gly Trp Trp Thr Val Thr Val Pro Val Val Gly Tyr Gly Asp Thr
    295                 300                 305

acc caa ggc gga acc tcc aaa atc ttg ccc gtg ggt tcc aaa gaa ctc   1075
Thr Gln Gly Gly Thr Ser Lys Ile Leu Pro Val Gly Ser Lys Glu Leu
310                 315                 320                 325

gca cta aaa gtc ctt gaa gcg gtg ggg cca cta aac agc gcc gac atc   1123
Ala Leu Lys Val Leu Glu Ala Val Gly Pro Leu Asn Ser Ala Asp Ile
                330                 335                 340

gcc gaa tct gca gac cca tca cat atg agc aga ccc cag tac aca cca   1171
Ala Glu Ser Ala Asp Pro Ser His Met Ser Arg Pro Gln Tyr Thr Pro
            345                 350                 355

cca gtt gct gca cgc ctg ctc aca cca gtc gat cgg acc cgc caa ggc   1219
Pro Val Ala Ala Arg Leu Leu Thr Pro Val Asp Arg Thr Arg Gln Gly
        360                 365                 370

gtc acg ttg att ggt gtg gct ggt gcc cct ggt gcg gtg gtc gtg cat   1267
Val Thr Leu Ile Gly Val Ala Gly Ala Pro Gly Ala Val Val Val His
    375                 380                 385

gaa ggc aga ttc atg cca cgt atg tct gtg att gat acc tcc cac atc   1315
Glu Gly Arg Phe Met Pro Arg Met Ser Val Ile Asp Thr Ser His Ile
390                 395                 400                 405

caa gaa ctc acc ctt aaa cac ggg ccg atc caa aga ata ctg gga ctc   1363
Gln Glu Leu Thr Leu Lys His Gly Pro Ile Gln Arg Ile Leu Gly Leu
                410                 415                 420

tcc acc gtt gtg ttt aac ctg gtc caa ggg cca gtg gga atg gcc gca   1411
Ser Thr Val Val Phe Asn Leu Val Gln Gly Pro Val Gly Met Ala Ala
            425                 430                 435

tcg gat ctc agt gca gct gat gga aaa gaa ctt ctc aac att ctc cgc   1459
Ser Asp Leu Ser Ala Ala Asp Gly Lys Glu Leu Leu Asn Ile Leu Arg
        440                 445                 450

aac aga aaa cta ccc gca ctg gaa tca gct ccg ctg gga caa aac agc   1507
Asn Arg Lys Leu Pro Ala Leu Glu Ser Ala Pro Leu Gly Gln Asn Ser
    455                 460                 465

ctg gac taaggtgtaa tcatgcacat ctc                                1536
Leu Asp
470
```

<210> 1744
<211> 471
<212> PRT
<213> Corynebacterium glutamicum

<400> 1744

```
Met Ser Ser Leu Glu Gly Phe Arg Lys Val His Arg Ala Thr Pro Phe
  1               5                  10                  15

Leu Arg Ile Trp Thr Ile Ile Val Ala Val Leu Ala Ala Phe Ala Phe
             20                  25                  30

Asn Ser Gly Ala Ser Val Leu Ser Phe Ile Trp Gly Val Val Thr Gly
         35                  40                  45

Glu Tyr Gly Phe Ala Val Leu Pro Ile Leu Leu Thr Val Gly Gly Ala
     50                  55                  60

Val Ile Val Val Ala Leu Ala Trp Ile Ile Thr Gly Ile Trp Trp Lys
 65                  70                  75                  80

Ala Val Gly Phe Arg Ile Thr Asn Glu Glu Val Gln Leu Gln Arg Gly
                 85                  90                  95

Val Ile Ser Lys Asp Leu Arg Thr Ala Arg Phe Asp Arg Ile Gln Ala
            100                 105                 110

Val Asp Leu Val Glu Ser Phe Ile Ala Arg Ile Phe Arg Leu Ala Glu
        115                 120                 125

Val Arg Ile Glu Thr Ala Gly Gly Ser Asp Ser Ala Ile Ser Ile Gly
    130                 135                 140

Phe Leu Arg Lys Ser Glu Ala Glu Ala Leu Lys Arg Glu Leu Leu Asp
145                 150                 155                 160

Ala Ser Gln His Ser Val Ala Thr Thr Pro Ala Gly Val Pro Ala Glu
                165                 170                 175

Pro Gly Val Gly Glu Thr Val Val Val Glu Ser Ala Gly Asp Val Leu
            180                 185                 190

Val Pro Gln Ile Pro Val Gln Arg Thr Leu Ala Ser Thr Ala Leu Ser
        195                 200                 205

Leu Ala Thr Ile Ile Thr Ala Ile Gly Ile Val Ile Leu Leu Phe Val
    210                 215                 220

Pro Phe Gly Val Ser Ile Ala Val Pro Phe Phe Val Gly Met Val Pro
225                 230                 235                 240

Ala Val Trp Asn Leu Ile Asp Lys Ser Trp Gln Phe Thr Ala Thr Gln
                245                 250                 255

Arg Asn Asp Val Leu His Val Ser Tyr Gly Leu Ala Asn Arg Arg Lys
            260                 265                 270

Gln Ser Ile Pro Leu Gly Arg Ile His Ala Val Lys Leu Lys Gln Pro
        275                 280                 285

Leu Leu Trp Arg Leu Val Gly Trp Trp Thr Val Thr Val Pro Val Val
    290                 295                 300

Gly Tyr Gly Asp Thr Thr Gln Gly Gly Thr Ser Lys Ile Leu Pro Val
305                 310                 315                 320
```

```
Gly Ser Lys Glu Leu Ala Leu Lys Val Leu Glu Ala Val Gly Pro Leu
                325                 330                 335

Asn Ser Ala Asp Ile Ala Glu Ser Ala Asp Pro Ser His Met Ser Arg
            340                 345                 350

Pro Gln Tyr Thr Pro Pro Val Ala Ala Arg Leu Leu Thr Pro Val Asp
        355                 360                 365

Arg Thr Arg Gln Gly Val Thr Leu Ile Gly Val Ala Gly Ala Pro Gly
    370                 375                 380

Ala Val Val Val His Glu Gly Arg Phe Met Pro Arg Met Ser Val Ile
385                 390                 395                 400

Asp Thr Ser His Ile Gln Glu Leu Thr Leu Lys His Gly Pro Ile Gln
                405                 410                 415

Arg Ile Leu Gly Leu Ser Thr Val Val Phe Asn Leu Val Gln Gly Pro
            420                 425                 430

Val Gly Met Ala Ala Ser Asp Leu Ser Ala Ala Asp Gly Lys Glu Leu
        435                 440                 445

Leu Asn Ile Leu Arg Asn Arg Lys Leu Pro Ala Leu Glu Ser Ala Pro
    450                 455                 460

Leu Gly Gln Asn Ser Leu Asp
465                 470


<210> 1745
<211> 798
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> RXA00411

<400> 1745
catttggcaa aatgactgtt cgactcaccg gcaacaccgc tgcgattgaa gagttctatc 60

aaaccttgac caagaccacg accatcaagg agatcacccg atg aac gag atg atc   115
                                              Met Asn Glu Met Ile
                                                1               5

ctc gca gct gac tgg aac cgg cta gga ccc acc ttc caa aca gcc atc   163
Leu Ala Ala Asp Trp Asn Arg Leu Gly Pro Thr Phe Gln Thr Ala Ile
                10                  15                  20

att gac acc ctg ttg atg gtc atc atc acc atg gtg gtg gct ggc tta   211
Ile Asp Thr Leu Leu Met Val Ile Ile Thr Met Val Val Ala Gly Leu
            25                  30                  35

ctg ggt ctt gtc gtc ggc ctg ctg ctt tac acc acc cgc gct ggt gga   259
Leu Gly Leu Val Val Gly Leu Leu Leu Tyr Thr Thr Arg Ala Gly Gly
        40                  45                  50
```

```
atc ttg aag aac aag gtc atc tac acc att ttg aat gtg ctg gtg aac   307
Ile Leu Lys Asn Lys Val Ile Tyr Thr Ile Leu Asn Val Leu Val Asn
     55                  60                  65

ttt gtt cga ccc atc cca ttc att att ttg atc gcc gcc atc aag cca   355
Phe Val Arg Pro Ile Pro Phe Ile Ile Leu Ile Ala Ala Ile Lys Pro
 70                  75                  80                  85

cta acg gtc gcc gtc atg ggc acc tcc atc ggc cga gat gcc ggc atc   403
Leu Thr Val Ala Val Met Gly Thr Ser Ile Gly Arg Asp Ala Gly Ile
                 90                  95                 100

ttc gtc atg gtt gtc gca gcg att ttc tct gtg gct cga atc gtg gag   451
Phe Val Met Val Val Ala Ala Ile Phe Ser Val Ala Arg Ile Val Glu
            105                 110                 115

caa aac ttg gtc tcc att gat cct ggt gtc atc gag gca gct cgc tcc   499
Gln Asn Leu Val Ser Ile Asp Pro Gly Val Ile Glu Ala Ala Arg Ser
        120                 125                 130

atg ggt gcg tcc ccg atg cgc atc atc gcc acc gtg atc att cca gaa   547
Met Gly Ala Ser Pro Met Arg Ile Ile Ala Thr Val Ile Ile Pro Glu
    135                 140                 145

gca ctt gga cca ttg gtt ctg ggt tac acc ttc ctg ttc atc gcg atc   595
Ala Leu Gly Pro Leu Val Leu Gly Tyr Thr Phe Leu Phe Ile Ala Ile
150                 155                 160                 165

gtc gat atg tcc gca atg gtc ggc tac atc ggt ggc ggt ggt ctt ggt   643
Val Asp Met Ser Ala Met Val Gly Tyr Ile Gly Gly Gly Gly Leu Gly
                170                 175                 180

gac ttc gcc att gtt tac ggc tac cgc gcc ttc gac aac gaa gtt atg   691
Asp Phe Ala Ile Val Tyr Gly Tyr Arg Ala Phe Asp Asn Glu Val Met
            185                 190                 195

tac gtt gcc gtc ctg gtt atc gtc atc atc gtg cag gca gcc cag ctt   739
Tyr Val Ala Val Leu Val Ile Val Ile Ile Val Gln Ala Ala Gln Leu
        200                 205                 210

ctg ggc aat tgg ctg tcc aag aag atc atg cgc cgc taaacctctt        785
Leu Gly Asn Trp Leu Ser Lys Lys Ile Met Arg Arg
    215                 220                 225

gcatagaaaa acc                                                   798
```

<210> 1746
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 1746

```
Met Asn Glu Met Ile Leu Ala Ala Asp Trp Asn Arg Leu Gly Pro Thr
  1               5                  10                  15

Phe Gln Thr Ala Ile Ile Asp Thr Leu Leu Met Val Ile Ile Thr Met
             20                  25                  30

Val Val Ala Gly Leu Leu Gly Leu Val Val Gly Leu Leu Leu Tyr Thr
         35                  40                  45
```

```
Thr Arg Ala Gly Gly Ile Leu Lys Asn Lys Val Ile Tyr Thr Ile Leu
     50                  55                  60

Asn Val Leu Val Asn Phe Val Arg Pro Ile Pro Phe Ile Ile Leu Ile
 65                  70                  75                  80

Ala Ala Ile Lys Pro Leu Thr Val Ala Val Met Gly Thr Ser Ile Gly
                 85                  90                  95

Arg Asp Ala Gly Ile Phe Val Met Val Val Ala Ala Ile Phe Ser Val
            100                 105                 110

Ala Arg Ile Val Glu Gln Asn Leu Val Ser Ile Asp Pro Gly Val Ile
        115                 120                 125

Glu Ala Ala Arg Ser Met Gly Ala Ser Pro Met Arg Ile Ile Ala Thr
    130                 135                 140

Val Ile Ile Pro Glu Ala Leu Gly Pro Leu Val Leu Gly Tyr Thr Phe
145                 150                 155                 160

Leu Phe Ile Ala Ile Val Asp Met Ser Ala Met Val Gly Tyr Ile Gly
                165                 170                 175

Gly Gly Gly Leu Gly Asp Phe Ala Ile Val Tyr Gly Tyr Arg Ala Phe
            180                 185                 190

Asp Asn Glu Val Met Tyr Val Ala Val Leu Val Ile Val Ile Ile Val
        195                 200                 205

Gln Ala Ala Gln Leu Leu Gly Asn Trp Leu Ser Lys Lys Ile Met Arg
    210                 215                 220

Arg
225
```

09350350.090501

<210> 1747
<211> 576
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(553)
<223> RXA00423

<400> 1747
agttctttga aaaacgtggc gcttccaggc cattcacctg cactggcatg gtgtacgccg 60

cttttattta cgcaatctgt gagctggagg cccgcacaaa atg acc tat ccc gtg 115
                                              Met Thr Tyr Pro Val
                                                1   5

ttg agt gtt ttg gat aat tct ggc gat cac aac atc atc tgg cat gtg 163
Leu Ser Val Leu Asp Asn Ser Gly Asp His Asn Ile Ile Trp His Val
                10   15   20

caa act tat ccc gcg gcg ctg ccc acc ggg gcg tgg att gcc gat gag 211
Gln Thr Tyr Pro Ala Ala Leu Pro Thr Gly Ala Trp Ile Ala Asp Glu

```
            25                  30                  35

caa caa ctg act gac ctg ctg aaa gac aca gta gtg ttc ctt acc cct   259
Gln Gln Leu Thr Asp Leu Leu Lys Asp Thr Val Val Phe Leu Thr Pro
         40                  45                  50

ggg agc acc gct ccg gaa aat gcc ccc gtg gcg acg ata gaa ggg gtg   307
Gly Ser Thr Ala Pro Glu Asn Ala Pro Val Ala Thr Ile Glu Gly Val
     55                  60                  65

cgg gtt gac gtc gat aag cag gtg gca gag tac aac aaa cat ggg atc   355
Arg Val Asp Val Asp Lys Gln Val Ala Glu Tyr Asn Lys His Gly Ile
 70                  75                  80                  85

cgc ctg ccc agc ttg ggc gcg cgc act gtg gag gcg cag tac cgc ggc   403
Arg Leu Pro Ser Leu Gly Ala Arg Thr Val Glu Ala Gln Tyr Arg Gly
                 90                  95                 100

gag ccg gag gca gag gct gcg tgg cgc acg gcg atg gag ctc gta gag   451
Glu Pro Glu Ala Glu Ala Ala Trp Arg Thr Ala Met Glu Leu Val Glu
            105                 110                 115

atc gca ggc ggc tgg cta gaa att gaa gcc aag cgc cgg gcg cgg aag   499
Ile Ala Gly Gly Trp Leu Glu Ile Glu Ala Lys Arg Arg Ala Arg Lys
        120                 125                 130

gcg ctg gct gag gcc ttc ggc gcg gag gtc cag cca ctg ccg ctt gac   547
Ala Leu Ala Glu Ala Phe Gly Ala Glu Val Gln Pro Leu Pro Leu Asp
    135                 140                 145

acc gaa taggacaaat gggtctatcc tgg                                576
Thr Glu
150
```

0000000000000000000

```
<210> 1748
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 1748
Met Thr Tyr Pro Val Leu Ser Val Leu Asp Asn Ser Gly Asp His Asn
  1               5                  10                  15

Ile Ile Trp His Val Gln Thr Tyr Pro Ala Ala Leu Pro Thr Gly Ala
             20                  25                  30

Trp Ile Ala Asp Glu Gln Gln Leu Thr Asp Leu Leu Lys Asp Thr Val
         35                  40                  45

Val Phe Leu Thr Pro Gly Ser Thr Ala Pro Glu Asn Ala Pro Val Ala
     50                  55                  60

Thr Ile Glu Gly Val Arg Val Asp Val Asp Lys Gln Val Ala Glu Tyr
 65                  70                  75                  80

Asn Lys His Gly Ile Arg Leu Pro Ser Leu Gly Ala Arg Thr Val Glu
                 85                  90                  95

Ala Gln Tyr Arg Gly Glu Pro Glu Ala Glu Ala Ala Trp Arg Thr Ala
            100                 105                 110
```

```
Met Glu Leu Val Glu Ile Ala Gly Gly Trp Leu Glu Ile Glu Ala Lys
        115                 120                 125

Arg Arg Ala Arg Lys Ala Leu Ala Glu Ala Phe Gly Ala Glu Val Gln
    130                 135                 140

Pro Leu Pro Leu Asp Thr Glu
145                 150


<210> 1749
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXA00424

<400> 1749
gcgatgtgga cctcgggagc cttggctttt ttgaatcttt caaacatgcc caccacctta 60

atcagtgagt agtcttggca acatggatac caggatgaga ttg cag gta gca gca   115
                                          Leu Gln Val Ala Ala
                                            1               5

ggt tcc gcg ctg att ggt gct ggg gtt gcg gtt aat gat tac gta caa   163
Gly Ser Ala Leu Ile Gly Ala Gly Val Ala Val Asn Asp Tyr Val Gln
                  10                  15                  20

agc cca gtc cgc cgg gcc atc agt tat ggt gcg ttg gcg ctt tct ggg   211
Ser Pro Val Arg Arg Ala Ile Ser Tyr Gly Ala Leu Ala Leu Ser Gly
              25                  30                  35

gcg acg gtg att gcg atg ggt cag gac ccg act ggg gag cgg tcc atc   259
Ala Thr Val Ile Ala Met Gly Gln Asp Pro Thr Gly Glu Arg Ser Ile
          40                  45                  50

att gcg aaa gat tcc gcg acg atg gtt gat caa atc cgc cag gag atc   307
Ile Ala Lys Asp Ser Ala Thr Met Val Asp Gln Ile Arg Gln Glu Ile
      55                  60                  65

ggc gat ttg ggt gtc acg cct ggt cca gaa tct gat gtg gat gcc atc   355
Gly Asp Leu Gly Val Thr Pro Gly Pro Glu Ser Asp Val Asp Ala Ile
  70                  75                  80                  85

acg gag cga ggt ccg ctg gtg acg tgg ctg ttg ctt gct gtt ttt gtc   403
Thr Glu Arg Gly Pro Leu Val Thr Trp Leu Leu Leu Ala Val Phe Val
                  90                  95                 100

gtg gca ttt ttc acc ttg gcg tat ttc tcc atg cgc atg gat gtg gcg   451
Val Ala Phe Phe Thr Leu Ala Tyr Phe Ser Met Arg Met Asp Val Ala
              105                 110                 115

gtg atg aga agg atc gct aag ttc ttt gaa aaa cgt ggc gct tcc agg   499
Val Met Arg Arg Ile Ala Lys Phe Phe Glu Lys Arg Gly Ala Ser Arg
          120                 125                 130

cca ttc acc tgc act ggc atg gtg tac gcc gct ttt att tac gca atc   547
```

```
Pro Phe Thr Cys Thr Gly Met Val Tyr Ala Ala Phe Ile Tyr Ala Ile
    135                 140                 145

tgt gag ctg gag gcc cgc aca aaa tgacctatcc cgtgttgagt gtt         594
Cys Glu Leu Glu Ala Arg Thr Lys
150                 155


<210> 1750
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 1750
Leu Gln Val Ala Ala Gly Ser Ala Leu Ile Gly Ala Gly Val Ala Val
  1               5                  10                  15

Asn Asp Tyr Val Gln Ser Pro Val Arg Arg Ala Ile Ser Tyr Gly Ala
             20                  25                  30

Leu Ala Leu Ser Gly Ala Thr Val Ile Ala Met Gly Gln Asp Pro Thr
         35                  40                  45

Gly Glu Arg Ser Ile Ile Ala Lys Asp Ser Ala Thr Met Val Asp Gln
     50                  55                  60

Ile Arg Gln Glu Ile Gly Asp Leu Gly Val Thr Pro Gly Pro Glu Ser
 65                  70                  75                  80

Asp Val Asp Ala Ile Thr Glu Arg Gly Pro Leu Val Thr Trp Leu Leu
                 85                  90                  95

Leu Ala Val Phe Val Val Ala Phe Phe Thr Leu Ala Tyr Phe Ser Met
            100                 105                 110

Arg Met Asp Val Ala Val Met Arg Arg Ile Ala Lys Phe Phe Glu Lys
        115                 120                 125

Arg Gly Ala Ser Arg Pro Phe Thr Cys Thr Gly Met Val Tyr Ala Ala
    130                 135                 140

Phe Ile Tyr Ala Ile Cys Glu Leu Glu Ala Arg Thr Lys
145                 150                 155


<210> 1751
<211> 348
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(325)
<223> RXA00425

<400> 1751
accgcaaccc cagcaccaat cagcgcggaa cctgctgcta cctgcaatct catcctggta 60

tccatgttgc caagactact cactgattaa ggtggtgggc atg ttt gaa aga ttc   115
                                              Met Phe Glu Arg Phe
                                                1               5
```

```
aaa aaa gcc aag gct ccc gag gtc cac atc gcg gcg gaa cgc acc aac   163
Lys Lys Ala Lys Ala Pro Glu Val His Ile Ala Ala Glu Arg Thr Asn
                 10                  15                  20

ctt ccg ctt aac gat ttc atg acc cgc ctc ttc gcc cag gaa ctc ccc   211
Leu Pro Leu Asn Asp Phe Met Thr Arg Leu Phe Ala Gln Glu Leu Pro
             25                  30                  35

ctg ctc gat agc acc tca cgt tca gag gtc tac cgc ctg ctt cgg gaa   259
Leu Leu Asp Ser Thr Ser Arg Ser Glu Val Tyr Arg Leu Leu Arg Glu
         40                  45                  50

tac gac ggc cca aca att agc tcc cag gaa gaa atc ccc gca gag att   307
Tyr Asp Gly Pro Thr Ile Ser Ser Gln Glu Glu Ile Pro Ala Glu Ile
     55                  60                  65

cgt gaa ctc atg gat ctt taggcaataa atgtgagatt gga                348
Arg Glu Leu Met Asp Leu
 70                  75
```

5,955,076 - 5,955,076

<210> 1752
<211> 75
<212> PRT
<213> Corynebacterium glutamicum

<400> 1752

```
Met Phe Glu Arg Phe Lys Lys Ala Lys Ala Pro Glu Val His Ile Ala
  1               5                  10                  15

Ala Glu Arg Thr Asn Leu Pro Leu Asn Asp Phe Met Thr Arg Leu Phe
             20                  25                  30

Ala Gln Glu Leu Pro Leu Leu Asp Ser Thr Ser Arg Ser Glu Val Tyr
         35                  40                  45

Arg Leu Leu Arg Glu Tyr Asp Gly Pro Thr Ile Ser Ser Gln Glu Glu
     50                  55                  60

Ile Pro Ala Glu Ile Arg Glu Leu Met Asp Leu
 65                  70                  75
```

<210> 1753
<211> 756
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)
<223> RXA00428

<400> 1753

```
agcgtcgcag ggatcggcgc gatcttcctc cttccgatcg gcatcatcat gtgcctcatc 60

gccggattca accgctacta cgcagccctt aaggtctaaa atg ccc ggt cta gtt   115
                                               Met Pro Gly Leu Val
                                                 1               5
```

```
ctc tcc aca aac gtc gcc cat atc caa caa gac cca ggt ggc gat gac   163
Leu Ser Thr Asn Val Ala His Ile Gln Gln Asp Pro Gly Gly Asp Asp
                 10                  15                  20

cgc atc agc ggc atc aac aaa ctc ccc gtc gcc acc ggc atc gat gta   211
Arg Ile Ser Gly Ile Asn Lys Leu Pro Val Ala Thr Gly Ile Asp Val
             25                  30                  35

ttc atc ccc gga ccc aac tac ggc gac ggc tcc ggc gta gtc ggc gac   259
Phe Ile Pro Gly Pro Asn Tyr Gly Asp Gly Ser Gly Val Val Gly Asp
         40                  45                  50

gcc atc ggc gat tcc ctc cac cac ggc ggc gcc cac aaa gcc atc tac   307
Ala Ile Gly Asp Ser Leu His His Gly Gly Ala His Lys Ala Ile Tyr
     55                  60                  65

gcc tac agc cgc gaa gaa ctc gac ttc ttt gac ccc acc tac cgc aac   355
Ala Tyr Ser Arg Glu Glu Leu Asp Phe Phe Asp Pro Thr Tyr Arg Asn
 70                  75                  80                  85

gga tac ttc ggc gaa aac ctc acc acc agc gga atc gtg ttg gaa gac   403
Gly Tyr Phe Gly Glu Asn Leu Thr Thr Ser Gly Ile Val Leu Glu Asp
                 90                  95                 100

ctc ctg atc aac caa caa gtg cgc atc ggc acc acg ctg ctc gaa gtc   451
Leu Leu Ile Asn Gln Gln Val Arg Ile Gly Thr Thr Leu Leu Glu Val
             105                 110                 115

tcc att ccc cgc cga ccc tgc cgc acg ttc gcc cac tgg ctc gac atc   499
Ser Ile Pro Arg Arg Pro Cys Arg Thr Phe Ala His Trp Leu Asp Ile
         120                 125                 130

aaa ggc tgg cta aaa acc ttc acc caa cgc ggc ctc ccc ggc agc tac   547
Lys Gly Trp Leu Lys Thr Phe Thr Gln Arg Gly Leu Pro Gly Ser Tyr
     135                 140                 145

ttc cga gtc atc gaa gaa ggc cac atc aac ccc ggc gac ccc att gaa   595
Phe Arg Val Ile Glu Glu Gly His Ile Asn Pro Gly Asp Pro Ile Glu
150                 155                 160                 165

gtt ctg cag gcc ccc gac cac gac atc acc atg tcc atg gcc ttc cgt   643
Val Leu Gln Ala Pro Asp His Asp Ile Thr Met Ser Met Ala Phe Arg
                 170                 175                 180

gca aaa atg gga aac aaa gac ctc gcg cgc cgg gtt gtt gca gcc aac   691
Ala Lys Met Gly Asn Lys Asp Leu Ala Arg Arg Val Val Ala Ala Asn
             185                 190                 195

tgt ctc cca gcg cgc tac cac gag gaa cta cta aaa ctg atc           733
Cys Leu Pro Ala Arg Tyr His Glu Glu Leu Leu Lys Leu Ile
         200                 205                 210

tagggcctat tgaatttctc gtc                                       756
```

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<210> 1754
<211> 211
<212> PRT
<213> Corynebacterium glutamicum

<400> 1754

```
Met Pro Gly Leu Val Leu Ser Thr Asn Val Ala His Ile Gln Gln Asp
  1               5                  10                  15

Pro Gly Gly Asp Asp Arg Ile Ser Gly Ile Asn Lys Leu Pro Val Ala
            20                  25                  30

Thr Gly Ile Asp Val Phe Ile Pro Gly Pro Asn Tyr Gly Asp Gly Ser
        35                  40                  45

Gly Val Val Gly Asp Ala Ile Gly Asp Ser Leu His His Gly Gly Ala
    50                  55                  60

His Lys Ala Ile Tyr Ala Tyr Ser Arg Glu Glu Leu Asp Phe Phe Asp
65                  70                  75                  80

Pro Thr Tyr Arg Asn Gly Tyr Phe Gly Glu Asn Leu Thr Thr Ser Gly
                85                  90                  95

Ile Val Leu Glu Asp Leu Leu Ile Asn Gln Gln Val Arg Ile Gly Thr
            100                 105                 110

Thr Leu Leu Glu Val Ser Ile Pro Arg Arg Pro Cys Arg Thr Phe Ala
        115                 120                 125

His Trp Leu Asp Ile Lys Gly Trp Leu Lys Thr Phe Thr Gln Arg Gly
    130                 135                 140

Leu Pro Gly Ser Tyr Phe Arg Val Ile Glu Glu Gly His Ile Asn Pro
145                 150                 155                 160

Gly Asp Pro Ile Glu Val Leu Gln Ala Pro Asp His Asp Ile Thr Met
                165                 170                 175

Ser Met Ala Phe Arg Ala Lys Met Gly Asn Lys Asp Leu Ala Arg Arg
            180                 185                 190

Val Val Ala Ala Asn Cys Leu Pro Ala Arg Tyr His Glu Glu Leu Leu
        195                 200                 205

Lys Leu Ile
    210
```

<210> 1755
<211> 525
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(502)
<223> RXA00429

<400> 1755
cgatggtggt cgccttcgtg atcgcccaag gcacccggaa cggtcatcaa cttcatcgtc 60

caaagaacca tcattttccg agtgaagtaa ggtacccctc atg aag acc ttc aat 115
                                              Met Lys Thr Phe Asn
                                                1   5

ccc acc atg att gcc gga ctc atc ggc gta ctc tac ttc gtg ctg ctc 163

```
Pro Thr Met Ile Ala Gly Leu Ile Gly Val Leu Tyr Phe Val Leu Leu
                  10                  15                  20

acc ctg att ttc tcc atc caa gac atg gaa cta gca gca gaa atc gcc   211
Thr Leu Ile Phe Ser Ile Gln Asp Met Glu Leu Ala Ala Glu Ile Ala
             25                  30                  35

ttc gga atc gtc acc atc gtc ggc ctg atc gcg gtg tgg gac aac ttc   259
Phe Gly Ile Val Thr Ile Val Gly Leu Ile Ala Val Trp Asp Asn Phe
         40                  45                  50

cgc gac cgc aac aac tcc acc tgg aaa acc tgg acc ggc ctc gtc ggc   307
Arg Asp Arg Asn Asn Ser Thr Trp Lys Thr Trp Thr Gly Leu Val Gly
     55                  60                  65

gga ctg cta atc gcc gtc ccc gga atc tgc ctt ctt gtg gga aac ctc   355
Gly Leu Leu Ile Ala Val Pro Gly Ile Cys Leu Leu Val Gly Asn Leu
 70                  75                  80                  85

gtg ctc ctc gca gtc gac ggc aac ccc tca acc atg gtg aac acc ctg   403
Val Leu Leu Ala Val Asp Gly Asn Pro Ser Thr Met Val Asn Thr Leu
                 90                  95                 100

ctc agc gtc gca ggg atc ggc gcg atc ttc ctc ctt ccg atc ggc atc   451
Leu Ser Val Ala Gly Ile Gly Ala Ile Phe Leu Leu Pro Ile Gly Ile
            105                 110                 115

atc atg tgc ctc atc gcc gga ttc aac cgc tac tac gca gcc ctt aag   499
Ile Met Cys Leu Ile Ala Gly Phe Asn Arg Tyr Tyr Ala Ala Leu Lys
        120                 125                 130

gtc taaaatgccc ggtctagttc tct                                    525
Val
```

```
<210> 1756
<211> 134
<212> PRT
<213> Corynebacterium glutamicum

<400> 1756
Met Lys Thr Phe Asn Pro Thr Met Ile Ala Gly Leu Ile Gly Val Leu
  1               5                  10                  15

Tyr Phe Val Leu Leu Thr Leu Ile Phe Ser Ile Gln Asp Met Glu Leu
             20                  25                  30

Ala Ala Glu Ile Ala Phe Gly Ile Val Thr Ile Val Gly Leu Ile Ala
         35                  40                  45

Val Trp Asp Asn Phe Arg Asp Arg Asn Asn Ser Thr Trp Lys Thr Trp
     50                  55                  60

Thr Gly Leu Val Gly Gly Leu Leu Ile Ala Val Pro Gly Ile Cys Leu
 65                  70                  75                  80

Leu Val Gly Asn Leu Val Leu Leu Ala Val Asp Gly Asn Pro Ser Thr
                 85                  90                  95

Met Val Asn Thr Leu Leu Ser Val Ala Gly Ile Gly Ala Ile Phe Leu
```

```
            100                 105                 110

Leu Pro Ile Gly Ile Ile Met Cys Leu Ile Ala Gly Phe Asn Arg Tyr
        115                 120                 125

Tyr Ala Ala Leu Lys Val
    130


<210> 1757
<211> 534
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> RXA00430

<400> 1757
tgcccccgtg gatcgcctgg acatttatag ggagctgctg tgtttctagg tattgtgtaa 60

cctcgtgtcc gaaaatcttg atgttacgat cgtccgacca atg agc ctg aaa acc   115
                                            Met Ser Leu Lys Thr
                                              1               5

caa gct ttc cgg ttc atc ctc acc ggt ggc ctc tca gcc atc gtg gac   163
Gln Ala Phe Arg Phe Ile Leu Thr Gly Gly Leu Ser Ala Ile Val Asp
                  10                  15                  20

ctc ggc ctg ctg tca ctt ttg cag cta gtg ttc ggc ctt ccc gta cct   211
Leu Gly Leu Leu Ser Leu Leu Gln Leu Val Phe Gly Leu Pro Val Pro
              25                  30                  35

gtt gcc cgc acg atc tcc ttc atc gcc ggc acc acc acc gcc tac atg   259
Val Ala Arg Thr Ile Ser Phe Ile Ala Gly Thr Thr Thr Ala Tyr Met
          40                  45                  50

atc aac cgc cgg tgg acc ttc caa gca gaa agc tcc acc tcc agg ttc   307
Ile Asn Arg Arg Trp Thr Phe Gln Ala Glu Ser Ser Thr Ser Arg Phe
      55                  60                  65

ctt gct gtg gtg gcc ctc tac ggc gtg acc ttc ctg atc aac att gga   355
Leu Ala Val Val Ala Leu Tyr Gly Val Thr Phe Leu Ile Asn Ile Gly
  70                  75                  80                  85

ctg caa acc ctc tgc tcc gca ttg ttt gag aat tgg ggc tgg aac gaa   403
Leu Gln Thr Leu Cys Ser Ala Leu Phe Glu Asn Trp Gly Trp Asn Glu
                  90                  95                 100

gcc gtc gcg atg gtg gtc gcc ttc gtg atc gcc caa ggc acc cgg aac   451
Ala Val Ala Met Val Val Ala Phe Val Ile Ala Gln Gly Thr Arg Asn
              105                 110                 115

ggt cat caa ctt cat cgt cca aag aac cat cat ttt ccg agt gaa gta   499
Gly His Gln Leu His Arg Pro Lys Asn His His Phe Pro Ser Glu Val
          120                 125                 130

agg tac ccc tca tgaagacctt caatcccacc atg                        534
Arg Tyr Pro Ser
    135
```

<210> 1758
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 1758
```
Met Ser Leu Lys Thr Gln Ala Phe Arg Phe Ile Leu Thr Gly Gly Leu
  1               5                  10                  15

Ser Ala Ile Val Asp Leu Gly Leu Leu Ser Leu Leu Gln Leu Val Phe
             20                  25                  30

Gly Leu Pro Val Pro Val Ala Arg Thr Ile Ser Phe Ile Ala Gly Thr
         35                  40                  45

Thr Thr Ala Tyr Met Ile Asn Arg Arg Trp Thr Phe Gln Ala Glu Ser
     50                  55                  60

Ser Thr Ser Arg Phe Leu Ala Val Val Ala Leu Tyr Gly Val Thr Phe
 65                  70                  75                  80

Leu Ile Asn Ile Gly Leu Gln Thr Leu Cys Ser Ala Leu Phe Glu Asn
                 85                  90                  95

Trp Gly Trp Asn Glu Ala Val Ala Met Val Val Ala Phe Val Ile Ala
            100                 105                 110

Gln Gly Thr Arg Asn Gly His Gln Leu His Arg Pro Lys Asn His His
        115                 120                 125

Phe Pro Ser Glu Val Arg Tyr Pro Ser
    130                 135
```

<210> 1759
<211> 648
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(625)
<223> RXA00433

<400> 1759
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gtctccagcg actcaaacat caaaaattga tatttgcgac aagttgaaat catacccgat 60

agtctcgaac atactaaatc acctaatcag ggggaattac atg gat gtg tta aag   115
                                          Met Asp Val Leu Lys
                                            1               5

atc gcc atc atc gct gca gcc atg att ggt gtg ccg gtt ctg gtg gtt   163
Ile Ala Ile Ile Ala Ala Ala Met Ile Gly Val Pro Val Leu Val Val
                10                  15                  20

ttc ctc att gtg ttt gcg gtg cac aag ttg gct aag gaa gtg ccg cgg   211
Phe Leu Ile Val Phe Ala Val His Lys Leu Ala Lys Glu Val Pro Arg
            25                  30                  35
```

```
tct ggt cgt cgt ccg ggt att ggg ttg ggg ttg ttg ctt ggt ttt gtt   259
Ser Gly Arg Arg Pro Gly Ile Gly Leu Gly Leu Leu Leu Gly Phe Val
         40                  45                  50

gcg ggg ctc atc gtg tgg ttt gtg tgg ttg agt tgg ggt ggt tat tac   307
Ala Gly Leu Ile Val Trp Phe Val Trp Leu Ser Trp Gly Gly Tyr Tyr
     55                  60                  65

gag aat gag ttt ggg cag atg caa ggt ccg tat cgt ccg tgg cag gtt   355
Glu Asn Glu Phe Gly Gln Met Gln Gly Pro Tyr Arg Pro Trp Gln Val
 70                  75                  80                  85

gtt gct tgt ggt gtc acg atg gtc gcg gtc act gtg att ctt ggt ctg   403
Val Ala Cys Gly Val Thr Met Val Ala Val Thr Val Ile Leu Gly Leu
                 90                  95                 100

tgg act agg tgg act gcg tct ggt ccg ttt tat tcg gcg ttg ggt ggt   451
Trp Thr Arg Trp Thr Ala Ser Gly Pro Phe Tyr Ser Ala Leu Gly Gly
            105                 110                 115

gcg tcg ggg ttt agt ttc gcg tgg gcc atg gat gcc att cct cag gat   499
Ala Ser Gly Phe Ser Phe Ala Trp Ala Met Asp Ala Ile Pro Gln Asp
        120                 125                 130

gaa acc gga ttg tcg gcg ttt ggc tta gtg atg gtc att gtt ggt gtt   547
Glu Thr Gly Leu Ser Ala Phe Gly Leu Val Met Val Ile Val Gly Val
    135                 140                 145

ggt gcg ggg cta aat gtg gtg gca act ctg acg tca atc ggc gca acg   595
Gly Ala Gly Leu Asn Val Val Ala Thr Leu Thr Ser Ile Gly Ala Thr
150                 155                 160                 165

atc tgg aat aac cgg cta ccc tcg aat gca tgactaaaac cacgcgccaa     645
Ile Trp Asn Asn Arg Leu Pro Ser Asn Ala
                170                 175

acc                                                              648
```

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<210> 1760
<211> 175
<212> PRT
<213> Corynebacterium glutamicum

<400> 1760

```
Met Asp Val Leu Lys Ile Ala Ile Ile Ala Ala Ala Met Ile Gly Val
  1               5                  10                  15

Pro Val Leu Val Val Phe Leu Ile Val Phe Ala Val His Lys Leu Ala
             20                  25                  30

Lys Glu Val Pro Arg Ser Gly Arg Arg Pro Gly Ile Gly Leu Gly Leu
         35                  40                  45

Leu Leu Gly Phe Val Ala Gly Leu Ile Val Trp Phe Val Trp Leu Ser
     50                  55                  60

Trp Gly Gly Tyr Tyr Glu Asn Glu Phe Gly Gln Met Gln Gly Pro Tyr
 65                  70                  75                  80

Arg Pro Trp Gln Val Val Ala Cys Gly Val Thr Met Val Ala Val Thr
```

```
                85                  90                  95

Val Ile Leu Gly Leu Trp Thr Arg Trp Thr Ala Ser Gly Pro Phe Tyr
            100                 105                 110

Ser Ala Leu Gly Gly Ala Ser Gly Phe Ser Phe Ala Trp Ala Met Asp
        115                 120                 125

Ala Ile Pro Gln Asp Glu Thr Gly Leu Ser Ala Phe Gly Leu Val Met
    130                 135                 140

Val Ile Val Gly Val Gly Ala Gly Leu Asn Val Val Ala Thr Leu Thr
145                 150                 155                 160

Ser Ile Gly Ala Thr Ile Trp Asn Asn Arg Leu Pro Ser Asn Ala
                165                 170                 175


<210> 1761
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(592)
<223> RXA00451

<400> 1761
ggatccgccg atgaggccga ggcccaggat gcatactggg cgggaaatgt ctttggtagt 60

cacctgacaa gtgtggcaca tacctactac ggttatctct atg aac act gaa gag   115
                                          Met Asn Thr Glu Glu
                                            1               5

gat ggc ctg agc ttt gca gtt acg gct acc tta gtt gaa ggt aaa tgg   163
Asp Gly Leu Ser Phe Ala Val Thr Ala Thr Leu Val Glu Gly Lys Trp
                10                  15                  20

cag gta cgc gag ttt gag gat cac ttc tcc aag ctc tct acc tct att   211
Gln Val Arg Glu Phe Glu Asp His Phe Ser Lys Leu Ser Thr Ser Ile
            25                  30                  35

aat gcg gtt cgc tcg ctg cgt agc gag ggg ccg gcg ttt gcg ctg ttg   259
Asn Ala Val Arg Ser Leu Arg Ser Glu Gly Pro Ala Phe Ala Leu Leu
        40                  45                  50

tgc gtt gat gat gaa tat ttt gtg atg gtg cgt ccc acc cca agt agg   307
Cys Val Asp Asp Glu Tyr Phe Val Met Val Arg Pro Thr Pro Ser Arg
    55                  60                  65

gta ttc ctt ttc ctt tcg gat gcg ccg atg gct gtc gac gat gat ttc   355
Val Phe Leu Phe Leu Ser Asp Ala Pro Met Ala Val Asp Asp Asp Phe
70                  75                  80                  85

gcc gcc gcg gtg atg gat gaa ctc gat gcg gat ctt cca gat atc aac   403
Ala Ala Ala Val Met Asp Glu Leu Asp Ala Asp Leu Pro Asp Ile Asn
                90                  95                  100

cct gat gat ttg gac gac atc gat cca tgg cca gaa ggt gat ttc gat   451
Pro Asp Asp Leu Asp Asp Ile Asp Pro Trp Pro Glu Gly Asp Phe Asp
```

```
            105                 110                 115

att ttg gcg gat ttg ggg ctg tct gag gag gtt ctt tcc gtg att tgc   499
Ile Leu Ala Asp Leu Gly Leu Ser Glu Glu Val Leu Ser Val Ile Cys
        120                 125                 130

gat gac atg gat ttg gat cct tcc gaa caa ttg ctg cgc atc gcg gaa   547
Asp Asp Met Asp Leu Asp Pro Ser Glu Gln Leu Leu Arg Ile Ala Glu
    135                 140                 145

gaa ctc ggt ttt gat aat gat ctg gct cgg gtg gtg gga ttc gac       592
Glu Leu Gly Phe Asp Asn Asp Leu Ala Arg Val Val Gly Phe Asp
150                 155                 160

tagtgggcgt tttacctgtg cag                                        615
```

<210> 1762
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 1762

```
Met Asn Thr Glu Glu Asp Gly Leu Ser Phe Ala Val Thr Ala Thr Leu
  1               5                  10                  15

Val Glu Gly Lys Trp Gln Val Arg Glu Phe Glu Asp His Phe Ser Lys
             20                  25                  30

Leu Ser Thr Ser Ile Asn Ala Val Arg Ser Leu Arg Ser Glu Gly Pro
         35                  40                  45

Ala Phe Ala Leu Leu Cys Val Asp Asp Glu Tyr Phe Val Met Val Arg
     50                  55                  60

Pro Thr Pro Ser Arg Val Phe Leu Phe Leu Ser Asp Ala Pro Met Ala
 65                  70                  75                  80

Val Asp Asp Asp Phe Ala Ala Ala Val Met Asp Glu Leu Asp Ala Asp
                 85                  90                  95

Leu Pro Asp Ile Asn Pro Asp Asp Leu Asp Asp Ile Asp Pro Trp Pro
            100                 105                 110

Glu Gly Asp Phe Asp Ile Leu Ala Asp Leu Gly Leu Ser Glu Glu Val
        115                 120                 125

Leu Ser Val Ile Cys Asp Asp Met Asp Leu Asp Pro Ser Glu Gln Leu
    130                 135                 140

Leu Arg Ile Ala Glu Glu Leu Gly Phe Asp Asn Asp Leu Ala Arg Val
145                 150                 155                 160

Val Gly Phe Asp
```

<210> 1763
<211> 1203
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1180)
<223> RXA00457

<400> 1763
aaactctcat gttggtttca tcgtggtttc atgaggcggg atttaactag agattgttag 60

ccaatcggcc agacacttcc tcctagaaag gtccctcctc atg acc att gct ctt 115
Met Thr Ile Ala Leu
1 5

gaa cac cca gta ctg cac tcc acg gcg atc gcg ttg cct gct cgt ttt 163
Glu His Pro Val Leu His Ser Thr Ala Ile Ala Leu Pro Ala Arg Phe
10 15 20

cag gcg agc tat acg acg cgt ttg gtg gcg gtg ggc gtc gat aag cgt 211
Gln Ala Ser Tyr Thr Thr Arg Leu Val Ala Val Gly Val Asp Lys Arg
25 30 35

cct tct gat ttt tgg ttg gaa aca gcc ggc acg ccg cag gcg ggc gat 259
Pro Ser Asp Phe Trp Leu Glu Thr Ala Gly Thr Pro Gln Ala Gly Asp
40 45 50

gtg gtg att gcg cgg gtg acg gcg att aat aat cac aag cgg gtg gag 307
Val Val Ile Ala Arg Val Thr Ala Ile Asn Asn His Lys Arg Val Glu
55 60 65

acg ccg gag tcg cgc aag gcc att ttg ttt gag ggg gtg ttg gtg atg 355
Thr Pro Glu Ser Arg Lys Ala Ile Leu Phe Glu Gly Val Leu Val Met
70 75 80 85

ttg gcg tat ggg cac cgg tat gcg gcg gat cag ttt tta gcg cat gta 403
Leu Ala Tyr Gly His Arg Tyr Ala Ala Asp Gln Phe Leu Ala His Val
90 95 100

ccg gag gat ttg ggg cca tgc cat ttg gtg gcg gct ggt ggc atc gcg 451
Pro Glu Asp Leu Gly Pro Cys His Leu Val Ala Ala Gly Gly Ile Ala
105 110 115

gga acg gtg acg gcg ctg cac gat cgg gtg gat gaa ccc aca gag att 499
Gly Thr Val Thr Ala Leu His Asp Arg Val Asp Glu Pro Thr Glu Ile
120 125 130

gaa ccg ttg gga ttg ctc acc aat gcg cgc gga act gtg aat gta cgg 547
Glu Pro Leu Gly Leu Leu Thr Asn Ala Arg Gly Thr Val Asn Val Arg
135 140 145

gac ttt gcg gct ttt gat aat cct ttg aaa gtg gag gct ccc aac aag 595
Asp Phe Ala Ala Phe Asp Asn Pro Leu Lys Val Glu Ala Pro Asn Lys
150 155 160 165

cgt gcg cag gtg atc gcg gtg ctg gga acg tcg atg aac tct gga aaa 643
Arg Ala Gln Val Ile Ala Val Leu Gly Thr Ser Met Asn Ser Gly Lys
170 175 180

tcc acc acg ctt gcc tgc ttg gtc aat ggt ttg gct gcg gcg ggg cag 691
Ser Thr Thr Leu Ala Cys Leu Val Asn Gly Leu Ala Ala Ala Gly Gln
185 190 195

```
aag gtg gcg gct gga aag atc acg ggc act ggt gct gga aat gac cgc   739
Lys Val Ala Ala Gly Lys Ile Thr Gly Thr Gly Ala Gly Asn Asp Arg
        200                 205                 210

atg att tat cac gat gct ggt gct cac agc gtt att gat ttc acc gac   787
Met Ile Tyr His Asp Ala Gly Ala His Ser Val Ile Asp Phe Thr Asp
    215                 220                 225

ttt ggc tac cca act acg ttc aag ctg aat ttc gcg gag att cgt gcg   835
Phe Gly Tyr Pro Thr Thr Phe Lys Leu Asn Phe Ala Glu Ile Arg Ala
230                 235                 240                 245

ctg agc gtc aac atg att aat gtg ctg gct gat tct ggt gcg gat acc   883
Leu Ser Val Asn Met Ile Asn Val Leu Ala Asp Ser Gly Ala Asp Thr
                250                 255                 260

gtg atc gtg gaa atc gcg gac gga att tat cag ggc gaa acc tcg cgg   931
Val Ile Val Glu Ile Ala Asp Gly Ile Tyr Gln Gly Glu Thr Ser Arg
            265                 270                 275

ctg ttg cgc gat caa gtg ttc cag gaa gcc gtg gat cat gtg gtg ttc   979
Leu Leu Arg Asp Gln Val Phe Gln Glu Ala Val Asp His Val Val Phe
        280                 285                 290

tcc gct gtt gat gcc ttg ggc gcg aag gcc ggt gtg cag gaa ctg cag   1027
Ser Ala Val Asp Ala Leu Gly Ala Lys Ala Gly Val Gln Glu Leu Gln
    295                 300                 305

gcg gcg ggg ctt cat gtg gct gcg gcc tcc gga gtg atg acg gct tcg   1075
Ala Ala Gly Leu His Val Ala Ala Ala Ser Gly Val Met Thr Ala Ser
310                 315                 320                 325

ccg ctg gcc acc gcg gaa gct gcc gct gtg ctt gaa gtt cca gtg gtg   1123
Pro Leu Ala Thr Ala Glu Ala Ala Ala Val Leu Glu Val Pro Val Val
                330                 335                 340

ccc act ttt gat ctc acc aac ccg gag atc gtc aca gcg gtg cta acg   1171
Pro Thr Phe Asp Leu Thr Asn Pro Glu Ile Val Thr Ala Val Leu Thr
            345                 350                 355

gat cat gcc tagcttatgg cgtgctcgtc gca                            1203
Asp His Ala
        360
```

<210> 1764
<211> 360
<212> PRT
<213> Corynebacterium glutamicum

<400> 1764

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Met Thr Ile Ala Leu Glu His Pro Val Leu His Ser Thr Ala Ile Ala
  1               5                  10                  15

Leu Pro Ala Arg Phe Gln Ala Ser Tyr Thr Thr Arg Leu Val Ala Val
             20                  25                  30

Gly Val Asp Lys Arg Pro Ser Asp Phe Trp Leu Glu Thr Ala Gly Thr
         35                  40                  45

Pro Gln Ala Gly Asp Val Val Ile Ala Arg Val Thr Ala Ile Asn Asn
```

```
     50                  55                  60

His Lys Arg Val Glu Thr Pro Glu Ser Arg Lys Ala Ile Leu Phe Glu
 65                  70                  75                  80

Gly Val Leu Val Met Leu Ala Tyr Gly His Arg Tyr Ala Ala Asp Gln
                 85                  90                  95

Phe Leu Ala His Val Pro Glu Asp Leu Gly Pro Cys His Leu Val Ala
            100                 105                 110

Ala Gly Gly Ile Ala Gly Thr Val Thr Ala Leu His Asp Arg Val Asp
        115                 120                 125

Glu Pro Thr Glu Ile Glu Pro Leu Gly Leu Leu Thr Asn Ala Arg Gly
    130                 135                 140

Thr Val Asn Val Arg Asp Phe Ala Ala Phe Asp Asn Pro Leu Lys Val
145                 150                 155                 160

Glu Ala Pro Asn Lys Arg Ala Gln Val Ile Ala Val Leu Gly Thr Ser
                165                 170                 175

Met Asn Ser Gly Lys Ser Thr Thr Leu Ala Cys Leu Val Asn Gly Leu
            180                 185                 190

Ala Ala Ala Gly Gln Lys Val Ala Ala Gly Lys Ile Thr Gly Thr Gly
        195                 200                 205

Ala Gly Asn Asp Arg Met Ile Tyr His Asp Ala Gly Ala His Ser Val
    210                 215                 220

Ile Asp Phe Thr Asp Phe Gly Tyr Pro Thr Thr Phe Lys Leu Asn Phe
225                 230                 235                 240

Ala Glu Ile Arg Ala Leu Ser Val Asn Met Ile Asn Val Leu Ala Asp
                245                 250                 255

Ser Gly Ala Asp Thr Val Ile Val Glu Ile Ala Asp Gly Ile Tyr Gln
            260                 265                 270

Gly Glu Thr Ser Arg Leu Leu Arg Asp Gln Val Phe Gln Glu Ala Val
        275                 280                 285

Asp His Val Val Phe Ser Ala Val Asp Ala Leu Gly Ala Lys Ala Gly
    290                 295                 300

Val Gln Glu Leu Gln Ala Ala Gly Leu His Val Ala Ala Ala Ser Gly
305                 310                 315                 320

Val Met Thr Ala Ser Pro Leu Ala Thr Ala Glu Ala Ala Ala Val Leu
                325                 330                 335

Glu Val Pro Val Val Pro Thr Phe Asp Leu Thr Asn Pro Glu Ile Val
            340                 345                 350

Thr Ala Val Leu Thr Asp His Ala
        355                 360
```

<210> 1765

<211> 1503
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1480)
<223> RXA00462

<400> 1765
tgaagccttg tcatttttcta catgtgcatc cgctttgact accgcccttt tccgcccagt 60

```
ccttttagaa accagcaaca cagaaagcaa gtgatcattt atg gaa gct att gcc   115
                                            Met Glu Ala Ile Ala
                                              1               5

ata cta ttt gtc att ggg gcg att ctt gtc gtc gcg gtc att gtc ctc   163
Ile Leu Phe Val Ile Gly Ala Ile Leu Val Val Ala Val Ile Val Leu
                 10                  15                  20

ggt att ttc ttc tta act tca cgc acc tgg atc aag gtg gct gca gct   211
Gly Ile Phe Phe Leu Thr Ser Arg Thr Trp Ile Lys Val Ala Ala Ala
             25                  30                  35

gat gaa gcg ctc att gtc tct gcg aag aag aag ggg gaa tcg cag gtc   259
Asp Glu Ala Leu Ile Val Ser Ala Lys Lys Lys Gly Glu Ser Gln Val
         40                  45                  50

att gtc cac ggc aaa gct gtg gta atg cct att acc cag act cac cag   307
Ile Val His Gly Lys Ala Val Val Met Pro Ile Thr Gln Thr His Gln
     55                  60                  65

aag atc tct ctg cgt tcc cgt cag gta aat atg cag gtg acg gca caa   355
Lys Ile Ser Leu Arg Ser Arg Gln Val Asn Met Gln Val Thr Ala Gln
 70                  75                  80                  85

agc gat gac aat gtc acg ttg aat gtc gag gct gtt gcg ctg gtg aag   403
Ser Asp Asp Asn Val Thr Leu Asn Val Glu Ala Val Ala Leu Val Lys
                 90                  95                 100

atc ggt tcc gaa gct gag ttt att cgt cgc gct gcc cag cgc ttc gct   451
Ile Gly Ser Glu Ala Glu Phe Ile Arg Arg Ala Ala Gln Arg Phe Ala
            105                 110                 115

tcc agt gac aaa gaa att gtt cgg ttc aca cag gat cag ctg gaa ggt   499
Ser Ser Asp Lys Glu Ile Val Arg Phe Thr Gln Asp Gln Leu Glu Gly
        120                 125                 130

gtg ctt cgt ggt gtc gtg gcg cag caa aca gtc acg tcg ctc atg cgt   547
Val Leu Arg Gly Val Val Ala Gln Gln Thr Val Thr Ser Leu Met Arg
    135                 140                 145

gag cgt aaa aaa ttc tcc gag cag atc gct gaa aca gtc atc ccc gag   595
Glu Arg Lys Lys Phe Ser Glu Gln Ile Ala Glu Thr Val Ile Pro Glu
150                 155                 160                 165

cta gag aag cag ggt ttg att ctt gac tcc ttc cag att cgt ggc atc   643
Leu Glu Lys Gln Gly Leu Ile Leu Asp Ser Phe Gln Ile Arg Gly Ile
                170                 175                 180

acc gat gat gtg gga tac atc aaa tcc ctc ggc gca ccg gaa att cag   691
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```
Thr Asp Asp Val Gly Tyr Ile Lys Ser Leu Gly Ala Pro Glu Ile Gln
            185                 190                 195

gca aag aag cag gct gcg gaa att gca gaa act gaa gct gct cgt gcg   739
Ala Lys Lys Gln Ala Ala Glu Ile Ala Glu Thr Glu Ala Ala Arg Ala
        200                 205                 210

atc gct aaa tca cgc att gct aac caa gag gca gat ctg gtt gaa cag   787
Ile Ala Lys Ser Arg Ile Ala Asn Gln Glu Ala Asp Leu Val Glu Gln
    215                 220                 225

acc caa ctt gat gcc aac aag gct gcc gct gat gct cag gtc ggt gaa   835
Thr Gln Leu Asp Ala Asn Lys Ala Ala Ala Asp Ala Gln Val Gly Glu
230                 235                 240                 245

gcc cgt gcc cag gct atg cag gct gaa cgc ctt gcc gat gaa aaa gct   883
Ala Arg Ala Gln Ala Met Gln Ala Glu Arg Leu Ala Asp Glu Lys Ala
                250                 255                 260

cga cta gag gtt ctt cgc caa cag gct gaa aat aag cag atc gag ctg   931
Arg Leu Glu Val Leu Arg Gln Gln Ala Glu Asn Lys Gln Ile Glu Leu
            265                 270                 275

gaa gcc gaa gtg aac aag gtg gcc gac gct gaa cgc tac cgc cgc aag   979
Glu Ala Glu Val Asn Lys Val Ala Asp Ala Glu Arg Tyr Arg Arg Lys
        280                 285                 290

cag gaa gtc gaa gcc gat act ttc gag caa acc agg cgc gca cag gct  1027
Gln Glu Val Glu Ala Asp Thr Phe Glu Gln Thr Arg Arg Ala Gln Ala
    295                 300                 305

cag gtc gaa atc gca gaa gcc gaa gct acc gct gca aag gtt cgt gca  1075
Gln Val Glu Ile Ala Glu Ala Glu Ala Thr Ala Ala Lys Val Arg Ala
310                 315                 320                 325

atg gct gaa gcc gaa gct gtt cga ttg aag gga cag gca gag gca gac  1123
Met Ala Glu Ala Glu Ala Val Arg Leu Lys Gly Gln Ala Glu Ala Asp
                330                 335                 340

gct atc aag gca aag gcc gag gcc tac cgc gaa aac caa gaa gca cta  1171
Ala Ile Lys Ala Lys Ala Glu Ala Tyr Arg Glu Asn Gln Glu Ala Leu
            345                 350                 355

ctc gcc cag caa gcc atg gaa atc ctg ccg gaa ctc atg agc aac ttc  1219
Leu Ala Gln Gln Ala Met Glu Ile Leu Pro Glu Leu Met Ser Asn Phe
        360                 365                 370

gcc tct gga tac gca aac att gga tcc atg aca gtg ctc tcc ggt gga  1267
Ala Ser Gly Tyr Ala Asn Ile Gly Ser Met Thr Val Leu Ser Gly Gly
    375                 380                 385

gaa gga tcc gag aat tcc gtg ggt tca cgt ttt gcc ggt gaa caa gca  1315
Glu Gly Ser Glu Asn Ser Val Gly Ser Arg Phe Ala Gly Glu Gln Ala
390                 395                 400                 405

ctt gga ctg aaa tcc att att gaa tca gtc aag caa acc acc ggc att  1363
Leu Gly Leu Lys Ser Ile Ile Glu Ser Val Lys Gln Thr Thr Gly Ile
                410                 415                 420

gat cta gct gag atc atc caa ggc cgt gct gct gga cat gca cag ggc  1411
Asp Leu Ala Glu Ile Ile Gln Gly Arg Ala Ala Gly His Ala Gln Gly
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            425                 430                 435

tcc gct cag ggt gca gcg att gct gaa gcg ctt tca cgc gat gaa act   1459
Ser Ala Gln Gly Ala Ala Ile Ala Glu Ala Leu Ser Arg Asp Glu Thr
        440                 445                 450

gtg gaa gat cgc tct gaa aaa taatctagct gcccagcgca tcg             1503
Val Glu Asp Arg Ser Glu Lys
    455                 460


<210> 1766
<211> 460
<212> PRT
<213> Corynebacterium glutamicum

<400> 1766
Met Glu Ala Ile Ala Ile Leu Phe Val Ile Gly Ala Ile Leu Val Val
  1               5                  10                  15

Ala Val Ile Val Leu Gly Ile Phe Phe Leu Thr Ser Arg Thr Trp Ile
             20                  25                  30

Lys Val Ala Ala Ala Asp Glu Ala Leu Ile Val Ser Ala Lys Lys Lys
         35                  40                  45

Gly Glu Ser Gln Val Ile Val His Gly Lys Ala Val Val Met Pro Ile
     50                  55                  60

Thr Gln Thr His Gln Lys Ile Ser Leu Arg Ser Arg Gln Val Asn Met
 65                  70                  75                  80

Gln Val Thr Ala Gln Ser Asp Asp Asn Val Thr Leu Asn Val Glu Ala
                 85                  90                  95

Val Ala Leu Val Lys Ile Gly Ser Glu Ala Glu Phe Ile Arg Arg Ala
            100                 105                 110

Ala Gln Arg Phe Ala Ser Ser Asp Lys Glu Ile Val Arg Phe Thr Gln
        115                 120                 125

Asp Gln Leu Glu Gly Val Leu Arg Gly Val Val Ala Gln Gln Thr Val
    130                 135                 140

Thr Ser Leu Met Arg Glu Arg Lys Lys Phe Ser Glu Gln Ile Ala Glu
145                 150                 155                 160

Thr Val Ile Pro Glu Leu Glu Lys Gln Gly Leu Ile Leu Asp Ser Phe
                165                 170                 175

Gln Ile Arg Gly Ile Thr Asp Asp Val Gly Tyr Ile Lys Ser Leu Gly
            180                 185                 190

Ala Pro Glu Ile Gln Ala Lys Lys Gln Ala Ala Glu Ile Ala Glu Thr
        195                 200                 205

Glu Ala Ala Arg Ala Ile Ala Lys Ser Arg Ile Ala Asn Gln Glu Ala
    210                 215                 220

Asp Leu Val Glu Gln Thr Gln Leu Asp Ala Asn Lys Ala Ala Ala Asp
225                 230                 235                 240
```

```
Ala Gln Val Gly Glu Ala Arg Ala Gln Ala Met Gln Ala Glu Arg Leu
                245                 250                 255

Ala Asp Glu Lys Ala Arg Leu Glu Val Leu Arg Gln Gln Ala Glu Asn
            260                 265                 270

Lys Gln Ile Glu Leu Glu Ala Glu Val Asn Lys Val Ala Asp Ala Glu
        275                 280                 285

Arg Tyr Arg Arg Lys Gln Glu Val Glu Ala Asp Thr Phe Glu Gln Thr
    290                 295                 300

Arg Arg Ala Gln Ala Gln Val Glu Ile Ala Glu Ala Glu Ala Thr Ala
305                 310                 315                 320

Ala Lys Val Arg Ala Met Ala Glu Ala Glu Ala Val Arg Leu Lys Gly
                325                 330                 335

Gln Ala Glu Ala Asp Ala Ile Lys Ala Lys Ala Glu Ala Tyr Arg Glu
            340                 345                 350

Asn Gln Glu Ala Leu Leu Ala Gln Gln Ala Met Glu Ile Leu Pro Glu
        355                 360                 365

Leu Met Ser Asn Phe Ala Ser Gly Tyr Ala Asn Ile Gly Ser Met Thr
    370                 375                 380

Val Leu Ser Gly Gly Glu Gly Ser Glu Asn Ser Val Gly Ser Arg Phe
385                 390                 395                 400

Ala Gly Glu Gln Ala Leu Gly Leu Lys Ser Ile Ile Glu Ser Val Lys
                405                 410                 415

Gln Thr Thr Gly Ile Asp Leu Ala Glu Ile Ile Gln Gly Arg Ala Ala
            420                 425                 430

Gly His Ala Gln Gly Ser Ala Gln Gly Ala Ala Ile Ala Glu Ala Leu
        435                 440                 445

Ser Arg Asp Glu Thr Val Glu Asp Arg Ser Glu Lys
    450                 455                 460


<210> 1767
<211> 945
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(922)
<223> RXA00463

<400> 1767
taccacgcta gtcgccagca ctctcggatt aagcggatgt acctccgtaa cttccagtgc 60

tacgagctcc cctgaaccgc cgactaaagt tgcggcggca atg cag aca acg act   115
                                              Met Gln Thr Thr Thr
                                                1               5
```

```
ggg gag acg tcg ata agc aat gaa acc tcg ttt aac gcc tca cgc gaa   163
Gly Glu Thr Ser Ile Ser Asn Glu Thr Ser Phe Asn Ala Ser Arg Glu
                 10                  15                  20

acc tcg ctg acg gcg ctg ggt ttc ttg gac tat ctt gac gag gag caa   211
Thr Ser Leu Thr Ala Leu Gly Phe Leu Asp Tyr Leu Asp Glu Glu Gln
             25                  30                  35

cgc gcc gcc ttg ctc ggt gaa ggc ctg gac atc agc acg ctg acc tgg   259
Arg Ala Ala Leu Leu Gly Glu Gly Leu Asp Ile Ser Thr Leu Thr Trp
         40                  45                  50

gcc aac cag gtt acc gcg ctg cgt gtg ctg gaa tcc ctc ttc aat gag   307
Ala Asn Gln Val Thr Ala Leu Arg Val Leu Glu Ser Leu Phe Asn Glu
     55                  60                  65

cat gca tac gag ctg gtt tct gca gtg att cag cat gta gct caa gaa   355
His Ala Tyr Glu Leu Val Ser Ala Val Ile Gln His Val Ala Gln Glu
 70                  75                  80                  85

cct ggc gat aat cca cac cac ttt ctg aag ttc tcg cct gaa cca tcc   403
Pro Gly Asp Asn Pro His His Phe Leu Lys Phe Ser Pro Glu Pro Ser
                 90                  95                 100

acc gag aat tct tgg gaa ttg acc ctg gat gga cca act gtc gga ttg   451
Thr Glu Asn Ser Trp Glu Leu Thr Leu Asp Gly Pro Thr Val Gly Leu
             105                 110                 115

aaa gtc act ttc gat ccg gac ggt cag atc act ttc aag gat gct cat   499
Lys Val Thr Phe Asp Pro Asp Gly Gln Ile Thr Phe Lys Asp Ala His
         120                 125                 130

ttg ggc ctg agc cca gct gag gtc gtt agt gtc act gag gcg tta gat   547
Leu Gly Leu Ser Pro Ala Glu Val Val Ser Val Thr Glu Ala Leu Asp
     135                 140                 145

acc tcc tat tcg gaa tcg caa atc aaa aaa gct gcg gaa caa ctg gtg   595
Thr Ser Tyr Ser Glu Ser Gln Ile Lys Lys Ala Ala Glu Gln Leu Val
150                 155                 160                 165

gga agc ctc aat cca acc cag cag gca gcg ctc caa gga tcc ggt ttg   643
Gly Ser Leu Asn Pro Thr Gln Gln Ala Ala Leu Gln Gly Ser Gly Leu
                 170                 175                 180

cga gga gca cag ctc act gaa gag caa aag acc ctg ttc tta aag atg   691
Arg Gly Ala Gln Leu Thr Glu Glu Gln Lys Thr Leu Phe Leu Lys Met
             185                 190                 195

acc tcc aac tgg atc gac ctt gcc aat ggc gat tcc ggc tct gaa cag   739
Thr Ser Asn Trp Ile Asp Leu Ala Asn Gly Asp Ser Gly Ser Glu Gln
         200                 205                 210

caa gaa gaa atc gct gat acg ttc agt gat acc tac atc att tgg aat   787
Gln Glu Glu Ile Ala Asp Thr Phe Ser Asp Thr Tyr Ile Ile Trp Asn
     215                 220                 225

gag cag aaa gat ggc tca gca ttc ttc cag atg aaa ggc cct gag ctc   835
Glu Gln Lys Asp Gly Ser Ala Phe Phe Gln Met Lys Gly Pro Glu Leu
230                 235                 240                 245

gac ttc agc tat aaa gag agc gtg cct gaa aac gct gaa ctc tct gca   883
```

```
Asp Phe Ser Tyr Lys Glu Ser Val Pro Glu Asn Ala Glu Leu Ser Ala
                250                 255                 260

cgg gga gtc ccc aat att cag acc tct ttt cag tca cct taactggcat    932
Arg Gly Val Pro Asn Ile Gln Thr Ser Phe Gln Ser Pro
            265                 270

tggtttagtt tgg                                                   945


<210> 1768
<211> 274
<212> PRT
<213> Corynebacterium glutamicum

<400> 1768
Met Gln Thr Thr Thr Gly Glu Thr Ser Ile Ser Asn Glu Thr Ser Phe
  1               5                  10                  15

Asn Ala Ser Arg Glu Thr Ser Leu Thr Ala Leu Gly Phe Leu Asp Tyr
             20                  25                  30

Leu Asp Glu Glu Gln Arg Ala Ala Leu Leu Gly Glu Gly Leu Asp Ile
         35                  40                  45

Ser Thr Leu Thr Trp Ala Asn Gln Val Thr Ala Leu Arg Val Leu Glu
     50                  55                  60

Ser Leu Phe Asn Glu His Ala Tyr Glu Leu Val Ser Ala Val Ile Gln
 65                  70                  75                  80

His Val Ala Gln Glu Pro Gly Asp Asn Pro His His Phe Leu Lys Phe
                85                  90                  95

Ser Pro Glu Pro Ser Thr Glu Asn Ser Trp Glu Leu Thr Leu Asp Gly
            100                 105                 110

Pro Thr Val Gly Leu Lys Val Thr Phe Asp Pro Asp Gly Gln Ile Thr
        115                 120                 125

Phe Lys Asp Ala His Leu Gly Leu Ser Pro Ala Glu Val Val Ser Val
    130                 135                 140

Thr Glu Ala Leu Asp Thr Ser Tyr Ser Glu Ser Gln Ile Lys Lys Ala
145                 150                 155                 160

Ala Glu Gln Leu Val Gly Ser Leu Asn Pro Thr Gln Gln Ala Ala Leu
                165                 170                 175

Gln Gly Ser Gly Leu Arg Gly Ala Gln Leu Thr Glu Glu Gln Lys Thr
            180                 185                 190

Leu Phe Leu Lys Met Thr Ser Asn Trp Ile Asp Leu Ala Asn Gly Asp
        195                 200                 205

Ser Gly Ser Glu Gln Gln Glu Glu Ile Ala Asp Thr Phe Ser Asp Thr
    210                 215                 220

Tyr Ile Ile Trp Asn Glu Gln Lys Asp Gly Ser Ala Phe Phe Gln Met
225                 230                 235                 240
```

```
Lys Gly Pro Glu Leu Asp Phe Ser Tyr Lys Glu Ser Val Pro Glu Asn
                245                 250                 255

Ala Glu Leu Ser Ala Arg Gly Val Pro Asn Ile Gln Thr Ser Phe Gln
            260                 265                 270

Ser Pro
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<210> 1769
<211> 942
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(919)
<223> RXA00468

<400> 1769

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ggcagaattt tgctcaagtt gcctaaatca agcacccgtt cgaataagtg tccacccttt 60

ggtttattct tgaactcact taagttttga atttttagtt gtg aaa gta gtt gat   115
                                          Val Lys Val Val Asp
                                            1               5

gca caa gtg gtt atg ggg cca acc cac gct atg agc ggt gca gcc gtg   163
Ala Gln Val Val Met Gly Pro Thr His Ala Met Ser Gly Ala Ala Val
                  10                  15                  20

ggg ctt gct gtt gct caa att ctc cca gca gaa tgg ggt ggg gtt acc   211
Gly Leu Ala Val Ala Gln Ile Leu Pro Ala Glu Trp Gly Gly Val Thr
              25                  30                  35

acc gcc acg gag gct ttt att tat gcg ggt tta gcg gcg ggt gca gcg   259
Thr Ala Thr Glu Ala Phe Ile Tyr Ala Gly Leu Ala Ala Gly Ala Ala
          40                  45                  50

ctg ctc ccg gac ctt gat tca ccg cag gcc acg gtg tcg cgt tct ttt   307
Leu Leu Pro Asp Leu Asp Ser Pro Gln Ala Thr Val Ser Arg Ser Phe
      55                  60                  65

ggt ccg att acc caa gtg att tcg cgt ttt aca gag aat att tgc caa   355
Gly Pro Ile Thr Gln Val Ile Ser Arg Phe Thr Glu Asn Ile Cys Gln
  70                  75                  80                  85

act ttc gtc aat gtc acc agg ggc agg aaa gac aaa cac tgc aac aac   403
Thr Phe Val Asn Val Thr Arg Gly Arg Lys Asp Lys His Cys Asn Asn
                  90                  95                 100

ggg cac cgc acg ttg aca cat acg gtg tgg agc gct gct gcc aca ggc   451
Gly His Arg Thr Leu Thr His Thr Val Trp Ser Ala Ala Ala Thr Gly
            105                 110                 115

gct ggt gcc aca gcg cta att ggc gcc tat gga aaa cct gcg gtg att   499
Ala Gly Ala Thr Ala Leu Ile Gly Ala Tyr Gly Lys Pro Ala Val Ile
        120                 125                 130

ggt ttg ctg ttt ttc ttc ctc ggg ctc gcc att aga ggt ctc atg cct   547
Gly Leu Leu Phe Phe Phe Leu Gly Leu Ala Ile Arg Gly Leu Met Pro
```

```
    135                 140                 145

gaa tgg tca aag aac gca gat tgg ctt tta gtt act gga gct tcc gct   595
Glu Trp Ser Lys Asn Ala Asp Trp Leu Leu Val Thr Gly Ala Ser Ala
150                 155                 160                 165

gca tta gca gtg gga gta tgg aat tat gct ccc gaa agt tca ttc ggc   643
Ala Leu Ala Val Gly Val Trp Asn Tyr Ala Pro Glu Ser Ser Phe Gly
                170                 175                 180

att gtg tta ggc tcc gcc att aca gtt gga agc ctg acc cac ttg gct   691
Ile Val Leu Gly Ser Ala Ile Thr Val Gly Ser Leu Thr His Leu Ala
            185                 190                 195

ggc gat atg gcc act aag gcc ggt atc cca gca ttt gcc ccg gtc att   739
Gly Asp Met Ala Thr Lys Ala Gly Ile Pro Ala Phe Ala Pro Val Ile
        200                 205                 210

ccg ctg aag ggc aaa cgc tgg tgg aac ctc aaa ttg cct aag ttt tta   787
Pro Leu Lys Gly Lys Arg Trp Trp Asn Leu Lys Leu Pro Lys Phe Leu
    215                 220                 225

agc att cgt gcc aac ggt cct gcc gat aag ttc tta ctg ttc gta ttc   835
Ser Ile Arg Ala Asn Gly Pro Ala Asp Lys Phe Leu Leu Phe Val Phe
230                 235                 240                 245

tcg gtg gcg gtc atc att cag att ggt ttg gtc tca tcg gga aat atg   883
Ser Val Ala Val Ile Ile Gln Ile Gly Leu Val Ser Ser Gly Asn Met
                250                 255                 260

agc acc att atg atg aat ctg ctt agt cct gca ctg taattaatgg       929
Ser Thr Ile Met Met Asn Leu Leu Ser Pro Ala Leu
            265                 270

cagttgcgtt tcg                                                   942


<210> 1770
<211> 273
<212> PRT
<213> Corynebacterium glutamicum

<400> 1770
Val Lys Val Val Asp Ala Gln Val Val Met Gly Pro Thr His Ala Met
  1               5                  10                  15

Ser Gly Ala Ala Val Gly Leu Ala Val Ala Gln Ile Leu Pro Ala Glu
             20                  25                  30

Trp Gly Gly Val Thr Thr Ala Thr Glu Ala Phe Ile Tyr Ala Gly Leu
         35                  40                  45

Ala Ala Gly Ala Ala Leu Leu Pro Asp Leu Asp Ser Pro Gln Ala Thr
     50                  55                  60

Val Ser Arg Ser Phe Gly Pro Ile Thr Gln Val Ile Ser Arg Phe Thr
 65                  70                  75                  80

Glu Asn Ile Cys Gln Thr Phe Val Asn Val Thr Arg Gly Arg Lys Asp
                 85                  90                  95
```

```
Lys His Cys Asn Asn Gly His Arg Thr Leu Thr His Thr Val Trp Ser
            100                 105                 110

Ala Ala Ala Thr Gly Ala Gly Ala Thr Ala Leu Ile Gly Ala Tyr Gly
        115                 120                 125

Lys Pro Ala Val Ile Gly Leu Leu Phe Phe Phe Leu Gly Leu Ala Ile
    130                 135                 140

Arg Gly Leu Met Pro Glu Trp Ser Lys Asn Ala Asp Trp Leu Leu Val
145                 150                 155                 160

Thr Gly Ala Ser Ala Ala Leu Ala Val Gly Val Trp Asn Tyr Ala Pro
                165                 170                 175

Glu Ser Ser Phe Gly Ile Val Leu Gly Ser Ala Ile Thr Val Gly Ser
            180                 185                 190

Leu Thr His Leu Ala Gly Asp Met Ala Thr Lys Ala Gly Ile Pro Ala
        195                 200                 205

Phe Ala Pro Val Ile Pro Leu Lys Gly Lys Arg Trp Trp Asn Leu Lys
    210                 215                 220

Leu Pro Lys Phe Leu Ser Ile Arg Ala Asn Gly Pro Ala Asp Lys Phe
225                 230                 235                 240

Leu Leu Phe Val Phe Ser Val Ala Val Ile Ile Gln Ile Gly Leu Val
                245                 250                 255

Ser Ser Gly Asn Met Ser Thr Ile Met Met Asn Leu Leu Ser Pro Ala
            260                 265                 270

Leu
```

US20220267807A1

<210> 1771
<211> 1299
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1276)
<223> RXA00469

<400> 1771

```
tgcccctgcg acaccaaacc atcagggaag accctgaacg ccacctttc agggctttcc 60

cccattcact tatcagcctc aacactccac aatagagtct atg agt act ttt cag   115
                                            Met Ser Thr Phe Gln
                                              1               5

gag ccc cac cac aac cag gga ttc atc cct ttt gcc caa cct ggt tat   163
Glu Pro His His Asn Gln Gly Phe Ile Pro Phe Ala Gln Pro Gly Tyr
                 10                  15                  20

gaa gct cca aca cca cac ctt gca act ggt act ttt cag caa atg tgg   211
Glu Ala Pro Thr Pro His Leu Ala Thr Gly Thr Phe Gln Gln Met Trp
             25                  30                  35
```

```
cag acc cgc ccc gca cgc atc cct gcc aag caa ggt ggt cac gcc aaa   259
Gln Thr Arg Pro Ala Arg Ile Pro Ala Lys Gln Gly Gly His Ala Lys
         40                  45                  50

gta gct ggt gtc tgt gaa ggc att ggt gtg cgt tat caa atc gac ccg   307
Val Ala Gly Val Cys Glu Gly Ile Gly Val Arg Tyr Gln Ile Asp Pro
     55                  60                  65

gtg ctc att cgt cta ttt ttc gtg gtc act ggt gtc ttc ggc gcc ggt   355
Val Leu Ile Arg Leu Phe Phe Val Val Thr Gly Val Phe Gly Ala Gly
 70                  75                  80                  85

gtc gca gcc tat ctc att gca tgg ctg tgc atg ccc cgc tac tcc gtt   403
Val Ala Ala Tyr Leu Ile Ala Trp Leu Cys Met Pro Arg Tyr Ser Val
                 90                  95                 100

ccg gtc tcc ccc atc gaa gct ctc tgg acc ccg ggc cac acc aaa gac   451
Pro Val Ser Pro Ile Glu Ala Leu Trp Thr Pro Gly His Thr Lys Asp
            105                 110                 115

cgc aac cac ggc tgg tgg ctg gtc atc gcg ttc ttt atg ttc tca ggt   499
Arg Asn His Gly Trp Trp Leu Val Ile Ala Phe Phe Met Phe Ser Gly
        120                 125                 130

gtt tta tcc tcc ggc gct gga gga ata tcc ggc cca gca gca gcc att   547
Val Leu Ser Ser Gly Ala Gly Gly Ile Ser Gly Pro Ala Ala Ala Ile
    135                 140                 145

act tac ctt tgc ctt tta gcc atg tgg tgg gcg ttg cat aag aaa caa   595
Thr Tyr Leu Cys Leu Leu Ala Met Trp Trp Ala Leu His Lys Lys Gln
150                 155                 160                 165

cca ctt cca ccc cgc gga cta ctc acc act gaa ttc act gtt tct gag   643
Pro Leu Pro Pro Arg Gly Leu Leu Thr Thr Glu Phe Thr Val Ser Glu
                170                 175                 180

gat gcc acc atg aaa aac gaa gat ctc tac cca cga ccc caa cca gat   691
Asp Ala Thr Met Lys Asn Glu Asp Leu Tyr Pro Arg Pro Gln Pro Asp
            185                 190                 195

cta agc act atc acc ccc gtt gag ggc tac tat gca ccc ttc gcg caa   739
Leu Ser Thr Ile Thr Pro Val Glu Gly Tyr Tyr Ala Pro Phe Ala Gln
        200                 205                 210

caa acc ccc gaa gcg cct cat tgg gat cca ctt gcc caa aac caa tac   787
Gln Thr Pro Glu Ala Pro His Trp Asp Pro Leu Ala Gln Asn Gln Tyr
    215                 220                 225

aac acc tgg gat gta caa gtc cct cca caa aag cct cag aaa aag cgc   835
Asn Thr Trp Asp Val Gln Val Pro Pro Gln Lys Pro Gln Lys Lys Arg
230                 235                 240                 245

cat gtg tgg cca tgg att gtc ggc ggt gta gtt ggt acc gga gtt gtc   883
His Val Trp Pro Trp Ile Val Gly Gly Val Val Gly Thr Gly Val Val
                250                 255                 260

atg agc gcc ctc gca ggc ctg ttt att tca aat atc gat ccc atc tac   931
Met Ser Ala Leu Ala Gly Leu Phe Ile Ser Asn Ile Asp Pro Ile Tyr
            265                 270                 275
```

```
ttt gaa gac gac cct gga atc ggc gat gtc aat ctc atc ccc acc aac   979
Phe Glu Asp Asp Pro Gly Ile Gly Asp Val Asn Leu Ile Pro Thr Asn
        280                 285                 290

gat gaa ctc ctc agc agc tac acc tct ggt gtg ggc gaa atg aac cta   1027
Asp Glu Leu Leu Ser Ser Tyr Thr Ser Gly Val Gly Glu Met Asn Leu
    295                 300                 305

gat ttc agc aac ctc acc caa ctt gat cag gaa caa aac gtt caa atc   1075
Asp Phe Ser Asn Leu Thr Gln Leu Asp Gln Glu Gln Asn Val Gln Ile
310                 315                 320                 325

acc tca ggt atc ggt gaa gtc atg gtg acc ctg cct gat gac gtg cca   1123
Thr Ser Gly Ile Gly Glu Val Met Val Thr Leu Pro Asp Asp Val Pro
                330                 335                 340

gta agc ttg agt tgc tcc gcc ggt gtg ggc aca gcg cgc tgt gat gtt   1171
Val Ser Leu Ser Cys Ser Ala Gly Val Gly Thr Ala Arg Cys Asp Val
            345                 350                 355

gga gac ctc gcc gcc cac aat gct gat ttg gaa ggt ccg atg ttg aat   1219
Gly Asp Leu Ala Ala His Asn Ala Asp Leu Glu Gly Pro Met Leu Asn
        360                 365                 370

ctg gtt gta aat tct gga atc ggc gat gtg aag gtg gag ttc gct gat   1267
Leu Val Val Asn Ser Gly Ile Gly Asp Val Lys Val Glu Phe Ala Asp
    375                 380                 385

cag aat gac tagcccgacc ctatgtgagt agt                            1299
Gln Asn Asp
390
```

US20090275096A1

<210> 1772
<211> 392
<212> PRT
<213> Corynebacterium glutamicum

<400> 1772

```
Met Ser Thr Phe Gln Glu Pro His His Asn Gln Gly Phe Ile Pro Phe
  1               5                  10                  15

Ala Gln Pro Gly Tyr Glu Ala Pro Thr Pro His Leu Ala Thr Gly Thr
             20                  25                  30

Phe Gln Gln Met Trp Gln Thr Arg Pro Ala Arg Ile Pro Ala Lys Gln
         35                  40                  45

Gly Gly His Ala Lys Val Ala Gly Val Cys Glu Gly Ile Gly Val Arg
     50                  55                  60

Tyr Gln Ile Asp Pro Val Leu Ile Arg Leu Phe Phe Val Val Thr Gly
 65                  70                  75                  80

Val Phe Gly Ala Gly Val Ala Ala Tyr Leu Ile Ala Trp Leu Cys Met
                 85                  90                  95

Pro Arg Tyr Ser Val Pro Val Ser Pro Ile Glu Ala Leu Trp Thr Pro
            100                 105                 110

Gly His Thr Lys Asp Arg Asn His Gly Trp Trp Leu Val Ile Ala Phe
```

```
        115                 120                 125

Phe Met Phe Ser Gly Val Leu Ser Ser Gly Ala Gly Gly Ile Ser Gly
    130                 135                 140

Pro Ala Ala Ala Ile Thr Tyr Leu Cys Leu Leu Ala Met Trp Trp Ala
145                 150                 155                 160

Leu His Lys Lys Gln Pro Leu Pro Pro Arg Gly Leu Leu Thr Thr Glu
                165                 170                 175

Phe Thr Val Ser Glu Asp Ala Thr Met Lys Asn Glu Asp Leu Tyr Pro
            180                 185                 190

Arg Pro Gln Pro Asp Leu Ser Thr Ile Thr Pro Val Glu Gly Tyr Tyr
        195                 200                 205

Ala Pro Phe Ala Gln Gln Thr Pro Glu Ala Pro His Trp Asp Pro Leu
    210                 215                 220

Ala Gln Asn Gln Tyr Asn Thr Trp Asp Val Gln Val Pro Pro Gln Lys
225                 230                 235                 240

Pro Gln Lys Lys Arg His Val Trp Pro Trp Ile Val Gly Gly Val Val
                245                 250                 255

Gly Thr Gly Val Val Met Ser Ala Leu Ala Gly Leu Phe Ile Ser Asn
            260                 265                 270

Ile Asp Pro Ile Tyr Phe Glu Asp Asp Pro Gly Ile Gly Asp Val Asn
        275                 280                 285

Leu Ile Pro Thr Asn Asp Glu Leu Leu Ser Ser Tyr Thr Ser Gly Val
    290                 295                 300

Gly Glu Met Asn Leu Asp Phe Ser Asn Leu Thr Gln Leu Asp Gln Glu
305                 310                 315                 320

Gln Asn Val Gln Ile Thr Ser Gly Ile Gly Glu Val Met Val Thr Leu
                325                 330                 335

Pro Asp Asp Val Pro Val Ser Leu Ser Cys Ser Ala Gly Val Gly Thr
            340                 345                 350

Ala Arg Cys Asp Val Gly Asp Leu Ala Ala His Asn Ala Asp Leu Glu
        355                 360                 365

Gly Pro Met Leu Asn Leu Val Val Asn Ser Gly Ile Gly Asp Val Lys
    370                 375                 380

Val Glu Phe Ala Asp Gln Asn Asp
385                 390
```

<210> 1773
<211> 984
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(961)
<223> RXA00472

<400> 1773
gtctaaacgc tcccgtgctt tcgccacagc attaatcgcc ttgggcctag ggctatcttc 60

ctgctctact acggaagata ccgctatatc ggagacgaca gtg tct agt gtt gca 115
Val Ser Ser Val Ala
1 5

acg aaa aca acc tcg act ctg cct gaa atg aac tcc gca gta tca gca 163
Thr Lys Thr Thr Ser Thr Leu Pro Glu Met Asn Ser Ala Val Ser Ala
10 15 20

gac ggc gtg acg atc act atc gat tct gcc ttc acg aca gac tct gta 211
Asp Gly Val Thr Ile Thr Ile Asp Ser Ala Phe Thr Thr Asp Ser Val
25 30 35

gaa atg gaa tcc cta gac aga cct tct ggc gac atc caa ccc gag atg 259
Glu Met Glu Ser Leu Asp Arg Pro Ser Gly Asp Ile Gln Pro Glu Met
40 45 50

tct aga gaa gac gga atc ttt gtc gta gtc gaa acc act ata aag aac 307
Ser Arg Glu Asp Gly Ile Phe Val Val Val Glu Thr Thr Ile Lys Asn
55 60 65

gag agt gga gca gat atg gac atc acc tgt gca tcc act ggt tca act 355
Glu Ser Gly Ala Asp Met Asp Ile Thr Cys Ala Ser Thr Gly Ser Thr
70 75 80 85

gtc tat gca gaa atc tcc act aat caa gag gcc gta tac caa cca ata 403
Val Tyr Ala Glu Ile Ser Thr Asn Gln Glu Ala Val Tyr Gln Pro Ile
90 95 100

cgc gat tta ttc ctc atc cca gga aac ccg gaa tgc aac cat aat cta 451
Arg Asp Leu Phe Leu Ile Pro Gly Asn Pro Glu Cys Asn His Asn Leu
105 110 115

gga tcc ggt ttc gac gca cca atg act tgg gta ttt caa atc cct aaa 499
Gly Ser Gly Phe Asp Ala Pro Met Thr Trp Val Phe Gln Ile Pro Lys
120 125 130

gat gcc act gcg gag cga ttt gga ttc aca cat agt gag ctc ggt gat 547
Asp Ala Thr Ala Glu Arg Phe Gly Phe Thr His Ser Glu Leu Gly Asp
135 140 145

ggg aaa cta act tgg att gca ctc aat gat ttg agt aat tcg gag cca 595
Gly Lys Leu Thr Trp Ile Ala Leu Asn Asp Leu Ser Asn Ser Glu Pro
150 155 160 165

gct act gaa tca act atg cga gac gaa gca gca atc gat ccg agc acc 643
Ala Thr Glu Ser Thr Met Arg Asp Glu Ala Ala Ile Asp Pro Ser Thr
170 175 180

cct cag caa act cca gta cag gaa act gtg atc tca caa aac acc att 691
Pro Gln Gln Thr Pro Val Gln Glu Thr Val Ile Ser Gln Asn Thr Ile
185 190 195

gaa act cct gta gcc cct gct cct gcg gta cct gct tat ggc gct tct 739
Glu Thr Pro Val Ala Pro Ala Pro Ala Val Pro Ala Tyr Gly Ala Ser
200 205 210

```
tgc cct gtc tcg atg ctc cag cag cca agt caa gct gca gat ggt tca   787
Cys Pro Val Ser Met Leu Gln Gln Pro Ser Gln Ala Ala Asp Gly Ser
    215                 220                 225

gct ttg gtc tgc att tat gca gga acc ccc aac cca atc tgg gtc tac   835
Ala Leu Val Cys Ile Tyr Ala Gly Thr Pro Asn Pro Ile Trp Val Tyr
230                 235                 240                 245

ggc cca gaa cct ctc gga gtc ggg act gct aca ccg ggt ggg gca tgc   883
Gly Pro Glu Pro Leu Gly Val Gly Thr Ala Thr Pro Gly Gly Ala Cys
                250                 255                 260

gaa gga tac gag gcc ggt ggg caa gat gct tct gga aat ata atg atg   931
Glu Gly Tyr Glu Ala Gly Gly Gln Asp Ala Ser Gly Asn Ile Met Met
            265                 270                 275

tgc tca ggc gga caa tgg gtc tat ggg cca taaatctaaa atcaaagagt     981
Cys Ser Gly Gly Gln Trp Val Tyr Gly Pro
        280                 285

gca                                                               984
```

US20090305363A1

<210> 1774
<211> 287
<212> PRT
<213> Corynebacterium glutamicum

<400> 1774

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Val Ser Ser Val Ala Thr Lys Thr Thr Ser Thr Leu Pro Glu Met Asn
  1               5                  10                  15

Ser Ala Val Ser Ala Asp Gly Val Thr Ile Thr Ile Asp Ser Ala Phe
             20                  25                  30

Thr Thr Asp Ser Val Glu Met Glu Ser Leu Asp Arg Pro Ser Gly Asp
         35                  40                  45

Ile Gln Pro Glu Met Ser Arg Glu Asp Gly Ile Phe Val Val Val Glu
     50                  55                  60

Thr Thr Ile Lys Asn Glu Ser Gly Ala Asp Met Asp Ile Thr Cys Ala
 65                  70                  75                  80

Ser Thr Gly Ser Thr Val Tyr Ala Glu Ile Ser Thr Asn Gln Glu Ala
                 85                  90                  95

Val Tyr Gln Pro Ile Arg Asp Leu Phe Leu Ile Pro Gly Asn Pro Glu
            100                 105                 110

Cys Asn His Asn Leu Gly Ser Gly Phe Asp Ala Pro Met Thr Trp Val
        115                 120                 125

Phe Gln Ile Pro Lys Asp Ala Thr Ala Glu Arg Phe Gly Phe Thr His
    130                 135                 140

Ser Glu Leu Gly Asp Gly Lys Leu Thr Trp Ile Ala Leu Asn Asp Leu
145                 150                 155                 160

Ser Asn Ser Glu Pro Ala Thr Glu Ser Thr Met Arg Asp Glu Ala Ala
```

```
                165                 170                 175

Ile Asp Pro Ser Thr Pro Gln Gln Thr Pro Val Gln Glu Thr Val Ile
            180                 185                 190

Ser Gln Asn Thr Ile Glu Thr Pro Val Ala Pro Ala Pro Ala Val Pro
        195                 200                 205

Ala Tyr Gly Ala Ser Cys Pro Val Ser Met Leu Gln Gln Pro Ser Gln
    210                 215                 220

Ala Ala Asp Gly Ser Ala Leu Val Cys Ile Tyr Ala Gly Thr Pro Asn
225                 230                 235                 240

Pro Ile Trp Val Tyr Gly Pro Glu Pro Leu Gly Val Gly Thr Ala Thr
                245                 250                 255

Pro Gly Gly Ala Cys Glu Gly Tyr Glu Ala Gly Gly Gln Asp Ala Ser
            260                 265                 270

Gly Asn Ile Met Met Cys Ser Gly Gly Gln Trp Val Tyr Gly Pro
        275                 280                 285
```

CN 1324129 C 2007.07.04

<210> 1775
<211> 1701
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1678)
<223> RXA00474

<400> 1775

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gtgtgcgcag cggaaaagtc ctgatcagta ggcctcagga tgcagcattg cttgagcctg 60

aacagccaac aacgttgcgg gcggtcccat gacgcgggtg atg gca ttg tgg ttt   115
                                          Met Ala Leu Trp Phe
                                            1               5

ccg gat tgg cct gtg cag gcg gtt cat ttg gat gaa gat gct ccc gcg   163
Pro Asp Trp Pro Val Gln Ala Val His Leu Asp Glu Asp Ala Pro Ala
                10                  15                  20

cac aat aaa cct gtg gcg att gct gcg cat tac cgc atc cag gtg tgt   211
His Asn Lys Pro Val Ala Ile Ala Ala His Tyr Arg Ile Gln Val Cys
            25                  30                  35

ggc gtg gct gcg cgc aag cgt ggg gtg cgt cgt ggg atg aag gtt cgg   259
Gly Val Ala Ala Arg Lys Arg Gly Val Arg Arg Gly Met Lys Val Arg
        40                  45                  50

cag gcg cag gct gtg tgc cct gag ctg gag gtt gtt gac gcg gat gca   307
Gln Ala Gln Ala Val Cys Pro Glu Leu Glu Val Val Asp Ala Asp Ala
    55                  60                  65

gat cgt gat gcc cgg atg ttt gag ggc atc gtg gca tcg ctc ggt gag   355
Asp Arg Asp Ala Arg Met Phe Glu Gly Ile Val Ala Ser Leu Gly Glu
70                  75                  80                  85
```

```
gtt gcc tcc agc gtc gag gtg ctt cgt ccg ggt ctg gtc gcg gtc gat   403
Val Ala Ser Ser Val Glu Val Leu Arg Pro Gly Leu Val Ala Val Asp
                 90                  95                 100

gcg gga gct gcc gcg cgc tat tac ggt tca gag gac atc gct gct cag   451
Ala Gly Ala Ala Ala Arg Tyr Tyr Gly Ser Glu Asp Ile Ala Ala Gln
            105                 110                 115

atg ctt atc gac gcc gcc ctg cgc caa ggc atc gac gtt ttc gcc ggg   499
Met Leu Ile Asp Ala Ala Leu Arg Gln Gly Ile Asp Val Phe Ala Gly
        120                 125                 130

gtt gcg gat gag atc acg acg gcc gtc atc gcg gcg agg gcg aat ggt   547
Val Ala Asp Glu Ile Thr Thr Ala Val Ile Ala Ala Arg Ala Asn Gly
    135                 140                 145

ggg act gtg gtg aag agg gag gcg tcg aga agc ttt tta cag cag caa   595
Gly Thr Val Val Lys Arg Glu Ala Ser Arg Ser Phe Leu Gln Gln Gln
150                 155                 160                 165

ccc ctg ggc gtg ctg gcg gcc gag gaa gcg ctg ggt tgt gag gcg gag   643
Pro Leu Gly Val Leu Ala Ala Glu Glu Ala Leu Gly Cys Glu Ala Glu
                170                 175                 180

gtg gtg cgc gcg ctg gcg gat ctg ggc atg cgc acg ctt ggt gag ctg   691
Val Val Arg Ala Leu Ala Asp Leu Gly Met Arg Thr Leu Gly Glu Leu
            185                 190                 195

gcg gaa ctg ccg gta gaa gcc gtg gcg acg cgt ttc ggc aac gct ggt   739
Ala Glu Leu Pro Val Glu Ala Val Ala Thr Arg Phe Gly Asn Ala Gly
        200                 205                 210

ctg cgg tgt cac aac att gcg cgt gcc agg cac gat cgt aag gtc gcg   787
Leu Arg Cys His Asn Ile Ala Arg Ala Arg His Asp Arg Lys Val Ala
    215                 220                 225

cca ccg atc acg cat gca gat tgg gag gtt tcg cat gtg ccg gag gag   835
Pro Pro Ile Thr His Ala Asp Trp Glu Val Ser His Val Pro Glu Glu
230                 235                 240                 245

cct att ttg cgt gtc gac gcc gcc tcg ttt gtt gcg cgc aac ctt gcc   883
Pro Ile Leu Arg Val Asp Ala Ala Ser Phe Val Ala Arg Asn Leu Ala
                250                 255                 260

tcg cgc ctg cat caa ctg ctg agc aaa ggt ggc gtg gtg tgc caa ttg   931
Ser Arg Leu His Gln Leu Leu Ser Lys Gly Gly Val Val Cys Gln Leu
            265                 270                 275

ctc aag gtc aca gcc gat ttc agt act ggt gat acg gtg agc aga att   979
Leu Lys Val Thr Ala Asp Phe Ser Thr Gly Asp Thr Val Ser Arg Ile
        280                 285                 290

tgg cgt acc ggt gaa cct tta acg gaa cag gca act gcg gat cgg gtg   1027
Trp Arg Thr Gly Glu Pro Leu Thr Glu Gln Ala Thr Ala Asp Arg Val
    295                 300                 305

cgt tgg cag ttg gat ggg tgg ttg act gcg cgc ggt gtg cat tcc gat   1075
Arg Trp Gln Leu Asp Gly Trp Leu Thr Ala Arg Gly Val His Ser Asp
310                 315                 320                 325

gat ccg aat gag cac gat ggg att acg gcg ttg tgg ctt att cct ttg   1123
```

```
Asp Pro Asn Glu His Asp Gly Ile Thr Ala Leu Trp Leu Ile Pro Leu
                330                 335                 340

gaa tgt gtg cca ccg gat atg gcc agc ggc gga ttg tgg gat acc ggg   1171
Glu Cys Val Pro Pro Asp Met Ala Ser Gly Gly Leu Trp Asp Thr Gly
            345                 350                 355

cgc agc cag cag cat gtg gcc aga caa gtc att gag cgt gtg caa tca   1219
Arg Ser Gln Gln His Val Ala Arg Gln Val Ile Glu Arg Val Gln Ser
        360                 365                 370

agc ttg ggc gtg gat gcg gtg ctg cag cct gtt ccg gct ggt ggt cgg   1267
Ser Leu Gly Val Asp Ala Val Leu Gln Pro Val Pro Ala Gly Gly Arg
    375                 380                 385

gga gta gaa gaa cgc att cat ttt gtt ccc tat ggt gaa aaa cgt gat   1315
Gly Val Glu Glu Arg Ile His Phe Val Pro Tyr Gly Glu Lys Arg Asp
390                 395                 400                 405

gct atc cgc aat cca gcg ggg tcg tgg cca ggg aaa ata cca ggt ccg   1363
Ala Ile Arg Asn Pro Ala Gly Ser Trp Pro Gly Lys Ile Pro Gly Pro
                410                 415                 420

ctg cct gct cgg ttg ggc ggt ggg atc aac cac ccg gcc tcg caa gtg   1411
Leu Pro Ala Arg Leu Gly Gly Gly Ile Asn His Pro Ala Ser Gln Val
            425                 430                 435

acc atg att gat aca gaa ggg cag cgt att tac gtc acc gca gag gca   1459
Thr Met Ile Asp Thr Glu Gly Gln Arg Ile Tyr Val Thr Ala Glu Ala
        440                 445                 450

ttg ctc agc tcg tcg ccg tat gcc ttg tcc tgg ggg ccg gcc cgc tat   1507
Leu Leu Ser Ser Ser Pro Tyr Ala Leu Ser Trp Gly Pro Ala Arg Tyr
    455                 460                 465

ttg atc act ggc tgg gct ggg cca tgg ccg gtg gat gat cga tgg tgg   1555
Leu Ile Thr Gly Trp Ala Gly Pro Trp Pro Val Asp Asp Arg Trp Trp
470                 475                 480                 485

gag aaa aac ggc aca aaa tat gcc cgc ctc caa gtg gtg gga cgg gca   1603
Glu Lys Asn Gly Thr Lys Tyr Ala Arg Leu Gln Val Val Gly Arg Ala
                490                 495                 500

gta tct gaa gaa agg cag ctc aat gcg tgg ctg ttg atg tgg aaa gac   1651
Val Ser Glu Glu Arg Gln Leu Asn Ala Trp Leu Leu Met Trp Lys Asp
            505                 510                 515

aac aag tgg cgg att gag gcc aca tat taggaaacta ctgcgctaaa         1698
Asn Lys Trp Arg Ile Glu Ala Thr Tyr
        520                 525

aca                                                               1701
```

<210> 1776
<211> 526
<212> PRT
<213> Corynebacterium glutamicum

<400> 1776
Met Ala Leu Trp Phe Pro Asp Trp Pro Val Gln Ala Val His Leu Asp

```
  1               5                  10                  15
Glu Asp Ala Pro Ala His Asn Lys Pro Val Ala Ile Ala Ala His Tyr
            20                  25                  30
Arg Ile Gln Val Cys Gly Val Ala Ala Arg Lys Arg Gly Val Arg Arg
        35                  40                  45
Gly Met Lys Val Arg Gln Ala Gln Ala Val Cys Pro Glu Leu Glu Val
    50                  55                  60
Val Asp Ala Asp Ala Asp Arg Asp Ala Arg Met Phe Glu Gly Ile Val
65                  70                  75                  80
Ala Ser Leu Gly Glu Val Ala Ser Ser Val Glu Val Leu Arg Pro Gly
                85                  90                  95
Leu Val Ala Val Asp Ala Gly Ala Ala Ala Arg Tyr Tyr Gly Ser Glu
            100                 105                 110
Asp Ile Ala Ala Gln Met Leu Ile Asp Ala Ala Leu Arg Gln Gly Ile
        115                 120                 125
Asp Val Phe Ala Gly Val Ala Asp Glu Ile Thr Thr Ala Val Ile Ala
    130                 135                 140
Ala Arg Ala Asn Gly Gly Thr Val Val Lys Arg Glu Ala Ser Arg Ser
145                 150                 155                 160
Phe Leu Gln Gln Gln Pro Leu Gly Val Leu Ala Ala Glu Glu Ala Leu
                165                 170                 175
Gly Cys Glu Ala Glu Val Val Arg Ala Leu Ala Asp Leu Gly Met Arg
            180                 185                 190
Thr Leu Gly Glu Leu Ala Glu Leu Pro Val Glu Ala Val Ala Thr Arg
        195                 200                 205
Phe Gly Asn Ala Gly Leu Arg Cys His Asn Ile Ala Arg Ala Arg His
    210                 215                 220
Asp Arg Lys Val Ala Pro Pro Ile Thr His Ala Asp Trp Glu Val Ser
225                 230                 235                 240
His Val Pro Glu Glu Pro Ile Leu Arg Val Asp Ala Ala Ser Phe Val
                245                 250                 255
Ala Arg Asn Leu Ala Ser Arg Leu His Gln Leu Leu Ser Lys Gly Gly
            260                 265                 270
Val Val Cys Gln Leu Leu Lys Val Thr Ala Asp Phe Ser Thr Gly Asp
        275                 280                 285
Thr Val Ser Arg Ile Trp Arg Thr Gly Glu Pro Leu Thr Glu Gln Ala
    290                 295                 300
Thr Ala Asp Arg Val Arg Trp Gln Leu Asp Gly Trp Leu Thr Ala Arg
305                 310                 315                 320
Gly Val His Ser Asp Asp Pro Asn Glu His Asp Gly Ile Thr Ala Leu
                325                 330                 335
```

CN 102250858 A 20111123

```
Trp Leu Ile Pro Leu Glu Cys Val Pro Pro Asp Met Ala Ser Gly Gly
            340                 345                 350

Leu Trp Asp Thr Gly Arg Ser Gln Gln His Val Ala Arg Gln Val Ile
        355                 360                 365

Glu Arg Val Gln Ser Ser Leu Gly Val Asp Ala Val Leu Gln Pro Val
    370                 375                 380

Pro Ala Gly Gly Arg Gly Val Glu Glu Arg Ile His Phe Val Pro Tyr
385                 390                 395                 400

Gly Glu Lys Arg Asp Ala Ile Arg Asn Pro Ala Gly Ser Trp Pro Gly
                405                 410                 415

Lys Ile Pro Gly Pro Leu Pro Ala Arg Leu Gly Gly Gly Ile Asn His
            420                 425                 430

Pro Ala Ser Gln Val Thr Met Ile Asp Thr Glu Gly Gln Arg Ile Tyr
        435                 440                 445

Val Thr Ala Glu Ala Leu Leu Ser Ser Ser Pro Tyr Ala Leu Ser Trp
    450                 455                 460

Gly Pro Ala Arg Tyr Leu Ile Thr Gly Trp Ala Gly Pro Trp Pro Val
465                 470                 475                 480

Asp Asp Arg Trp Trp Glu Lys Asn Gly Thr Lys Tyr Ala Arg Leu Gln
                485                 490                 495

Val Val Gly Arg Ala Val Ser Glu Glu Arg Gln Leu Asn Ala Trp Leu
            500                 505                 510

Leu Met Trp Lys Asp Asn Lys Trp Arg Ile Glu Ala Thr Tyr
        515                 520                 525
```

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<210> 1777
<211> 783
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(760)
<223> RXA00475

<400> 1777

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ggggtgtctg taattttcac gtctcctggc gtttttaaga cgaattacaa caattcgttc 60

acgattgagc gaaattgggc gtcttgctta ggtttcgggg gtg acc cag ggt tac   115
                                              Val Thr Gln Gly Tyr
                                                1               5

ggt gtg tgc atg att gtg cag cca act tct cat tca aag cat cgt gcc   163
Gly Val Cys Met Ile Val Gln Pro Thr Ser His Ser Lys His Arg Ala
                 10                  15                  20

cgc ctg aag act cta gcg att gtc ggc gct agc gcg ttg act ctt gcg   211
Arg Leu Lys Thr Leu Ala Ile Val Gly Ala Ser Ala Leu Thr Leu Ala
```

```
            25                  30                  35

ggt tgt gga acc tcc aat tcc acc acc aac gat gct tct tct gta acc   259
Gly Cys Gly Thr Ser Asn Ser Thr Thr Asn Asp Ala Ser Ser Val Thr
         40                  45                  50

caa act atg tcc gca act gcg gat ggc gca cag ttg tcc aac gaa gct   307
Gln Thr Met Ser Ala Thr Ala Asp Gly Ala Gln Leu Ser Asn Glu Ala
     55                  60                  65

tcc acc ggc cca acc gca ttg ggc gaa gcc gat gta gca atg aag act   355
Ser Thr Gly Pro Thr Ala Leu Gly Glu Ala Asp Val Ala Met Lys Thr
 70                  75                  80                  85

ctc cga cct gat gcg cct gca cag ctc atg gtc acc gat gtt cgg att   403
Leu Arg Pro Asp Ala Pro Ala Gln Leu Met Val Thr Asp Val Arg Ile
                 90                  95                 100

ggc tct cac agt ggc ttt gac cgc gtg gta ttt gat ctc act ggc acc   451
Gly Ser His Ser Gly Phe Asp Arg Val Val Phe Asp Leu Thr Gly Thr
            105                 110                 115

gga act cct ggt tgg ttc att gat tac acc tcc aat ccc acc cag cag   499
Gly Thr Pro Gly Trp Phe Ile Asp Tyr Thr Ser Asn Pro Thr Gln Gln
        120                 125                 130

ggc agc gga aac acc atc aac ttc acg ggc gat aca gcg ctg aac gta   547
Gly Ser Gly Asn Thr Ile Asn Phe Thr Gly Asp Thr Ala Leu Asn Val
    135                 140                 145

aat att gac ggt act gtt tat cct ttc gat ttg ggc ctt gag gat cca   595
Asn Ile Asp Gly Thr Val Tyr Pro Phe Asp Leu Gly Leu Glu Asp Pro
150                 155                 160                 165

gag atc ggc acc gtg gat ggc tcc ggc agc att gtc acc cag gtc gtc   643
Glu Ile Gly Thr Val Asp Gly Ser Gly Ser Ile Val Thr Gln Val Val
                170                 175                 180

agc gca ggt act ttt gag gga cgc tcc cag ttc gtc atc ggc ctc aac   691
Ser Ala Gly Thr Phe Glu Gly Arg Ser Gln Phe Val Ile Gly Leu Asn
            185                 190                 195

ggc aag cac cgc tac tcg gtc act gag ttg cag gat ccg cac cgt ctc   739
Gly Lys His Arg Tyr Ser Val Thr Glu Leu Gln Asp Pro His Arg Leu
        200                 205                 210

gtt gtg gat gtt tta gcg cag tagtttccta atatgtggcc tca             783
Val Val Asp Val Leu Ala Gln
    215                 220
```

<210> 1778
<211> 220
<212> PRT
<213> Corynebacterium glutamicum

<400> 1778

```
Val Thr Gln Gly Tyr Gly Val Cys Met Ile Val Gln Pro Thr Ser His
  1               5                  10                  15

Ser Lys His Arg Ala Arg Leu Lys Thr Leu Ala Ile Val Gly Ala Ser
```

```
             20                  25                  30

Ala Leu Thr Leu Ala Gly Cys Gly Thr Ser Asn Ser Thr Thr Asn Asp
         35                  40                  45

Ala Ser Ser Val Thr Gln Thr Met Ser Ala Thr Ala Asp Gly Ala Gln
     50                  55                  60

Leu Ser Asn Glu Ala Ser Thr Gly Pro Thr Ala Leu Gly Glu Ala Asp
 65                  70                  75                  80

Val Ala Met Lys Thr Leu Arg Pro Asp Ala Pro Ala Gln Leu Met Val
                 85                  90                  95

Thr Asp Val Arg Ile Gly Ser His Ser Gly Phe Asp Arg Val Val Phe
            100                 105                 110

Asp Leu Thr Gly Thr Gly Thr Pro Gly Trp Phe Ile Asp Tyr Thr Ser
        115                 120                 125

Asn Pro Thr Gln Gln Gly Ser Gly Asn Thr Ile Asn Phe Thr Gly Asp
    130                 135                 140

Thr Ala Leu Asn Val Asn Ile Asp Gly Thr Val Tyr Pro Phe Asp Leu
145                 150                 155                 160

Gly Leu Glu Asp Pro Glu Ile Gly Thr Val Asp Gly Ser Gly Ser Ile
                165                 170                 175

Val Thr Gln Val Val Ser Ala Gly Thr Phe Glu Gly Arg Ser Gln Phe
            180                 185                 190

Val Ile Gly Leu Asn Gly Lys His Arg Tyr Ser Val Thr Glu Leu Gln
        195                 200                 205

Asp Pro His Arg Leu Val Val Asp Val Leu Ala Gln
    210                 215                 220


<210> 1779
<211> 984
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(961)
<223> RXA00476

<400> 1779
gtgaacgaat tgttgtaatt cgtcttaaaa acgccaggag acgtgaaaat tacagacacc 60

ccagacatca gatggaggcg gcgatactag ggtagaggac atg act ctt cgc tgt   115
                                            Met Thr Leu Arg Cys
                                              1               5

tct gac gtc aat gtt gaa ccc ctg ccg gga acg gca aaa aca ggt tct   163
Ser Asp Val Asn Val Glu Pro Leu Pro Gly Thr Ala Lys Thr Gly Ser
                 10                  15                  20

ggg ttt gtt ctc ctt gaa cat gct ggc tcg tgg agc cgt gat gtt tta   211
```

```
Gly Phe Val Leu Leu Glu His Ala Gly Ser Trp Ser Arg Asp Val Leu
             25                  30                  35

gac ggc gga aca ttt gat cct gag ttg act gat caa ttg aag agg cac   259
Asp Gly Gly Thr Phe Asp Pro Glu Leu Thr Asp Gln Leu Lys Arg His
         40                  45                  50

ctg aaa gct tcc gga atg ggt ctg caa tta att agg aag ccg gga agg   307
Leu Lys Ala Ser Gly Met Gly Leu Gln Leu Ile Arg Lys Pro Gly Arg
     55                  60                  65

gag ggt cga aac gtc gaa aag cat aat ctt ttt ctc gtt ttt gct gag   355
Glu Gly Arg Asn Val Glu Lys His Asn Leu Phe Leu Val Phe Ala Glu
 70                  75                  80                  85

gcc tca att att gag cac ctg gtg gtg gac gcg ccg gct gat gtt ttg   403
Ala Ser Ile Ile Glu His Leu Val Val Asp Ala Pro Ala Asp Val Leu
                 90                  95                 100

gat ctt gat tta agc ggg ccg ggc aaa aac aat gcg cag cgc atg gat   451
Asp Leu Asp Leu Ser Gly Pro Gly Lys Asn Asn Ala Gln Arg Met Asp
            105                 110                 115

gat ccg atg ctg ctg att tgt acg cat tcg aag cgc gat gtg tgc tgc   499
Asp Pro Met Leu Leu Ile Cys Thr His Ser Lys Arg Asp Val Cys Cys
        120                 125                 130

gcg atc aag ggg cgt ccg ctg gca gct gcc gtg gag cca caa ttt ggg   547
Ala Ile Lys Gly Arg Pro Leu Ala Ala Ala Val Glu Pro Gln Phe Gly
    135                 140                 145

ccg ctg cat gtg tgg gag gct tcg cac acc aag ggc cac cgt ttt gcg   595
Pro Leu His Val Trp Glu Ala Ser His Thr Lys Gly His Arg Phe Ala
150                 155                 160                 165

cca tcg atg ctg ctc atg ccg tgg aat tac tct tat ggc cta ctt gat   643
Pro Ser Met Leu Leu Met Pro Trp Asn Tyr Ser Tyr Gly Leu Leu Asp
                170                 175                 180

gag gcc gaa acc gtg cag ctt ttc caa ggc gcg ttg gac aac aaa ctc   691
Glu Ala Glu Thr Val Gln Leu Phe Gln Gly Ala Leu Asp Asn Lys Leu
            185                 190                 195

ttc ctg ccg ggc aac cgt ggc cga gga acc tta gat gct cgt ggc cag   739
Phe Leu Pro Gly Asn Arg Gly Arg Gly Thr Leu Asp Ala Arg Gly Gln
        200                 205                 210

gtt gca gaa att gcc gtg gcg gaa gct ttc ggc gag gcg gtt gct cct   787
Val Ala Glu Ile Ala Val Ala Glu Ala Phe Gly Glu Ala Val Ala Pro
    215                 220                 225

gcg agt ttg cag gtt gaa ttc gaa gat gat tct gtt ttg gtt act cat   835
Ala Ser Leu Gln Val Glu Phe Glu Asp Asp Ser Val Leu Val Thr His
230                 235                 240                 245

ccc gat ggg cgc acg tgg gtt gtg gag ctt gaa cgc atc gag gtc gac   883
Pro Asp Gly Arg Thr Trp Val Val Glu Leu Glu Arg Ile Glu Val Asp
                250                 255                 260

ggc gtg gtg tcc tcg tgt ggt gat cag ccg aaa act gga aaa gcg tgg   931
Gly Val Val Ser Ser Cys Gly Asp Gln Pro Lys Thr Gly Lys Ala Trp
```

```
            265                 270                 275

gtg gct agg caa gtt aca gaa ctg atc gga taaaagcaga gttatatctg     981
Val Ala Arg Gln Val Thr Glu Leu Ile Gly
        280                 285

atg                                                               984
```

<210> 1780
<211> 287
<212> PRT
<213> Corynebacterium glutamicum

<400> 1780

```
Met Thr Leu Arg Cys Ser Asp Val Asn Val Glu Pro Leu Pro Gly Thr
  1               5                  10                  15

Ala Lys Thr Gly Ser Gly Phe Val Leu Leu Glu His Ala Gly Ser Trp
             20                  25                  30

Ser Arg Asp Val Leu Asp Gly Gly Thr Phe Asp Pro Glu Leu Thr Asp
         35                  40                  45

Gln Leu Lys Arg His Leu Lys Ala Ser Gly Met Gly Leu Gln Leu Ile
     50                  55                  60

Arg Lys Pro Gly Arg Glu Gly Arg Asn Val Glu Lys His Asn Leu Phe
 65                  70                  75                  80

Leu Val Phe Ala Glu Ala Ser Ile Ile Glu His Leu Val Val Asp Ala
                 85                  90                  95

Pro Ala Asp Val Leu Asp Leu Asp Leu Ser Gly Pro Gly Lys Asn Asn
            100                 105                 110

Ala Gln Arg Met Asp Asp Pro Met Leu Leu Ile Cys Thr His Ser Lys
        115                 120                 125

Arg Asp Val Cys Cys Ala Ile Lys Gly Arg Pro Leu Ala Ala Ala Val
    130                 135                 140

Glu Pro Gln Phe Gly Pro Leu His Val Trp Glu Ala Ser His Thr Lys
145                 150                 155                 160

Gly His Arg Phe Ala Pro Ser Met Leu Leu Met Pro Trp Asn Tyr Ser
                165                 170                 175

Tyr Gly Leu Leu Asp Glu Ala Glu Thr Val Gln Leu Phe Gln Gly Ala
            180                 185                 190

Leu Asp Asn Lys Leu Phe Leu Pro Gly Asn Arg Gly Arg Gly Thr Leu
        195                 200                 205

Asp Ala Arg Gly Gln Val Ala Glu Ile Ala Val Ala Glu Ala Phe Gly
    210                 215                 220

Glu Ala Val Ala Pro Ala Ser Leu Gln Val Glu Phe Glu Asp Asp Ser
225                 230                 235                 240

Val Leu Val Thr His Pro Asp Gly Arg Thr Trp Val Val Glu Leu Glu
```

```
                245                 250                 255

Arg Ile Glu Val Asp Gly Val Val Ser Ser Cys Gly Asp Gln Pro Lys
            260                 265                 270

Thr Gly Lys Ala Trp Val Ala Arg Gln Val Thr Glu Leu Ile Gly
        275                 280                 285


<210> 1781
<211> 708
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(685)
<223> RXA00481

<400> 1781
gtccataaaa ataatgtgcc tacaagaaat ttatagtatc ccatgagtta atatttttaa 60

aaataaactt tatctgactt tgtagaaaaa ggtgattact atg ctg aat atg cag   115
                                            Met Leu Asn Met Gln
                                              1               5

gaa cca gat aaa atc cat ccg gca gaa cct aca ctt cgt aat att tat   163
Glu Pro Asp Lys Ile His Pro Ala Glu Pro Thr Leu Arg Asn Ile Tyr
                  10                  15                  20

gac gtt aaa act agt gat ccc aaa agt gaa tta gtt gat cgt tct ggc   211
Asp Val Lys Thr Ser Asp Pro Lys Ser Glu Leu Val Asp Arg Ser Gly
              25                  30                  35

atg tcg gaa gaa gac att gcg caa att ggg cgg cta atg aaa tcg ttg   259
Met Ser Glu Glu Asp Ile Ala Gln Ile Gly Arg Leu Met Lys Ser Leu
          40                  45                  50

gcc agt ctt cgc gat gtg gaa cgt agt att ggt gaa gcc tcg gca cgt   307
Ala Ser Leu Arg Asp Val Glu Arg Ser Ile Gly Glu Ala Ser Ala Arg
      55                  60                  65

tat atg gag cta agt gcc cct gat atg cga gct ttg cac tat ttg att   355
Tyr Met Glu Leu Ser Ala Pro Asp Met Arg Ala Leu His Tyr Leu Ile
  70                  75                  80                  85

gtg gcg ggc aat gcg ggc gaa gtg gtg act cca gga atg ctt gga gct   403
Val Ala Gly Asn Ala Gly Glu Val Val Thr Pro Gly Met Leu Gly Ala
                  90                  95                 100

cac ctt aag ctt tcc ccg gca tct gta aca aag acg ctt aat agg cta   451
His Leu Lys Leu Ser Pro Ala Ser Val Thr Lys Thr Leu Asn Arg Leu
              105                 110                 115

gaa aaa ggt ggg cat att gtt cgt aat gtg cac ccc gtc gac cgc agg   499
Glu Lys Gly Gly His Ile Val Arg Asn Val His Pro Val Asp Arg Arg
          120                 125                 130

gct ttc gcc ctc atg gtc act gat gcc act cgt gga gag gcg atg cgg   547
Ala Phe Ala Leu Met Val Thr Asp Ala Thr Arg Gly Glu Ala Met Arg
      135                 140                 145
```

```
acg ctt ggt aag cat cag gcg cgt cgt ttt gat gct gct aaa cga tta   595
Thr Leu Gly Lys His Gln Ala Arg Arg Phe Asp Ala Ala Lys Arg Leu
150                 155                 160                 165

act cca caa gag cgt gaa gtg gtt atc cga ttc ctt cag gat atg gca   643
Thr Pro Gln Glu Arg Glu Val Val Ile Arg Phe Leu Gln Asp Met Ala
                170                 175                 180

cag gag tta tcc ctt aat aat gca cca tgg ctc aac acg gag           685
Gln Glu Leu Ser Leu Asn Asn Ala Pro Trp Leu Asn Thr Glu
            185                 190                 195

tagatgacca tctacgttaa tta                                        708


<210> 1782
<211> 195
<212> PRT
<213> Corynebacterium glutamicum

<400> 1782
Met Leu Asn Met Gln Glu Pro Asp Lys Ile His Pro Ala Glu Pro Thr
  1               5                  10                  15

Leu Arg Asn Ile Tyr Asp Val Lys Thr Ser Asp Pro Lys Ser Glu Leu
             20                  25                  30

Val Asp Arg Ser Gly Met Ser Glu Glu Asp Ile Ala Gln Ile Gly Arg
         35                  40                  45

Leu Met Lys Ser Leu Ala Ser Leu Arg Asp Val Glu Arg Ser Ile Gly
     50                  55                  60

Glu Ala Ser Ala Arg Tyr Met Glu Leu Ser Ala Pro Asp Met Arg Ala
 65                  70                  75                  80

Leu His Tyr Leu Ile Val Ala Gly Asn Ala Gly Glu Val Val Thr Pro
                 85                  90                  95

Gly Met Leu Gly Ala His Leu Lys Leu Ser Pro Ala Ser Val Thr Lys
            100                 105                 110

Thr Leu Asn Arg Leu Glu Lys Gly Gly His Ile Val Arg Asn Val His
        115                 120                 125

Pro Val Asp Arg Arg Ala Phe Ala Leu Met Val Thr Asp Ala Thr Arg
    130                 135                 140

Gly Glu Ala Met Arg Thr Leu Gly Lys His Gln Ala Arg Arg Phe Asp
145                 150                 155                 160

Ala Ala Lys Arg Leu Thr Pro Gln Glu Arg Glu Val Val Ile Arg Phe
                165                 170                 175

Leu Gln Asp Met Ala Gln Glu Leu Ser Leu Asn Asn Ala Pro Trp Leu
            180                 185                 190

Asn Thr Glu
        195
```

<210> 1783
<211> 725
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(702)
<223> RXA00486

<400> 1783

```
cat gcg atc atg gca gca gtc gac cat gcc cgc gca gcc gtt cta gat   48
His Ala Ile Met Ala Ala Val Asp His Ala Arg Ala Ala Val Leu Asp
  1               5                  10                  15

tcg ctg tct gaa gtg tcc gga acg ttg aaa gtc acc tcc ttc caa tcc   96
Ser Leu Ser Glu Val Ser Gly Thr Leu Lys Val Thr Ser Phe Gln Ser
             20                  25                  30

ctg ctg ttc acc ctt gcc ccg aaa gcc atc gcg cgc ctg acc gag aaa   144
Leu Leu Phe Thr Leu Ala Pro Lys Ala Ile Ala Arg Leu Thr Glu Lys
         35                  40                  45

tac cca cac ctg caa gta gaa atc tcc caa cta gaa gtc acc gca gcg   192
Tyr Pro His Leu Gln Val Glu Ile Ser Gln Leu Glu Val Thr Ala Ala
     50                  55                  60

ctc gaa gaa ctc cgc gcc cgc cgc gtc gac gtc gca ctc ggc gag gaa   240
Leu Glu Glu Leu Arg Ala Arg Arg Val Asp Val Ala Leu Gly Glu Glu
 65                  70                  75                  80

tac ccc gtg gaa gtc ccc ctt gtt gag gcc agc att cac cgc gaa gtc   288
Tyr Pro Val Glu Val Pro Leu Val Glu Ala Ser Ile His Arg Glu Val
                 85                  90                  95

ctc ttc gaa gac ccc atg ctg ctc gtc acc cca gca agc ggc cca tac   336
Leu Phe Glu Asp Pro Met Leu Leu Val Thr Pro Ala Ser Gly Pro Tyr
            100                 105                 110

tct ggc ctc acc ctg cca gaa ctc cgc gac atc ccc atc gcc atc gat   384
Ser Gly Leu Thr Leu Pro Glu Leu Arg Asp Ile Pro Ile Ala Ile Asp
        115                 120                 125

cca ccc gac ctt ccc gcg ggc gaa tgg gtc cat agg ctc tgc cgg cgc   432
Pro Pro Asp Leu Pro Ala Gly Glu Trp Val His Arg Leu Cys Arg Arg
    130                 135                 140

gcc ggg ttt gag ccc cgc gtg acc ttt gaa acc agc gat ccc atg ctc   480
Ala Gly Phe Glu Pro Arg Val Thr Phe Glu Thr Ser Asp Pro Met Leu
145                 150                 155                 160

caa gca cac ctc gtg cgt agc ggc ttg gcc gtg aca ttt tcc ccc aca   528
Gln Ala His Leu Val Arg Ser Gly Leu Ala Val Thr Phe Ser Pro Thr
                165                 170                 175

ctg ctc acc ccg atg ctg gaa agc gtg cac atc cag ccg ctg ccc ggc   576
Leu Leu Thr Pro Met Leu Glu Ser Val His Ile Gln Pro Leu Pro Gly
            180                 185                 190

aac ccc acg cgc acg ctc tac acc gcg gtc agg gaa ggg cgc cag ggg   624
```

```
Asn Pro Thr Arg Thr Leu Tyr Thr Ala Val Arg Glu Gly Arg Gln Gly
        195                 200                 205

cat cca gcc att aaa gct ttt cga cga gcc ctc gcc cat gtg gcc aaa   672
His Pro Ala Ile Lys Ala Phe Arg Arg Ala Leu Ala His Val Ala Lys
    210                 215                 220

gaa tct tat ttg gag gct cgt cta gta gag tgagttcttg tgagccttca     722
Glu Ser Tyr Leu Glu Ala Arg Leu Val Glu
225                 230

gac                                                               725
```

<210> 1784
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 1784

```
His Ala Ile Met Ala Ala Val Asp His Ala Arg Ala Ala Val Leu Asp
  1               5                  10                  15

Ser Leu Ser Glu Val Ser Gly Thr Leu Lys Val Thr Ser Phe Gln Ser
             20                  25                  30

Leu Leu Phe Thr Leu Ala Pro Lys Ala Ile Ala Arg Leu Thr Glu Lys
         35                  40                  45

Tyr Pro His Leu Gln Val Glu Ile Ser Gln Leu Glu Val Thr Ala Ala
     50                  55                  60

Leu Glu Glu Leu Arg Ala Arg Arg Val Asp Val Ala Leu Gly Glu Glu
 65                  70                  75                  80

Tyr Pro Val Glu Val Pro Leu Val Glu Ala Ser Ile His Arg Glu Val
                 85                  90                  95

Leu Phe Glu Asp Pro Met Leu Leu Val Thr Pro Ala Ser Gly Pro Tyr
            100                 105                 110

Ser Gly Leu Thr Leu Pro Glu Leu Arg Asp Ile Pro Ile Ala Ile Asp
        115                 120                 125

Pro Pro Asp Leu Pro Ala Gly Glu Trp Val His Arg Leu Cys Arg Arg
    130                 135                 140

Ala Gly Phe Glu Pro Arg Val Thr Phe Glu Thr Ser Asp Pro Met Leu
145                 150                 155                 160

Gln Ala His Leu Val Arg Ser Gly Leu Ala Val Thr Phe Ser Pro Thr
                165                 170                 175

Leu Leu Thr Pro Met Leu Glu Ser Val His Ile Gln Pro Leu Pro Gly
            180                 185                 190

Asn Pro Thr Arg Thr Leu Tyr Thr Ala Val Arg Glu Gly Arg Gln Gly
        195                 200                 205

His Pro Ala Ile Lys Ala Phe Arg Arg Ala Leu Ala His Val Ala Lys
    210                 215                 220
```

```
Glu Ser Tyr Leu Glu Ala Arg Leu Val Glu
225                 230


<210> 1785
<211> 1026
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1003)
<223> RXA00490

<400> 1785
gattgagcac gacacctcca aaattgttca gtattactta actatagttg gctgtttttc 60

gatctagtcc ttaaaggttt ctttggcaat aatcaagggc atg aat aaa cag tcc   115
                                          Met Asn Lys Gln Ser
                                            1               5

gct gca gtg ttg atg gtg atg ggt tcc gcc cta tcc ctg caa ttt ggt   163
Ala Ala Val Leu Met Val Met Gly Ser Ala Leu Ser Leu Gln Phe Gly
                 10                  15                  20

gct gcc att gga acg cag ctt ttc ccc ctc aac ggc ccc tgg gct gtc   211
Ala Ala Ile Gly Thr Gln Leu Phe Pro Leu Asn Gly Pro Trp Ala Val
             25                  30                  35

acc tct tta agg ctg ttc atc gca ggc ttg atc atg tgc ctg gtg atc   259
Thr Ser Leu Arg Leu Phe Ile Ala Gly Leu Ile Met Cys Leu Val Ile
         40                  45                  50

cgc ccg cga ctt cgt tcc tgg act aaa aaa caa tgg atc gcc gtg ctg   307
Arg Pro Arg Leu Arg Ser Trp Thr Lys Lys Gln Trp Ile Ala Val Leu
     55                  60                  65

ctg ttg gga tta tct ctt ggc gga atg aac agc ctg ttt tac gca tcc   355
Leu Leu Gly Leu Ser Leu Gly Gly Met Asn Ser Leu Phe Tyr Ala Ser
 70                  75                  80                  85

atc gaa ctc atc ccg ctg ggt acc gcc gtg acc att gag ttc ctc ggc   403
Ile Glu Leu Ile Pro Leu Gly Thr Ala Val Thr Ile Glu Phe Leu Gly
                 90                  95                 100

ccc ctg att ttc tcc gcg gtg tta gcc cgc acg ctg aaa aac gga ttg   451
Pro Leu Ile Phe Ser Ala Val Leu Ala Arg Thr Leu Lys Asn Gly Leu
            105                 110                 115

tgc gtg gct tta gcg ttt ctc ggc atg gca cta ctg ggt atc gat tcc   499
Cys Val Ala Leu Ala Phe Leu Gly Met Ala Leu Leu Gly Ile Asp Ser
        120                 125                 130

ctc agc ggc gaa acc ctt gac cca ctc ggc gtc att ttc gca gcc gtc   547
Leu Ser Gly Glu Thr Leu Asp Pro Leu Gly Val Ile Phe Ala Ala Val
    135                 140                 145

gca gga atc ttc tgg gtg tgc tac atc ctg gca tca aag aaa atc ggc   595
Ala Gly Ile Phe Trp Val Cys Tyr Ile Leu Ala Ser Lys Lys Ile Gly
150                 155                 160                 165
```

```
caa ctc atc ccc gga aca agc ggc ctg gcc gtc gca ctg att atc ggc   643
Gln Leu Ile Pro Gly Thr Ser Gly Leu Ala Val Ala Leu Ile Ile Gly
                170                 175                 180

gca gtg gca gta ttt cca ctg ggt gct aca cac atg ggc ccg att ttc   691
Ala Val Ala Val Phe Pro Leu Gly Ala Thr His Met Gly Pro Ile Phe
            185                 190                 195

cag acc cca acc cta ctc atc ctg gcg ctt ggc aca gca ctt ctc ggg   739
Gln Thr Pro Thr Leu Leu Ile Leu Ala Leu Gly Thr Ala Leu Leu Gly
        200                 205                 210

tcg ctt atc ccc tat tcg ctg gaa tta tcg gca ctg cgc cga ctc ccc   787
Ser Leu Ile Pro Tyr Ser Leu Glu Leu Ser Ala Leu Arg Arg Leu Pro
    215                 220                 225

gcc ccc att ttc agt att ctg ctc agc ctc gaa ccg gca ttc gcc gcc   835
Ala Pro Ile Phe Ser Ile Leu Leu Ser Leu Glu Pro Ala Phe Ala Ala
230                 235                 240                 245

gcc gtc ggc tgg atc ctg ctt gat caa acc ccc acc gcg ctc aag tgg   883
Ala Val Gly Trp Ile Leu Leu Asp Gln Thr Pro Thr Ala Leu Lys Trp
                250                 255                 260

gcc gcg atc atc ctt gtc atc gcg gcc agc atc ggc gtc acg tgg gag   931
Ala Ala Ile Ile Leu Val Ile Ala Ala Ser Ile Gly Val Thr Trp Glu
            265                 270                 275

cct aaa aag atg ctt gtc gac gcg ccc ctc cac tca aaa tgc aac gcg   979
Pro Lys Lys Met Leu Val Asp Ala Pro Leu His Ser Lys Cys Asn Ala
        280                 285                 290

aag agg cga gta cac aca cct agt taacgtgcag gcttaccttt tgg        1026
Lys Arg Arg Val His Thr Pro Ser
    295                 300
```

<210> 1786
<211> 301
<212> PRT
<213> Corynebacterium glutamicum

<400> 1786

```
Met Asn Lys Gln Ser Ala Ala Val Leu Met Val Met Gly Ser Ala Leu
  1               5                  10                  15

Ser Leu Gln Phe Gly Ala Ala Ile Gly Thr Gln Leu Phe Pro Leu Asn
             20                  25                  30

Gly Pro Trp Ala Val Thr Ser Leu Arg Leu Phe Ile Ala Gly Leu Ile
         35                  40                  45

Met Cys Leu Val Ile Arg Pro Arg Leu Arg Ser Trp Thr Lys Lys Gln
     50                  55                  60

Trp Ile Ala Val Leu Leu Leu Gly Leu Ser Leu Gly Gly Met Asn Ser
 65                  70                  75                  80

Leu Phe Tyr Ala Ser Ile Glu Leu Ile Pro Leu Gly Thr Ala Val Thr
                 85                  90                  95
```

```
Ile Glu Phe Leu Gly Pro Leu Ile Phe Ser Ala Val Leu Ala Arg Thr
            100                 105                 110

Leu Lys Asn Gly Leu Cys Val Ala Leu Ala Phe Leu Gly Met Ala Leu
        115                 120                 125

Leu Gly Ile Asp Ser Leu Ser Gly Glu Thr Leu Asp Pro Leu Gly Val
    130                 135                 140

Ile Phe Ala Ala Val Ala Gly Ile Phe Trp Val Cys Tyr Ile Leu Ala
145                 150                 155                 160

Ser Lys Lys Ile Gly Gln Leu Ile Pro Gly Thr Ser Gly Leu Ala Val
                165                 170                 175

Ala Leu Ile Ile Gly Ala Val Ala Val Phe Pro Leu Gly Ala Thr His
            180                 185                 190

Met Gly Pro Ile Phe Gln Thr Pro Thr Leu Leu Ile Leu Ala Leu Gly
        195                 200                 205

Thr Ala Leu Leu Gly Ser Leu Ile Pro Tyr Ser Leu Glu Leu Ser Ala
    210                 215                 220

Leu Arg Arg Leu Pro Ala Pro Ile Phe Ser Ile Leu Leu Ser Leu Glu
225                 230                 235                 240

Pro Ala Phe Ala Ala Ala Val Gly Trp Ile Leu Leu Asp Gln Thr Pro
                245                 250                 255

Thr Ala Leu Lys Trp Ala Ala Ile Ile Leu Val Ile Ala Ala Ser Ile
            260                 265                 270

Gly Val Thr Trp Glu Pro Lys Lys Met Leu Val Asp Ala Pro Leu His
        275                 280                 285

Ser Lys Cys Asn Ala Lys Arg Arg Val His Thr Pro Ser
    290                 295                 300
```

09550-0045-00000

<210> 1787
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> RXA00491

<400> 1787
tcctcatagt gtgtccacaa ttatctaaac tttagtagct tgtccttaaa tcggataacc 60

gctgcagctc acacgctatt ccacaaccgg aaatctggca gtg tat tgg gtt tta 115
                                                Val Tyr Trp Val Leu
                                                  1   5

gca acc tct gcc aat agg gtg gaa gat gtg aac ttt gat gcg atg atg 163
Ala Thr Ser Ala Asn Arg Val Glu Asp Val Asn Phe Asp Ala Met Met
                  10   15   20

```
ccc cgc gac ccg ttt gcc gat gat ccc aat gac ccg gca tcg ttt att   211
Pro Arg Asp Pro Phe Ala Asp Asp Pro Asn Asp Pro Ala Ser Phe Ile
             25                  30                  35

acc gac gat gac cct tat gat cat ccc gaa ccg ctt tct gaa gaa gag   259
Thr Asp Asp Asp Pro Tyr Asp His Pro Glu Pro Leu Ser Glu Glu Glu
         40                  45                  50

cga atc cac gtg agc caa gac ctt cgc ctc gtg atg gaa ttt aaa aaa   307
Arg Ile His Val Ser Gln Asp Leu Arg Leu Val Met Glu Phe Lys Lys
     55                  60                  65

gtt tta ggt ccc cga gga atc gaa ggc gtg ttc ttc atg tgc gaa gac   355
Val Leu Gly Pro Arg Gly Ile Glu Gly Val Phe Phe Met Cys Glu Asp
 70                  75                  80                  85

tgc gaa gag ttc cac tac tac gac tgg gac atc atg gca gca aac atg   403
Cys Glu Glu Phe His Tyr Tyr Asp Trp Asp Ile Met Ala Ala Asn Met
                 90                  95                 100

cgc gcc acc ttg gct ggg gaa ctc agc ccc gtg cat gaa cca agt gcg   451
Arg Ala Thr Leu Ala Gly Glu Leu Ser Pro Val His Glu Pro Ser Ala
            105                 110                 115

caa ccc aat att gat gcc tat gtg ccg tgg gac tac tgc att ggt tac   499
Gln Pro Asn Ile Asp Ala Tyr Val Pro Trp Asp Tyr Cys Ile Gly Tyr
        120                 125                 130

cta gac gga ctt gaa gcc aaa taaaaactgc tagcaactaa aga             543
Leu Asp Gly Leu Glu Ala Lys
    135                 140
```

<210> 1788
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 1788

```
Val Tyr Trp Val Leu Ala Thr Ser Ala Asn Arg Val Glu Asp Val Asn
  1               5                  10                  15

Phe Asp Ala Met Met Pro Arg Asp Pro Phe Ala Asp Asp Pro Asn Asp
             20                  25                  30

Pro Ala Ser Phe Ile Thr Asp Asp Asp Pro Tyr Asp His Pro Glu Pro
         35                  40                  45

Leu Ser Glu Glu Glu Arg Ile His Val Ser Gln Asp Leu Arg Leu Val
     50                  55                  60

Met Glu Phe Lys Lys Val Leu Gly Pro Arg Gly Ile Glu Gly Val Phe
 65                  70                  75                  80

Phe Met Cys Glu Asp Cys Glu Glu Phe His Tyr Tyr Asp Trp Asp Ile
                 85                  90                  95

Met Ala Ala Asn Met Arg Ala Thr Leu Ala Gly Glu Leu Ser Pro Val
            100                 105                 110
```

```
His Glu Pro Ser Ala Gln Pro Asn Ile Asp Ala Tyr Val Pro Trp Asp
        115                 120                 125

Tyr Cys Ile Gly Tyr Leu Asp Gly Leu Glu Ala Lys
    130                 135                 140


<210> 1789
<211> 347
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(324)
<223> RXA00493

<400> 1789
ttc gaa ggc gac cag aag gtc ggc gtt cgc gca ctg gct act gct ttg   48
Phe Glu Gly Asp Gln Lys Val Gly Val Arg Ala Leu Ala Thr Ala Leu
  1               5                  10                  15

ggc aag cca gcg tac tgg atc gcc tcc aac gca ggt ctt gac ggc tct   96
Gly Lys Pro Ala Tyr Trp Ile Ala Ser Asn Ala Gly Leu Asp Gly Ser
             20                  25                  30

gtt gtt gtt gca cgc act gct gct ctg cca aac ggc gag ggc ttc aac   144
Val Val Val Ala Arg Thr Ala Ala Leu Pro Asn Gly Glu Gly Phe Asn
         35                  40                  45

gct gca act ttg gaa tac gga aac ctg atc aac gac ggt gtc atc gac   192
Ala Ala Thr Leu Glu Tyr Gly Asn Leu Ile Asn Asp Gly Val Ile Asp
     50                  55                  60

cca gtc aag gtc acc cat tcc gca gta gtg aat gca acc tct gtt gca   240
Pro Val Lys Val Thr His Ser Ala Val Val Asn Ala Thr Ser Val Ala
 65                  70                  75                  80

cgc atg gtt ctg acc act gag gct tct gtt gtt gag aag cct gca gaa   288
Arg Met Val Leu Thr Thr Glu Ala Ser Val Val Glu Lys Pro Ala Glu
                 85                  90                  95

gaa gca gcc gat gca cat gca gga cat cat cac cac taaagttctg        334
Glu Ala Ala Asp Ala His Ala Gly His His His His
            100                 105

tgaaaaacac cgt                                                   347


<210> 1790
<211> 108
<212> PRT
<213> Corynebacterium glutamicum

<400> 1790
Phe Glu Gly Asp Gln Lys Val Gly Val Arg Ala Leu Ala Thr Ala Leu
  1               5                  10                  15

Gly Lys Pro Ala Tyr Trp Ile Ala Ser Asn Ala Gly Leu Asp Gly Ser
             20                  25                  30
```

```
Val Val Val Ala Arg Thr Ala Ala Leu Pro Asn Gly Glu Gly Phe Asn
         35                  40                  45

Ala Ala Thr Leu Glu Tyr Gly Asn Leu Ile Asn Asp Gly Val Ile Asp
     50                  55                  60

Pro Val Lys Val Thr His Ser Ala Val Val Asn Ala Thr Ser Val Ala
 65                  70                  75                  80

Arg Met Val Leu Thr Thr Glu Ala Ser Val Val Glu Lys Pro Ala Glu
                 85                  90                  95

Glu Ala Ala Asp Ala His Ala Gly His His His His
            100                 105


<210> 1791
<211> 536
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(513)
<223> RXA00519

<400> 1791
atg gct ggc ggc gga ctg ttc gag acc ggt gct ggt gga tct gct cct   48
Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser Ala Pro
  1               5                  10                  15

aag cac gtc cag cag gtt cag gaa gaa aac cac ctg cgt tgg gat tcc   96
Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp Asp Ser
             20                  25                  30

ctc ggt gag ttc ctc gca ctg gct gag tcc ttc cgc cac gag ctc aac  144
Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu Leu Asn
         35                  40                  45

aac aac ggc aac acc aag gcc ggc gtt ctg gct gac gct ctg gac aag  192
Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu Asp Lys
     50                  55                  60

gca act gag aag ctg ctg aac gaa gag aag tcc cca tcc cgc aag gtt  240
Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg Lys Val
 65                  70                  75                  80

ggc gag atc gac aac cgt ggc tcc cac ttc tgg ctg acc aag ttc tgg  288
Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys Phe Trp
                 85                  90                  95

gct gac gag ctc gct gct cag acc gag gac gca gat ctg gct gct acc  336
Ala Asp Glu Leu Ala Ala Gln Thr Glu Asp Ala Asp Leu Ala Ala Thr
            100                 105                 110

ttc gca cca gtc gca gaa gca ctg aac aca ggc gct gca gac atc gat  384
Phe Ala Pro Val Ala Glu Ala Leu Asn Thr Gly Ala Ala Asp Ile Asp
        115                 120                 125

gct gca ctg ctc gca gtt cag ggt gga gca act gac ctt ggt ggc tac  432
Ala Ala Leu Leu Ala Val Gln Gly Gly Ala Thr Asp Leu Gly Gly Tyr
```

```
    130                 135                 140

tac tcc cct aac gag gag aag ctc acc aac atc atg cgc cca gtc gca   480
Tyr Ser Pro Asn Glu Glu Lys Leu Thr Asn Ile Met Arg Pro Val Ala
145                 150                 155                 160

cag ttc aac gag atc gtt gac gca ctg aag aag taaagtctct tcacaaaaag 533
Gln Phe Asn Glu Ile Val Asp Ala Leu Lys Lys
                165                 170

cgc                                                               536
```

<210> 1792
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 1792

```
Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser Ala Pro
  1               5                  10                  15

Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp Asp Ser
             20                  25                  30

Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu Leu Asn
         35                  40                  45

Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu Asp Lys
     50                  55                  60

Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg Lys Val
 65                  70                  75                  80

Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys Phe Trp
                 85                  90                  95

Ala Asp Glu Leu Ala Ala Gln Thr Glu Asp Ala Asp Leu Ala Ala Thr
            100                 105                 110

Phe Ala Pro Val Ala Glu Ala Leu Asn Thr Gly Ala Ala Asp Ile Asp
        115                 120                 125

Ala Ala Leu Leu Ala Val Gln Gly Gly Ala Thr Asp Leu Gly Gly Tyr
    130                 135                 140

Tyr Ser Pro Asn Glu Glu Lys Leu Thr Asn Ile Met Arg Pro Val Ala
145                 150                 155                 160

Gln Phe Asn Glu Ile Val Asp Ala Leu Lys Lys
                165                 170
```

<210> 1793
<211> 1212
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1189)

<223> RXA00528

<400> 1793

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ttctgctggg aatccccaca ttttggaacg tagcgtcgat aagcgtgcgg cgaagctttt 60

tcggtcgcgg ccgttatctt tttaagagga gaaattttag atg agc acg tcc acc   115
                                            Met Ser Thr Ser Thr
                                              1               5

atc agg gtt gcc att gcc gga gtc gga aac tgc gcg acc tcc ctc att   163
Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys Ala Thr Ser Leu Ile
                 10                  15                  20

cag ggt gtg gaa tat tac cga aat gcg gat cct tcc gaa act gtc ccg   211
Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro Ser Glu Thr Val Pro
             25                  30                  35

ggt ttg atg cac gtc aaa ttc ggt gat tac cac gtt ggc gac att gaa   259
Gly Leu Met His Val Lys Phe Gly Asp Tyr His Val Gly Asp Ile Glu
         40                  45                  50

ttc gtg gcc gcg ttc gac gtc gac gcc gaa aaa gta ggc atc gat ctt   307
Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys Val Gly Ile Asp Leu
     55                  60                  65

gcc gac gcc acc gag gct tca caa aac tgc act atc aaa atc gcc gat   355
Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr Ile Lys Ile Ala Asp
 70                  75                  80                  85

gtc cca cag acc ggc atc aac gtg ctg cgt ggc ccg act ctc gac ggc   403
Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly Pro Thr Leu Asp Gly
                 90                  95                 100

ctg ggc gat cat tac cgc gcg acc atc gac gag tcc acc gcc gag cca   451
Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu Ser Thr Ala Glu Pro
             105                 110                 115

gtc gac gtt gtc cag gcg ctt atc gac gca aaa gcc gat gtt ttg gtg   499
Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys Ala Asp Val Leu Val
         120                 125                 130

tcc tac ctc cca gtg ggc tcc gaa gaa gcc gac aaa ttc tac gca caa   547
Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp Lys Phe Tyr Ala Gln
     135                 140                 145

gcc gcc atc gat gca ggc tgc gcc ttt gtc aac gct ctc cca gta ttc   595
Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn Ala Leu Pro Val Phe
150                 155                 160                 165

atc gcc tcc gac cct gag tgg gct aag aag ttc act gac gct ggc atc   643
Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe Thr Asp Ala Gly Ile
                170                 175                 180

cca att gtt ggc gat gac atc aaa tcc cag atc ggt gca acc atc acc   691
Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile Gly Ala Thr Ile Thr
            185                 190                 195

cac cgt gtc ctc gca cgc ctt ttt gaa gaa cgt ggc gtt cgc gta gat   739
His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg Gly Val Arg Val Asp
        200                 205                 210
```

```
cgc acc atg cag ctc aac gtc ggc ggc aac atg gac ttc aaa aac atg   787
Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met Asp Phe Lys Asn Met
    215                 220                 225

ctt gac cgc aat cgc ttg gaa tcc aag aag gtc tcc aaa acc caa gca   835
Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val Ser Lys Thr Gln Ala
230                 235                 240                 245

gtg acc tcc aac att cca gat ggt cca ctg tct gga aag gtg gaa gac   883
Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser Gly Lys Val Glu Asp
                250                 255                 260

cgc aac gtc cac atc gga cca tcc gac cac gtc caa tgg ctc gat gac   931
Arg Asn Val His Ile Gly Pro Ser Asp His Val Gln Trp Leu Asp Asp
            265                 270                 275

cgc aag tgg gct tat gtc cgc ctc gaa ggc acc gca ttc ggt gga gtt   979
Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr Ala Phe Gly Gly Val
        280                 285                 290

ccc ctc aac ctt gag tac aaa ctc gag gtg tgg gat tca ccc aac tct   1027
Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp Asp Ser Pro Asn Ser
    295                 300                 305

gcc ggc atc atc atc gac gct gtt cgc gcc gcc aag atc gcc ctc gat   1075
Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala Lys Ile Ala Leu Asp
310                 315                 320                 325

cgc ggt atc ggc gga ccg atc atg cca gca agc tcc tac ctg atg aag   1123
Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser Ser Tyr Leu Met Lys
                330                 335                 340

tcc cca cct gag cag ctt cca gac gat gtt gct tgt gaa cgc cta gag   1171
Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala Cys Glu Arg Leu Glu
            345                 350                 355

gca ttc atc atc gag gcg taaaattagg ctaaaaattt ggg                1212
Ala Phe Ile Ile Glu Ala
        360
```

<210> 1794
<211> 363
<212> PRT
<213> Corynebacterium glutamicum

<400> 1794

```
Met Ser Thr Ser Thr Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys
  1               5                  10                  15

Ala Thr Ser Leu Ile Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro
             20                  25                  30

Ser Glu Thr Val Pro Gly Leu Met His Val Lys Phe Gly Asp Tyr His
         35                  40                  45

Val Gly Asp Ile Glu Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys
     50                  55                  60

Val Gly Ile Asp Leu Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr
 65                  70                  75                  80
```

```
Ile Lys Ile Ala Asp Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly
                  85                  90                  95

Pro Thr Leu Asp Gly Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu
             100                 105                 110

Ser Thr Ala Glu Pro Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys
         115                 120                 125

Ala Asp Val Leu Val Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp
     130                 135                 140

Lys Phe Tyr Ala Gln Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn
145                 150                 155                 160

Ala Leu Pro Val Phe Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe
                 165                 170                 175

Thr Asp Ala Gly Ile Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile
             180                 185                 190

Gly Ala Thr Ile Thr His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg
         195                 200                 205

Gly Val Arg Val Asp Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met
     210                 215                 220

Asp Phe Lys Asn Met Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val
225                 230                 235                 240

Ser Lys Thr Gln Ala Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser
                 245                 250                 255

Gly Lys Val Glu Asp Arg Asn Val His Ile Gly Pro Ser Asp His Val
             260                 265                 270

Gln Trp Leu Asp Asp Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr
         275                 280                 285

Ala Phe Gly Gly Val Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp
     290                 295                 300

Asp Ser Pro Asn Ser Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala
305                 310                 315                 320

Lys Ile Ala Leu Asp Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser
                 325                 330                 335

Ser Tyr Leu Met Lys Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala
             340                 345                 350

Cys Glu Arg Leu Glu Ala Phe Ile Ile Glu Ala
         355                 360
```

<210> 1795
<211> 666
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(643)
<223> RXA00529

<400> 1795
gcaaagcttt gtaccggaag cgttaaggca ctggattttg tcgagcagtt tcaggctgtt 60

tagcgggcga gttcttatag agatgtataa ggtgaagctc atg aag ttg aag tgg 115
Met Lys Leu Lys Trp
1 5

att gca cca att ctt ccg gtt ttg gcc ctt gca ggc tgc gga aac tac 163
Ile Ala Pro Ile Leu Pro Val Leu Ala Leu Ala Gly Cys Gly Asn Tyr
10 15 20

gtc aac gta gag tcg caa ggg aaa tct gga att tcc cat gat gag gac 211
Val Asn Val Glu Ser Gln Gly Lys Ser Gly Ile Ser His Asp Glu Asp
25 30 35

gga aat ata agc gtt cac atg tac atc tgt ggt gat aat gcg gtg gat 259
Gly Asn Ile Ser Val His Met Tyr Ile Cys Gly Asp Asn Ala Val Asp
40 45 50

gaa ctg ata ctt agc ggt ggt ttt tac gat ggc cca cct ggg aca aac 307
Glu Leu Ile Leu Ser Gly Gly Phe Tyr Asp Gly Pro Pro Gly Thr Asn
55 60 65

aac cca gcc ctt ggg atg ttg aaa act tcc aac cct gag tcg ggt tat 355
Asn Pro Ala Leu Gly Met Leu Lys Thr Ser Asn Pro Glu Ser Gly Tyr
70 75 80 85

gtt gta gtc aac atc gct gat cca gca ccg tgg gaa gtt gtt gag cca 403
Val Val Val Asn Ile Ala Asp Pro Ala Pro Trp Glu Val Val Glu Pro
90 95 100

atc aat ttg ccc acg gaa cag gga aag tac att att gcc aat ccg agg 451
Ile Asn Leu Pro Thr Glu Gln Gly Lys Tyr Ile Ile Ala Asn Pro Arg
105 110 115

ttg gta gat aaa ggt tgg ccg att cct ttc gca aaa gaa aag tat atg 499
Leu Val Asp Lys Gly Trp Pro Ile Pro Phe Ala Lys Glu Lys Tyr Met
120 125 130

ccg agt gtt tcc aca tca gta gga atg ctt gaa gga ata gat cca ggt 547
Pro Ser Val Ser Thr Ser Val Gly Met Leu Glu Gly Ile Asp Pro Gly
135 140 145

cta gtc atg cgg gat atg tat acc gag tcg act cat gtg ttc ggt act 595
Leu Val Met Arg Asp Met Tyr Thr Glu Ser Thr His Val Phe Gly Thr
150 155 160 165

gcc gaa gac ttt gtt gaa gcc ggt caa cag tgg tgc gag gat tat ttc 643
Ala Glu Asp Phe Val Glu Ala Gly Gln Gln Trp Cys Glu Asp Tyr Phe
170 175 180

taaaacgtga atctggcaaa aga 666

<210> 1796
<211> 181

<212> PRT
<213> Corynebacterium glutamicum

<400> 1796

```
Met Lys Leu Lys Trp Ile Ala Pro Ile Leu Pro Val Leu Ala Leu Ala
  1               5                  10                  15

Gly Cys Gly Asn Tyr Val Asn Val Glu Ser Gln Gly Lys Ser Gly Ile
             20                  25                  30

Ser His Asp Glu Asp Gly Asn Ile Ser Val His Met Tyr Ile Cys Gly
         35                  40                  45

Asp Asn Ala Val Asp Glu Leu Ile Leu Ser Gly Gly Phe Tyr Asp Gly
     50                  55                  60

Pro Pro Gly Thr Asn Asn Pro Ala Leu Gly Met Leu Lys Thr Ser Asn
 65                  70                  75                  80

Pro Glu Ser Gly Tyr Val Val Val Asn Ile Ala Asp Pro Ala Pro Trp
                 85                  90                  95

Glu Val Val Glu Pro Ile Asn Leu Pro Thr Glu Gln Gly Lys Tyr Ile
            100                 105                 110

Ile Ala Asn Pro Arg Leu Val Asp Lys Gly Trp Pro Ile Pro Phe Ala
        115                 120                 125

Lys Glu Lys Tyr Met Pro Ser Val Ser Thr Ser Val Gly Met Leu Glu
    130                 135                 140

Gly Ile Asp Pro Gly Leu Val Met Arg Asp Met Tyr Thr Glu Ser Thr
145                 150                 155                 160

His Val Phe Gly Thr Ala Glu Asp Phe Val Glu Ala Gly Gln Gln Trp
                165                 170                 175

Cys Glu Asp Tyr Phe
            180
```

<210> 1797
<211> 1404
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1381)
<223> RXA00530

<400> 1797

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ggcgataagc ctcctccctg gggccttgcc catttcatag ggtgtccagg taatgtttca 60

ggggttagat ttcagctgaa gcaactgggg agttggcgct atg agc atc gga ttc   115
                                           Met Ser Ile Gly Phe
                                             1               5

gac cgc gac ctt tat att aag atg cag tcg cag cac atc aat gag cgc   163
Asp Arg Asp Leu Tyr Ile Lys Met Gln Ser Gln His Ile Asn Glu Arg
                 10                  15                  20
```

```
cgc gag cag atc ggc ggc aag ctg tat ctg gaa atg ggc ggc aag ctt   211
Arg Glu Gln Ile Gly Gly Lys Leu Tyr Leu Glu Met Gly Gly Lys Leu
            25                  30                  35

ttc gac gac atg cac gct tcc cgt gtg ctg cca ggt ttc acg cct gac   259
Phe Asp Asp Met His Ala Ser Arg Val Leu Pro Gly Phe Thr Pro Asp
        40                  45                  50

aac aag atc gct atg ctc act gag ctt aaa gat gag ctg gaa atc ctc   307
Asn Lys Ile Ala Met Leu Thr Glu Leu Lys Asp Glu Leu Glu Ile Leu
    55                  60                  65

gtc gca atc aat gcg aag gat ctg gag cgc aag aaa acc cgc gcc gac   355
Val Ala Ile Asn Ala Lys Asp Leu Glu Arg Lys Lys Thr Arg Ala Asp
70                  75                  80                  85

ctc gac att tct tat gag gaa gat gtt tta cgc ctc att gat gtg ttc   403
Leu Asp Ile Ser Tyr Glu Glu Asp Val Leu Arg Leu Ile Asp Val Phe
                90                  95                  100

cgt gag ctg ggc ttt ttg gcg gag cat gtg gtg ctc aca cag ttg gag   451
Arg Glu Leu Gly Phe Leu Ala Glu His Val Val Leu Thr Gln Leu Glu
            105                 110                 115

gat gac aac tat cag gca ctc gcg ttc aag cag cgc cta gag cgc ctt   499
Asp Asp Asn Tyr Gln Ala Leu Ala Phe Lys Gln Arg Leu Glu Arg Leu
        120                 125                 130

ggc ctg aag gtt gct gtt cac cgc gtg att cca ggt tac cca act gat   547
Gly Leu Lys Val Ala Val His Arg Val Ile Pro Gly Tyr Pro Thr Asp
    135                 140                 145

gct cgc cgc att gtt agc gag gaa ggt ttc ggc atc aac gag tat gtg   595
Ala Arg Arg Ile Val Ser Glu Glu Gly Phe Gly Ile Asn Glu Tyr Val
150                 155                 160                 165

gaa acc acc cgc aat ttg gtt gtt gtg acc gca ccg ggc cca ggt tct   643
Glu Thr Thr Arg Asn Leu Val Val Val Thr Ala Pro Gly Pro Gly Ser
                170                 175                 180

gga aag ctc gct acc tgc ttg agc cag att tat ggc gat cac cag cgc   691
Gly Lys Leu Ala Thr Cys Leu Ser Gln Ile Tyr Gly Asp His Gln Arg
            185                 190                 195

gga atc aag tcc ggc tac gca aag ttt gaa act ttc ccc att tgg aac   739
Gly Ile Lys Ser Gly Tyr Ala Lys Phe Glu Thr Phe Pro Ile Trp Asn
        200                 205                 210

ctg cct ctt gag cac cca gtt aac ttg gct tat gag gct gcc acg gca   787
Leu Pro Leu Glu His Pro Val Asn Leu Ala Tyr Glu Ala Ala Thr Ala
    215                 220                 225

gat ctc gat gac atc aac atc atc gat cct ttc cac ctc gcc gcc tat   835
Asp Leu Asp Asp Ile Asn Ile Ile Asp Pro Phe His Leu Ala Ala Tyr
230                 235                 240                 245

gac acc aaa gcc acc agc tac aac cgc gac gtg gaa gtc ttc ccg ctg   883
Asp Thr Lys Ala Thr Ser Tyr Asn Arg Asp Val Glu Val Phe Pro Leu
                250                 255                 260
```

```
ctg aaa acc atg ctg gaa atg ctg tcg ggc tca tcg ccg tac aaa tcc   931
Leu Lys Thr Met Leu Glu Met Leu Ser Gly Ser Ser Pro Tyr Lys Ser
            265                 270                 275

ccc acc gac atg ggt gtc aac atg gtc gga agc gca att atc gac gac   979
Pro Thr Asp Met Gly Val Asn Met Val Gly Ser Ala Ile Ile Asp Asp
        280                 285                 290

gcc gcg tgc cag gaa gcc gcc cgc caa gaa att gtt cgg cgt tac ttc   1027
Ala Ala Cys Gln Glu Ala Ala Arg Gln Glu Ile Val Arg Arg Tyr Phe
    295                 300                 305

aag gcg ctt gtc gac gag cgt cgc gag gag cag gac gat acc att tca   1075
Lys Ala Leu Val Asp Glu Arg Arg Glu Glu Gln Asp Asp Thr Ile Ser
310                 315                 320                 325

gcg cgc atc gcc att gtc atg agc aag gcc ggt tgc acc gtt gaa gac   1123
Ala Arg Ile Ala Ile Val Met Ser Lys Ala Gly Cys Thr Val Glu Asp
                330                 335                 340

cgc cgc gtg gtt gcc cga gca ctt gat gtt gaa gaa tcc acc ggc gcg   1171
Arg Arg Val Val Ala Arg Ala Leu Asp Val Glu Glu Ser Thr Gly Ala
            345                 350                 355

ccg ggt tgt gcc att gaa ctt aac gat ggt cga ctc gtc acc ggc aag   1219
Pro Gly Cys Ala Ile Glu Leu Asn Asp Gly Arg Leu Val Thr Gly Lys
        360                 365                 370

act tca gaa ctt ctc gga tgc tcc gca gcg atg gtg ctt aat gca ctg   1267
Thr Ser Glu Leu Leu Gly Cys Ser Ala Ala Met Val Leu Asn Ala Leu
    375                 380                 385

aag gaa ctc gct ggc att gat cgc agc gtg gat ctc ctc tcc cct gaa   1315
Lys Glu Leu Ala Gly Ile Asp Arg Ser Val Asp Leu Leu Ser Pro Glu
390                 395                 400                 405

tcc atc gag cca atc caa tcg ctg aag acc cag cac ctg gga tcc cgc   1363
Ser Ile Glu Pro Ile Gln Ser Leu Lys Thr Gln His Leu Gly Ser Arg
                410                 415                 420

aac ccc tcg cct gca cac tgatgaagtg cttattgctt tgt                 1404
Asn Pro Ser Pro Ala His
            425
```

<210> 1798
<211> 427
<212> PRT
<213> Corynebacterium glutamicum

<400> 1798

```
Met Ser Ile Gly Phe Asp Arg Asp Leu Tyr Ile Lys Met Gln Ser Gln
  1               5                  10                  15

His Ile Asn Glu Arg Arg Glu Gln Ile Gly Gly Lys Leu Tyr Leu Glu
             20                  25                  30

Met Gly Gly Lys Leu Phe Asp Asp Met His Ala Ser Arg Val Leu Pro
         35                  40                  45

Gly Phe Thr Pro Asp Asn Lys Ile Ala Met Leu Thr Glu Leu Lys Asp
```

```
     50                  55                  60

Glu Leu Glu Ile Leu Val Ala Ile Asn Ala Lys Asp Leu Glu Arg Lys
 65                  70                  75                  80

Lys Thr Arg Ala Asp Leu Asp Ile Ser Tyr Glu Glu Asp Val Leu Arg
                 85                  90                  95

Leu Ile Asp Val Phe Arg Glu Leu Gly Phe Leu Ala Glu His Val Val
            100                 105                 110

Leu Thr Gln Leu Glu Asp Asp Asn Tyr Gln Ala Leu Ala Phe Lys Gln
        115                 120                 125

Arg Leu Glu Arg Leu Gly Leu Lys Val Ala Val His Arg Val Ile Pro
    130                 135                 140

Gly Tyr Pro Thr Asp Ala Arg Arg Ile Val Ser Glu Glu Gly Phe Gly
145                 150                 155                 160

Ile Asn Glu Tyr Val Glu Thr Thr Arg Asn Leu Val Val Val Thr Ala
                165                 170                 175

Pro Gly Pro Gly Ser Gly Lys Leu Ala Thr Cys Leu Ser Gln Ile Tyr
            180                 185                 190

Gly Asp His Gln Arg Gly Ile Lys Ser Gly Tyr Ala Lys Phe Glu Thr
        195                 200                 205

Phe Pro Ile Trp Asn Leu Pro Leu Glu His Pro Val Asn Leu Ala Tyr
    210                 215                 220

Glu Ala Ala Thr Ala Asp Leu Asp Asp Ile Asn Ile Ile Asp Pro Phe
225                 230                 235                 240

His Leu Ala Ala Tyr Asp Thr Lys Ala Thr Ser Tyr Asn Arg Asp Val
                245                 250                 255

Glu Val Phe Pro Leu Leu Lys Thr Met Leu Glu Met Leu Ser Gly Ser
            260                 265                 270

Ser Pro Tyr Lys Ser Pro Thr Asp Met Gly Val Asn Met Val Gly Ser
        275                 280                 285

Ala Ile Ile Asp Asp Ala Ala Cys Gln Glu Ala Ala Arg Gln Glu Ile
    290                 295                 300

Val Arg Arg Tyr Phe Lys Ala Leu Val Asp Glu Arg Arg Glu Glu Gln
305                 310                 315                 320

Asp Asp Thr Ile Ser Ala Arg Ile Ala Ile Val Met Ser Lys Ala Gly
                325                 330                 335

Cys Thr Val Glu Asp Arg Arg Val Val Ala Arg Ala Leu Asp Val Glu
            340                 345                 350

Glu Ser Thr Gly Ala Pro Gly Cys Ala Ile Glu Leu Asn Asp Gly Arg
        355                 360                 365

Leu Val Thr Gly Lys Thr Ser Glu Leu Leu Gly Cys Ser Ala Ala Met
    370                 375                 380
```

```
Val Leu Asn Ala Leu Lys Glu Leu Ala Gly Ile Asp Arg Ser Val Asp
385                 390                 395                 400

Leu Leu Ser Pro Glu Ser Ile Glu Pro Ile Gln Ser Leu Lys Thr Gln
                405                 410                 415

His Leu Gly Ser Arg Asn Pro Ser Pro Ala His
            420                 425


<210> 1799
<211> 840
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(817)
<223> RXA00535

<400> 1799
aatcgcatgg ggcaccgtgg tcagacaccg gatcgcgctc cgcaccccaa aagatggctc 60

cctaaggagc tcacctttac tcaatgctct gatgacaccg atg tgg tgg gca ggc   115
                                              Met Trp Trp Ala Gly
                                                1               5

atg agt acc gcg atg ctg gca tat ttc tta caa aca gta gca ctt ggt   163
Met Ser Thr Ala Met Leu Ala Tyr Phe Leu Gln Thr Val Ala Leu Gly
                10                  15                  20

ttc ggc acc ctc ttg gta gtg caa cca gtg ctt gtc ctg tcg ctg atg   211
Phe Gly Thr Leu Leu Val Val Gln Pro Val Leu Val Leu Ser Leu Met
            25                  30                  35

ttc acg ctg ccg ctc tca gca cga ttc aat ggc tac cga cta cgc cga   259
Phe Thr Leu Pro Leu Ser Ala Arg Phe Asn Gly Tyr Arg Leu Arg Arg
        40                  45                  50

act gaa atc ttc tgg gct acc ctc ctc acc gta gcc gtg ggc atc atg   307
Thr Glu Ile Phe Trp Ala Thr Leu Leu Thr Val Ala Val Gly Ile Met
    55                  60                  65

atc gtt ttg gga cgc ccc ctt ccc gga aac ccc cac ccc cca ctc gat   355
Ile Val Leu Gly Arg Pro Leu Pro Gly Asn Pro His Pro Pro Leu Asp
70                  75                  80                  85

cga tgg att cca gta ctt tta gtc ggc gtt gca gta atg ggt gga atg   403
Arg Trp Ile Pro Val Leu Leu Val Gly Val Ala Val Met Gly Gly Met
                90                  95                  100

tgg ctg ctt gcg gaa tac gta tta aag aag gac aaa gcc ctc atc ctt   451
Trp Leu Leu Ala Glu Tyr Val Leu Lys Lys Asp Lys Ala Leu Ile Leu
            105                 110                 115

ggt ctt gtg acg ggt gca ttg ttt ggc tac gta gca gtg atg tcc aaa   499
Gly Leu Val Thr Gly Ala Leu Phe Gly Tyr Val Ala Val Met Ser Lys
        120                 125                 130

gcc gcg gtg gat ctt ttt gtc cat caa ggc ata acg gga ctc atc ttg   547
```

```
Ala Ala Val Asp Leu Phe Val His Gln Gly Ile Thr Gly Leu Ile Leu
    135                 140                 145

aac tgg gaa ggc tac ggc cta atc ctc acc gca tta ctt gga aca atc   595
Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala Leu Leu Gly Thr Ile
150                 155                 160                 165

gtg cag cag tat tcc ttt aac gct ggc gaa cta caa aaa tcg cta ccc   643
Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu Gln Lys Ser Leu Pro
                170                 175                 180

gcc atg acc att gcc gaa cca att gtt gcc ttc agt ttg ggc tac ttg   691
Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe Ser Leu Gly Tyr Leu
            185                 190                 195

gtt ctg ggc gaa aaa ttc caa gtc gtg gac tgg gaa tgg atc gcc atg   739
Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp Glu Trp Ile Ala Met
        200                 205                 210

ggc atc gca cta ctg gtg atg att gtt tcc acc att gca ctg tct cgt   787
Gly Ile Ala Leu Leu Val Met Ile Val Ser Thr Ile Ala Leu Ser Arg
    215                 220                 225

aca agc aca atg ccg gcc gga tcg aaa agg taaaactcca aagttccccc     837
Thr Ser Thr Met Pro Ala Gly Ser Lys Arg
230                 235

cga                                                              840
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SEQUENCE LISTING

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<210> 1800
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 1800

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Met Trp Trp Ala Gly Met Ser Thr Ala Met Leu Ala Tyr Phe Leu Gln
  1               5                  10                  15

Thr Val Ala Leu Gly Phe Gly Thr Leu Leu Val Val Gln Pro Val Leu
            20                  25                  30

Val Leu Ser Leu Met Phe Thr Leu Pro Leu Ser Ala Arg Phe Asn Gly
        35                  40                  45

Tyr Arg Leu Arg Arg Thr Glu Ile Phe Trp Ala Thr Leu Leu Thr Val
    50                  55                  60

Ala Val Gly Ile Met Ile Val Leu Gly Arg Pro Leu Pro Gly Asn Pro
65                  70                  75                  80

His Pro Pro Leu Asp Arg Trp Ile Pro Val Leu Leu Val Gly Val Ala
                85                  90                  95

Val Met Gly Gly Met Trp Leu Leu Ala Glu Tyr Val Leu Lys Lys Asp
            100                 105                 110

Lys Ala Leu Ile Leu Gly Leu Val Thr Gly Ala Leu Phe Gly Tyr Val
        115                 120                 125

Ala Val Met Ser Lys Ala Ala Val Asp Leu Phe Val His Gln Gly Ile
```

```
    130                 135                 140

Thr Gly Leu Ile Leu Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala
145                 150                 155                 160

Leu Leu Gly Thr Ile Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu
                165                 170                 175

Gln Lys Ser Leu Pro Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe
            180                 185                 190

Ser Leu Gly Tyr Leu Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp
        195                 200                 205

Glu Trp Ile Ala Met Gly Ile Ala Leu Leu Val Met Ile Val Ser Thr
    210                 215                 220

Ile Ala Leu Ser Arg Thr Ser Thr Met Pro Ala Gly Ser Lys Arg
225                 230                 235


<210> 1801
<211> 366
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(343)
<223> RXA00540

<400> 1801
tctccctatc taagggctgg ctaggtttga ccagtggcaa cagttacact tgtgctcgta 60

aaacattgtc ctccccattt cttgagtaag ggaaaatacc gtg gcc cgt gta gtt   115
                                          Val Ala Arg Val Val
                                            1               5

gtc aat gtc atg cct aag gct gag att ctg gat ccc cag ggg cag gcg   163
Val Asn Val Met Pro Lys Ala Glu Ile Leu Asp Pro Gln Gly Gln Ala
                10                  15                  20

gta cac cgc gcc ctc gga cgt atc gga gtt tct ggc gtt tcc gat gtc   211
Val His Arg Ala Leu Gly Arg Ile Gly Val Ser Gly Val Ser Asp Val
            25                  30                  35

cgt cag gga aag cgc ttc gag ctt gag gta gat gat tcc gtc acc gaa   259
Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp Asp Ser Val Thr Glu
        40                  45                  50

gct gac cta aag aaa att gct gaa acc ctc ctc gca aac acc gtc atc   307
Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu Ala Asn Thr Val Ile
    55                  60                  65

gaa gac ttc gat gtg gtg gga gtt gag gtc gcg aag tgagcgccaa        353
Glu Asp Phe Asp Val Val Gly Val Glu Val Ala Lys
70                  75                  80

aatcggtgtc att                                                   366
```

<210> 1802
<211> 81
<212> PRT
<213> Corynebacterium glutamicum

<400> 1802
Val Ala Arg Val Val Val Asn Val Met Pro Lys Ala Glu Ile Leu Asp
1 5 10 15

Pro Gln Gly Gln Ala Val His Arg Ala Leu Gly Arg Ile Gly Val Ser
20 25 30

Gly Val Ser Asp Val Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp
35 40 45

Asp Ser Val Thr Glu Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu
50 55 60

Ala Asn Thr Val Ile Glu Asp Phe Asp Val Val Gly Val Glu Val Ala
65 70 75 80

Lys

<210> 1803
<211> 519
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(496)
<223> RXA00549

<400> 1803
attcgtttgc agcaggatct ggaaaatggt tcacaggata ctgcggacat ggcgcatgct 60

ttgggtatcg cgaagtcttt gccaactatc cctgagacac ttg act gaa aac gga 115
Leu Thr Glu Asn Gly
1 5

gag acc cct tat gag ggc atc atc ttg ggt cag tat gag tcc cgc cca 163
Glu Thr Pro Tyr Glu Gly Ile Ile Leu Gly Gln Tyr Glu Ser Arg Pro
10 15 20

ctt gat atg gct tct gcg atg gca act atc gct aat gaa ggt gtc tgg 211
Leu Asp Met Ala Ser Ala Met Ala Thr Ile Ala Asn Glu Gly Val Trp
25 30 35

cac cgc ccg cac ttc gtg tcc aag gtg gag act gtc agc ggt gag gtt 259
His Arg Pro His Phe Val Ser Lys Val Glu Thr Val Ser Gly Glu Val
40 45 50

ctc tac gag ttc gag gat ggc gac ggc gag cgt cgt gtt tct gaa aag 307
Leu Tyr Glu Phe Glu Asp Gly Asp Gly Glu Arg Arg Val Ser Glu Lys
55 60 65

gtt gca ctg aat ctg ctc aag gcc atg ggg cca atc gct gca tac tcc 355
Val Ala Leu Asn Leu Leu Lys Ala Met Gly Pro Ile Ala Ala Tyr Ser
70 75 80 85

```
aac gga aac gct ctg gct gat ggc cag gtt tct gca tcc aag act ggt   403
Asn Gly Asn Ala Leu Ala Asp Gly Gln Val Ser Ala Ser Lys Thr Gly
                 90                  95                 100

acc act cag ctt ggt gat acc ggt gca aac aag gat gcg tgg atg ttg   451
Thr Thr Gln Leu Gly Asp Thr Gly Ala Asn Lys Asp Ala Trp Met Leu
            105                 110                 115

ggt gcg gca cct cag cta gct act gcg gtg tgg gtc gga act gct       496
Gly Ala Ala Pro Gln Leu Ala Thr Ala Val Trp Val Gly Thr Ala
        120                 125                 130

tgataacact gcattgtata aca                                        519
```

<210> 1804
<211> 132
<212> PRT
<213> Corynebacterium glutamicum

<400> 1804

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Leu Thr Glu Asn Gly Glu Thr Pro Tyr Glu Gly Ile Ile Leu Gly Gln
  1               5                  10                  15

Tyr Glu Ser Arg Pro Leu Asp Met Ala Ser Ala Met Ala Thr Ile Ala
             20                  25                  30

Asn Glu Gly Val Trp His Arg Pro His Phe Val Ser Lys Val Glu Thr
         35                  40                  45

Val Ser Gly Glu Val Leu Tyr Glu Phe Glu Asp Gly Asp Gly Glu Arg
     50                  55                  60

Arg Val Ser Glu Lys Val Ala Leu Asn Leu Leu Lys Ala Met Gly Pro
 65                  70                  75                  80

Ile Ala Ala Tyr Ser Asn Gly Asn Ala Leu Ala Asp Gly Gln Val Ser
                 85                  90                  95

Ala Ser Lys Thr Gly Thr Thr Gln Leu Gly Asp Thr Gly Ala Asn Lys
            100                 105                 110

Asp Ala Trp Met Leu Gly Ala Ala Pro Gln Leu Ala Thr Ala Val Trp
        115                 120                 125

Val Gly Thr Ala
    130
```

<210> 1805
<211> 444
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(421)
<223> RXA00550

<400> 1805

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aaggatgcgt ggatgttggg tgcggcacct cagctagcta ctgcggtgtg ggtcggaact 60

gcttgataac actgcattgt ataacacctg gggtggcagt atg tat ggt tct aac   115
                                            Met Tyr Gly Ser Asn
                                              1               5

tcc cct gcc acg atc tgg aag cag acc atg gat aac gcc ctc gag aac   163
Ser Pro Ala Thr Ile Trp Lys Gln Thr Met Asp Asn Ala Leu Glu Asn
                 10                  15                  20

tcc cct ctc gaa act tgg gat atc gct cca gca ttg ggg tac ggt aac   211
Ser Pro Leu Glu Thr Trp Asp Ile Ala Pro Ala Leu Gly Tyr Gly Asn
             25                  30                  35

cca cca gtt ccg gaa tat gtg tgg act cca agt cca aac atc gcg act   259
Pro Pro Val Pro Glu Tyr Val Trp Thr Pro Ser Pro Asn Ile Ala Thr
         40                  45                  50

aat gat cca gaa gga gca acc gag gaa gct cca gtg gag gat cca aat   307
Asn Asp Pro Glu Gly Ala Thr Glu Glu Ala Pro Val Glu Asp Pro Asn
     55                  60                  65

gca gta atc gat acc cct gct gta gat ccc act gca cct gca gag gag   355
Ala Val Ile Asp Thr Pro Ala Val Asp Pro Thr Ala Pro Ala Glu Glu
 70                  75                  80                  85

acc ggt aac ggt cag gta gaa atc ctg ccg ggg ctg act atc ccg gga   403
Thr Gly Asn Gly Gln Val Glu Ile Leu Pro Gly Leu Thr Ile Pro Gly
                 90                  95                 100

gat ctc tta ggg atc ggc taaaatccgg tcgtagccta aac                 444
Asp Leu Leu Gly Ile Gly
            105
```

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<210> 1806
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

<400> 1806

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Met Tyr Gly Ser Asn Ser Pro Ala Thr Ile Trp Lys Gln Thr Met Asp
  1               5                  10                  15

Asn Ala Leu Glu Asn Ser Pro Leu Glu Thr Trp Asp Ile Ala Pro Ala
             20                  25                  30

Leu Gly Tyr Gly Asn Pro Pro Val Pro Glu Tyr Val Trp Thr Pro Ser
         35                  40                  45

Pro Asn Ile Ala Thr Asn Asp Pro Glu Gly Ala Thr Glu Glu Ala Pro
     50                  55                  60

Val Glu Asp Pro Asn Ala Val Ile Asp Thr Pro Ala Val Asp Pro Thr
 65                  70                  75                  80

Ala Pro Ala Glu Glu Thr Gly Asn Gly Gln Val Glu Ile Leu Pro Gly
                 85                  90                  95

Leu Thr Ile Pro Gly Asp Leu Leu Gly Ile Gly
            100                 105
```

<210> 1807
<211> 444
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(421)
<223> RXA00553

<400> 1807
gtcattgcaa gcgcgaacgc tgtgcagcaa ttgctgcgga tttcgctgag caaggaattg 60

atccgctcgt tacttcttaa aaagggtatg gtggctgggt atg agc atc gtt aag 115
Met Ser Ile Val Lys
1 5

atc aac gca att tcc gta ccc gaa ggc gct ggt gaa gag ctt gag aag 163
Ile Asn Ala Ile Ser Val Pro Glu Gly Ala Gly Glu Glu Leu Glu Lys
10 15 20

cgc ttc gca gcc cgc caa aat gcc gtg gat tcc gct ccg gga ttt gag 211
Arg Phe Ala Ala Arg Gln Asn Ala Val Asp Ser Ala Pro Gly Phe Glu
25 30 35

ggc ttt caa ctg tta cgc cct gtt tcc ggt gaa gac cgc tac ttt gta 259
Gly Phe Gln Leu Leu Arg Pro Val Ser Gly Glu Asp Arg Tyr Phe Val
40 45 50

gtc acc cag tgg gct gat gaa gac agc tat aac gcg tgg cgt gat gcc 307
Val Thr Gln Trp Ala Asp Glu Asp Ser Tyr Asn Ala Trp Arg Asp Ala
55 60 65

gaa aag gcc aag ggc ggt cat ggc cag gga gcc cac ggc tca gat aag 355
Glu Lys Ala Lys Gly Gly His Gly Gln Gly Ala His Gly Ser Asp Lys
70 75 80 85

aag cct gtc gct tcc ggc gct tcc ctg ctg gag ttc gaa gta gtc cta 403
Lys Pro Val Ala Ser Gly Ala Ser Leu Leu Glu Phe Glu Val Val Leu
90 95 100

gga tct acc ggc gct aag tagggaaaga gaaaagtcgg aac 444
Gly Ser Thr Gly Ala Lys
105

<210> 1808
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

<400> 1808
Met Ser Ile Val Lys Ile Asn Ala Ile Ser Val Pro Glu Gly Ala Gly
1 5 10 15

Glu Glu Leu Glu Lys Arg Phe Ala Ala Arg Gln Asn Ala Val Asp Ser
20 25 30

Ala Pro Gly Phe Glu Gly Phe Gln Leu Leu Arg Pro Val Ser Gly Glu

```
         35                  40                  45

Asp Arg Tyr Phe Val Val Thr Gln Trp Ala Asp Glu Asp Ser Tyr Asn
     50                  55                  60

Ala Trp Arg Asp Ala Glu Lys Ala Lys Gly Gly His Gly Gln Gly Ala
 65                  70                  75                  80

His Gly Ser Asp Lys Lys Pro Val Ala Ser Gly Ala Ser Leu Leu Glu
                 85                  90                  95

Phe Glu Val Val Leu Gly Ser Thr Gly Ala Lys
            100                 105


<210> 1809
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXA00554

<400> 1809
atccgaaact ctcctgtacc gaccatcatt tatcccggtc tttaggctct ccaacagcag 60

aggactagac ttaagtatgc ctgcaaagga ggacaacttc atg aac acc caa cca   115
                                            Met Asn Thr Gln Pro
                                              1               5

gag cat cca gaa aat gat cta gtc gac gaa gcc gat ttt tct aac cgg   163
Glu His Pro Glu Asn Asp Leu Val Asp Glu Ala Asp Phe Ser Asn Arg
                 10                  15                  20

ccc agg atc tac tcg gac gat cct gat tcc ttg gct gat gcg cca gac   211
Pro Arg Ile Tyr Ser Asp Asp Pro Asp Ser Leu Ala Asp Ala Pro Asp
            25                  30                  35

cca gcg ctg gag cat gag aag aac aag aaa tct tca cgc caa gca ctc   259
Pro Ala Leu Glu His Glu Lys Asn Lys Lys Ser Ser Arg Gln Ala Leu
        40                  45                  50

att tat ctg ttg cag gtt cca cta gtt aca ttc gtt tct gca tac gta   307
Ile Tyr Leu Leu Gln Val Pro Leu Val Thr Phe Val Ser Ala Tyr Val
    55                  60                  65

ttg gcc tgg gtg tca cga ctc cag ggc ggt ccc atc tgt gac gcc ggt   355
Leu Ala Trp Val Ser Arg Leu Gln Gly Gly Pro Ile Cys Asp Ala Gly
70                  75                  80                  85

gag gct gtg tgg att tgt tcc cgt gct gca gaa ctg tgg tgg cca att   403
Glu Ala Val Trp Ile Cys Ser Arg Ala Ala Glu Leu Trp Trp Pro Ile
                90                  95                 100

acc act agc gtc atc gca ttt ggt ggc atg ctt gga tct gca tgg atc   451
Thr Thr Ser Val Ile Ala Phe Gly Gly Met Leu Gly Ser Ala Trp Ile
            105                 110                 115

ctc tat gac aaa tac cga aat tac cta cgc tgg cgt cct tgg atg ggc   499
```

```
Leu Tyr Asp Lys Tyr Arg Asn Tyr Leu Arg Trp Arg Pro Trp Met Gly
        120                 125                 130

gtg ttg tgg att ttg att cca ttc agc atg ctg tgg gga acc tcg gtg   547
Val Leu Trp Ile Leu Ile Pro Phe Ser Met Leu Trp Gly Thr Ser Val
    135                 140                 145

ctc acc ttg tcc atc ttg ggg cac taaaaacttc acataaatga caa         594
Leu Thr Leu Ser Ile Leu Gly His
150                 155


<210> 1810
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 1810
Met Asn Thr Gln Pro Glu His Pro Glu Asn Asp Leu Val Asp Glu Ala
  1               5                  10                  15

Asp Phe Ser Asn Arg Pro Arg Ile Tyr Ser Asp Asp Pro Asp Ser Leu
             20                  25                  30

Ala Asp Ala Pro Asp Pro Ala Leu Glu His Glu Lys Asn Lys Lys Ser
         35                  40                  45

Ser Arg Gln Ala Leu Ile Tyr Leu Leu Gln Val Pro Leu Val Thr Phe
     50                  55                  60

Val Ser Ala Tyr Val Leu Ala Trp Val Ser Arg Leu Gln Gly Gly Pro
 65                  70                  75                  80

Ile Cys Asp Ala Gly Glu Ala Val Trp Ile Cys Ser Arg Ala Ala Glu
                 85                  90                  95

Leu Trp Trp Pro Ile Thr Thr Ser Val Ile Ala Phe Gly Gly Met Leu
            100                 105                 110

Gly Ser Ala Trp Ile Leu Tyr Asp Lys Tyr Arg Asn Tyr Leu Arg Trp
        115                 120                 125

Arg Pro Trp Met Gly Val Leu Trp Ile Leu Ile Pro Phe Ser Met Leu
    130                 135                 140

Trp Gly Thr Ser Val Leu Thr Leu Ser Ile Leu Gly His
145                 150                 155


<210> 1811
<211> 2762
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(2739)
<223> RXA00563

<400> 1811
ttc tac aag gat ctc tac gca cgt tcc gca cgc ggc acg gca gca ctg   48
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Phe Tyr Lys Asp Leu Tyr Ala Arg Ser Ala Arg Gly Thr Ala Ala Leu
  1               5                  10                  15

tgg atc gtg gcg gct aac ttg agc tcc tac tca gac atc gac gcc atc   96
Trp Ile Val Ala Ala Asn Leu Ser Ser Tyr Ser Asp Ile Asp Ala Ile
             20                  25                  30

atc aac tgg gtc gga tcc gag cag acc acc acc gtc aac ggc gca tcc   144
Ile Asn Trp Val Gly Ser Glu Gln Thr Thr Thr Val Asn Gly Ala Ser
         35                  40                  45

aag ctg gtc aag cca gct ttg gtc cct acc ttg ctg ttc cca ttc gcg   192
Lys Leu Val Lys Pro Ala Leu Val Pro Thr Leu Leu Phe Pro Phe Ala
     50                  55                  60

gca cct cgc gtg tcc gga tcc atg gca gat gca ggc cca cag gca gaa   240
Ala Pro Arg Val Ser Gly Ser Met Ala Asp Ala Gly Pro Gln Ala Glu
 65                  70                  75                  80

tcc cag atg cga ctt ctg ctc tgg tct gtt gag cgc ctc atc gca ggt   288
Ser Gln Met Arg Leu Leu Leu Trp Ser Val Glu Arg Leu Ile Ala Gly
                 85                  90                  95

ctt gcg cca ttg ggc tcc tcc atc aac gtg ggt cac cgc ctg cac gtg   336
Leu Ala Pro Leu Gly Ser Ser Ile Asn Val Gly His Arg Leu His Val
            100                 105                 110

gtc atc cca ggt tca cca aac cgt gga cgc ttc ggt ggc gat ggt gca   384
Val Ile Pro Gly Ser Pro Asn Arg Gly Arg Phe Gly Gly Asp Gly Ala
        115                 120                 125

tac ggt gaa tcc aag gca gct ctc gac gcc gtg gtt acc cgt tgg aac   432
Tyr Gly Glu Ser Lys Ala Ala Leu Asp Ala Val Val Thr Arg Trp Asn
    130                 135                 140

gca gag caa gct gca tgg gga gca cac acc tcc ctc gtg cac gct cac   480
Ala Glu Gln Ala Ala Trp Gly Ala His Thr Ser Leu Val His Ala His
145                 150                 155                 160

atc ggt tgg gtt cgc ggc acc ggc ctc atg ggc ggc aac gat cct ttg   528
Ile Gly Trp Val Arg Gly Thr Gly Leu Met Gly Gly Asn Asp Pro Leu
                165                 170                 175

gtc aag gca gct gaa gaa gca ggc gtg gaa acc tac tcc acc caa gaa   576
Val Lys Ala Ala Glu Glu Ala Gly Val Glu Thr Tyr Ser Thr Gln Glu
            180                 185                 190

att gca gag aaa ctg ctg tcc cag gca act tcc act gtt cgc gag cag   624
Ile Ala Glu Lys Leu Leu Ser Gln Ala Thr Ser Thr Val Arg Glu Gln
        195                 200                 205

gca gca tcc gcg cca atc acc gtc gac ttc act ggc gga ctt ggt gaa   672
Ala Ala Ser Ala Pro Ile Thr Val Asp Phe Thr Gly Gly Leu Gly Glu
    210                 215                 220

tct gat ctg aac ctg gcg gaa atg gca cgt gca gaa gca gct aag gca   720
Ser Asp Leu Asn Leu Ala Glu Met Ala Arg Ala Glu Ala Ala Lys Ala
225                 230                 235                 240

gct aac gca cca gtg gtt gag gct cca cgc aca gtg gca gca ctg cca   768
Ala Asn Ala Pro Val Val Glu Ala Pro Arg Thr Val Ala Ala Leu Pro
```

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                245                 250                 255

act cct tac cga cca gtg gtt caa acc acc cct gat ttc gca ggt caa   816
Thr Pro Tyr Arg Pro Val Val Gln Thr Thr Pro Asp Phe Ala Gly Gln
            260                 265                 270

gtc acc caa aac ctt gac gag atg gtc gtc atc gtt ggc gcc ggc gag   864
Val Thr Gln Asn Leu Asp Glu Met Val Val Ile Val Gly Ala Gly Glu
        275                 280                 285

ctc ggc cca ctg ggt tct gca cgt acg cgt ttc gac gcc gaa ctc aac   912
Leu Gly Pro Leu Gly Ser Ala Arg Thr Arg Phe Asp Ala Glu Leu Asn
    290                 295                 300

ggt tcc ctc tcc gcc gcg ggt gtc atc gaa ctt gca tgg acg atg gga   960
Gly Ser Leu Ser Ala Ala Gly Val Ile Glu Leu Ala Trp Thr Met Gly
305                 310                 315                 320

ctt atc cac tgg gat gaa gat cca aag cca ggc tgg tac gac gac tcc  1008
Leu Ile His Trp Asp Glu Asp Pro Lys Pro Gly Trp Tyr Asp Asp Ser
                325                 330                 335

gac gac gca gtg gcc gaa gaa gac atc ttc gac cgc tac cac gac gaa  1056
Asp Asp Ala Val Ala Glu Glu Asp Ile Phe Asp Arg Tyr His Asp Glu
            340                 345                 350

gtc atg gca cgc gtt ggt gtc cgc aag tac aat gac atg cct gag tac  1104
Val Met Ala Arg Val Gly Val Arg Lys Tyr Asn Asp Met Pro Glu Tyr
        355                 360                 365

ggc atg atc gac aac ttt gca cca gag ctg acc acc gtc tac ctc gac  1152
Gly Met Ile Asp Asn Phe Ala Pro Glu Leu Thr Thr Val Tyr Leu Asp
    370                 375                 380

cag gac ctc acc ttc aac gtg gga tcc cgc gaa gag gca ctg acc tac  1200
Gln Asp Leu Thr Phe Asn Val Gly Ser Arg Glu Glu Ala Leu Thr Tyr
385                 390                 395                 400

gtc gac tcc gag cca gaa ctc acc ttt gct tct ttc gac gaa gca gca  1248
Val Asp Ser Glu Pro Glu Leu Thr Phe Ala Ser Phe Asp Glu Ala Ala
                405                 410                 415

ggg gag tgg aag gtc act cgc aag gca ggc tcc gca atc cgc gta cct  1296
Gly Glu Trp Lys Val Thr Arg Lys Ala Gly Ser Ala Ile Arg Val Pro
            420                 425                 430

cgc cgc atg gcg atg acc cgc ttc gtt ggt gga cag gtt cct aag gac  1344
Arg Arg Met Ala Met Thr Arg Phe Val Gly Gly Gln Val Pro Lys Asp
        435                 440                 445

ttc gac cca gct gtg tgg ggc att cca gct gac atg gtg gac aac ctg  1392
Phe Asp Pro Ala Val Trp Gly Ile Pro Ala Asp Met Val Asp Asn Leu
    450                 455                 460

gac acc gtc gcg ctg tgg aac att gtc tgt act gtc gac gcc ttc ctg  1440
Asp Thr Val Ala Leu Trp Asn Ile Val Cys Thr Val Asp Ala Phe Leu
465                 470                 475                 480

tcc gct gga ttc acc cca gca gag ctg ctt gct tcc gtt cac cca gca  1488
Ser Ala Gly Phe Thr Pro Ala Glu Leu Leu Ala Ser Val His Pro Ala
                485                 490                 495
```

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cgc gtg tcc tct acc caa ggc acc ggc atg ggc ggc atg gaa tcc ctc   1536
Arg Val Ser Ser Thr Gln Gly Thr Gly Met Gly Gly Met Glu Ser Leu
            500                 505                 510

cgt ggc atc tac gtc gac cgc att ctg gca gag cca cgc gcc aac gac   1584
Arg Gly Ile Tyr Val Asp Arg Ile Leu Ala Glu Pro Arg Ala Asn Asp
        515                 520                 525

gtt ctg cag gaa gca ctg ccc aac gtt gtt gca gct cac gtc atg cag   1632
Val Leu Gln Glu Ala Leu Pro Asn Val Val Ala Ala His Val Met Gln
    530                 535                 540

tcc tac gtc ggt ggc tac gga cag atg atc cac cca gtc gca gct tgt   1680
Ser Tyr Val Gly Gly Tyr Gly Gln Met Ile His Pro Val Ala Ala Cys
545                 550                 555                 560

gca acc gca gct gtt tct gtg gaa gaa gca ctg gac aag atc cgc atc   1728
Ala Thr Ala Ala Val Ser Val Glu Glu Ala Leu Asp Lys Ile Arg Ile
                565                 570                 575

ggc aag tcc gac ttc gtt gtc gca ggt ggc ttc gat gcc ctg tcc gtt   1776
Gly Lys Ser Asp Phe Val Val Ala Gly Gly Phe Asp Ala Leu Ser Val
            580                 585                 590

gaa ggc atc acc ggc ttc ggc gac atg gca gca acc gcc gac tcc gca   1824
Glu Gly Ile Thr Gly Phe Gly Asp Met Ala Ala Thr Ala Asp Ser Ala
        595                 600                 605

gag atg gaa ggc aag gga att gag cac cgc ttc ttc tcc cgc gcc aac   1872
Glu Met Glu Gly Lys Gly Ile Glu His Arg Phe Phe Ser Arg Ala Asn
    610                 615                 620

gac cgg cgc cgc ggt gga ttc atc gaa tcc gaa ggt ggc gga acc gtc   1920
Asp Arg Arg Arg Gly Gly Phe Ile Glu Ser Glu Gly Gly Gly Thr Val
625                 630                 635                 640

ctt ctg gca cgc gga tca ctc gca gct gac ctg ggc ctt cca gta ctc   1968
Leu Leu Ala Arg Gly Ser Leu Ala Ala Asp Leu Gly Leu Pro Val Leu
                645                 650                 655

ggt gtc atc gga ttc gca gag tcc ttt gca gat ggt gcc cac acc tcc   2016
Gly Val Ile Gly Phe Ala Glu Ser Phe Ala Asp Gly Ala His Thr Ser
            660                 665                 670

atc cca gcc cca ggc ctc ggt gcc ctt ggt gct gct cgc gat ggt gtg   2064
Ile Pro Ala Pro Gly Leu Gly Ala Leu Gly Ala Ala Arg Asp Gly Val
        675                 680                 685

gaa tct cgc ctt gca gta gca ctg cgt tcc gtc ggt gtc tct gct gat   2112
Glu Ser Arg Leu Ala Val Ala Leu Arg Ser Val Gly Val Ser Ala Asp
    690                 695                 700

gag atc tcc att atc tcc aag cac gac acc tcc acc aac gcg aat gat   2160
Glu Ile Ser Ile Ile Ser Lys His Asp Thr Ser Thr Asn Ala Asn Asp
705                 710                 715                 720

cca aac gag tcc gac ctg cac gag cgc atc gca tcc gct atc ggt cgt   2208
Pro Asn Glu Ser Asp Leu His Glu Arg Ile Ala Ser Ala Ile Gly Arg
                725                 730                 735
```

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gca gac ggc aac ccg atg tac gtg att tcc cag aag tca ctc acc gga   2256
Ala Asp Gly Asn Pro Met Tyr Val Ile Ser Gln Lys Ser Leu Thr Gly
            740                 745                 750

cac gcc aag ggt ggt gca gca gca ttc cag atg atc ggt ctc acc cag   2304
His Ala Lys Gly Gly Ala Ala Ala Phe Gln Met Ile Gly Leu Thr Gln
        755                 760                 765

gtc ctc cga tcc gga ctg gtg cca gcc aac cgc gca ctc gac tgc gtt   2352
Val Leu Arg Ser Gly Leu Val Pro Ala Asn Arg Ala Leu Asp Cys Val
    770                 775                 780

gac cca gta ctg tcc aag cat tcc cac ctc gtc tgg ctg cgc aag cca   2400
Asp Pro Val Leu Ser Lys His Ser His Leu Val Trp Leu Arg Lys Pro
785                 790                 795                 800

cta gac ctt cgt gcg aag gca cca aag gca ggt ctt gtt acc tcc ctt   2448
Leu Asp Leu Arg Ala Lys Ala Pro Lys Ala Gly Leu Val Thr Ser Leu
                805                 810                 815

ggc ttc gga cac gtc tcc gct ctg gtt gcg att gtt cac cca gac gcc   2496
Gly Phe Gly His Val Ser Ala Leu Val Ala Ile Val His Pro Asp Ala
            820                 825                 830

ttc tat gag gca gtt cgt gtg gca cgt ggt gct gag gca gct gac gta   2544
Phe Tyr Glu Ala Val Arg Val Ala Arg Gly Ala Glu Ala Ala Asp Val
        835                 840                 845

tgg cgc gca tcc gcg atc gct cgc gaa gaa gca ggc ctt cgt acc atc   2592
Trp Arg Ala Ser Ala Ile Ala Arg Glu Glu Ala Gly Leu Arg Thr Ile
    850                 855                 860

gtc gcc ggt atg cac ggt ggc gta ctg tac gaa cgc cca gtc gag cgc   2640
Val Ala Gly Met His Gly Gly Val Leu Tyr Glu Arg Pro Val Glu Arg
865                 870                 875                 880

aac ctc ggt gtc cac gga gac gca gct aag gaa gtt gaa gct gca gtc   2688
Asn Leu Gly Val His Gly Asp Ala Ala Lys Glu Val Glu Ala Ala Val
                885                 890                 895

ctc ctg gat tcc cgc gcc cgc cta gtt gac ggt gtc ctc cgc gcc gaa   2736
Leu Leu Asp Ser Arg Ala Arg Leu Val Asp Gly Val Leu Arg Ala Glu
            900                 905                 910

ggc tagttggtta ttgcgttgag ccc                                    2762
Gly
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<210> 1812
<211> 913
<212> PRT
<213> Corynebacterium glutamicum

<400> 1812

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Phe Tyr Lys Asp Leu Tyr Ala Arg Ser Ala Arg Gly Thr Ala Ala Leu
  1               5                  10                  15

Trp Ile Val Ala Ala Asn Leu Ser Ser Tyr Ser Asp Ile Asp Ala Ile
             20                  25                  30
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Ile Asn Trp Val Gly Ser Glu Gln Thr Thr Thr Val Asn Gly Ala Ser
          35                  40                  45

Lys Leu Val Lys Pro Ala Leu Val Pro Thr Leu Leu Phe Pro Phe Ala
     50                  55                  60

Ala Pro Arg Val Ser Gly Ser Met Ala Asp Ala Gly Pro Gln Ala Glu
 65                  70                  75                  80

Ser Gln Met Arg Leu Leu Leu Trp Ser Val Glu Arg Leu Ile Ala Gly
                 85                  90                  95

Leu Ala Pro Leu Gly Ser Ser Ile Asn Val Gly His Arg Leu His Val
            100                 105                 110

Val Ile Pro Gly Ser Pro Asn Arg Gly Arg Phe Gly Gly Asp Gly Ala
        115                 120                 125

Tyr Gly Glu Ser Lys Ala Ala Leu Asp Ala Val Val Thr Arg Trp Asn
    130                 135                 140

Ala Glu Gln Ala Ala Trp Gly Ala His Thr Ser Leu Val His Ala His
145                 150                 155                 160

Ile Gly Trp Val Arg Gly Thr Gly Leu Met Gly Gly Asn Asp Pro Leu
                165                 170                 175

Val Lys Ala Ala Glu Glu Ala Gly Val Glu Thr Tyr Ser Thr Gln Glu
            180                 185                 190

Ile Ala Glu Lys Leu Leu Ser Gln Ala Thr Ser Thr Val Arg Glu Gln
        195                 200                 205

Ala Ala Ser Ala Pro Ile Thr Val Asp Phe Thr Gly Gly Leu Gly Glu
    210                 215                 220

Ser Asp Leu Asn Leu Ala Glu Met Ala Arg Ala Glu Ala Ala Lys Ala
225                 230                 235                 240

Ala Asn Ala Pro Val Val Glu Ala Pro Arg Thr Val Ala Ala Leu Pro
                245                 250                 255

Thr Pro Tyr Arg Pro Val Val Gln Thr Thr Pro Asp Phe Ala Gly Gln
            260                 265                 270

Val Thr Gln Asn Leu Asp Glu Met Val Val Ile Val Gly Ala Gly Glu
        275                 280                 285

Leu Gly Pro Leu Gly Ser Ala Arg Thr Arg Phe Asp Ala Glu Leu Asn
    290                 295                 300

Gly Ser Leu Ser Ala Ala Gly Val Ile Glu Leu Ala Trp Thr Met Gly
305                 310                 315                 320

Leu Ile His Trp Asp Glu Asp Pro Lys Pro Gly Trp Tyr Asp Asp Ser
                325                 330                 335

Asp Asp Ala Val Ala Glu Glu Asp Ile Phe Asp Arg Tyr His Asp Glu
            340                 345                 350

Val Met Ala Arg Val Gly Val Arg Lys Tyr Asn Asp Met Pro Glu Tyr
```

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        355                 360                 365

Gly Met Ile Asp Asn Phe Ala Pro Glu Leu Thr Thr Val Tyr Leu Asp
    370                 375                 380

Gln Asp Leu Thr Phe Asn Val Gly Ser Arg Glu Glu Ala Leu Thr Tyr
385                 390                 395                 400

Val Asp Ser Glu Pro Glu Leu Thr Phe Ala Ser Phe Asp Glu Ala Ala
                405                 410                 415

Gly Glu Trp Lys Val Thr Arg Lys Ala Gly Ser Ala Ile Arg Val Pro
            420                 425                 430

Arg Arg Met Ala Met Thr Arg Phe Val Gly Gly Gln Val Pro Lys Asp
        435                 440                 445

Phe Asp Pro Ala Val Trp Gly Ile Pro Ala Asp Met Val Asp Asn Leu
    450                 455                 460

Asp Thr Val Ala Leu Trp Asn Ile Val Cys Thr Val Asp Ala Phe Leu
465                 470                 475                 480

Ser Ala Gly Phe Thr Pro Ala Glu Leu Leu Ala Ser Val His Pro Ala
                485                 490                 495

Arg Val Ser Ser Thr Gln Gly Thr Gly Met Gly Gly Met Glu Ser Leu
            500                 505                 510

Arg Gly Ile Tyr Val Asp Arg Ile Leu Ala Glu Pro Arg Ala Asn Asp
        515                 520                 525

Val Leu Gln Glu Ala Leu Pro Asn Val Val Ala Ala His Val Met Gln
    530                 535                 540

Ser Tyr Val Gly Gly Tyr Gly Gln Met Ile His Pro Val Ala Ala Cys
545                 550                 555                 560

Ala Thr Ala Ala Val Ser Val Glu Glu Ala Leu Asp Lys Ile Arg Ile
                565                 570                 575

Gly Lys Ser Asp Phe Val Val Ala Gly Gly Phe Asp Ala Leu Ser Val
            580                 585                 590

Glu Gly Ile Thr Gly Phe Gly Asp Met Ala Ala Thr Ala Asp Ser Ala
        595                 600                 605

Glu Met Glu Gly Lys Gly Ile Glu His Arg Phe Phe Ser Arg Ala Asn
    610                 615                 620

Asp Arg Arg Arg Gly Gly Phe Ile Glu Ser Glu Gly Gly Gly Thr Val
625                 630                 635                 640

Leu Leu Ala Arg Gly Ser Leu Ala Ala Asp Leu Gly Leu Pro Val Leu
                645                 650                 655

Gly Val Ile Gly Phe Ala Glu Ser Phe Ala Asp Gly Ala His Thr Ser
            660                 665                 670

Ile Pro Ala Pro Gly Leu Gly Ala Leu Gly Ala Ala Arg Asp Gly Val
        675                 680                 685
```

```
Glu Ser Arg Leu Ala Val Ala Leu Arg Ser Val Gly Val Ser Ala Asp
    690                 695                 700

Glu Ile Ser Ile Ile Ser Lys His Asp Thr Ser Thr Asn Ala Asn Asp
705                 710                 715                 720

Pro Asn Glu Ser Asp Leu His Glu Arg Ile Ala Ser Ala Ile Gly Arg
                725                 730                 735

Ala Asp Gly Asn Pro Met Tyr Val Ile Ser Gln Lys Ser Leu Thr Gly
            740                 745                 750

His Ala Lys Gly Gly Ala Ala Ala Phe Gln Met Ile Gly Leu Thr Gln
        755                 760                 765

Val Leu Arg Ser Gly Leu Val Pro Ala Asn Arg Ala Leu Asp Cys Val
    770                 775                 780

Asp Pro Val Leu Ser Lys His Ser His Leu Val Trp Leu Arg Lys Pro
785                 790                 795                 800

Leu Asp Leu Arg Ala Lys Ala Pro Lys Ala Gly Leu Val Thr Ser Leu
                805                 810                 815

Gly Phe Gly His Val Ser Ala Leu Val Ala Ile Val His Pro Asp Ala
            820                 825                 830

Phe Tyr Glu Ala Val Arg Val Ala Arg Gly Ala Glu Ala Ala Asp Val
        835                 840                 845

Trp Arg Ala Ser Ala Ile Ala Arg Glu Glu Ala Gly Leu Arg Thr Ile
    850                 855                 860

Val Ala Gly Met His Gly Gly Val Leu Tyr Glu Arg Pro Val Glu Arg
865                 870                 875                 880

Asn Leu Gly Val His Gly Asp Ala Ala Lys Glu Val Glu Ala Ala Val
                885                 890                 895

Leu Leu Asp Ser Arg Ala Arg Leu Val Asp Gly Val Leu Arg Ala Glu
            900                 905                 910

Gly
```

<210> 1813
<211> 528
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(505)
<223> RXA00564

<400> 1813
caacgatgga gtgctattcg taacgaggtg acattcccac cggcaccttg atccagatag 60

aaaaacggat ggaaccagta ttgggaaaag gatggttgcg atg aaa tac aac gtc 115

```
                                                    Met Lys Tyr Asn Val
                                                      1               5

gat gtc tct cgt gaa agc gag gac tgg ctc gcc acc gtc acc aat ctc   163
Asp Val Ser Arg Glu Ser Glu Asp Trp Leu Ala Thr Val Thr Asn Leu
                 10                  15                  20

gaa ggc gta tcc acg tgg gcg aca acc ttc gcc aac ctt gat cgc aac   211
Glu Gly Val Ser Thr Trp Ala Thr Thr Phe Ala Asn Leu Asp Arg Asn
             25                  30                  35

ggc cgg gaa gcc att gct cta gct gaa gat ctc ccc gaa ggt gcg gaa   259
Gly Arg Glu Ala Ile Ala Leu Ala Glu Asp Leu Pro Glu Gly Ala Glu
         40                  45                  50

agc tca ctg acc atc tct tgg tcg gtt cct aca gat tcc cac ccc gaa   307
Ser Ser Leu Thr Ile Ser Trp Ser Val Pro Thr Asp Ser His Pro Glu
     55                  60                  65

ctg gac act gca att caa att gct caa cag cgt cgc tat cta gtg caa   355
Leu Asp Thr Ala Ile Gln Ile Ala Gln Gln Arg Arg Tyr Leu Val Gln
 70                  75                  80                  85

gcc caa caa gac tta gag ccc aaa gtt cga tcc gct att tcc gct ctc   403
Ala Gln Gln Asp Leu Glu Pro Lys Val Arg Ser Ala Ile Ser Ala Leu
                 90                  95                 100

acc caa gct gcg ctg cta ggt atg act gca ggt cga gta tcc cca act   451
Thr Gln Ala Ala Leu Leu Gly Met Thr Ala Gly Arg Val Ser Pro Thr
             105                 110                 115

cac aac ccg ggt agc aga gct atc tca ttg gat cag gtg tca gga gtt   499
His Asn Pro Gly Ser Arg Ala Ile Ser Leu Asp Gln Val Ser Gly Val
         120                 125                 130

tta aac tagcgtgcgc aattcccgtg tga                                 528
Leu Asn
    135
```

5a2b5a2b5a2b

```
Arg Tyr Leu Val Gln Ala Gln Gln Asp Leu Glu Pro Lys Val Arg Ser
                 85                  90                  95

Ala Ile Ser Ala Leu Thr Gln Ala Ala Leu Leu Gly Met Thr Ala Gly
            100                 105                 110

Arg Val Ser Pro Thr His Asn Pro Gly Ser Arg Ala Ile Ser Leu Asp
        115                 120                 125

Gln Val Ser Gly Val Leu Asn
    130                 135


<210> 1815
<211> 774
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> RXA00573

<400> 1815
gacgccaact ccatctgtgt tcatggggat aatccgcaag ctctcgcatt ggtggagaaa 60

atcgtgacca cccttgcagc tcatgaggtt caggtttccc atg ctc gtt agg cca   115
                                            Met Leu Val Arg Pro
                                              1               5

tgt ggt gag caa gca gtc atc atc gat ttg ctt gct gaa gat gcc gaa   163
Cys Gly Glu Gln Ala Val Ile Ile Asp Leu Leu Ala Glu Asp Ala Glu
                 10                  15                  20

gcc gtc caa ggc agc atc ttg gat gct gtt ctt gca ctc aac cgc tct   211
Ala Val Gln Gly Ser Ile Leu Asp Ala Val Leu Ala Leu Asn Arg Ser
             25                  30                  35

ttg gtg ggc atg cag gtc cct gga atc atc gat act att ccc gct gcg   259
Leu Val Gly Met Gln Val Pro Gly Ile Ile Asp Thr Ile Pro Ala Ala
         40                  45                  50

caa aca ctg tta gtg acg ttt gac acc aag cag atc acc ccg aat cgt   307
Gln Thr Leu Leu Val Thr Phe Asp Thr Lys Gln Ile Thr Pro Asn Arg
     55                  60                  65

ttc gca gag atc gtt gat tca att gcg ctg acc cca gcc gca aag ggc   355
Phe Ala Glu Ile Val Asp Ser Ile Ala Leu Thr Pro Ala Ala Lys Gly
 70                  75                  80                  85

gca gca gag ctt acc gac acc att gag att ccc gtg gtc tac gac ggc   403
Ala Ala Glu Leu Thr Asp Thr Ile Glu Ile Pro Val Val Tyr Asp Gly
                 90                  95                 100

cct gat cta gaa acc gta gct caa cac aca ggt ctg agc gtg gag gaa   451
Pro Asp Leu Glu Thr Val Ala Gln His Thr Gly Leu Ser Val Glu Glu
            105                 110                 115

gtt atc gcc acg cat tct ggc acc gtg tgg act gct gct ttc ggt gga   499
Val Ile Ala Thr His Ser Gly Thr Val Trp Thr Ala Ala Phe Gly Gly
        120                 125                 130
```

```
ttt gca cca ggt ttt tac tat ctg atc ccc cag act ccc ctg tgg gat   547
Phe Ala Pro Gly Phe Tyr Tyr Leu Ile Pro Gln Thr Pro Leu Trp Asp
    135                 140                 145

att ccc cgc ttg gaa tcg cca cgc acc aag att cct gca ggt tct gtc   595
Ile Pro Arg Leu Glu Ser Pro Arg Thr Lys Ile Pro Ala Gly Ser Val
150                 155                 160                 165

gca gtg gcc ggt gaa ttc agc gct gtg tac ccg cag cag tcc cct ggt   643
Ala Val Ala Gly Glu Phe Ser Ala Val Tyr Pro Gln Gln Ser Pro Gly
                170                 175                 180

ggt tgg caa ctg ctg ggc act act gag att ccc atg tgg gat gtg gac   691
Gly Trp Gln Leu Leu Gly Thr Thr Glu Ile Pro Met Trp Asp Val Asp
            185                 190                 195

cgg tgg caa cca tcg ctt ctc aag ccc ggt gat tca gtt cga ttt gtg   739
Arg Trp Gln Pro Ser Leu Leu Lys Pro Gly Asp Ser Val Arg Phe Val
        200                 205                 210

cag gtg aag aaa tgagcttcaa agtaatttcc act                        774
Gln Val Lys Lys
    215
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20050070699

<210> 1816
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 1816

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Met Leu Val Arg Pro Cys Gly Glu Gln Ala Val Ile Ile Asp Leu Leu
  1               5                  10                  15

Ala Glu Asp Ala Glu Ala Val Gln Gly Ser Ile Leu Asp Ala Val Leu
             20                  25                  30

Ala Leu Asn Arg Ser Leu Val Gly Met Gln Val Pro Gly Ile Ile Asp
         35                  40                  45

Thr Ile Pro Ala Ala Gln Thr Leu Leu Val Thr Phe Asp Thr Lys Gln
     50                  55                  60

Ile Thr Pro Asn Arg Phe Ala Glu Ile Val Asp Ser Ile Ala Leu Thr
 65                  70                  75                  80

Pro Ala Ala Lys Gly Ala Ala Glu Leu Thr Asp Thr Ile Glu Ile Pro
                 85                  90                  95

Val Val Tyr Asp Gly Pro Asp Leu Glu Thr Val Ala Gln His Thr Gly
            100                 105                 110

Leu Ser Val Glu Glu Val Ile Ala Thr His Ser Gly Thr Val Trp Thr
        115                 120                 125

Ala Ala Phe Gly Gly Phe Ala Pro Gly Phe Tyr Tyr Leu Ile Pro Gln
    130                 135                 140

Thr Pro Leu Trp Asp Ile Pro Arg Leu Glu Ser Pro Arg Thr Lys Ile
145                 150                 155                 160
```

```
Pro Ala Gly Ser Val Ala Val Ala Gly Glu Phe Ser Ala Val Tyr Pro
                165                 170                 175

Gln Gln Ser Pro Gly Gly Trp Gln Leu Leu Gly Thr Thr Glu Ile Pro
            180                 185                 190

Met Trp Asp Val Asp Arg Trp Gln Pro Ser Leu Leu Lys Pro Gly Asp
        195                 200                 205

Ser Val Arg Phe Val Gln Val Lys Lys
    210                 215


<210> 1817
<211> 795
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(772)
<223> RXA00576

<400> 1817
acagtccgag cttcttagcg gcggtctgtg gcttcatagc cctgcccgat ggctggcgta 60

cagattcttc gttcacgccc acaacggtag cattgttttc atg ctg acc tta agt   115
                                            Met Leu Thr Leu Ser
                                              1               5

ttc atc act ggc acg gag cca gga aag tgg ttt acc cga ttc cga gat   163
Phe Ile Thr Gly Thr Glu Pro Gly Lys Trp Phe Thr Arg Phe Arg Asp
                  10                  15                  20

cgg act cat cac ggt gga ctt gag acc ctt gat tcg gac gac gcc cta   211
Arg Thr His His Gly Gly Leu Glu Thr Leu Asp Ser Asp Asp Ala Leu
              25                  30                  35

ggc ctc atg ctc gct ggc cag gca caa ctc gcc tta acc agg ctt cca   259
Gly Leu Met Leu Ala Gly Gln Ala Gln Leu Ala Leu Thr Arg Leu Pro
          40                  45                  50

gat gcg cgt atc gac gcc tcc ctc cac gtg gtc act ctt tat cag gaa   307
Asp Ala Arg Ile Asp Ala Ser Leu His Val Val Thr Leu Tyr Gln Glu
      55                  60                  65

caa ccc gga gtc gct ttt cca aaa gac ttt ttc ctc agt gcc gaa gaa   355
Gln Pro Gly Val Ala Phe Pro Lys Asp Phe Phe Leu Ser Ala Glu Glu
  70                  75                  80                  85

ggc gcg gtg gac ctt gcg gac tta gat ggg gag atc atc aac tgg tcc   403
Gly Ala Val Asp Leu Ala Asp Leu Asp Gly Glu Ile Ile Asn Trp Ser
                  90                  95                 100

atg ccc gat agt ggg gaa gtc gat gcc gct gct gtt cgc gat gct ctg   451
Met Pro Asp Ser Gly Glu Val Asp Ala Ala Ala Val Arg Asp Ala Leu
              105                 110                 115

caa atc gtg gca gcg aac gtc ggt gtg gtg atc gcc ccc agg cca ctt   499
Gln Ile Val Ala Ala Asn Val Gly Val Val Ile Ala Pro Arg Pro Leu
```

```
        120                 125                 130

ctc aag gtg ttg agc aag aaa ttg gtg gag cac cgg gac atc aag ggt   547
Leu Lys Val Leu Ser Lys Lys Leu Val Glu His Arg Asp Ile Lys Gly
    135                 140                 145

gga act gaa aca tct atc gcc ctg gta tgg aag aaa gat gag gat tct   595
Gly Thr Glu Thr Ser Ile Ala Leu Val Trp Lys Lys Asp Glu Asp Ser
150                 155                 160                 165

gaa gag att caa gac ttc gtc ggt att gct cgc ggt cga acg cgg aat   643
Glu Glu Ile Gln Asp Phe Val Gly Ile Ala Arg Gly Arg Thr Arg Asn
                170                 175                 180

tcc agc agg cag caa acg gta aag ctc agt gct cgt gaa aaa aca ctg   691
Ser Ser Arg Gln Gln Thr Val Lys Leu Ser Ala Arg Glu Lys Thr Leu
            185                 190                 195

gca aaa caa gcc cgc agg cag ggg gag aaa cca aaa act ccg aag cgt   739
Ala Lys Gln Ala Arg Arg Gln Gly Glu Lys Pro Lys Thr Pro Lys Arg
        200                 205                 210

ccg cag gca aga aaa cgt ccc gga aaa cgg cga taggggtcac ccgcgcatgt 792
Pro Gln Ala Arg Lys Arg Pro Gly Lys Arg Arg
    215                 220

ccg                                                               795


<210> 1818
<211> 224
<212> PRT
<213> Corynebacterium glutamicum

<400> 1818
Met Leu Thr Leu Ser Phe Ile Thr Gly Thr Glu Pro Gly Lys Trp Phe
  1               5                  10                  15

Thr Arg Phe Arg Asp Arg Thr His His Gly Gly Leu Glu Thr Leu Asp
            20                  25                  30

Ser Asp Asp Ala Leu Gly Leu Met Leu Ala Gly Gln Ala Gln Leu Ala
        35                  40                  45

Leu Thr Arg Leu Pro Asp Ala Arg Ile Asp Ala Ser Leu His Val Val
    50                  55                  60

Thr Leu Tyr Gln Glu Gln Pro Gly Val Ala Phe Pro Lys Asp Phe Phe
65                  70                  75                  80

Leu Ser Ala Glu Glu Gly Ala Val Asp Leu Ala Asp Leu Asp Gly Glu
                85                  90                  95

Ile Ile Asn Trp Ser Met Pro Asp Ser Gly Glu Val Asp Ala Ala Ala
            100                 105                 110

Val Arg Asp Ala Leu Gln Ile Val Ala Ala Asn Val Gly Val Val Ile
        115                 120                 125

Ala Pro Arg Pro Leu Leu Lys Val Leu Ser Lys Lys Leu Val Glu His
    130                 135                 140
```

```
Arg Asp Ile Lys Gly Gly Thr Glu Thr Ser Ile Ala Leu Val Trp Lys
145                 150                 155                 160

Lys Asp Glu Asp Ser Glu Glu Ile Gln Asp Phe Val Gly Ile Ala Arg
                165                 170                 175

Gly Arg Thr Arg Asn Ser Ser Arg Gln Gln Thr Val Lys Leu Ser Ala
            180                 185                 190

Arg Glu Lys Thr Leu Ala Lys Gln Ala Arg Arg Gln Gly Glu Lys Pro
        195                 200                 205

Lys Thr Pro Lys Arg Pro Gln Ala Arg Lys Arg Pro Gly Lys Arg Arg
    210                 215                 220
```

CONFIDENTIAL

<210> 1819
<211> 471
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(448)
<223> RXA00577

<400> 1819

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ctggctccgt gccagtgatg aaacttaagg tcagcatgaa aacaatgcta ccgttgtggg 60

cgtgaacgaa gaatctgtac gccagccatc gggcagggct atg aag cca cag acc   115
                                              Met Lys Pro Gln Thr
                                                1               5

gcc gct aag aag ctc gga ctg ttt ttg ccc gcc acg cca gag gag ttc   163
Ala Ala Lys Lys Leu Gly Leu Phe Leu Pro Ala Thr Pro Glu Glu Phe
                10                  15                  20

caa aca ggt gca ttg act cac caa gag ttc aag aac ctg cag gaa aac   211
Gln Thr Gly Ala Leu Thr His Gln Glu Phe Lys Asn Leu Gln Glu Asn
            25                  30                  35

cca ccg gag tgg ctc caa acc cta cgc cgc gag ggc cca cac cct cgt   259
Pro Pro Glu Trp Leu Gln Thr Leu Arg Arg Glu Gly Pro His Pro Arg
        40                  45                  50

cca gtg gtc gcc caa aaa ttg ggc atc acc atc gcg gct ctg aaa aag   307
Pro Val Val Ala Gln Lys Leu Gly Ile Thr Ile Ala Ala Leu Lys Lys
    55                  60                  65

aac gac atg gac aaa cca ctg acc acc gcc gag atc aag gca ctt ctg   355
Asn Asp Met Asp Lys Pro Leu Thr Thr Ala Glu Ile Lys Ala Leu Leu
70                  75                  80                  85

gaa aac cag cca gaa tgg ttg cgc acc gca cgc aca cag ctt gct gaa   403
Glu Asn Gln Pro Glu Trp Leu Arg Thr Ala Arg Thr Gln Leu Ala Glu
                90                  95                  100
```

```
ggt cgc gaa acc gca aag aaa gaa act gaa gaa act acc gaa gac       448
Gly Arg Glu Thr Ala Lys Lys Glu Thr Glu Glu Thr Thr Glu Asp
            105                 110                 115

taaatcttca caaagactgc gct                                       471


<210> 1820
<211> 116
<212> PRT
<213> Corynebacterium glutamicum

<400> 1820
Met Lys Pro Gln Thr Ala Ala Lys Lys Leu Gly Leu Phe Leu Pro Ala
  1               5                  10                  15

Thr Pro Glu Glu Phe Gln Thr Gly Ala Leu Thr His Gln Glu Phe Lys
             20                  25                  30

Asn Leu Gln Glu Asn Pro Pro Glu Trp Leu Gln Thr Leu Arg Arg Glu
         35                  40                  45

Gly Pro His Pro Arg Pro Val Val Ala Gln Lys Leu Gly Ile Thr Ile
     50                  55                  60

Ala Ala Leu Lys Lys Asn Asp Met Asp Lys Pro Leu Thr Thr Ala Glu
 65                  70                  75                  80

Ile Lys Ala Leu Leu Glu Asn Gln Pro Glu Trp Leu Arg Thr Ala Arg
                85                  90                  95

Thr Gln Leu Ala Glu Gly Arg Glu Thr Ala Lys Lys Glu Thr Glu Glu
            100                 105                 110

Thr Thr Glu Asp
        115


<210> 1821
<211> 846
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(823)
<223> RXA00578

<400> 1821
tgggcggtgc acttcttgct ctgtctgatc cggaggctga gtgggaggaa atccgcgtta 60

aatcacggcc tctgctgaat ttgtttgggg ttgaattccc atg acg tac ctc gtg   115
                                              Met Thr Tyr Leu Val
                                                1               5

tgg gac ggt gca aca ctc gta gaa ggc gcg ctg gaa tca aca ccc aca   163
Trp Asp Gly Ala Thr Leu Val Glu Gly Ala Leu Glu Ser Thr Pro Thr
                10                  15                  20

gtt gtt gat tcc tac cta gcc aaa gac cac cgc gtg gtg cgc tgg gat   211
Val Val Asp Ser Tyr Leu Ala Lys Asp His Arg Val Val Arg Trp Asp
```

```
            25                  30                  35

ctt cat gaa cag cgc ttc gcc act agc gtg gac gtg gac ccg tgg gat   259
Leu His Glu Gln Arg Phe Ala Thr Ser Val Asp Val Asp Pro Trp Asp
         40                  45                  50

ttt ctc cac gca gta agg gaa gca att cca cgc cag ggc tca tgg ttt   307
Phe Leu His Ala Val Arg Glu Ala Ile Pro Arg Gln Gly Ser Trp Phe
     55                  60                  65

ccc aaa gtt gaa tgg cat ggc gat gat ctt ttc gca gtc aat att cgc   355
Pro Lys Val Glu Trp His Gly Asp Asp Leu Phe Ala Val Asn Ile Arg
 70                  75                  80                  85

ccg gca cca aca ctg cga aag gcc aca tca ttg tgg ctt tcc gaa gac   403
Pro Ala Pro Thr Leu Arg Lys Ala Thr Ser Leu Trp Leu Ser Glu Asp
                 90                  95                 100

cca gat cca cgc aca cag cca acc att aaa ggc cca gac cta gat gtg   451
Pro Asp Pro Arg Thr Gln Pro Thr Ile Lys Gly Pro Asp Leu Asp Val
            105                 110                 115

ctt gct cac ctt cgc agt cgc gcc aac gat aac ggc tgc gat gat gcg   499
Leu Ala His Leu Arg Ser Arg Ala Asn Asp Asn Gly Cys Asp Asp Ala
        120                 125                 130

ctg ttg atc agc gcg gat ggg ttc att ctg gaa gct gcc aac gcc acc   547
Leu Leu Ile Ser Ala Asp Gly Phe Ile Leu Glu Ala Ala Asn Ala Thr
    135                 140                 145

gtg gtg ttt tgg gcg gat cca cag acg gtc atc gtg ccc agg gga gat   595
Val Val Phe Trp Ala Asp Pro Gln Thr Val Ile Val Pro Arg Gly Asp
150                 155                 160                 165

gtg ctc cca tcg gtg aca ctc gcc gca acc att ccg ctg tgg gaa aaa   643
Val Leu Pro Ser Val Thr Leu Ala Ala Thr Ile Pro Leu Trp Glu Lys
                170                 175                 180

gcc gga atc aca ttg cgc tat caa aac att cgg cac att ggt ttt ccc   691
Ala Gly Ile Thr Leu Arg Tyr Gln Asn Ile Arg His Ile Gly Phe Pro
            185                 190                 195

gcg tgg tgc ggt agt tcg ctg cat ggt tgg aca cct gtg gtc agt tgg   739
Ala Trp Cys Gly Ser Ser Leu His Gly Trp Thr Pro Val Val Ser Trp
        200                 205                 210

ggc agg gga ttg ggc aaa att gca gca gcg aaa gct cca tcg gtg aag   787
Gly Arg Gly Leu Gly Lys Ile Ala Ala Ala Lys Ala Pro Ser Val Lys
    215                 220                 225

ccc tgg aat gaa aaa ttg cgc cca acc att ttt ctg tgaggaaaag       833
Pro Trp Asn Glu Lys Leu Arg Pro Thr Ile Phe Leu
230                 235                 240

gttgagcgca gtc                                                  846


<210> 1822
<211> 241
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 1822
Met Thr Tyr Leu Val Trp Asp Gly Ala Thr Leu Val Glu Gly Ala Leu
1 5 10 15

Glu Ser Thr Pro Thr Val Val Asp Ser Tyr Leu Ala Lys Asp His Arg
20 25 30

Val Val Arg Trp Asp Leu His Glu Gln Arg Phe Ala Thr Ser Val Asp
35 40 45

Val Asp Pro Trp Asp Phe Leu His Ala Val Arg Glu Ala Ile Pro Arg
50 55 60

Gln Gly Ser Trp Phe Pro Lys Val Glu Trp His Gly Asp Asp Leu Phe
65 70 75 80

Ala Val Asn Ile Arg Pro Ala Pro Thr Leu Arg Lys Ala Thr Ser Leu
85 90 95

Trp Leu Ser Glu Asp Pro Asp Pro Arg Thr Gln Pro Thr Ile Lys Gly
100 105 110

Pro Asp Leu Asp Val Leu Ala His Leu Arg Ser Arg Ala Asn Asp Asn
115 120 125

Gly Cys Asp Asp Ala Leu Leu Ile Ser Ala Asp Gly Phe Ile Leu Glu
130 135 140

Ala Ala Asn Ala Thr Val Val Phe Trp Ala Asp Pro Gln Thr Val Ile
145 150 155 160

Val Pro Arg Gly Asp Val Leu Pro Ser Val Thr Leu Ala Ala Thr Ile
165 170 175

Pro Leu Trp Glu Lys Ala Gly Ile Thr Leu Arg Tyr Gln Asn Ile Arg
180 185 190

His Ile Gly Phe Pro Ala Trp Cys Gly Ser Ser Leu His Gly Trp Thr
195 200 205

Pro Val Val Ser Trp Gly Arg Gly Leu Gly Lys Ile Ala Ala Ala Lys
210 215 220

Ala Pro Ser Val Lys Pro Trp Asn Glu Lys Leu Arg Pro Thr Ile Phe
225 230 235 240

Leu

<210> 1823
<211> 642
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(619)
<223> RXA00582

<400> 1823
actggccagc cttccgacgc atcgacttcc tccgcgccat tcgcgactac tcgcagcgca 60

gcagaagatt cggtaaataa cttattctcc aaggagagac atg tct gac tac atc 115
Met Ser Asp Tyr Ile
1 5

gtc gca ttt gaa tcc gca tac ggc tct acc aag cag tac gca gaa tct 163
Val Ala Phe Glu Ser Ala Tyr Gly Ser Thr Lys Gln Tyr Ala Glu Ser
10 15 20

ctg gcg caa cgc ctc ggc gta gat gcc tta aat ttt gaa caa gcg tgt 211
Leu Ala Gln Arg Leu Gly Val Asp Ala Leu Asn Phe Glu Gln Ala Cys
25 30 35

gcg gaa ctc gcg gcg aac ccg acc gca gca atc gtg gtt ttg agc ttt 259
Ala Glu Leu Ala Ala Asn Pro Thr Ala Ala Ile Val Val Leu Ser Phe
40 45 50

gtt cac ggc cca tcc cat cca ggt gcg aaa ttc att acc gat acc gat 307
Val His Gly Pro Ser His Pro Gly Ala Lys Phe Ile Thr Asp Thr Asp
55 60 65

ctc tcc ggc cac cgc gtc gca ctg tgc acc gtc ggc atg acg ctt gat 355
Leu Ser Gly His Arg Val Ala Leu Cys Thr Val Gly Met Thr Leu Asp
70 75 80 85

gat gtc gtg caa aag aag gac ggc gca gct cga tca ctg gga aac aag 403
Asp Val Val Gln Lys Lys Asp Gly Ala Ala Arg Ser Leu Gly Asn Lys
90 95 100

gca gac gat gtc acc cgt ttc tac ctt ccg gga cgc ctt aat tac tca 451
Ala Asp Asp Val Thr Arg Phe Tyr Leu Pro Gly Arg Leu Asn Tyr Ser
105 110 115

gag ctc tcg acc gcg cac cgc acc acc atg tgg acg atc gtc aac atg 499
Glu Leu Ser Thr Ala His Arg Thr Thr Met Trp Thr Ile Val Asn Met
120 125 130

ctg aaa gcg aag ccg ttg aag aat gac aac gac aaa atg atg atc aac 547
Leu Lys Ala Lys Pro Leu Lys Asn Asp Asn Asp Lys Met Met Ile Asn
135 140 145

act ttt gat acc gat gtt gac cgc gtc gat gag tcc cgc ctg gac gca 595
Thr Phe Asp Thr Asp Val Asp Arg Val Asp Glu Ser Arg Leu Asp Ala
150 155 160 165

gtg gag gag tgg gcg agg ggc ctc tagagtgggc gttgcaaaaa ctc 642
Val Glu Glu Trp Ala Arg Gly Leu
170

<210> 1824
<211> 173
<212> PRT
<213> Corynebacterium glutamicum

<400> 1824
Met Ser Asp Tyr Ile Val Ala Phe Glu Ser Ala Tyr Gly Ser Thr Lys
1 5 10 15

```
Gln Tyr Ala Glu Ser Leu Ala Gln Arg Leu Gly Val Asp Ala Leu Asn
              20                  25                  30

Phe Glu Gln Ala Cys Ala Glu Leu Ala Ala Asn Pro Thr Ala Ala Ile
          35                  40                  45

Val Val Leu Ser Phe Val His Gly Pro Ser His Pro Gly Ala Lys Phe
     50                  55                  60

Ile Thr Asp Thr Asp Leu Ser Gly His Arg Val Ala Leu Cys Thr Val
 65                  70                  75                  80

Gly Met Thr Leu Asp Asp Val Val Gln Lys Lys Asp Gly Ala Ala Arg
                 85                  90                  95

Ser Leu Gly Asn Lys Ala Asp Asp Val Thr Arg Phe Tyr Leu Pro Gly
            100                 105                 110

Arg Leu Asn Tyr Ser Glu Leu Ser Thr Ala His Arg Thr Thr Met Trp
        115                 120                 125

Thr Ile Val Asn Met Leu Lys Ala Lys Pro Leu Lys Asn Asp Asn Asp
    130                 135                 140

Lys Met Met Ile Asn Thr Phe Asp Thr Asp Val Asp Arg Val Asp Glu
145                 150                 155                 160

Ser Arg Leu Asp Ala Val Glu Glu Trp Ala Arg Gly Leu
                165                 170
```

<210> 1825
<211> 441
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(418)
<223> RXA00585

<400> 1825

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tgtgaagacg tcgatcccag aagatgacct gtttgccgga atcacacccg atgcagaata 60

atgcagttag accacatcct ttaggaagga ccttttcggc gtg att gac ctc agc   115
                                            Val Ile Asp Leu Ser
                                              1               5

cct gta ttc aat aca gct gcc ggc gta tac aac gac acc aac gca atc   163
Pro Val Phe Asn Thr Ala Ala Gly Val Tyr Asn Asp Thr Asn Ala Ile
                 10                  15                  20

atc ttg gct cag cag cag caa ggt gga cca ctt gga cct gag ttt gga   211
Ile Leu Ala Gln Gln Gln Gly Gly Pro Leu Gly Pro Glu Phe Gly
             25                  30                  35

aag gcc tcg ccg gtt ggt ttg cta ctg atc gtc gcg atg ctc gtt gcc   259
Lys Ala Ser Pro Val Gly Leu Leu Ile Val Ala Met Leu Val Ala
         40                  45                  50

att ctt gtt ctc ggc tgg gcg ttc cac cga cgc tgg tca cgg atg aat   307
```

```
Ile Leu Val Leu Gly Trp Ala Phe His Arg Arg Trp Ser Arg Met Asn
     55                  60                  65

cgt cgt cgt att ttc gca gag cgc aac ggc ctt gat ccc ttc gat att   355
Arg Arg Arg Ile Phe Ala Glu Arg Asn Gly Leu Asp Pro Phe Asp Ile
 70                  75                  80                  85

gag ggt gtt cgc aag gca atg gct gag gcc ggc ttg aat gaa aag tcc   403
Glu Gly Val Arg Lys Ala Met Ala Glu Ala Gly Leu Asn Glu Lys Ser
                 90                  95                 100

aaa aag ggc ttc ctt taaaaagaaa gtgtgttaag gtt                    441
Lys Lys Gly Phe Leu
            105


<210> 1826
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 1826
Val Ile Asp Leu Ser Pro Val Phe Asn Thr Ala Ala Gly Val Tyr Asn
  1               5                  10                  15

Asp Thr Asn Ala Ile Ile Leu Ala Gln Gln Gln Gln Gly Gly Pro Leu
             20                  25                  30

Gly Pro Glu Phe Gly Lys Ala Ser Pro Val Gly Leu Leu Leu Ile Val
         35                  40                  45

Ala Met Leu Val Ala Ile Leu Val Leu Gly Trp Ala Phe His Arg Arg
     50                  55                  60

Trp Ser Arg Met Asn Arg Arg Arg Ile Phe Ala Glu Arg Asn Gly Leu
 65                  70                  75                  80

Asp Pro Phe Asp Ile Glu Gly Val Arg Lys Ala Met Ala Glu Ala Gly
                 85                  90                  95

Leu Asn Glu Lys Ser Lys Lys Gly Phe Leu
            100                 105


<210> 1827
<211> 1005
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(982)
<223> RXA00586

<400> 1827
tcatccaagg ggtaaatagg tatgacggcg gaaacgacta tcatgaatgc aatacacatc 60

aactaaaccc tgcggaagca tataaagctt caaggaaagg atg aaa cac gtg agt   115
                                               Met Lys His Val Ser
                                                 1               5
```

```
ggt cta cgc cta atg gcg atc cac gcc cac cct gac gac gag tca agc   163
Gly Leu Arg Leu Met Ala Ile His Ala His Pro Asp Asp Glu Ser Ser
                 10                  15                  20

aag ggc gca gca acc atg gcg cgc tat gca gct gag ggc aat caa gta   211
Lys Gly Ala Ala Thr Met Ala Arg Tyr Ala Ala Glu Gly Asn Gln Val
             25                  30                  35

atg gtt gtt acc tgc act ggt ggt gag cgt gga gac att ctc aac cct   259
Met Val Val Thr Cys Thr Gly Gly Glu Arg Gly Asp Ile Leu Asn Pro
         40                  45                  50

gct atg gat aag cca gga atc ctg gac aat att ttt gct gtg cgt cag   307
Ala Met Asp Lys Pro Gly Ile Leu Asp Asn Ile Phe Ala Val Arg Gln
     55                  60                  65

gaa gag atg gcg aag gcc atg gaa att ctt ggc act gag cac aga tgg   355
Glu Glu Met Ala Lys Ala Met Glu Ile Leu Gly Thr Glu His Arg Trp
 70                  75                  80                  85

cta ggt tat gag gac tct ggg ctg ccc caa ggt gat cct ttg cct cct   403
Leu Gly Tyr Glu Asp Ser Gly Leu Pro Gln Gly Asp Pro Leu Pro Pro
                 90                  95                 100

ctg cct gag ggc tgt ttt gct tta gaa gac tcg gat aaa gtc acc caa   451
Leu Pro Glu Gly Cys Phe Ala Leu Glu Asp Ser Asp Lys Val Thr Gln
             105                 110                 115

gat tta gtg aag att ctg cgc gag ttc cgc cca cac gtc atc att acc   499
Asp Leu Val Lys Ile Leu Arg Glu Phe Arg Pro His Val Ile Ile Thr
         120                 125                 130

tat gat gag aac ggc ggt tac cca cac ccg gat cac ctc aag gtt cat   547
Tyr Asp Glu Asn Gly Gly Tyr Pro His Pro Asp His Leu Lys Val His
     135                 140                 145

gag gtg tcg atg ctt gca tgg gag aag tcc ggc gat gca gcg tat gca   595
Glu Val Ser Met Leu Ala Trp Glu Lys Ser Gly Asp Ala Ala Tyr Ala
150                 155                 160                 165

cct gag ttg ggc gca ccg tgg gag cca ctg aag ctt tat tac acc cac   643
Pro Glu Leu Gly Ala Pro Trp Glu Pro Leu Lys Leu Tyr Tyr Thr His
                 170                 175                 180

ggc ttt atc cgt cag cgc atg gaa atg ttc cat gat ctg ctc att gaa   691
Gly Phe Ile Arg Gln Arg Met Glu Met Phe His Asp Leu Leu Ile Glu
             185                 190                 195

cag ggc aag ccc agc cca tac acc ccg atg ctt gag cgt tgg aag gca   739
Gln Gly Lys Pro Ser Pro Tyr Thr Pro Met Leu Glu Arg Trp Lys Ala
         200                 205                 210

aat gag gct gat gtg atg gct cga gtt acc act cag gtt cct tgt gag   787
Asn Glu Ala Asp Val Met Ala Arg Val Thr Thr Gln Val Pro Cys Glu
     215                 220                 225

cgc ttc ttt gat cag cgt gat gac gcc ctg cgt gcg cac gca act cag   835
Arg Phe Phe Asp Gln Arg Asp Asp Ala Leu Arg Ala His Ala Thr Gln
230                 235                 240                 245

att gat cct gcg ggt gct ttc ttt gga act ccc gtt gag gtg cag cgt   883
```

```
Ile Asp Pro Ala Gly Ala Phe Phe Gly Thr Pro Val Glu Val Gln Arg
                250                 255                 260

cgc ctg tgg ccg act gaa gag ttc gaa tta gct aaa act cgt gtg aag   931
Arg Leu Trp Pro Thr Glu Glu Phe Glu Leu Ala Lys Thr Arg Val Lys
            265                 270                 275

acg tcg atc cca gaa gat gac ctg ttt gcc gga atc aca ccc gat gca   979
Thr Ser Ile Pro Glu Asp Asp Leu Phe Ala Gly Ile Thr Pro Asp Ala
        280                 285                 290

gaa taatgcagtt agaccacatc ctt                                    1005
Glu
```

<210> 1828
<211> 294
<212> PRT
<213> Corynebacterium glutamicum

<400> 1828

```
Met Lys His Val Ser Gly Leu Arg Leu Met Ala Ile His Ala His Pro
  1               5                  10                  15

Asp Asp Glu Ser Ser Lys Gly Ala Ala Thr Met Ala Arg Tyr Ala Ala
             20                  25                  30

Glu Gly Asn Gln Val Met Val Val Thr Cys Thr Gly Gly Glu Arg Gly
         35                  40                  45

Asp Ile Leu Asn Pro Ala Met Asp Lys Pro Gly Ile Leu Asp Asn Ile
     50                  55                  60

Phe Ala Val Arg Gln Glu Glu Met Ala Lys Ala Met Glu Ile Leu Gly
 65                  70                  75                  80

Thr Glu His Arg Trp Leu Gly Tyr Glu Asp Ser Gly Leu Pro Gln Gly
                 85                  90                  95

Asp Pro Leu Pro Pro Leu Pro Glu Gly Cys Phe Ala Leu Glu Asp Ser
            100                 105                 110

Asp Lys Val Thr Gln Asp Leu Val Lys Ile Leu Arg Glu Phe Arg Pro
        115                 120                 125

His Val Ile Ile Thr Tyr Asp Glu Asn Gly Gly Tyr Pro His Pro Asp
    130                 135                 140

His Leu Lys Val His Glu Val Ser Met Leu Ala Trp Glu Lys Ser Gly
145                 150                 155                 160

Asp Ala Ala Tyr Ala Pro Glu Leu Gly Ala Pro Trp Glu Pro Leu Lys
                165                 170                 175

Leu Tyr Tyr Thr His Gly Phe Ile Arg Gln Arg Met Glu Met Phe His
            180                 185                 190

Asp Leu Leu Ile Glu Gln Gly Lys Pro Ser Pro Tyr Thr Pro Met Leu
        195                 200                 205
```

```
Glu Arg Trp Lys Ala Asn Glu Ala Asp Val Met Ala Arg Val Thr Thr
    210                 215                 220

Gln Val Pro Cys Glu Arg Phe Phe Asp Gln Arg Asp Asp Ala Leu Arg
225                 230                 235                 240

Ala His Ala Thr Gln Ile Asp Pro Ala Gly Ala Phe Phe Gly Thr Pro
                245                 250                 255

Val Glu Val Gln Arg Arg Leu Trp Pro Thr Glu Glu Phe Glu Leu Ala
            260                 265                 270

Lys Thr Arg Val Lys Thr Ser Ile Pro Glu Asp Asp Leu Phe Ala Gly
        275                 280                 285

Ile Thr Pro Asp Ala Glu
    290
```

<210> 1829
<211> 606
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(583)
<223> RXA00587

<400> 1829

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cccttggatg acctcggtta acagtttttc ctgaggtgac taagatgtat aggtgaccaa 60

ctcgattcgg ctttgaagag gatgcagaca gacttccatc atg agt aca aat tcc   115
                                            Met Ser Thr Asn Ser
                                              1               5

aac tct cca tcc aac gca tca ggc gct tcg aac att cca aac acc caa   163
Asn Ser Pro Ser Asn Ala Ser Gly Ala Ser Asn Ile Pro Asn Thr Gln
                  10                  15                  20

cgt ccg gct agc cga tac aat tcg cct cgc ccg gaa gct gct gca ggc   211
Arg Pro Ala Ser Arg Tyr Asn Ser Pro Arg Pro Glu Ala Ala Ala Gly
              25                  30                  35

agg aac atc agc gga aaa atc atc gca gtc att ggc gtg ctg ctg gtg   259
Arg Asn Ile Ser Gly Lys Ile Ile Ala Val Ile Gly Val Leu Leu Val
          40                  45                  50

atc gcc att gtg att gtt ggc gca aac ttc ctc aaa aac cgc gat gca   307
Ile Ala Ile Val Ile Val Gly Ala Asn Phe Leu Lys Asn Arg Asp Ala
      55                  60                  65

caa aca gtg tcc ggc caa atg ggt tca ttt gaa cgc atc gac gac gac   355
Gln Thr Val Ser Gly Gln Met Gly Ser Phe Glu Arg Ile Asp Asp Asp
  70                  75                  80                  85

acc ttc cgc ttt gaa gtt gac gtc acc cgc gat gac cca agc caa gtc   403
Thr Phe Arg Phe Glu Val Asp Val Thr Arg Asp Asp Pro Ser Gln Val
                  90                  95                 100

gcc tac tgc atc gtg acc gca aag gac tac tcg cac gca gaa gtc ggg   451
```

```
Ala Tyr Cys Ile Val Thr Ala Lys Asp Tyr Ser His Ala Glu Val Gly
            105                 110                 115

cgt cga gaa gtg ctt gtg gag ccc agc gac cac tca acg gtg cgt atc   499
Arg Arg Glu Val Leu Val Glu Pro Ser Asp His Ser Thr Val Arg Ile
        120                 125                 130

tcc acg ctg atc ccc acc cgc gaa cca gca gtt tcc ggt ggt gtt tac   547
Ser Thr Leu Ile Pro Thr Arg Glu Pro Ala Val Ser Gly Gly Val Tyr
    135                 140                 145

ggt tgt tca acc gtg atc cca tca cat atg aac ctg taaaactaga        593
Gly Cys Ser Thr Val Ile Pro Ser His Met Asn Leu
150                 155                 160

aaattttgct gtg                                                   606


<210> 1830
<211> 161
<212> PRT
<213> Corynebacterium glutamicum

<400> 1830
Met Ser Thr Asn Ser Asn Ser Pro Ser Asn Ala Ser Gly Ala Ser Asn
  1               5                  10                  15

Ile Pro Asn Thr Gln Arg Pro Ala Ser Arg Tyr Asn Ser Pro Arg Pro
             20                  25                  30

Glu Ala Ala Ala Gly Arg Asn Ile Ser Gly Lys Ile Ile Ala Val Ile
         35                  40                  45

Gly Val Leu Leu Val Ile Ala Ile Val Ile Val Gly Ala Asn Phe Leu
     50                  55                  60

Lys Asn Arg Asp Ala Gln Thr Val Ser Gly Gln Met Gly Ser Phe Glu
 65                  70                  75                  80

Arg Ile Asp Asp Asp Thr Phe Arg Phe Glu Val Asp Val Thr Arg Asp
                 85                  90                  95

Asp Pro Ser Gln Val Ala Tyr Cys Ile Val Thr Ala Lys Asp Tyr Ser
            100                 105                 110

His Ala Glu Val Gly Arg Arg Glu Val Leu Val Glu Pro Ser Asp His
        115                 120                 125

Ser Thr Val Arg Ile Ser Thr Leu Ile Pro Thr Arg Glu Pro Ala Val
    130                 135                 140

Ser Gly Gly Val Tyr Gly Cys Ser Thr Val Ile Pro Ser His Met Asn
145                 150                 155                 160

Leu


<210> 1831
<211> 353
<212> DNA
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<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(330)
<223> RXA00595

<400> 1831

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cgc aat att gca gca tgg atc gca atc gcc gcc atc atc atc gcc agc   48
Arg Asn Ile Ala Ala Trp Ile Ala Ile Ala Ala Ile Ile Ile Ala Ser
  1               5                  10                  15

ctg ggc gca ctg ctc tcg atg atc cgc gtg tgg cgt gaa gtc ttc tgg   96
Leu Gly Ala Leu Leu Ser Met Ile Arg Val Trp Arg Glu Val Phe Trp
             20                  25                  30

ggt ggc gca atg cac cag cgc ggc gtc tcg ccg cag ctg cgc atc agc   144
Gly Gly Ala Met His Gln Arg Gly Val Ser Pro Gln Leu Arg Ile Ser
         35                  40                  45

cca gca aaa atc gcc cca gcg ctc agc ctg atc att tta tcg gta ggc   192
Pro Ala Lys Ile Ala Pro Ala Leu Ser Leu Ile Ile Leu Ser Val Gly
     50                  55                  60

atg ttc atc ttc gcg ggc ccg ctt atc gac gcg acc ctc acc gcc acc   240
Met Phe Ile Phe Ala Gly Pro Leu Ile Asp Ala Thr Leu Thr Ala Thr
 65                  70                  75                  80

gac ggc ctc ttg aac acc gat gca tac caa cag gct gtg ctc ggt gaa   288
Asp Gly Leu Leu Asn Thr Asp Ala Tyr Gln Gln Ala Val Leu Gly Glu
                 85                  90                  95

aat gcc atc gga gtg cca agc cct agc tac cag gga gga aac           330
Asn Ala Ile Gly Val Pro Ser Pro Ser Tyr Gln Gly Gly Asn
            100                 105                 110

taatgcttaa cgccctgaaa ttc                                        353
```

<210> 1832
<211> 110
<212> PRT
<213> Corynebacterium glutamicum

<400> 1832

```
Arg Asn Ile Ala Ala Trp Ile Ala Ile Ala Ala Ile Ile Ile Ala Ser
  1               5                  10                  15

Leu Gly Ala Leu Leu Ser Met Ile Arg Val Trp Arg Glu Val Phe Trp
             20                  25                  30

Gly Gly Ala Met His Gln Arg Gly Val Ser Pro Gln Leu Arg Ile Ser
         35                  40                  45

Pro Ala Lys Ile Ala Pro Ala Leu Ser Leu Ile Ile Leu Ser Val Gly
     50                  55                  60

Met Phe Ile Phe Ala Gly Pro Leu Ile Asp Ala Thr Leu Thr Ala Thr
 65                  70                  75                  80

Asp Gly Leu Leu Asn Thr Asp Ala Tyr Gln Gln Ala Val Leu Gly Glu
```

```
                85                  90                  95

Asn Ala Ile Gly Val Pro Ser Pro Ser Tyr Gln Gly Gly Asn
            100                 105                 110


<210> 1833
<211> 393
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(370)
<223> RXA00597

<400> 1833
caaggagatc cgccccagcg atgctgagtg gccaagtcgc gagatcgctg acaccgccca 60

aaacaccgtc agccaagaca agagggagtt ttaaaacaac atg act gct ttt gga   115
                                            Met Thr Ala Phe Gly
                                              1               5

att gtc acc aca gtt ggc atc tgc atg ttt gcg ttc tcc ctc tta tct   163
Ile Val Thr Thr Val Gly Ile Cys Met Phe Ala Phe Ser Leu Leu Ser
                  10                  15                  20

gcc ctg gtc ctt att ctg cgc acc aaa gat ttc ctc acc cgc gtg gtg   211
Ala Leu Val Leu Ile Leu Arg Thr Lys Asp Phe Leu Thr Arg Val Val
              25                  30                  35

ctt tcc gac atg gtt ttc tac tct atg atc gcg atc tac ctc atc tgg   259
Leu Ser Asp Met Val Phe Tyr Ser Met Ile Ala Ile Tyr Leu Ile Trp
          40                  45                  50

gtg ctc aac aac cca acc tca atc gcc ttt gag att gct ctt ctc gca   307
Val Leu Asn Asn Pro Thr Ser Ile Ala Phe Glu Ile Ala Leu Leu Ala
      55                  60                  65

gca gtc ctc ggc ggc gta ctt cca acc ctg tcc atg gct cgc atc att   355
Ala Val Leu Gly Gly Val Leu Pro Thr Leu Ser Met Ala Arg Ile Ile
  70                  75                  80                  85

tcg aag gga cgc agg taaatgacca ttccagagat cat                    393
Ser Lys Gly Arg Arg
                  90


<210> 1834
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

<400> 1834
Met Thr Ala Phe Gly Ile Val Thr Thr Val Gly Ile Cys Met Phe Ala
  1               5                  10                  15

Phe Ser Leu Leu Ser Ala Leu Val Leu Ile Leu Arg Thr Lys Asp Phe
            20                  25                  30

Leu Thr Arg Val Val Leu Ser Asp Met Val Phe Tyr Ser Met Ile Ala
```

```
         35                  40                  45

Ile Tyr Leu Ile Trp Val Leu Asn Asn Pro Thr Ser Ile Ala Phe Glu
     50                  55                  60

Ile Ala Leu Leu Ala Ala Val Leu Gly Gly Val Leu Pro Thr Leu Ser
 65                  70                  75                  80

Met Ala Arg Ile Ile Ser Lys Gly Arg Arg
                 85                  90


<210> 1835
<211> 441
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(418)
<223> RXA00598

<400> 1835
aacctcaatc gcctttgaga ttgctcttct cgcagcagtc ctcggcggcg tacttccaac 60

cctgtccatg gctcgcatca tttcgaaggg acgcaggtaa atg acc att cca gag   115
                                          Met Thr Ile Pro Glu
                                            1               5

atc atc gtc tcc atc ctc gtg atc ctc gca ggc ctg ttt tct cta ggt   163
Ile Ile Val Ser Ile Leu Val Ile Leu Ala Gly Leu Phe Ser Leu Gly
                 10                  15                  20

act gca atc gct ttg tgg cgc gca ccg gat ccg ctc acc cga gcc aac   211
Thr Ala Ile Ala Leu Trp Arg Ala Pro Asp Pro Leu Thr Arg Ala Asn
             25                  30                  35

ctg ctt ggc acc acc gtg ggt gtc tcc ata ccg ctg ctc atc att gcg   259
Leu Leu Gly Thr Thr Val Gly Val Ser Ile Pro Leu Leu Ile Ile Ala
         40                  45                  50

ctg ctg att cac acc tgg tcc gtc gac gga ttt aac ccc aac aat ttc   307
Leu Leu Ile His Thr Trp Ser Val Asp Gly Phe Asn Pro Asn Asn Phe
     55                  60                  65

atc cga gcg atc atc gcc atc atc ggc gtc tgg gtc atc ggt tcc gtt   355
Ile Arg Ala Ile Ile Ala Ile Ile Gly Val Trp Val Ile Gly Ser Val
 70                  75                  80                  85

ggt tcc tac tac atg gga cgc gcc atc tat ggt gtg acc gta gtg gat   403
Gly Ser Tyr Tyr Met Gly Arg Ala Ile Tyr Gly Val Thr Val Val Asp
                 90                  95                 100

aac aga cga tcc aaa taaactgctt ttagaaaaaa agg                    441
Asn Arg Arg Ser Lys
            105


<210> 1836
<211> 106
<212> PRT
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<213> Corynebacterium glutamicum

<400> 1836

```
Met Thr Ile Pro Glu Ile Ile Val Ser Ile Leu Val Ile Leu Ala Gly
  1               5                  10                  15

Leu Phe Ser Leu Gly Thr Ala Ile Ala Leu Trp Arg Ala Pro Asp Pro
             20                  25                  30

Leu Thr Arg Ala Asn Leu Leu Gly Thr Thr Val Gly Val Ser Ile Pro
         35                  40                  45

Leu Leu Ile Ile Ala Leu Leu Ile His Thr Trp Ser Val Asp Gly Phe
     50                  55                  60

Asn Pro Asn Asn Phe Ile Arg Ala Ile Ile Ala Ile Ile Gly Val Trp
 65                  70                  75                  80

Val Ile Gly Ser Val Gly Ser Tyr Tyr Met Gly Arg Ala Ile Tyr Gly
                 85                  90                  95

Val Thr Val Val Asp Asn Arg Arg Ser Lys
            100                 105
```

<210> 1837
<211> 414
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(391)
<223> RXA00601

<400> 1837

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tagatataga acacattcta ttgcagggaa ttatcaagtt tcatacattg tcctcgtagg 60

ggcaagtata tttcccatgc aatatttttt aggagtccca atg cgt ttc aag tca   115
                                            Met Arg Phe Lys Ser
                                              1               5

gtt gca gct atc gca ctt tcc acc gca atg atc agg ggt gga acc gca   163
Val Ala Ala Ile Ala Leu Ser Thr Ala Met Ile Arg Gly Gly Thr Ala
                 10                  15                  20

agc gtt gct aat gct cag cag gtt agc cct agt tcc acg att gag atc   211
Ser Val Ala Asn Ala Gln Gln Val Ser Pro Ser Ser Thr Ile Glu Ile
             25                  30                  35

cct caa gaa ttc gtc cac acc gtg cag aac ttc gtg cca ggt atg act   259
Pro Gln Glu Phe Val His Thr Val Gln Asn Phe Val Pro Gly Met Thr
         40                  45                  50

tac ggc gat gca ggg tcc gct atc cag agc acc gct ggt tct gtg gca   307
Tyr Gly Asp Ala Gly Ser Ala Ile Gln Ser Thr Ala Gly Ser Val Ala
     55                  60                  65

ctg aac agt acc gct gga atc atc ctt cca atc gtt ctt cca ttc ctt   355
Leu Asn Ser Thr Ala Gly Ile Ile Leu Pro Ile Val Leu Pro Phe Leu
 70                  75                  80                  85
```

```
ggt ctg gga gct gtt ggt tct gca gcg ctg tct gct taagcctttt        401
Gly Leu Gly Ala Val Gly Ser Ala Ala Leu Ser Ala
                 90                  95

ctaggttcct taa                                                   414


<210> 1838
<211> 97
<212> PRT
<213> Corynebacterium glutamicum

<400> 1838
Met Arg Phe Lys Ser Val Ala Ala Ile Ala Leu Ser Thr Ala Met Ile
  1               5                  10                  15

Arg Gly Gly Thr Ala Ser Val Ala Asn Ala Gln Gln Val Ser Pro Ser
             20                  25                  30

Ser Thr Ile Glu Ile Pro Gln Glu Phe Val His Thr Val Gln Asn Phe
         35                  40                  45

Val Pro Gly Met Thr Tyr Gly Asp Ala Gly Ser Ala Ile Gln Ser Thr
     50                  55                  60

Ala Gly Ser Val Ala Leu Asn Ser Thr Ala Gly Ile Ile Leu Pro Ile
 65                  70                  75                  80

Val Leu Pro Phe Leu Gly Leu Gly Ala Val Gly Ser Ala Ala Leu Ser
                 85                  90                  95

Ala



<210> 1839
<211> 876
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(853)
<223> RXA00602

<400> 1839
gcgcgatcaa tggaatctag cttcatatat tgcacaatag cctagttgag gtgcgcaaac 60

tggcaacaaa actacccggc aattgtgtga tgattgtagt gtg caa aaa acg caa   115
                                            Val Gln Lys Thr Gln
                                              1               5

gag att cat tca agc ctg gag gtg tcg cca tcc aag gca gcc ctg gaa   163
Glu Ile His Ser Ser Leu Glu Val Ser Pro Ser Lys Ala Ala Leu Glu
                 10                  15                  20

cca gat gat aaa ggt tat cgg cgc tac gaa atc gcg caa ggt cta aaa   211
Pro Asp Asp Lys Gly Tyr Arg Arg Tyr Glu Ile Ala Gln Gly Leu Lys
             25                  30                  35
```

```
acc tcc ctt gct gca ggt ttg ggc atg tac ccg att ggt att gcg ttt   259
Thr Ser Leu Ala Ala Gly Leu Gly Met Tyr Pro Ile Gly Ile Ala Phe
         40                  45                  50

ggt ctc ttg gtt att caa tac ggc tac gaa tgg tgg gca gcc cca ctg   307
Gly Leu Leu Val Ile Gln Tyr Gly Tyr Glu Trp Trp Ala Ala Pro Leu
     55                  60                  65

ttt tcc ggc ctg att ttc gcg ggc tcc acc gaa atg ctg gtc atc gcc   355
Phe Ser Gly Leu Ile Phe Ala Gly Ser Thr Glu Met Leu Val Ile Ala
 70                  75                  80                  85

ctc gtt gtg ggc gca gcg ccc ctg ggc gcc atc gcg ctc acc aca ttg   403
Leu Val Val Gly Ala Ala Pro Leu Gly Ala Ile Ala Leu Thr Thr Leu
                 90                  95                 100

ctg gtg aac ttc cgc cac gta ttc tat gcg ttt tca ttc ccg ctg cat   451
Leu Val Asn Phe Arg His Val Phe Tyr Ala Phe Ser Phe Pro Leu His
            105                 110                 115

gtg gtc aaa aac ccc att gcc cgt ttc tat tcg gtt ttc gcg ctt atc   499
Val Val Lys Asn Pro Ile Ala Arg Phe Tyr Ser Val Phe Ala Leu Ile
        120                 125                 130

gac gaa gcc tac gca gtc act gcg gcc agg ccc gca ggc tgg tcg gcg   547
Asp Glu Ala Tyr Ala Val Thr Ala Ala Arg Pro Ala Gly Trp Ser Ala
    135                 140                 145

tgg cga ctt atc tca atg caa ata gcg ttt cac tcc tac tgg gta ttc   595
Trp Arg Leu Ile Ser Met Gln Ile Ala Phe His Ser Tyr Trp Val Phe
150                 155                 160                 165

ggc ggt ctc acc gga gtg gcg atc gca gag ttg att cct ttt gaa att   643
Gly Gly Leu Thr Gly Val Ala Ile Ala Glu Leu Ile Pro Phe Glu Ile
                170                 175                 180

aag ggc ctc gag ttc gcc ctt tgc tct ctc ttt gtc acg ctg act ttg   691
Lys Gly Leu Glu Phe Ala Leu Cys Ser Leu Phe Val Thr Leu Thr Leu
            185                 190                 195

gat tcc tgc cga acg aaa aag cag atc cct tct ctg ctg ctc gca ggt   739
Asp Ser Cys Arg Thr Lys Lys Gln Ile Pro Ser Leu Leu Leu Ala Gly
        200                 205                 210

ttg agc ttc acc att gct ctt gtg gta att cca ggt cag gcc cta ttt   787
Leu Ser Phe Thr Ile Ala Leu Val Val Ile Pro Gly Gln Ala Leu Phe
    215                 220                 225

gcg gcg ctg ctg atc ttc ttg ggt ctg ttg acc atc cgg tac ttc ttc   835
Ala Ala Leu Leu Ile Phe Leu Gly Leu Leu Thr Ile Arg Tyr Phe Phe
230                 235                 240                 245

ttg gga aag gct gct aaa tgacaactga tttctcctgt att                 876
Leu Gly Lys Ala Ala Lys
                250
```

<210> 1840
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

<400> 1840

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Val Gln Lys Thr Gln Glu Ile His Ser Ser Leu Glu Val Ser Pro Ser
  1               5                  10                  15

Lys Ala Ala Leu Glu Pro Asp Asp Lys Gly Tyr Arg Arg Tyr Glu Ile
             20                  25                  30

Ala Gln Gly Leu Lys Thr Ser Leu Ala Ala Gly Leu Gly Met Tyr Pro
         35                  40                  45

Ile Gly Ile Ala Phe Gly Leu Leu Val Ile Gln Tyr Gly Tyr Glu Trp
     50                  55                  60

Trp Ala Ala Pro Leu Phe Ser Gly Leu Ile Phe Ala Gly Ser Thr Glu
 65                  70                  75                  80

Met Leu Val Ile Ala Leu Val Val Gly Ala Ala Pro Leu Gly Ala Ile
                 85                  90                  95

Ala Leu Thr Thr Leu Leu Val Asn Phe Arg His Val Phe Tyr Ala Phe
            100                 105                 110

Ser Phe Pro Leu His Val Val Lys Asn Pro Ile Ala Arg Phe Tyr Ser
        115                 120                 125

Val Phe Ala Leu Ile Asp Glu Ala Tyr Ala Val Thr Ala Ala Arg Pro
    130                 135                 140

Ala Gly Trp Ser Ala Trp Arg Leu Ile Ser Met Gln Ile Ala Phe His
145                 150                 155                 160

Ser Tyr Trp Val Phe Gly Gly Leu Thr Gly Val Ala Ile Ala Glu Leu
                165                 170                 175

Ile Pro Phe Glu Ile Lys Gly Leu Glu Phe Ala Leu Cys Ser Leu Phe
            180                 185                 190

Val Thr Leu Thr Leu Asp Ser Cys Arg Thr Lys Lys Gln Ile Pro Ser
        195                 200                 205

Leu Leu Leu Ala Gly Leu Ser Phe Thr Ile Ala Leu Val Val Ile Pro
    210                 215                 220

Gly Gln Ala Leu Phe Ala Ala Leu Leu Ile Phe Leu Gly Leu Leu Thr
225                 230                 235                 240

Ile Arg Tyr Phe Phe Leu Gly Lys Ala Ala Lys
                245                 250
```

<210> 1841
<211> 414
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(391)
<223> RXA00604

<400> 1841
atcacgtttt gctatgaaag tggtgaaacc agctcgcccc caggtgtgaa gcatgcattt 60

tgaagcatga atctttttca tctagtgaag gactgatccc atg cgt atg aaa tca 115
Met Arg Met Lys Ser
1 5

atc gca gca att gca atc gct acc gcc gcc ctg gct ggt ggc act gga 163
Ile Ala Ala Ile Ala Ile Ala Thr Ala Ala Leu Ala Gly Gly Thr Gly
10 15 20

gtc gct agc gca cag gaa gct ggc tcg act gct ggt tcc tcc aac ctc 211
Val Ala Ser Ala Gln Glu Ala Gly Ser Thr Ala Gly Ser Ser Asn Leu
25 30 35

agc tct ggg atc cag ctt cca caa gaa gcc acc gat ctg ttg agc ttc 259
Ser Ser Gly Ile Gln Leu Pro Gln Glu Ala Thr Asp Leu Leu Ser Phe
40 45 50

ctg cct gct gct cag gct gcg cag gtt gaa gga gca att cag agc acc 307
Leu Pro Ala Ala Gln Ala Ala Gln Val Glu Gly Ala Ile Gln Ser Thr
55 60 65

gct ggt ttc ttt gcc gtt gga ctc ggc tcg acc gcc att ggt tcc act 355
Ala Gly Phe Phe Ala Val Gly Leu Gly Ser Thr Ala Ile Gly Ser Thr
70 75 80 85

gca gtg acc ttg gga att gcg gat ctg ctg tct agc taatttcctc 401
Ala Val Thr Leu Gly Ile Ala Asp Leu Leu Ser Ser
90 95

tcaatagctt caa 414

<210> 1842
<211> 97
<212> PRT
<213> Corynebacterium glutamicum

<400> 1842
Met Arg Met Lys Ser Ile Ala Ala Ile Ala Ile Ala Thr Ala Ala Leu
1 5 10 15

Ala Gly Gly Thr Gly Val Ala Ser Ala Gln Glu Ala Gly Ser Thr Ala
20 25 30

Gly Ser Ser Asn Leu Ser Ser Gly Ile Gln Leu Pro Gln Glu Ala Thr
35 40 45

Asp Leu Leu Ser Phe Leu Pro Ala Ala Gln Ala Ala Gln Val Glu Gly
50 55 60

Ala Ile Gln Ser Thr Ala Gly Phe Phe Ala Val Gly Leu Gly Ser Thr
65 70 75 80

Ala Ile Gly Ser Thr Ala Val Thr Leu Gly Ile Ala Asp Leu Leu Ser
85 90 95

Ser

<210> 1843
<211> 987
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(964)
<223> RXA00610

<400> 1843
caagcactcc caggggaacg ttcattcgaa aaactcgacg ccttatacga gcttctagag 60

cctcggaacc aattgctcga gatcgcagtc taactagagt atg gaa ccg aaa aaa 115
Met Glu Pro Lys Lys
1 5

cct gtc aca tat aaa gaa ctt gcc cac gaa tat tca aga aga acg ttt 163
Pro Val Thr Tyr Lys Glu Leu Ala His Glu Tyr Ser Arg Arg Thr Phe
10 15 20

aac aaa ctc ttc acc aaa att act ggc ttc gtc tat cta aaa aac gat 211
Asn Lys Leu Phe Thr Lys Ile Thr Gly Phe Val Tyr Leu Lys Asn Asp
25 30 35

cta atc aac gat ccc aac tta gtg acc caa gca ctg ctc aaa aga tgc 259
Leu Ile Asn Asp Pro Asn Leu Val Thr Gln Ala Leu Leu Lys Arg Cys
40 45 50

cca gaa gga gta ctt cgc gga tat gca gca tta aag caa cgt ggc tat 307
Pro Glu Gly Val Leu Arg Gly Tyr Ala Ala Leu Lys Gln Arg Gly Tyr
55 60 65

cag ctt tta gac gat cag tgg atg cca atc atc agt gtt tcc gga gat 355
Gln Leu Leu Asp Asp Gln Trp Met Pro Ile Ile Ser Val Ser Gly Asp
70 75 80 85

cta aac agg agg gac tgc tca cga ggt gaa att ctc agg cgg att gaa 403
Leu Asn Arg Arg Asp Cys Ser Arg Gly Glu Ile Leu Arg Arg Ile Glu
90 95 100

cca gaa aac acc ctg ctc agt ggc aac att agg ttc gtt aat gat gtt 451
Pro Glu Asn Thr Leu Leu Ser Gly Asn Ile Arg Phe Val Asn Asp Val
105 110 115

caa gcg atc caa gac gtc ttc gac ctg cat tct ctc aac gac ttt gaa 499
Gln Ala Ile Gln Asp Val Phe Asp Leu His Ser Leu Asn Asp Phe Glu
120 125 130

gac caa gta gct ctc atc gat cat ctc atc agg cag cgc ccc gaa tta 547
Asp Gln Val Ala Leu Ile Asp His Leu Ile Arg Gln Arg Pro Glu Leu
135 140 145

ttc caa gaa ctc ata caa gag cca aaa ctt aag aaa cac act caa tac 595
Phe Gln Glu Leu Ile Gln Glu Pro Lys Leu Lys Lys His Thr Gln Tyr
150 155 160 165

gcc aat cct ttt gct gaa tct ccg caa gaa tca cga ctt cgg gtc aga 643
Ala Asn Pro Phe Ala Glu Ser Pro Gln Glu Ser Arg Leu Arg Val Arg
170 175 180

```
ctt cat tca ctg ggt tac cac ggc ttc atc cca cag att cat gtt gaa   691
Leu His Ser Leu Gly Tyr His Gly Phe Ile Pro Gln Ile His Val Glu
            185                 190                 195

tac gac ggt caa tcc tat ttt cta gat ctc gca gat ccg ctg tgg cag   739
Tyr Asp Gly Gln Ser Tyr Phe Leu Asp Leu Ala Asp Pro Leu Trp Gln
        200                 205                 210

gtt gcc ctc gaa tac aac ggc gga tgg cac tac acc tct gag cag cga   787
Val Ala Leu Glu Tyr Asn Gly Gly Trp His Tyr Thr Ser Glu Gln Arg
    215                 220                 225

gag aaa gat tct cat cgg aag aat gct ctg aaa agt gcg gga tgg gat   835
Glu Lys Asp Ser His Arg Lys Asn Ala Leu Lys Ser Ala Gly Trp Asp
230                 235                 240                 245

gtc cta gaa gtg aca tca aaa act ctg cag aat ccg aat tcc tgg aac   883
Val Leu Glu Val Thr Ser Lys Thr Leu Gln Asn Pro Asn Ser Trp Asn
                250                 255                 260

aac ctg ata caa cag atc aat agc tct ctc cgc cga aag cag gct cag   931
Asn Leu Ile Gln Gln Ile Asn Ser Ser Leu Arg Arg Lys Gln Ala Gln
            265                 270                 275

cga cgc cga agg tta ccc atg caa acg gtg ggc taacggcatc actgaaaaag 984
Arg Arg Arg Arg Leu Pro Met Gln Thr Val Gly
        280                 285

acc                                                               987


<210> 1844
<211> 288
<212> PRT
<213> Corynebacterium glutamicum

<400> 1844
Met Glu Pro Lys Lys Pro Val Thr Tyr Lys Glu Leu Ala His Glu Tyr
  1               5                  10                  15

Ser Arg Arg Thr Phe Asn Lys Leu Phe Thr Lys Ile Thr Gly Phe Val
             20                  25                  30

Tyr Leu Lys Asn Asp Leu Ile Asn Asp Pro Asn Leu Val Thr Gln Ala
         35                  40                  45

Leu Leu Lys Arg Cys Pro Glu Gly Val Leu Arg Gly Tyr Ala Ala Leu
     50                  55                  60

Lys Gln Arg Gly Tyr Gln Leu Leu Asp Asp Gln Trp Met Pro Ile Ile
 65                  70                  75                  80

Ser Val Ser Gly Asp Leu Asn Arg Arg Asp Cys Ser Arg Gly Glu Ile
                 85                  90                  95

Leu Arg Arg Ile Glu Pro Glu Asn Thr Leu Leu Ser Gly Asn Ile Arg
            100                 105                 110

Phe Val Asn Asp Val Gln Ala Ile Gln Asp Val Phe Asp Leu His Ser
        115                 120                 125
```

```
Leu Asn Asp Phe Glu Asp Gln Val Ala Leu Ile Asp His Leu Ile Arg
    130                 135                 140

Gln Arg Pro Glu Leu Phe Gln Glu Leu Ile Gln Glu Pro Lys Leu Lys
145                 150                 155                 160

Lys His Thr Gln Tyr Ala Asn Pro Phe Ala Glu Ser Pro Gln Glu Ser
                165                 170                 175

Arg Leu Arg Val Arg Leu His Ser Leu Gly Tyr His Gly Phe Ile Pro
            180                 185                 190

Gln Ile His Val Glu Tyr Asp Gly Gln Ser Tyr Phe Leu Asp Leu Ala
        195                 200                 205

Asp Pro Leu Trp Gln Val Ala Leu Glu Tyr Asn Gly Gly Trp His Tyr
    210                 215                 220

Thr Ser Glu Gln Arg Glu Lys Asp Ser His Arg Lys Asn Ala Leu Lys
225                 230                 235                 240

Ser Ala Gly Trp Asp Val Leu Glu Val Thr Ser Lys Thr Leu Gln Asn
                245                 250                 255

Pro Asn Ser Trp Asn Asn Leu Ile Gln Gln Ile Asn Ser Ser Leu Arg
            260                 265                 270

Arg Lys Gln Ala Gln Arg Arg Arg Arg Leu Pro Met Gln Thr Val Gly
        275                 280                 285
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<210> 1845
<211> 1599
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1576)
<223> RXA00611

<400> 1845

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ctttaaattg actatttaca aaactacttg atgagttagc aagagcacat ttcggtgcgc 60

ctccctgcta aacctcgaaa caataactag attgcacact atg tct gcc gct gct   115
                                               Met Ser Ala Ala Ala
                                                 1               5

tct cga tca aga aac atc ttg act gcc ctc ctg cta ttg gtc ccg ctc   163
Ser Arg Ser Arg Asn Ile Leu Thr Ala Leu Leu Leu Leu Val Pro Leu
                 10                  15                  20

atc gca ggt acc atc tac gcc tcc gcc atg ggc ttg gac gtc tcc cgc   211
Ile Ala Gly Thr Ile Tyr Ala Ser Ala Met Gly Leu Asp Val Ser Arg
             25                  30                  35

gca tgg tcc tca gca gat gaa gta acg ggg gca cct gca gcc tcc gta   259
```

```
Ala Trp Ser Ser Ala Asp Glu Val Thr Gly Ala Pro Ala Ala Ser Val
          40                  45                  50

gcc acc aac aac cag gag ctt atc gaa gcc cgt cgc gcc gcc gga gaa   307
Ala Thr Asn Asn Gln Glu Leu Ile Glu Ala Arg Arg Ala Ala Gly Glu
     55                  60                  65

gcc ggc gcc caa gcg ggg ttc ctc acc tca gga act gaa gag cta acc   355
Ala Gly Ala Gln Ala Gly Phe Leu Thr Ser Gly Thr Glu Glu Leu Thr
 70                  75                  80                  85

agc gga aca caa gag ctt atc gac ggc gca gcc cca ctc gaa gaa ggc   403
Ser Gly Thr Gln Glu Leu Ile Asp Gly Ala Ala Pro Leu Glu Glu Gly
                 90                  95                 100

gtc tca gcc gcg gct gac ggt gca gcg caa ctc cac gat ggc ctc atc   451
Val Ser Ala Ala Ala Asp Gly Ala Ala Gln Leu His Asp Gly Leu Ile
            105                 110                 115

caa ctc cag gcc ggc act gga caa atg gga acc ggc gcc acc gaa att   499
Gln Leu Gln Ala Gly Thr Gly Gln Met Gly Thr Gly Ala Thr Glu Ile
        120                 125                 130

gcc gac ggc gtc caa aac gca gtc gaa caa ctt ggc ggt ctt gtc gtt   547
Ala Asp Gly Val Gln Asn Ala Val Glu Gln Leu Gly Gly Leu Val Val
    135                 140                 145

gta cag cag caa ctc tta ggc gcc ctc aac gaa gca gac aaa caa ctc   595
Val Gln Gln Gln Leu Leu Gly Ala Leu Asn Glu Ala Asp Lys Gln Leu
150                 155                 160                 165

gcc tcg agc aaa atc ccc gaa gcc gaa gac ctg cgc aaa caa atc acc   643
Ala Ser Ser Lys Ile Pro Glu Ala Glu Asp Leu Arg Lys Gln Ile Thr
                170                 175                 180

gaa gtc cga gga cac ctc gaa aac ttc ggc atc tcc gta gaa atg acc   691
Glu Val Arg Gly His Leu Glu Asn Phe Gly Ile Ser Val Glu Met Thr
            185                 190                 195

gac caa ctc gat caa cta cgt tcc ggc acc cgc gac ctg gct aac caa   739
Asp Gln Leu Asp Gln Leu Arg Ser Gly Thr Arg Asp Leu Ala Asn Gln
        200                 205                 210

ctc gca gtc ccc ggc tac gga ttc cac gat ggt att tac agc gcc acc   787
Leu Ala Val Pro Gly Tyr Gly Phe His Asp Gly Ile Tyr Ser Ala Thr
    215                 220                 225

aat gga gca gcc gaa tta tct gca ggt ttg caa gag cta gaa gca ggc   835
Asn Gly Ala Ala Glu Leu Ser Ala Gly Leu Gln Glu Leu Glu Ala Gly
230                 235                 240                 245

gtt ggg act gcc gtc gaa ggc ttc acc gca ctc gat gaa ggt gca aac   883
Val Gly Thr Ala Val Glu Gly Phe Thr Ala Leu Asp Glu Gly Ala Asn
                250                 255                 260

cga tta gac tcc atg gcc acc ctc aac gaa gaa aaa acc tcc gca gtc   931
Arg Leu Asp Ser Met Ala Thr Leu Asn Glu Glu Lys Thr Ser Ala Val
            265                 270                 275

caa cga gcc ctc ccg gta ccc caa gta ccc gcc ggc aca atc gaa ggc   979
Gln Arg Ala Leu Pro Val Pro Gln Val Pro Ala Gly Thr Ile Glu Gly
```

```
        280                 285                 290

acc gca gac gaa gaa cgc acc agc gca cta gcg ccc atg tac gcc ttc   1027
Thr Ala Asp Glu Glu Arg Thr Ser Ala Leu Ala Pro Met Tyr Ala Phe
    295                 300                 305

tta att tca gca ttg gtc atg ctg gcc ggt gca gca ctt gga tgg gca   1075
Leu Ile Ser Ala Leu Val Met Leu Ala Gly Ala Ala Leu Gly Trp Ala
310                 315                 320                 325

aca cta aaa aac aag tgg ctg atg gcc ttt gct gtc att ggt gtc act   1123
Thr Leu Lys Asn Lys Trp Leu Met Ala Phe Ala Val Ile Gly Val Thr
                330                 335                 340

gca atc ggt ggc att atc ttg ttc acc gta gct ttg ggc ata tcc att   1171
Ala Ile Gly Gly Ile Ile Leu Phe Thr Val Ala Leu Gly Ile Ser Ile
            345                 350                 355

gga gct ttg ttt gga gcc tta gga att ttg ctt ctt gcc act gtt gtt   1219
Gly Ala Leu Phe Gly Ala Leu Gly Ile Leu Leu Leu Ala Thr Val Val
        360                 365                 370

gcc ggt att ctc tcc cgg att ttg ctt gac gtg ttg gga act acc ggg   1267
Ala Gly Ile Leu Ser Arg Ile Leu Leu Asp Val Leu Gly Thr Thr Gly
    375                 380                 385

gct att gtg gtt tct gtt ctg gga tgg gta gcc caa gct gca gta att   1315
Ala Ile Val Val Ser Val Leu Gly Trp Val Ala Gln Ala Ala Val Ile
390                 395                 400                 405

ggc cat gta tgg agt gtt acc gct gta tcc gat atc gca ctt gtt tgg   1363
Gly His Val Trp Ser Val Thr Ala Val Ser Asp Ile Ala Leu Val Trp
                410                 415                 420

cga gtc gtc gca ggc atg atg cca ctg cat tat cca acc ttt gca gtg   1411
Arg Val Val Ala Gly Met Met Pro Leu His Tyr Pro Thr Phe Ala Val
            425                 430                 435

acc tcc att ggt aat ggc gga tca gct gca gct atc tgg atg tct gtt   1459
Thr Ser Ile Gly Asn Gly Gly Ser Ala Ala Ala Ile Trp Met Ser Val
        440                 445                 450

gct gtc ttg ttg gca atg gga gcg atc gga gct gtt gcg ctt cgg aag   1507
Ala Val Leu Leu Ala Met Gly Ala Ile Gly Ala Val Ala Leu Arg Lys
    455                 460                 465

cca aag gcg gtt gcg gtt gag gtt gaa gaa gct gtt gat gct gat gca   1555
Pro Lys Ala Val Ala Val Glu Val Glu Glu Ala Val Asp Ala Asp Ala
470                 475                 480                 485

gac caa gca gcc tcg gaa tcc tgatggtttt ggtctgattc gac            1599
Asp Gln Ala Ala Ser Glu Ser
                490
```

<210> 1846
<211> 492
<212> PRT
<213> Corynebacterium glutamicum

<400> 1846

```
Met Ser Ala Ala Ala Ser Arg Ser Arg Asn Ile Leu Thr Ala Leu Leu
  1               5                  10                  15

Leu Leu Val Pro Leu Ile Ala Gly Thr Ile Tyr Ala Ser Ala Met Gly
            20                  25                  30

Leu Asp Val Ser Arg Ala Trp Ser Ser Ala Asp Glu Val Thr Gly Ala
        35                  40                  45

Pro Ala Ala Ser Val Ala Thr Asn Asn Gln Glu Leu Ile Glu Ala Arg
    50                  55                  60

Arg Ala Ala Gly Glu Ala Gly Ala Gln Ala Gly Phe Leu Thr Ser Gly
65                  70                  75                  80

Thr Glu Glu Leu Thr Ser Gly Thr Gln Glu Leu Ile Asp Gly Ala Ala
                85                  90                  95

Pro Leu Glu Glu Gly Val Ser Ala Ala Ala Asp Gly Ala Ala Gln Leu
            100                 105                 110

His Asp Gly Leu Ile Gln Leu Gln Ala Gly Thr Gly Gln Met Gly Thr
        115                 120                 125

Gly Ala Thr Glu Ile Ala Asp Gly Val Gln Asn Ala Val Glu Gln Leu
    130                 135                 140

Gly Gly Leu Val Val Val Gln Gln Gln Leu Leu Gly Ala Leu Asn Glu
145                 150                 155                 160

Ala Asp Lys Gln Leu Ala Ser Ser Lys Ile Pro Glu Ala Glu Asp Leu
                165                 170                 175

Arg Lys Gln Ile Thr Glu Val Arg Gly His Leu Glu Asn Phe Gly Ile
            180                 185                 190

Ser Val Glu Met Thr Asp Gln Leu Asp Gln Leu Arg Ser Gly Thr Arg
        195                 200                 205

Asp Leu Ala Asn Gln Leu Ala Val Pro Gly Tyr Gly Phe His Asp Gly
    210                 215                 220

Ile Tyr Ser Ala Thr Asn Gly Ala Ala Glu Leu Ser Ala Gly Leu Gln
225                 230                 235                 240

Glu Leu Glu Ala Gly Val Gly Thr Ala Val Glu Gly Phe Thr Ala Leu
                245                 250                 255

Asp Glu Gly Ala Asn Arg Leu Asp Ser Met Ala Thr Leu Asn Glu Glu
            260                 265                 270

Lys Thr Ser Ala Val Gln Arg Ala Leu Pro Val Pro Gln Val Pro Ala
        275                 280                 285

Gly Thr Ile Glu Gly Thr Ala Asp Glu Glu Arg Thr Ser Ala Leu Ala
    290                 295                 300

Pro Met Tyr Ala Phe Leu Ile Ser Ala Leu Val Met Leu Ala Gly Ala
305                 310                 315                 320

Ala Leu Gly Trp Ala Thr Leu Lys Asn Lys Trp Leu Met Ala Phe Ala
```

```
                325                 330                 335

Val Ile Gly Val Thr Ala Ile Gly Gly Ile Ile Leu Phe Thr Val Ala
            340                 345                 350

Leu Gly Ile Ser Ile Gly Ala Leu Phe Gly Ala Leu Gly Ile Leu Leu
        355                 360                 365

Leu Ala Thr Val Val Ala Gly Ile Leu Ser Arg Ile Leu Leu Asp Val
    370                 375                 380

Leu Gly Thr Thr Gly Ala Ile Val Val Ser Val Leu Gly Trp Val Ala
385                 390                 395                 400

Gln Ala Ala Val Ile Gly His Val Trp Ser Val Thr Ala Val Ser Asp
                405                 410                 415

Ile Ala Leu Val Trp Arg Val Val Ala Gly Met Met Pro Leu His Tyr
            420                 425                 430

Pro Thr Phe Ala Val Thr Ser Ile Gly Asn Gly Gly Ser Ala Ala Ala
        435                 440                 445

Ile Trp Met Ser Val Ala Val Leu Leu Ala Met Gly Ala Ile Gly Ala
    450                 455                 460

Val Ala Leu Arg Lys Pro Lys Ala Val Ala Val Glu Val Glu Glu Ala
465                 470                 475                 480

Val Asp Ala Asp Ala Asp Gln Ala Ala Ser Glu Ser
                485                 490
```

09535050 = 09535050

```
<210> 1847
<211> 576
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(553)
<223> RXA00613

<400> 1847
tggcgatacc agctccgagt agggctgcac ttgaaaaagt gagtgtttta gcgatagttg 60

acaccttatt caccctacct ggggagtact ctgggcaaac atg agt gaa cta aaa   115
                                            Met Ser Glu Leu Lys
                                              1               5

gac aaa atc cgc gca gat ctg acc acc gct atg aag gcc cgc gac aag   163
Asp Lys Ile Arg Ala Asp Leu Thr Thr Ala Met Lys Ala Arg Asp Lys
                 10                  15                  20

gac acc act ggt acc ttg cgc atg ctg ctt tcc gca ttg acc cag gaa   211
Asp Thr Thr Gly Thr Leu Arg Met Leu Leu Ser Ala Leu Thr Gln Glu
             25                  30                  35

gaa aca tcg gga acc aag cac gaa ctc aat gat gaa gaa gtg ttg aag   259
Glu Thr Ser Gly Thr Lys His Glu Leu Asn Asp Glu Glu Val Leu Lys
         40                  45                  50
```

```
gtg att gct cgt gag att aag aag cgt cgc gag tcc gct gag gtg tac   307
Val Ile Ala Arg Glu Ile Lys Lys Arg Arg Glu Ser Ala Glu Val Tyr
     55                  60                  65

acc gaa aat ggt cgt cag gaa ttg gct gac gtt gag ctt aaa gag gct   355
Thr Glu Asn Gly Arg Gln Glu Leu Ala Asp Val Glu Leu Lys Glu Ala
 70                  75                  80                  85

gcc att ttg gag ggc tac cag cct gag cag ctt gat gat gat cag ctg   403
Ala Ile Leu Glu Gly Tyr Gln Pro Glu Gln Leu Asp Asp Asp Gln Leu
                 90                  95                 100

aac gcg ctg atc gat gag gct atc gct gaa gtc ggc ggc gag gcc gat   451
Asn Ala Leu Ile Asp Glu Ala Ile Ala Glu Val Gly Gly Glu Ala Asp
            105                 110                 115

atg aag aag atg ggc cag atc atg aag gct gct acc gct aag gct gct   499
Met Lys Lys Met Gly Gln Ile Met Lys Ala Ala Thr Ala Lys Ala Ala
        120                 125                 130

ggc cgt gca gat gga aaa cga ctc tcc acc gca gtg aag agc cgt ttg   547
Gly Arg Ala Asp Gly Lys Arg Leu Ser Thr Ala Val Lys Ser Arg Leu
    135                 140                 145

agc aac taggtatttc tagcggaaga act                                576
Ser Asn
150
```

EFS Web 2.2.0.D

<210> 1848
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 1848

```
Met Ser Glu Leu Lys Asp Lys Ile Arg Ala Asp Leu Thr Thr Ala Met
  1               5                  10                  15

Lys Ala Arg Asp Lys Asp Thr Thr Gly Thr Leu Arg Met Leu Leu Ser
             20                  25                  30

Ala Leu Thr Gln Glu Glu Thr Ser Gly Thr Lys His Glu Leu Asn Asp
         35                  40                  45

Glu Glu Val Leu Lys Val Ile Ala Arg Glu Ile Lys Lys Arg Arg Glu
     50                  55                  60

Ser Ala Glu Val Tyr Thr Glu Asn Gly Arg Gln Glu Leu Ala Asp Val
 65                  70                  75                  80

Glu Leu Lys Glu Ala Ala Ile Leu Glu Gly Tyr Gln Pro Glu Gln Leu
                 85                  90                  95

Asp Asp Asp Gln Leu Asn Ala Leu Ile Asp Glu Ala Ile Ala Glu Val
            100                 105                 110

Gly Gly Glu Ala Asp Met Lys Lys Met Gly Gln Ile Met Lys Ala Ala
        115                 120                 125

Thr Ala Lys Ala Ala Gly Arg Ala Asp Gly Lys Arg Leu Ser Thr Ala
```

```
    130                 135                 140

Val Lys Ser Arg Leu Ser Asn
145                 150


<210> 1849
<211> 1038
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1015)
<223> RXA00614

<400> 1849
cagtggtgtc cttgtcgcgg gccttcatag cggtggtcag atctgcgcgg attttgtctt 60

ttagttcact catgtttgcc cagagtactc cccaggtagg gtg aat aag gtg tca   115
                                            Val Asn Lys Val Ser
                                              1               5

act atc gct aaa aca ctc act ttt tca agt gca gcc cta ctc gga gct   163
Thr Ile Ala Lys Thr Leu Thr Phe Ser Ser Ala Ala Leu Leu Gly Ala
                  10                  15                  20

ggt atc gcc acc gct gca tgg gga tac tca gag ctc aaa aaa ttc gag   211
Gly Ile Ala Thr Ala Ala Trp Gly Tyr Ser Glu Leu Lys Lys Phe Glu
              25                  30                  35

ctc aaa aca gta gaa ctg cca att ttg aag cct gga acg ctc cgt gga   259
Leu Lys Thr Val Glu Leu Pro Ile Leu Lys Pro Gly Thr Leu Arg Gly
          40                  45                  50

aag aag gaa ttc cgc ctt ctc cac atc tct gat ctc cac atg atc cca   307
Lys Lys Glu Phe Arg Leu Leu His Ile Ser Asp Leu His Met Ile Pro
      55                  60                  65

ggc caa gaa acc aaa aaa gca tgg gtc tcc gca ctc gat tca cta agc   355
Gly Gln Glu Thr Lys Lys Ala Trp Val Ser Ala Leu Asp Ser Leu Ser
  70                  75                  80                  85

ccc gat ttg gtg atc aac acc ggt gac aac ctt agc gat gaa aaa gca   403
Pro Asp Leu Val Ile Asn Thr Gly Asp Asn Leu Ser Asp Glu Lys Ala
                  90                  95                 100

gtc ccc gac gtc ctc cgc gca ctc ggc cca ctg atg aac cgc ccc ggc   451
Val Pro Asp Val Leu Arg Ala Leu Gly Pro Leu Met Asn Arg Pro Gly
             105                 110                 115

gcg ttc gtc ttc gga acc aac gat tac tgg gca ccc cgc ccc gtc aat   499
Ala Phe Val Phe Gly Thr Asn Asp Tyr Trp Ala Pro Arg Pro Val Asn
         120                 125                 130

cct ttc ggc tac ctc ttc ggt aaa aaa cgc gaa gtg agc cac atc gac   547
Pro Phe Gly Tyr Leu Phe Gly Lys Lys Arg Glu Val Ser His Ile Asp
     135                 140                 145

ctc ccc tgg cga gcc atg cga gct gct ttc atc gaa cac gga tgg caa   595
Leu Pro Trp Arg Ala Met Arg Ala Ala Phe Ile Glu His Gly Trp Gln
```

```
150                 155                 160                 165

gac gcc aac caa aag cga ctc gaa ttc caa gta ggt tcc gtc cgc ctc   643
Asp Ala Asn Gln Lys Arg Leu Glu Phe Gln Val Gly Ser Val Arg Leu
                170                 175                 180

gcc atc tca ggt gtt gat gac ccc cac cat gac ctc gac gac tac aca   691
Ala Ile Ser Gly Val Asp Asp Pro His His Asp Leu Asp Asp Tyr Thr
            185                 190                 195

gag atc gca ggg gca cca aac gtg gac gct gat ctg tcc ata gcg ttg   739
Glu Ile Ala Gly Ala Pro Asn Val Asp Ala Asp Leu Ser Ile Ala Leu
        200                 205                 210

ctt cac gca cca gaa cct cga gtc ctc gct cag ttc gaa gcc gac ggc   787
Leu His Ala Pro Glu Pro Arg Val Leu Ala Gln Phe Glu Ala Asp Gly
    215                 220                 225

tac cag ctt tcc ctc tcc ggc cac acc cac ggc ggt cag ctt tgt ctt   835
Tyr Gln Leu Ser Leu Ser Gly His Thr His Gly Gly Gln Leu Cys Leu
230                 235                 240                 245

ccg ggc agc aag cca att gtc acc aac tgt gga atc gac cgc aaa cgc   883
Pro Gly Ser Lys Pro Ile Val Thr Asn Cys Gly Ile Asp Arg Lys Arg
                250                 255                 260

gcc acc ggc ctc aac aaa ttt ggc gac atg tgg atg cac gtt tcc aac   931
Ala Thr Gly Leu Asn Lys Phe Gly Asp Met Trp Met His Val Ser Asn
            265                 270                 275

ggc ctc ggc acc tca aaa ttc gtc cca ttc cgc atc ttc tgc cga ccc   979
Gly Leu Gly Thr Ser Lys Phe Val Pro Phe Arg Ile Phe Cys Arg Pro
        280                 285                 290

agc gcc acc cta ata aag atc act gaa cag gca ctt tgacctgaaa        1025
Ser Ala Thr Leu Ile Lys Ile Thr Glu Gln Ala Leu
    295                 300                 305

aacccacagg act                                                   1038
```

Sequence Listing.ST25.txt

<210> 1850
<211> 305
<212> PRT
<213> Corynebacterium glutamicum

<400> 1850

```
Val Asn Lys Val Ser Thr Ile Ala Lys Thr Leu Thr Phe Ser Ser Ala
  1               5                  10                  15

Ala Leu Leu Gly Ala Gly Ile Ala Thr Ala Ala Trp Gly Tyr Ser Glu
             20                  25                  30

Leu Lys Lys Phe Glu Leu Lys Thr Val Glu Leu Pro Ile Leu Lys Pro
         35                  40                  45

Gly Thr Leu Arg Gly Lys Lys Glu Phe Arg Leu Leu His Ile Ser Asp
     50                  55                  60

Leu His Met Ile Pro Gly Gln Glu Thr Lys Lys Ala Trp Val Ser Ala
 65                  70                  75                  80
```

```
Leu Asp Ser Leu Ser Pro Asp Leu Val Ile Asn Thr Gly Asp Asn Leu
                  85                  90                  95

Ser Asp Glu Lys Ala Val Pro Asp Val Leu Arg Ala Leu Gly Pro Leu
             100                 105                 110

Met Asn Arg Pro Gly Ala Phe Val Phe Gly Thr Asn Asp Tyr Trp Ala
         115                 120                 125

Pro Arg Pro Val Asn Pro Phe Gly Tyr Leu Phe Gly Lys Lys Arg Glu
     130                 135                 140

Val Ser His Ile Asp Leu Pro Trp Arg Ala Met Arg Ala Ala Phe Ile
145                 150                 155                 160

Glu His Gly Trp Gln Asp Ala Asn Gln Lys Arg Leu Glu Phe Gln Val
                 165                 170                 175

Gly Ser Val Arg Leu Ala Ile Ser Gly Val Asp Asp Pro His His Asp
             180                 185                 190

Leu Asp Asp Tyr Thr Glu Ile Ala Gly Ala Pro Asn Val Asp Ala Asp
         195                 200                 205

Leu Ser Ile Ala Leu Leu His Ala Pro Glu Pro Arg Val Leu Ala Gln
     210                 215                 220

Phe Glu Ala Asp Gly Tyr Gln Leu Ser Leu Ser Gly His Thr His Gly
225                 230                 235                 240

Gly Gln Leu Cys Leu Pro Gly Ser Lys Pro Ile Val Thr Asn Cys Gly
                 245                 250                 255

Ile Asp Arg Lys Arg Ala Thr Gly Leu Asn Lys Phe Gly Asp Met Trp
             260                 265                 270

Met His Val Ser Asn Gly Leu Gly Thr Ser Lys Phe Val Pro Phe Arg
         275                 280                 285

Ile Phe Cys Arg Pro Ser Ala Thr Leu Ile Lys Ile Thr Glu Gln Ala
     290                 295                 300

Leu
305
```

<210> 1851
<211> 1183
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1183)
<223> RXA00617

<400> 1851
acgactggga cgacgactaa ctaacccctg aggcactttc tatttcatgg ctaaatcaac 60

tcctttgatt gcatcgctac gctggcgaat tgtcctgtgg atg aca gcg gtt gtt 115

```
                                                    Met Thr Ala Val Val
                                                      1               5

ttc ttg acc cta gcc agc gtt gtg atc att acc cgt tcg gtg ctg ctt   163
Phe Leu Thr Leu Ala Ser Val Val Ile Ile Thr Arg Ser Val Leu Leu
                 10                  15                  20

tca gag gta acc aac acc gcg aac tcg gca gtt gag cag gaa att gag   211
Ser Glu Val Thr Asn Thr Ala Asn Ser Ala Val Glu Gln Glu Ile Glu
             25                  30                  35

gag ttt cgt cgc ttt gca gcc gaa gga att gat cca aca act gcg cag   259
Glu Phe Arg Arg Phe Ala Ala Glu Gly Ile Asp Pro Thr Thr Ala Gln
         40                  45                  50

cct ttt gag tca ggt cat cgc ctg atg gag gtt tac ctg tcg agg cag   307
Pro Phe Glu Ser Gly His Arg Leu Met Glu Val Tyr Leu Ser Arg Gln
     55                  60                  65

att ccg gat gaa aat gaa gcc att gtc ggc att ttc ccc gga gag ctc   355
Ile Pro Asp Glu Asn Glu Ala Ile Val Gly Ile Phe Pro Gly Glu Leu
 70                  75                  80                  85

att cag gtt gat tac tcc cag ctc agt ggc gcc cat ccg ctt cct ttg   403
Ile Gln Val Asp Tyr Ser Gln Leu Ser Gly Ala His Pro Leu Pro Leu
                 90                  95                 100

gaa cac tcc gat ccg ttg att tcg gaa atc cga cag acc acg ctg aat   451
Glu His Ser Asp Pro Leu Ile Ser Glu Ile Arg Gln Thr Thr Leu Asn
             105                 110                 115

tct gga gtt ttc agc gat ctt gaa cgc gga acc act cac tgg gga aag   499
Ser Gly Val Phe Ser Asp Leu Glu Arg Gly Thr Thr His Trp Gly Lys
         120                 125                 130

gtg aat ttc caa act gct tcc ggt gag gcc gat ggt gag ttc gtt gtc   547
Val Asn Phe Gln Thr Ala Ser Gly Glu Ala Asp Gly Glu Phe Val Val
     135                 140                 145

gca ttc ttc gct gat aat ctt aaa gac cag gtc aac ggc cag atc cag   595
Ala Phe Phe Ala Asp Asn Leu Lys Asp Gln Val Asn Gly Gln Ile Gln
150                 155                 160                 165

att ctt att ttg atc ggc aca ggg ggt ttg att gcc tca att ctg att   643
Ile Leu Ile Leu Ile Gly Thr Gly Gly Leu Ile Ala Ser Ile Leu Ile
                170                 175                 180

gct tgg ttg att gcg ggc cag atc att gcc ccg atc cgc aaa ttg agt   691
Ala Trp Leu Ile Ala Gly Gln Ile Ile Ala Pro Ile Arg Lys Leu Ser
            185                 190                 195

tcc gtg tcc gca aag atc agt aat tcg gat ctc acc tgg cgc gtc cct   739
Ser Val Ser Ala Lys Ile Ser Asn Ser Asp Leu Thr Trp Arg Val Pro
        200                 205                 210

gtg gag ggt cgt gat gag att gcg cag ctg gcc agg act ttt aat gcc   787
Val Glu Gly Arg Asp Glu Ile Ala Gln Leu Ala Arg Thr Phe Asn Ala
    215                 220                 225

atg ttg gat cgc atc gaa atc gcg tat aac gat cag cgc cag ttc gtt   835
Met Leu Asp Arg Ile Glu Ile Ala Tyr Asn Asp Gln Arg Gln Phe Val
```

```
230                 235                 240                 245

gat gat gcc ggc cac gag ctg cgc acc ccg atc aca gtg gtg cgt ggc   883
Asp Asp Ala Gly His Glu Leu Arg Thr Pro Ile Thr Val Val Arg Gly
                250                 255                 260

cag tta gag ctt ctc gcc acc acc ccg ccg gag gaa caa gcg cgg tcg   931
Gln Leu Glu Leu Leu Ala Thr Thr Pro Pro Glu Glu Gln Ala Arg Ser
            265                 270                 275

att gag ctg gcc acc act gag ttg gat cga atg tcg cga atg gtc aat   979
Ile Glu Leu Ala Thr Thr Glu Leu Asp Arg Met Ser Arg Met Val Asn
        280                 285                 290

gat ctg ctc acc ctc gca gtc gcc gat tct ggc acc ttc atc cac gcc   1027
Asp Leu Leu Thr Leu Ala Val Ala Asp Ser Gly Thr Phe Ile His Ala
    295                 300                 305

cac ccc acg gat gtc acg gat tta aca atc gat atc gaa gac aaa gcc   1075
His Pro Thr Asp Val Thr Asp Leu Thr Ile Asp Ile Glu Asp Lys Ala
310                 315                 320                 325

cgc acc atc agc gac cga att ttg ctt gtc gac gcc gcc gag ggc ctc   1123
Arg Thr Ile Ser Asp Arg Ile Leu Leu Val Asp Ala Ala Glu Gly Leu
                330                 335                 340

gtc agc ctc gac gag cag cgg gtc acc gag gca gtg ctg gag ttg ttc   1171
Val Ser Leu Asp Glu Gln Arg Val Thr Glu Ala Val Leu Glu Leu Phe
            345                 350                 355

ggc aat gcg ttg                                                  1183
Gly Asn Ala Leu
        360
```

20050130.0930

<210> 1852
<211> 361
<212> PRT
<213> Corynebacterium glutamicum

<400> 1852

```
Met Thr Ala Val Val Phe Leu Thr Leu Ala Ser Val Val Ile Ile Thr
  1               5                  10                  15

Arg Ser Val Leu Leu Ser Glu Val Thr Asn Thr Ala Asn Ser Ala Val
             20                  25                  30

Glu Gln Glu Ile Glu Glu Phe Arg Arg Phe Ala Ala Glu Gly Ile Asp
         35                  40                  45

Pro Thr Thr Ala Gln Pro Phe Glu Ser Gly His Arg Leu Met Glu Val
     50                  55                  60

Tyr Leu Ser Arg Gln Ile Pro Asp Glu Asn Glu Ala Ile Val Gly Ile
 65                  70                  75                  80

Phe Pro Gly Glu Leu Ile Gln Val Asp Tyr Ser Gln Leu Ser Gly Ala
                 85                  90                  95

His Pro Leu Pro Leu Glu His Ser Asp Pro Leu Ile Ser Glu Ile Arg
            100                 105                 110
```

```
Gln Thr Thr Leu Asn Ser Gly Val Phe Ser Asp Leu Glu Arg Gly Thr
        115                 120                 125

Thr His Trp Gly Lys Val Asn Phe Gln Thr Ala Ser Gly Glu Ala Asp
    130                 135                 140

Gly Glu Phe Val Val Ala Phe Phe Ala Asp Asn Leu Lys Asp Gln Val
145                 150                 155                 160

Asn Gly Gln Ile Gln Ile Leu Ile Leu Ile Gly Thr Gly Gly Leu Ile
                165                 170                 175

Ala Ser Ile Leu Ile Ala Trp Leu Ile Ala Gly Gln Ile Ile Ala Pro
            180                 185                 190

Ile Arg Lys Leu Ser Ser Val Ser Ala Lys Ile Ser Asn Ser Asp Leu
        195                 200                 205

Thr Trp Arg Val Pro Val Glu Gly Arg Asp Glu Ile Ala Gln Leu Ala
    210                 215                 220

Arg Thr Phe Asn Ala Met Leu Asp Arg Ile Glu Ile Ala Tyr Asn Asp
225                 230                 235                 240

Gln Arg Gln Phe Val Asp Asp Ala Gly His Glu Leu Arg Thr Pro Ile
                245                 250                 255

Thr Val Val Arg Gly Gln Leu Glu Leu Leu Ala Thr Thr Pro Pro Glu
            260                 265                 270

Glu Gln Ala Arg Ser Ile Glu Leu Ala Thr Thr Glu Leu Asp Arg Met
        275                 280                 285

Ser Arg Met Val Asn Asp Leu Leu Thr Leu Ala Val Ala Asp Ser Gly
    290                 295                 300

Thr Phe Ile His Ala His Pro Thr Asp Val Thr Asp Leu Thr Ile Asp
305                 310                 315                 320

Ile Glu Asp Lys Ala Arg Thr Ile Ser Asp Arg Ile Leu Leu Val Asp
                325                 330                 335

Ala Ala Glu Gly Leu Val Ser Leu Asp Glu Gln Arg Val Thr Glu Ala
            340                 345                 350

Val Leu Glu Leu Phe Gly Asn Ala Leu
        355                 360
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<210> 1853
<211> 531
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> RXA00628

<400> 1853

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ggttgaaagt ggcgtcgaaa agcgccttaa aatgaccggc tcacctgcat tattttatgc 60

aacctcaatt tggttgcacg ccaagtagta gtctgtgcat atg gct tct gta ttc   115
                                             Met Ala Ser Val Phe
                                               1               5

acg aaa att att aat ggc gag ctc ccc ggc cga ttt gtg tat cgt tcc   163
Thr Lys Ile Ile Asn Gly Glu Leu Pro Gly Arg Phe Val Tyr Arg Ser
                  10                  15                  20

gag aat gtc gtg gct ttt cta tcc atc gaa ccc ctc acc tac ggc cac   211
Glu Asn Val Val Ala Phe Leu Ser Ile Glu Pro Leu Thr Tyr Gly His
              25                  30                  35

acc cta gtc gta ccc gtt gca gaa gtt gac cgc tgg acc gac ctt cct   259
Thr Leu Val Val Pro Val Ala Glu Val Asp Arg Trp Thr Asp Leu Pro
          40                  45                  50

cag aac atc tgg agc gaa gta aac gag gcc tcc cag ctc atc gga aat   307
Gln Asn Ile Trp Ser Glu Val Asn Glu Ala Ser Gln Leu Ile Gly Asn
      55                  60                  65

gca atc cgc aca gca ttc gac gcc cct cga tgt ggt tac atc atc gca   355
Ala Ile Arg Thr Ala Phe Asp Ala Pro Arg Cys Gly Tyr Ile Ile Ala
  70                  75                  80                  85

gga ttc gat gtt ccc cac act cac atc cac ctc ttc ccc acc gac aaa   403
Gly Phe Asp Val Pro His Thr His Ile His Leu Phe Pro Thr Asp Lys
                  90                  95                 100

atg gcc gat tac gat ttc cgc aac gcc atg gcc gca gac gcc acc gac   451
Met Ala Asp Tyr Asp Phe Arg Asn Ala Met Ala Ala Asp Ala Thr Asp
              105                 110                 115

cct gca aaa atg gat gaa gct gca gag aag atc cgc gaa gcg ctg gac   499
Pro Ala Lys Met Asp Glu Ala Ala Glu Lys Ile Arg Glu Ala Leu Asp
          120                 125                 130

ggt ctg gtc tagttcttgt agttctaatt gct                            531
Gly Leu Val
    135


<210> 1854
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 1854
Met Ala Ser Val Phe Thr Lys Ile Ile Asn Gly Glu Leu Pro Gly Arg
  1               5                  10                  15

Phe Val Tyr Arg Ser Glu Asn Val Val Ala Phe Leu Ser Ile Glu Pro
              20                  25                  30

Leu Thr Tyr Gly His Thr Leu Val Val Pro Val Ala Glu Val Asp Arg
          35                  40                  45

Trp Thr Asp Leu Pro Gln Asn Ile Trp Ser Glu Val Asn Glu Ala Ser
      50                  55                  60
```

```
Gln Leu Ile Gly Asn Ala Ile Arg Thr Ala Phe Asp Ala Pro Arg Cys
 65                  70                  75                  80

Gly Tyr Ile Ile Ala Gly Phe Asp Val Pro His Thr His Ile His Leu
                 85                  90                  95

Phe Pro Thr Asp Lys Met Ala Asp Tyr Asp Phe Arg Asn Ala Met Ala
            100                 105                 110

Ala Asp Ala Thr Asp Pro Ala Lys Met Asp Glu Ala Ala Glu Lys Ile
        115                 120                 125

Arg Glu Ala Leu Asp Gly Leu Val
    130                 135


<210> 1855
<211> 1578
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1555)
<223> RXA00631

<400> 1855
cctacctgcg ccgcaaggtg gacacccagg atccgcagct aattcagact gttcgtggcg 60

ttggatatgt tctgcgcacc ccacgtagct aaattctcct atg gaa aat cct tat   115
                                              Met Glu Asn Pro Tyr
                                                1               5

gtt gct gcg ctc gat gac gaa aac caa gaa gtc ggc gta aaa aaa gaa   163
Val Ala Ala Leu Asp Asp Glu Asn Gln Glu Val Gly Val Lys Lys Glu
                 10                  15                  20

gca gaa aaa gaa cct gaa ata ggt ccc atc aga gct gcc gga cga gcc   211
Ala Glu Lys Glu Pro Glu Ile Gly Pro Ile Arg Ala Ala Gly Arg Ala
            25                  30                  35

ata ccg ctg cgc acc cgc atc att ttg atc gtg gtg ggt atc gcc ggg   259
Ile Pro Leu Arg Thr Arg Ile Ile Leu Ile Val Val Gly Ile Ala Gly
        40                  45                  50

ctt ggt ttg ctg gtc aac gcg att gct gtc tcc agc ctc atg cgt gaa   307
Leu Gly Leu Leu Val Asn Ala Ile Ala Val Ser Ser Leu Met Arg Glu
    55                  60                  65

gtt tcc tat acc cgc atg gat caa gag cta gag acc tcg atg ggg acg   355
Val Ser Tyr Thr Arg Met Asp Gln Glu Leu Glu Thr Ser Met Gly Thr
70                  75                  80                  85

tgg gcg cat aac gtt gag ctg ttt aat ttc gat ggc gtc cgc caa ggg   403
Trp Ala His Asn Val Glu Leu Phe Asn Phe Asp Gly Val Arg Gln Gly
                90                  95                 100

cca ccc agc gat tat tat gtg gcc aag gtt ttt cct gat gga tcc agc   451
Pro Pro Ser Asp Tyr Tyr Val Ala Lys Val Phe Pro Asp Gly Ser Ser
            105                 110                 115
```

```
atc atc ttc aac gat gca caa tcg gca ccc gat cta gct gaa acc acc   499
Ile Ile Phe Asn Asp Ala Gln Ser Ala Pro Asp Leu Ala Glu Thr Thr
        120                 125                 130

atc ggt act ggt cca cac act gtg gat gct gct agc ggt tct gcc tcc   547
Ile Gly Thr Gly Pro His Thr Val Asp Ala Ala Ser Gly Ser Ala Ser
    135                 140                 145

aac act ccg tgg cgt gtg atg gcg gaa aag aac ggt gac att atc acc   595
Asn Thr Pro Trp Arg Val Met Ala Glu Lys Asn Gly Asp Ile Ile Thr
150                 155                 160                 165

gtg gtg ggt aaa agc atg ggg cgt gaa aca aac ctg ctg tac cga ttg   643
Val Val Gly Lys Ser Met Gly Arg Glu Thr Asn Leu Leu Tyr Arg Leu
                170                 175                 180

gtg atg gtg cag atg atc atc ggc gcg ctg att ctg gtt gct att ttg   691
Val Met Val Gln Met Ile Ile Gly Ala Leu Ile Leu Val Ala Ile Leu
            185                 190                 195

att act tca ctc ttc cta gtc aga cgc tcg ttg cgg ccg ttg aga gaa   739
Ile Thr Ser Leu Phe Leu Val Arg Arg Ser Leu Arg Pro Leu Arg Glu
        200                 205                 210

gtt gaa gag acc gcc acc agg att gcg ggc ggt gat ttg gat cga cgt   787
Val Glu Glu Thr Ala Thr Arg Ile Ala Gly Gly Asp Leu Asp Arg Arg
    215                 220                 225

gtc ccg cag tgg cca atg acc aca gaa gtc gga cag ctg tcg aat gcc   835
Val Pro Gln Trp Pro Met Thr Thr Glu Val Gly Gln Leu Ser Asn Ala
230                 235                 240                 245

ctc aat atc atg ttg gag cag ctc caa gcc tca att ctg acc gcc cag   883
Leu Asn Ile Met Leu Glu Gln Leu Gln Ala Ser Ile Leu Thr Ala Gln
                250                 255                 260

caa aaa gaa gct cag atg cgc cga ttc gtt ggc gat gcc tcc cac gag   931
Gln Lys Glu Ala Gln Met Arg Arg Phe Val Gly Asp Ala Ser His Glu
            265                 270                 275

ctc cgc aca cca ctg acc tct gtg aag ggc ttc acc gag ctg tat tca   979
Leu Arg Thr Pro Leu Thr Ser Val Lys Gly Phe Thr Glu Leu Tyr Ser
        280                 285                 290

tca ggt gca aca gat gat gcc aac tgg gtc atg tcc aag atc ggt ggc   1027
Ser Gly Ala Thr Asp Asp Ala Asn Trp Val Met Ser Lys Ile Gly Gly
    295                 300                 305

gaa gcc caa cgc atg agt gtg ctt gtg gaa gac ctc ctg tca ctg acg   1075
Glu Ala Gln Arg Met Ser Val Leu Val Glu Asp Leu Leu Ser Leu Thr
310                 315                 320                 325

cgt gcc gaa ggc cag caa atg gag aag cac cgc gtt gac gtg ctg gaa   1123
Arg Ala Glu Gly Gln Gln Met Glu Lys His Arg Val Asp Val Leu Glu
                330                 335                 340

ctc gcc ttg gca gta cgc gga tcc atg cga gca gcc tgg cca gat cgc   1171
Leu Ala Leu Ala Val Arg Gly Ser Met Arg Ala Ala Trp Pro Asp Arg
            345                 350                 355

aca gtc aat gta tcc aac aaa gct gag tcc att ccg gtt gtc aaa ggc   1219
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Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile Pro Val Val Lys Gly
        360                 365                 370

gac cca act cgc ctc cac caa gtg ctt acc aac ctg gtt gcc aac gga   1267
Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn Leu Val Ala Asn Gly
    375                 380                 385

cta aac cac ggc gga ccg gac gcg gaa gtc agc att gag atc aac acc   1315
Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser Ile Glu Ile Asn Thr
390                 395                 400                 405

gat gga caa aac gtg agg att ctc gtg gca gac aac ggt gtc gga atg   1363
Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp Asn Gly Val Gly Met
                410                 415                 420

tct gaa gaa gat gct cag cat atc ttc gag cgt ttc tac cgc gcc gat   1411
Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg Phe Tyr Arg Ala Asp
            425                 430                 435

tcc tcc cgc tca cgc gca tcc ggc gga tcg ggc ctc ggc ctt gcg atc   1459
Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly Leu Gly Leu Ala Ile
        440                 445                 450

acg aaa tcc ctg gtc gaa ggc cac ggc ggc aca gtc acc gtc gac agc   1507
Thr Lys Ser Leu Val Glu Gly His Gly Gly Thr Val Thr Val Asp Ser
    455                 460                 465

gtg caa ggc gaa ggc acg gtg ttc acg atc acc ttg ccg gcg gtt tct   1555
Val Gln Gly Glu Gly Thr Val Phe Thr Ile Thr Leu Pro Ala Val Ser
470                 475                 480                 485

taaaggcatc aagggccgga aaa                                        1578


<210> 1856
<211> 485
<212> PRT
<213> Corynebacterium glutamicum

<400> 1856
Met Glu Asn Pro Tyr Val Ala Ala Leu Asp Asp Glu Asn Gln Glu Val
  1               5                  10                  15

Gly Val Lys Lys Glu Ala Glu Lys Glu Pro Glu Ile Gly Pro Ile Arg
            20                  25                  30

Ala Ala Gly Arg Ala Ile Pro Leu Arg Thr Arg Ile Ile Leu Ile Val
        35                  40                  45

Val Gly Ile Ala Gly Leu Gly Leu Leu Val Asn Ala Ile Ala Val Ser
    50                  55                  60

Ser Leu Met Arg Glu Val Ser Tyr Thr Arg Met Asp Gln Glu Leu Glu
65                  70                  75                  80

Thr Ser Met Gly Thr Trp Ala His Asn Val Glu Leu Phe Asn Phe Asp
                85                  90                  95

Gly Val Arg Gln Gly Pro Pro Ser Asp Tyr Tyr Val Ala Lys Val Phe
            100                 105                 110
```

```
Pro Asp Gly Ser Ser Ile Ile Phe Asn Asp Ala Gln Ser Ala Pro Asp
        115                 120                 125

Leu Ala Glu Thr Thr Ile Gly Thr Gly Pro His Thr Val Asp Ala Ala
    130                 135                 140

Ser Gly Ser Ala Ser Asn Thr Pro Trp Arg Val Met Ala Glu Lys Asn
145                 150                 155                 160

Gly Asp Ile Ile Thr Val Val Gly Lys Ser Met Gly Arg Glu Thr Asn
                165                 170                 175

Leu Leu Tyr Arg Leu Val Met Val Gln Met Ile Ile Gly Ala Leu Ile
            180                 185                 190

Leu Val Ala Ile Leu Ile Thr Ser Leu Phe Leu Val Arg Arg Ser Leu
        195                 200                 205

Arg Pro Leu Arg Glu Val Glu Glu Thr Ala Thr Arg Ile Ala Gly Gly
    210                 215                 220

Asp Leu Asp Arg Arg Val Pro Gln Trp Pro Met Thr Thr Glu Val Gly
225                 230                 235                 240

Gln Leu Ser Asn Ala Leu Asn Ile Met Leu Glu Gln Leu Gln Ala Ser
                245                 250                 255

Ile Leu Thr Ala Gln Gln Lys Glu Ala Gln Met Arg Arg Phe Val Gly
            260                 265                 270

Asp Ala Ser His Glu Leu Arg Thr Pro Leu Thr Ser Val Lys Gly Phe
        275                 280                 285

Thr Glu Leu Tyr Ser Ser Gly Ala Thr Asp Asp Ala Asn Trp Val Met
    290                 295                 300

Ser Lys Ile Gly Gly Glu Ala Gln Arg Met Ser Val Leu Val Glu Asp
305                 310                 315                 320

Leu Leu Ser Leu Thr Arg Ala Glu Gly Gln Gln Met Glu Lys His Arg
                325                 330                 335

Val Asp Val Leu Glu Leu Ala Leu Ala Val Arg Gly Ser Met Arg Ala
            340                 345                 350

Ala Trp Pro Asp Arg Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile
        355                 360                 365

Pro Val Val Lys Gly Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn
    370                 375                 380

Leu Val Ala Asn Gly Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser
385                 390                 395                 400

Ile Glu Ile Asn Thr Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp
                405                 410                 415

Asn Gly Val Gly Met Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg
            420                 425                 430

Phe Tyr Arg Ala Asp Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly
```

```
        435                 440                 445

Leu Gly Leu Ala Ile Thr Lys Ser Leu Val Glu Gly His Gly Gly Thr
    450                 455                 460

Val Thr Val Asp Ser Val Gln Gly Glu Gly Thr Val Phe Thr Ile Thr
465                 470                 475                 480

Leu Pro Ala Val Ser
                485


<210> 1857
<211> 876
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(853)
<223> RXA00637

<400> 1857
ccgatggcac tttccgtacc tggaaggtag ttgcccgcgg cagaaacaat tagggaaacc 60

tcttgacctt cacgcgacgt caaggattta actaacagtc atg aca gat cga acc   115
                                            Met Thr Asp Arg Thr
                                              1               5

att ggc gag gct gct gaa cta ctc ggt gtc acc acc cgc aca ctg cgg   163
Ile Gly Glu Ala Ala Glu Leu Leu Gly Val Thr Thr Arg Thr Leu Arg
                  10                  15                  20

cat tgg gac agc atc ggg ttg ctt caa ccg agc tgg cga acc aca acg   211
His Trp Asp Ser Ile Gly Leu Leu Gln Pro Ser Trp Arg Thr Thr Thr
              25                  30                  35

gat tat cgc ctt tac aca gaa gac gat gtc gag cgc gcc ctg cag att   259
Asp Tyr Arg Leu Tyr Thr Glu Asp Asp Val Glu Arg Ala Leu Gln Ile
          40                  45                  50

ctt att tac agg gcc gcc gga atc ggg ttg aag gat att gcg gag gtg   307
Leu Ile Tyr Arg Ala Ala Gly Ile Gly Leu Lys Asp Ile Ala Glu Val
      55                  60                  65

ctt gat cag ccg gat tcg gcc aat cag cac ctg cgc cgc cag cgg gaa   355
Leu Asp Gln Pro Asp Ser Ala Asn Gln His Leu Arg Arg Gln Arg Glu
  70                  75                  80                  85

ctc cta gtg gaa cag atc ggt cag ctg cat cgg atg gtc cgg gca gta   403
Leu Leu Val Glu Gln Ile Gly Gln Leu His Arg Met Val Arg Ala Val
                  90                  95                 100

gat gaa atc ctt gga aag gat gcg att agc gtg aag gaa aag att gag   451
Asp Glu Ile Leu Gly Lys Asp Ala Ile Ser Val Lys Glu Lys Ile Glu
             105                 110                 115

atc ttc ggc gag gat ctg ccc aag tac caa gag gag gct ttc cag cgc   499
Ile Phe Gly Glu Asp Leu Pro Lys Tyr Gln Glu Glu Ala Phe Gln Arg
         120                 125                 130
```

```
tgg ggc gac acc ccg gag tgg aaa gaa tcc caa aag atc cag gag aag   547
Trp Gly Asp Thr Pro Glu Trp Lys Glu Ser Gln Lys Ile Gln Glu Lys
    135                 140                 145

atg acc aag gag gat ttt cag agg gcg aaa gat gaa cat gag ggg ttc   595
Met Thr Lys Glu Asp Phe Gln Arg Ala Lys Asp Glu His Glu Gly Phe
150                 155                 160                 165

gtc gaa aag ctt atc gac gcc tcc ctg cgc ggc atc gcg ccc ggc tct   643
Val Glu Lys Leu Ile Asp Ala Ser Leu Arg Gly Ile Ala Pro Gly Ser
                170                 175                 180

gca gag ggc aat gag cta gcg ctt gcg cac cgc gca agc atc ggt cag   691
Ala Glu Gly Asn Glu Leu Ala Leu Ala His Arg Ala Ser Ile Gly Gln
            185                 190                 195

tgg tac acc gtg agt gca aac aag caa gta att ttg gct cgg atg tac   739
Trp Tyr Thr Val Ser Ala Asn Lys Gln Val Ile Leu Ala Arg Met Tyr
        200                 205                 210

gtg gaa gac gag cgt ttt aac gaa act tac aaa gga cac gcc tca tat   787
Val Glu Asp Glu Arg Phe Asn Glu Thr Tyr Lys Gly His Ala Ser Tyr
    215                 220                 225

ctt tta aca ctt att gaa gca ttg gcg cag gta gaa ggc gtg gac ttg   835
Leu Leu Thr Leu Ile Glu Ala Leu Ala Gln Val Glu Gly Val Asp Leu
230                 235                 240                 245

gag aat gtg gag tgg gaa taatcccaat ttcaactctt tca                876
Glu Asn Val Glu Trp Glu
                250
```

CCGCCGCCGC

```
        115                 120                 125

Glu Ala Phe Gln Arg Trp Gly Asp Thr Pro Glu Trp Lys Glu Ser Gln
    130                 135                 140

Lys Ile Gln Glu Lys Met Thr Lys Glu Asp Phe Gln Arg Ala Lys Asp
145                 150                 155                 160

Glu His Glu Gly Phe Val Glu Lys Leu Ile Asp Ala Ser Leu Arg Gly
                165                 170                 175

Ile Ala Pro Gly Ser Ala Glu Gly Asn Glu Leu Ala Leu Ala His Arg
            180                 185                 190

Ala Ser Ile Gly Gln Trp Tyr Thr Val Ser Ala Asn Lys Gln Val Ile
        195                 200                 205

Leu Ala Arg Met Tyr Val Glu Asp Glu Arg Phe Asn Glu Thr Tyr Lys
    210                 215                 220

Gly His Ala Ser Tyr Leu Leu Thr Leu Ile Glu Ala Leu Ala Gln Val
225                 230                 235                 240

Glu Gly Val Asp Leu Glu Asn Val Glu Trp Glu
                245                 250


<210> 1859
<211> 541
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(541)
<223> RXA00646

<400> 1859
aatgcaatcg gaacggttaa cgccaagtga tctggtggga tgtaggtacc gtcaggtcca 60

gcgcataaat ttcccagaaa tctctccttt acctgcaaca atg cag cgc agg gcc   115
                                               Met Gln Arg Arg Ala
                                                 1               5

cgc cgt gag gtt ggg ttg acg gaa gtt ttg gat cgt ctc cca gag cag   163
Arg Arg Glu Val Gly Leu Thr Glu Val Leu Asp Arg Leu Pro Glu Gln
                 10                  15                  20

ccc aaa aag cgg ggc cga att cct ttc acc agg gca gat cta gac aat   211
Pro Lys Lys Arg Gly Arg Ile Pro Phe Thr Arg Ala Asp Leu Asp Asn
             25                  30                  35

gac gct gaa ttg gcg gag ttt gaa acc ctc gaa gca att gca gcc ggc   259
Asp Ala Glu Leu Ala Glu Phe Glu Thr Leu Glu Ala Ile Ala Ala Gly
         40                  45                  50

gac acc ttg att acc ggc gca gtg ttc acg ggc acc ctc gaa ggg gtg   307
Asp Thr Leu Ile Thr Gly Ala Val Phe Thr Gly Thr Leu Glu Gly Val
     55                  60                  65

gca tgg gaa gtg caa gtg gat gtc ttg gtg cgc aac cct gat gga agc   355
```

```
Ala Trp Glu Val Gln Val Asp Val Leu Val Arg Asn Pro Asp Gly Ser
 70                  75                  80                  85

tac atg ccc gtg atg gtg agc aat cac cgt gtc gcc cgt ccg gat ccg   403
Tyr Met Pro Val Met Val Ser Asn His Arg Val Ala Arg Pro Asp Pro
                 90                  95                 100

cac aaa act atg cag ggc att gcc gtc acc cgc ctc ggt ttg ggt cag   451
His Lys Thr Met Gln Gly Ile Ala Val Thr Arg Leu Gly Leu Gly Gln
            105                 110                 115

ccg cta gag ctc aag gca acg ctg cgc cac cac acg atc gat ggc tat   499
Pro Leu Glu Leu Lys Ala Thr Leu Arg His His Thr Ile Asp Gly Tyr
        120                 125                 130

cgc ctc acc ctc gcg ttg atg ggt ttg gag gaa gct gga gca           541
Arg Leu Thr Leu Ala Leu Met Gly Leu Glu Glu Ala Gly Ala
    135                 140                 145


<210> 1860
<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 1860
Met Gln Arg Arg Ala Arg Arg Glu Val Gly Leu Thr Glu Val Leu Asp
  1               5                  10                  15

Arg Leu Pro Glu Gln Pro Lys Lys Arg Gly Arg Ile Pro Phe Thr Arg
            20                  25                  30

Ala Asp Leu Asp Asn Asp Ala Glu Leu Ala Glu Phe Glu Thr Leu Glu
        35                  40                  45

Ala Ile Ala Ala Gly Asp Thr Leu Ile Thr Gly Ala Val Phe Thr Gly
    50                  55                  60

Thr Leu Glu Gly Val Ala Trp Glu Val Gln Val Asp Val Leu Val Arg
65                  70                  75                  80

Asn Pro Asp Gly Ser Tyr Met Pro Val Met Val Ser Asn His Arg Val
                85                  90                  95

Ala Arg Pro Asp Pro His Lys Thr Met Gln Gly Ile Ala Val Thr Arg
            100                 105                 110

Leu Gly Leu Gly Gln Pro Leu Glu Leu Lys Ala Thr Leu Arg His His
        115                 120                 125

Thr Ile Asp Gly Tyr Arg Leu Thr Leu Ala Leu Met Gly Leu Glu Glu
    130                 135                 140

Ala Gly Ala
145


<210> 1861
<211> 579
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(556)
<223> RXA00649

<400> 1861
gtatttgatc tgtggtgtgg ctgattcggg aggactcgat gacattatgt gtatggtaca 60

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cattttgtgc aagatgcaat agctggcaaa ctggagagcc atg agc acc gac ccc   115
                                             Met Ser Thr Asp Pro
                                               1               5

atc gcg gcc ttg gaa tac gaa tcc acc atc ttc gcc cgt cac cgg aat   163
Ile Ala Ala Leu Glu Tyr Glu Ser Thr Ile Phe Ala Arg His Arg Asn
                 10                  15                  20

caa tac acc ggc caa gca ggt acg aat gct ggc gtc ctc gat tcc agc   211
Gln Tyr Thr Gly Gln Ala Gly Thr Asn Ala Gly Val Leu Asp Ser Ser
             25                  30                  35

ggc tac aac cta ctc acg ctg ctc cag tta cgt ggc ccc tcc acc atc   259
Gly Tyr Asn Leu Leu Thr Leu Leu Gln Leu Arg Gly Pro Ser Thr Ile
         40                  45                  50

ggc gaa ctc agc gcc atc acc ggc cta gac gca tct acc ctt aac cgt   307
Gly Glu Leu Ser Ala Ile Thr Gly Leu Asp Ala Ser Thr Leu Asn Arg
     55                  60                  65

cag aca aaa gcc cta cta acc aaa gga ttt gtc gaa cgc atc cca gat   355
Gln Thr Lys Ala Leu Leu Thr Lys Gly Phe Val Glu Arg Ile Pro Asp
 70                  75                  80                  85

ccc gac ggt gga atc gct cgg aaa ttc cac ccc acc gac ctc ggc aat   403
Pro Asp Gly Gly Ile Ala Arg Lys Phe His Pro Thr Asp Leu Gly Asn
                 90                  95                 100

gaa ctg ctc aac gag gaa cgc aca tcc agc caa gaa aaa tat gcc gag   451
Glu Leu Leu Asn Glu Glu Arg Thr Ser Ser Gln Glu Lys Tyr Ala Glu
            105                 110                 115

tta ctt tca gac tgg ccc gaa gag gat cta cgc acc ttc gtc aaa ctt   499
Leu Leu Ser Asp Trp Pro Glu Glu Asp Leu Arg Thr Phe Val Lys Leu
        120                 125                 130

ctt gaa aaa cta aat aaa gcc gtg gag aca cgc gtc gga aag cat tgg   547
Leu Glu Lys Leu Asn Lys Ala Val Glu Thr Arg Val Gly Lys His Trp
    135                 140                 145

ccg cgc ccc tgactcagcc caagccagag ccc                           579
Pro Arg Pro
150
```

<210> 1862
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 1862
Met Ser Thr Asp Pro Ile Ala Ala Leu Glu Tyr Glu Ser Thr Ile Phe

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  1               5                  10                  15

Ala Arg His Arg Asn Gln Tyr Thr Gly Gln Ala Gly Thr Asn Ala Gly
            20                  25                  30

Val Leu Asp Ser Ser Gly Tyr Asn Leu Leu Thr Leu Leu Gln Leu Arg
        35                  40                  45

Gly Pro Ser Thr Ile Gly Glu Leu Ser Ala Ile Thr Gly Leu Asp Ala
    50                  55                  60

Ser Thr Leu Asn Arg Gln Thr Lys Ala Leu Leu Thr Lys Gly Phe Val
65                  70                  75                  80

Glu Arg Ile Pro Asp Pro Asp Gly Gly Ile Ala Arg Lys Phe His Pro
                85                  90                  95

Thr Asp Leu Gly Asn Glu Leu Leu Asn Glu Glu Arg Thr Ser Ser Gln
            100                 105                 110

Glu Lys Tyr Ala Glu Leu Leu Ser Asp Trp Pro Glu Glu Asp Leu Arg
        115                 120                 125

Thr Phe Val Lys Leu Leu Glu Lys Leu Asn Lys Ala Val Glu Thr Arg
    130                 135                 140

Val Gly Lys His Trp Pro Arg Pro
145                 150


<210> 1863
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
<223> RXA00652

<400> 1863
gcgatagctc atcgcgcccg gttgattccc cttcttcaca agggtttcaa catcgagctc 60

attgcgtccg gtttccgaca cacgatctag gcttgactgc atg cgt cgt aca tta   115
                                            Met Arg Arg Thr Leu
                                              1               5

cct act atc ctc gct gct tcc atc atg ctc acc gct tgt acc ccg gcg   163
Pro Thr Ile Leu Ala Ala Ser Ile Met Leu Thr Ala Cys Thr Pro Ala
                10                  15                  20

gaa cct gaa gca acc cca gag acc acc acc gag gca gcc ccg gaa gta   211
Glu Pro Glu Ala Thr Pro Glu Thr Thr Thr Glu Ala Ala Pro Glu Val
            25                  30                  35

att act gac ggc ctt ccc atc gac gcg atg ccc gcg gtc gaa cgc acc   259
Ile Thr Asp Gly Leu Pro Ile Asp Ala Met Pro Ala Val Glu Arg Thr
        40                  45                  50

gca caa acc gca tgc ccc tac ctg ggc acc gac tgg gtc gcc gat acc   307
Ala Gln Thr Ala Cys Pro Tyr Leu Gly Thr Asp Trp Val Ala Asp Thr
```

```
     55                  60                  65

aac ggc cag cgc gtc acg ggt tac ggc aca gac gaa cgc ttt tcg acg   355
Asn Gly Gln Arg Val Thr Gly Tyr Gly Thr Asp Glu Arg Phe Ser Thr
 70                  75                  80                  85

ccc tcc tgc gtt ttt tac tcc tac ccc gaa gaa cca caa ctc acg gtg   403
Pro Ser Cys Val Phe Tyr Ser Tyr Pro Glu Glu Pro Gln Leu Thr Val
                 90                  95                 100

att gtc cgc gat atg gcc acc acg gat gac gct atc gcg gta gtg gat   451
Ile Val Arg Asp Met Ala Thr Thr Asp Asp Ala Ile Ala Val Val Asp
            105                 110                 115

tgg gca gcc ccc atc gat tcc act gag ccc gct gag gaa ccc gca ggg   499
Trp Ala Ala Pro Ile Asp Ser Thr Glu Pro Ala Glu Glu Pro Ala Gly
        120                 125                 130

tgg tcc ggt ggc cgc cga ggt gga aac gat act tca ggc gca ctc tac   547
Trp Ser Gly Gly Arg Arg Gly Gly Asn Asp Thr Ser Gly Ala Leu Tyr
    135                 140                 145

gcg gtt caa aac ggc ccc acc gcg gtc atc gtg ttc acc aat cag gat   595
Ala Val Gln Asn Gly Pro Thr Ala Val Ile Val Phe Thr Asn Gln Asp
150                 155                 160                 165

caa tcc ctc aaa gcg cag tta atc gct gag gaa gta atc cag aat ctt   643
Gln Ser Leu Lys Ala Gln Leu Ile Ala Glu Glu Val Ile Gln Asn Leu
                170                 175                 180

ggt ctc taactattag aaggccacat cgt                                672
Gly Leu
```

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<210> 1864
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 1864

```
Met Arg Arg Thr Leu Pro Thr Ile Leu Ala Ala Ser Ile Met Leu Thr
  1               5                  10                  15

Ala Cys Thr Pro Ala Glu Pro Glu Ala Thr Pro Glu Thr Thr Thr Glu
             20                  25                  30

Ala Ala Pro Glu Val Ile Thr Asp Gly Leu Pro Ile Asp Ala Met Pro
         35                  40                  45

Ala Val Glu Arg Thr Ala Gln Thr Ala Cys Pro Tyr Leu Gly Thr Asp
     50                  55                  60

Trp Val Ala Asp Thr Asn Gly Gln Arg Val Thr Gly Tyr Gly Thr Asp
 65                  70                  75                  80

Glu Arg Phe Ser Thr Pro Ser Cys Val Phe Tyr Ser Tyr Pro Glu Glu
                 85                  90                  95

Pro Gln Leu Thr Val Ile Val Arg Asp Met Ala Thr Thr Asp Asp Ala
            100                 105                 110
```

```
Ile Ala Val Val Asp Trp Ala Ala Pro Ile Asp Ser Thr Glu Pro Ala
        115                 120                 125

Glu Glu Pro Ala Gly Trp Ser Gly Gly Arg Arg Gly Gly Asn Asp Thr
    130                 135                 140

Ser Gly Ala Leu Tyr Ala Val Gln Asn Gly Pro Thr Ala Val Ile Val
145                 150                 155                 160

Phe Thr Asn Gln Asp Gln Ser Leu Lys Ala Gln Leu Ile Ala Glu Glu
                165                 170                 175

Val Ile Gln Asn Leu Gly Leu
            180
```

<210> 1865
<211> 1389
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1366)
<223> RXA00654

<400> 1865

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cagcaatagc gattattgct tgattgtgtg tttttagatc ttcggttctc ttcactcaac 60

tgctgtgaag tgccacctgt ttggaaaggc gaacacgata gtg ctc gat att ttg   115
                                              Val Leu Asp Ile Leu
                                                1               5

att tac ccg gtg tct gga gtg atg aag ctg tgg cac ctg ctt ctt cac   163
Ile Tyr Pro Val Ser Gly Val Met Lys Leu Trp His Leu Leu Leu His
            10                  15                  20

aac gtt gcg ggt ttg gac gat tca ctg gcg tgg ttc ttt tcc ctt ttc   211
Asn Val Ala Gly Leu Asp Asp Ser Leu Ala Trp Phe Phe Ser Leu Phe
        25                  30                  35

ggc ctt gtc atc acg atc cgt gca att atc gcg cct ttc acc tgg cag   259
Gly Leu Val Ile Thr Ile Arg Ala Ile Ile Ala Pro Phe Thr Trp Gln
    40                  45                  50

atg tat aag tcg ggc cgc act gcc gca cat att cgt cct cac cgc gct   307
Met Tyr Lys Ser Gly Arg Thr Ala Ala His Ile Arg Pro His Arg Ala
55                  60                  65

gcg ctc cgg gaa gaa tac aag gga aag tac gat gaa gcg tcc att cgg   355
Ala Leu Arg Glu Glu Tyr Lys Gly Lys Tyr Asp Glu Ala Ser Ile Arg
70                  75                  80                  85

gag ttg cag aag cgc cag aat gat ttg aat aag gaa tac ggc att aac   403
Glu Leu Gln Lys Arg Gln Asn Asp Leu Asn Lys Glu Tyr Gly Ile Asn
                90                  95                  100

ccg ctg gca ggt tgt gtg cct ggg ctg atc cag ata ccg att gtc ctt   451
Pro Leu Ala Gly Cys Val Pro Gly Leu Ile Gln Ile Pro Ile Val Leu
            105                 110                 115
```

```
ggt ctt tac tgg gca ctt ctc cgc atg gct cgc cct gaa ggt ggt ttg   499
Gly Leu Tyr Trp Ala Leu Leu Arg Met Ala Arg Pro Glu Gly Gly Leu
        120                 125                 130

gaa aat ccc gtc ttc cag tcg atc ggc ttc cta act cct gag gaa gtg   547
Glu Asn Pro Val Phe Gln Ser Ile Gly Phe Leu Thr Pro Glu Glu Val
    135                 140                 145

gaa tct ttc ctc gct ggt cgc gtg agc aat gtg cct ctg ccc gct tat   595
Glu Ser Phe Leu Ala Gly Arg Val Ser Asn Val Pro Leu Pro Ala Tyr
150                 155                 160                 165

gtt tcg atg ccc act gag cag cta aaa tat ttg agc acc acg cag gcg   643
Val Ser Met Pro Thr Glu Gln Leu Lys Tyr Leu Ser Thr Thr Gln Ala
                170                 175                 180

gaa gtt ctt agt ttc gtt ttg cca ctg ttc atc aca gcc gca atc ctc   691
Glu Val Leu Ser Phe Val Leu Pro Leu Phe Ile Thr Ala Ala Ile Leu
            185                 190                 195

acc gca atc aac atg gcg atg tcc atg tac cgc agc ttc caa acc aac   739
Thr Ala Ile Asn Met Ala Met Ser Met Tyr Arg Ser Phe Gln Thr Asn
        200                 205                 210

gat tac gca tcc gga ttc tct aac ggc atg ctg aag ttc atg atc gtg   787
Asp Tyr Ala Ser Gly Phe Ser Asn Gly Met Leu Lys Phe Met Ile Val
    215                 220                 225

atg tcg atc ctc gcg ccg atc ttc cca ctg tcc ctt ggc ctc aca gga   835
Met Ser Ile Leu Ala Pro Ile Phe Pro Leu Ser Leu Gly Leu Thr Gly
230                 235                 240                 245

cca ttc ccc aca gca atc gca ctc tat tgg gtc agc aac aac ctg tgg   883
Pro Phe Pro Thr Ala Ile Ala Leu Tyr Trp Val Ser Asn Asn Leu Trp
                250                 255                 260

acg ctc ctc caa aca atc atc atg atg gtc att ttg gaa cgc aaa tac   931
Thr Leu Leu Gln Thr Ile Ile Met Met Val Ile Leu Glu Arg Lys Tyr
            265                 270                 275

cca ctt acc gac gat ttc aaa gtg cac cac cta gag cag cgc gac atc   979
Pro Leu Thr Asp Asp Phe Lys Val His His Leu Glu Gln Arg Asp Ile
        280                 285                 290

tac cgc gca aaa caa aaa gaa aag cgc atc ttc ctg tgg aca cga cgc   1027
Tyr Arg Ala Lys Gln Lys Glu Lys Arg Ile Phe Leu Trp Thr Arg Arg
    295                 300                 305

aaa aac cgc gcc ctg atg att ctc acc cca tgg aac gcc tca acg ctt   1075
Lys Asn Arg Ala Leu Met Ile Leu Thr Pro Trp Asn Ala Ser Thr Leu
310                 315                 320                 325

cac gca aca aac gtg gaa ctc acc aaa acc cgt act gcc gaa atc aac   1123
His Ala Thr Asn Val Glu Leu Thr Lys Thr Arg Thr Ala Glu Ile Asn
                330                 335                 340

gaa gca aaa cag gcc cgc aaa gaa atc gcg aac aag agg cgc gaa acg   1171
Glu Ala Lys Gln Ala Arg Lys Glu Ile Ala Asn Lys Arg Arg Glu Thr
            345                 350                 355
```

```
caa cgt gaa atg aac cgc gcc gcc atg cag cgc tta aag cag cgt cgc   1219
Gln Arg Glu Met Asn Arg Ala Ala Met Gln Arg Leu Lys Gln Arg Arg
        360                 365                 370

gct gag gtt aaa gct aaa aag aag ggg ctt atc gac gcc tcc ccc aac   1267
Ala Glu Val Lys Ala Lys Lys Lys Gly Leu Ile Asp Ala Ser Pro Asn
    375                 380                 385

gaa gat acc cct tcg gaa aat gaa gaa act aaa ttg agt agt ccg cag   1315
Glu Asp Thr Pro Ser Glu Asn Glu Glu Thr Lys Leu Ser Ser Pro Gln
390                 395                 400                 405

gtg gag ccg aca aca act gcc gag cca aat cgc gag ccg tct caa gag   1363
Val Glu Pro Thr Thr Thr Ala Glu Pro Asn Arg Glu Pro Ser Gln Glu
                410                 415                 420

gac tgatgttgtg gaccaatcga gat                                    1389
Asp
```

<210> 1866
<211> 422
<212> PRT
<213> Corynebacterium glutamicum

<400> 1866

```
Val Leu Asp Ile Leu Ile Tyr Pro Val Ser Gly Val Met Lys Leu Trp
  1               5                  10                  15

His Leu Leu Leu His Asn Val Ala Gly Leu Asp Asp Ser Leu Ala Trp
             20                  25                  30

Phe Phe Ser Leu Phe Gly Leu Val Ile Thr Ile Arg Ala Ile Ile Ala
         35                  40                  45

Pro Phe Thr Trp Gln Met Tyr Lys Ser Gly Arg Thr Ala Ala His Ile
     50                  55                  60

Arg Pro His Arg Ala Ala Leu Arg Glu Glu Tyr Lys Gly Lys Tyr Asp
 65                  70                  75                  80

Glu Ala Ser Ile Arg Glu Leu Gln Lys Arg Gln Asn Asp Leu Asn Lys
                 85                  90                  95

Glu Tyr Gly Ile Asn Pro Leu Ala Gly Cys Val Pro Gly Leu Ile Gln
            100                 105                 110

Ile Pro Ile Val Leu Gly Leu Tyr Trp Ala Leu Leu Arg Met Ala Arg
        115                 120                 125

Pro Glu Gly Gly Leu Glu Asn Pro Val Phe Gln Ser Ile Gly Phe Leu
    130                 135                 140

Thr Pro Glu Glu Val Glu Ser Phe Leu Ala Gly Arg Val Ser Asn Val
145                 150                 155                 160

Pro Leu Pro Ala Tyr Val Ser Met Pro Thr Glu Gln Leu Lys Tyr Leu
                165                 170                 175

Ser Thr Thr Gln Ala Glu Val Leu Ser Phe Val Leu Pro Leu Phe Ile
```

```
            180                 185                 190

Thr Ala Ala Ile Leu Thr Ala Ile Asn Met Ala Met Ser Met Tyr Arg
        195                 200                 205

Ser Phe Gln Thr Asn Asp Tyr Ala Ser Gly Phe Ser Asn Gly Met Leu
    210                 215                 220

Lys Phe Met Ile Val Met Ser Ile Leu Ala Pro Ile Phe Pro Leu Ser
225                 230                 235                 240

Leu Gly Leu Thr Gly Pro Phe Pro Thr Ala Ile Ala Leu Tyr Trp Val
                245                 250                 255

Ser Asn Asn Leu Trp Thr Leu Leu Gln Thr Ile Ile Met Met Val Ile
            260                 265                 270

Leu Glu Arg Lys Tyr Pro Leu Thr Asp Asp Phe Lys Val His His Leu
        275                 280                 285

Glu Gln Arg Asp Ile Tyr Arg Ala Lys Gln Lys Glu Lys Arg Ile Phe
    290                 295                 300

Leu Trp Thr Arg Arg Lys Asn Arg Ala Leu Met Ile Leu Thr Pro Trp
305                 310                 315                 320

Asn Ala Ser Thr Leu His Ala Thr Asn Val Glu Leu Thr Lys Thr Arg
                325                 330                 335

Thr Ala Glu Ile Asn Glu Ala Lys Gln Ala Arg Lys Glu Ile Ala Asn
            340                 345                 350

Lys Arg Arg Glu Thr Gln Arg Glu Met Asn Arg Ala Ala Met Gln Arg
        355                 360                 365

Leu Lys Gln Arg Arg Ala Glu Val Lys Ala Lys Lys Lys Gly Leu Ile
    370                 375                 380

Asp Ala Ser Pro Asn Glu Asp Thr Pro Ser Glu Asn Glu Glu Thr Lys
385                 390                 395                 400

Leu Ser Ser Pro Gln Val Glu Pro Thr Thr Thr Ala Glu Pro Asn Arg
                405                 410                 415

Glu Pro Ser Gln Glu Asp
            420
```

<210> 1867
<211> 384
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(361)
<223> RXA00656

<400> 1867
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ccttttaata acaatacaat gaataattgg aataggtcga caccttgga gcggagccgg 60
```

```
ttaaaattgg cagcattcac cgaaagaaaa ggagaaccac atg ctt gcc cta ggt   115
                                            Met Leu Ala Leu Gly
                                              1               5

tgg att aca tgg atc att att ggt ggt cta gct ggt tgg att gcc tcc   163
Trp Ile Thr Trp Ile Ile Ile Gly Gly Leu Ala Gly Trp Ile Ala Ser
                 10                  15                  20

aag att aaa ggc act gat gct cag caa gga att ttg ctg aac ata gtc   211
Lys Ile Lys Gly Thr Asp Ala Gln Gln Gly Ile Leu Leu Asn Ile Val
             25                  30                  35

gtc ggt att atc ggt ggt ttg tta ggc ggc tgg ctg ctt gga atc ttc   259
Val Gly Ile Ile Gly Gly Leu Leu Gly Gly Trp Leu Leu Gly Ile Phe
         40                  45                  50

gga gtg gat gtt gcc ggt ggc ggc ttg atc ttc agc ttc atc aca tgt   307
Gly Val Asp Val Ala Gly Gly Gly Leu Ile Phe Ser Phe Ile Thr Cys
     55                  60                  65

ctg att ggt gct gtc att ttg ctg acg atc gtg cag ttc ttc act cgg   355
Leu Ile Gly Ala Val Ile Leu Leu Thr Ile Val Gln Phe Phe Thr Arg
 70                  75                  80                  85

aag aag taatctgctt taaatccgta ggg                                384
Lys Lys
```

Sequence Listing

<210> 1868
<211> 87
<212> PRT
<213> Corynebacterium glutamicum

<400> 1868

```
Met Leu Ala Leu Gly Trp Ile Thr Trp Ile Ile Ile Gly Gly Leu Ala
  1               5                  10                  15

Gly Trp Ile Ala Ser Lys Ile Lys Gly Thr Asp Ala Gln Gln Gly Ile
             20                  25                  30

Leu Leu Asn Ile Val Val Gly Ile Ile Gly Gly Leu Leu Gly Gly Trp
         35                  40                  45

Leu Leu Gly Ile Phe Gly Val Asp Val Ala Gly Gly Gly Leu Ile Phe
     50                  55                  60

Ser Phe Ile Thr Cys Leu Ile Gly Ala Val Ile Leu Leu Thr Ile Val
 65                  70                  75                  80

Gln Phe Phe Thr Arg Lys Lys
                 85
```

<210> 1869
<211> 986
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (61)..(963)
<223> RXA00657

<400> 1869
gatcatgagt ttccacgaac tgtaacgcag gattcaccaa tcaatgaaag gtcgaccgac 60

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atg agc act gaa gac att gtc gtc gta gca gta gat ggc tcg gac gcc   108
Met Ser Thr Glu Asp Ile Val Val Val Ala Val Asp Gly Ser Asp Ala
  1               5                  10                  15

tca aaa caa gct gtt cgg tgg gct gca aat acc gcc aac aaa cgt ggc   156
Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly
             20                  25                  30

att cca ctt cgc ttg gct tcc agc tac acc atg cct cag ttc ctc tac   204
Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr
         35                  40                  45

gca gag gga atg gtt cca cca caa gag ctt ttc gat gac ctc cag gcc   252
Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
     50                  55                  60

gaa gcc ctg gaa aag att aac gaa gcc cgt gac atc gcc cat gag gta   300
Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val
 65                  70                  75                  80

gcg cca gaa atc aag atc ggg cac acc atc gct gaa ggc agt ccc atc   348
Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile
                 85                  90                  95

gac atg ctg ttg gaa atg tct ccc gat gcc aca atg atc gtc atg ggt   396
Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
            100                 105                 110

tcc cgc gga ctc ggc gga ctc tcc gga atg gtc atg ggc tcc gtc tcc   444
Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
        115                 120                 125

ggt gca gtg gtc agc cac gca aag tgt cca gtc gtt gtt gtc cgt gaa   492
Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
    130                 135                 140

gac agc gca gtc aac gaa gac agc aag tac ggc cca gtc gtc gtc ggt   540
Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly
145                 150                 155                 160

gtg gat ggc tcc gaa gtc tcc caa cag gca acc gaa tac gca ttt gcg   588
Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala
                165                 170                 175

gaa gct gaa gct cgt ggc gcc gaa ctc gtt gca gtt cac acc tgg atg   636
Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met
            180                 185                 190

gac atg cag gta cag gca tca ctt gca ggt ctt gca gct gct caa cag   684
Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln
        195                 200                 205

cag tgg gat gaa gtg gaa cgt cag caa acc gac atg ctg atc gaa cgc   732
Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg
    210                 215                 220
```

```
ctc gca cca ctg gtg gaa aag tac cca agt gta acc gtc aag aag atc   780
Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
225                 230                 235                 240

atc acc cgt gac cgc cca gtt cgc gca ctt gca gaa gca tct gaa aac   828
Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn
                245                 250                 255

gcg cag ctc cta gtc gtt ggt tcc cat ggt cgt ggc gga ttt aag ggc   876
Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
            260                 265                 270

atg ctc ctt ggc tcc acc tcc cgc gca ctg ctg caa tcc gca ccg tgc   924
Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
        275                 280                 285

cca atg atg gtg gtt cgc cca cct gag aag att aag aag tagtttcttt   973
Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
    290                 295                 300

taagtttcga tgc                                                  986


<210> 1870
<211> 301
<212> PRT
<213> Corynebacterium glutamicum

<400> 1870
Met Ser Thr Glu Asp Ile Val Val Val Ala Val Asp Gly Ser Asp Ala
  1               5                  10                  15

Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly
             20                  25                  30

Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr
         35                  40                  45

Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
     50                  55                  60

Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val
 65                  70                  75                  80

Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile
                 85                  90                  95

Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
            100                 105                 110

Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
        115                 120                 125

Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
    130                 135                 140

Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly
145                 150                 155                 160

Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala
```

```
                165                 170                 175

Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met
            180                 185                 190

Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln
        195                 200                 205

Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg
    210                 215                 220

Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
225                 230                 235                 240

Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn
                245                 250                 255

Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
            260                 265                 270

Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
        275                 280                 285

Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
    290                 295                 300


<210> 1871
<211> 813
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(790)
<223> RXA00661

<400> 1871
cggatgcaag agaaccgtgg tttcgctgat ttttggcgaa cccggaatta aggccccgag 60

gattacatgc ttttaaatcc tttgaaaagg ggacaagatc atg aat cct ata acc   115
                                            Met Asn Pro Ile Thr
                                              1               5

gaa tta tta gac gca aca cta tgg atc ggc gga gtt ccg att ctg tgg   163
Glu Leu Leu Asp Ala Thr Leu Trp Ile Gly Gly Val Pro Ile Leu Trp
                  10                  15                  20

cgc gaa atc atc ggc aac gtt ttc gga tta ttt agc gcg tgg gca gga   211
Arg Glu Ile Ile Gly Asn Val Phe Gly Leu Phe Ser Ala Trp Ala Gly
              25                  30                  35

atg cga cgc atc gtg tgg gca tgg ccc atc ggc atc ata ggc aac gcg   259
Met Arg Arg Ile Val Trp Ala Trp Pro Ile Gly Ile Ile Gly Asn Ala
          40                  45                  50

ctg ctg ttc aca gta ttt atg ggc ggc ctt ttc cac act cca caa aac   307
Leu Leu Phe Thr Val Phe Met Gly Gly Leu Phe His Thr Pro Gln Asn
      55                  60                  65

ctc gat ctc tac ggc caa gcg ggt cgc cag atc atg ttc atc atc gtc   355
```

```
Leu Asp Leu Tyr Gly Gln Ala Gly Arg Gln Ile Met Phe Ile Ile Val
 70                  75                  80                  85

agt ggt tat ggc tgg tac caa tgg tcg gcc gca aaa cgt cgc gca ctc   403
Ser Gly Tyr Gly Trp Tyr Gln Trp Ser Ala Ala Lys Arg Arg Ala Leu
                 90                  95                 100

acc cca gaa aat gca gta gca gtg gtt cct cgc tgg gca agc acc aaa   451
Thr Pro Glu Asn Ala Val Ala Val Val Pro Arg Trp Ala Ser Thr Lys
            105                 110                 115

gaa cgc gcc ggc att gtg att gcg gcg gtt gtg gga aca ctc agc ttt   499
Glu Arg Ala Gly Ile Val Ile Ala Ala Val Val Gly Thr Leu Ser Phe
        120                 125                 130

gcc tgg att ttc caa gca ctc ggc tcc tgg ggg cca tgg gcc gac gcg   547
Ala Trp Ile Phe Gln Ala Leu Gly Ser Trp Gly Pro Trp Ala Asp Ala
    135                 140                 145

tgg att ttc gtc ggc tca atc ctg gct acc tac gga atg gct cgc gga   595
Trp Ile Phe Val Gly Ser Ile Leu Ala Thr Tyr Gly Met Ala Arg Gly
150                 155                 160                 165

tgg aca gag ttc tgg ctg atc tgg atc gcc gtc gac ata gtt ggc gtt   643
Trp Thr Glu Phe Trp Leu Ile Trp Ile Ala Val Asp Ile Val Gly Val
                170                 175                 180

cct cta ctt ttg act gct ggc tac tac cca tcc gcg gtg ctt tac ctg   691
Pro Leu Leu Leu Thr Ala Gly Tyr Tyr Pro Ser Ala Val Leu Tyr Leu
            185                 190                 195

gtg tac ggt gcg ttt gtc agc tgg gga ttt gtc gtg tgg ctg cgg gtg   739
Val Tyr Gly Ala Phe Val Ser Trp Gly Phe Val Val Trp Leu Arg Val
        200                 205                 210

caa aaa gca gac aag gct cgt gcg ctg gaa gct cag gag tct gtg aca   787
Gln Lys Ala Asp Lys Ala Arg Ala Leu Glu Ala Gln Glu Ser Val Thr
    215                 220                 225

gtc tgaaaagcgt ttactaaata gaa                                    813
Val
230
```

09550850.090705

<210> 1872
<211> 230
<212> PRT
<213> Corynebacterium glutamicum

<400> 1872

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Met Asn Pro Ile Thr Glu Leu Leu Asp Ala Thr Leu Trp Ile Gly Gly
  1               5                  10                  15

Val Pro Ile Leu Trp Arg Glu Ile Ile Gly Asn Val Phe Gly Leu Phe
             20                  25                  30

Ser Ala Trp Ala Gly Met Arg Arg Ile Val Trp Ala Trp Pro Ile Gly
         35                  40                  45

Ile Ile Gly Asn Ala Leu Leu Phe Thr Val Phe Met Gly Gly Leu Phe
     50                  55                  60
```

```
His Thr Pro Gln Asn Leu Asp Leu Tyr Gly Gln Ala Gly Arg Gln Ile
 65                  70                  75                  80

Met Phe Ile Ile Val Ser Gly Tyr Gly Trp Tyr Gln Trp Ser Ala Ala
                85                  90                  95

Lys Arg Arg Ala Leu Thr Pro Glu Asn Ala Val Ala Val Val Pro Arg
            100                 105                 110

Trp Ala Ser Thr Lys Glu Arg Ala Gly Ile Val Ile Ala Ala Val Val
        115                 120                 125

Gly Thr Leu Ser Phe Ala Trp Ile Phe Gln Ala Leu Gly Ser Trp Gly
    130                 135                 140

Pro Trp Ala Asp Ala Trp Ile Phe Val Gly Ser Ile Leu Ala Thr Tyr
145                 150                 155                 160

Gly Met Ala Arg Gly Trp Thr Glu Phe Trp Leu Ile Trp Ile Ala Val
                165                 170                 175

Asp Ile Val Gly Val Pro Leu Leu Leu Thr Ala Gly Tyr Tyr Pro Ser
            180                 185                 190

Ala Val Leu Tyr Leu Val Tyr Gly Ala Phe Val Ser Trp Gly Phe Val
        195                 200                 205

Val Trp Leu Arg Val Gln Lys Ala Asp Lys Ala Arg Ala Leu Glu Ala
    210                 215                 220

Gln Glu Ser Val Thr Val
225                 230
```

<210> 1873
<211> 685
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(685)
<223> RXA00667

<400> 1873

```
ggcatcagtg tttgaaggga aaagcaggtc aaacaaggtg cggctgattt gagcgatcac 60

agcaccgaga tctgtgctga agaattcaat gattgggttg atg att gcg ttg aag   115
                                            Met Ile Ala Leu Lys
                                              1               5

tcc atg tct aac agg gta gta caa aag cca aaa atg aaa gcg ccg cta   163
Ser Met Ser Asn Arg Val Val Gln Lys Pro Lys Met Lys Ala Pro Leu
                10                  15                  20

ccc atc cgc gac ggc ctc aac cct tcc cgt gtg cgc ttg ccg ctc gac   211
Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val Arg Leu Pro Leu Asp
            25                  30                  35

gcg gcg ccg atc cgc gcc atc gat ttt gtt gaa tac ctc att tcc acg   259
```

```
Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu Tyr Leu Ile Ser Thr
         40                  45                  50

cag cgc cac cgc aat ccg gcc gac aac gcc gaa gcg ctt caa gcg cgt   307
Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu Ala Leu Gln Ala Arg
     55                  60                  65

ttc gac gcc gac ctt gtt gtc aac cac tac ggc gag ccc tac gcc ccc   355
Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly Glu Pro Tyr Ala Pro
 70                  75                  80                  85

gac acc atg gtt cag ccc gac gac gac att tgg ttc tac cgc atg ccc   403
Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp Phe Tyr Arg Met Pro
                 90                  95                 100

gcc gcc gaa cgg ccg atc cct tac aaa att cat gtc att cac gaa gac   451
Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His Val Ile His Glu Asp
            105                 110                 115

gat gac atc ctc gtc att gac aag cca ccc tac cta gca acc atg cct   499
Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr Leu Ala Thr Met Pro
        120                 125                 130

cgt ggc cgc cac atc acc gaa acc gct ctg gtg aaa atg cgt gtg ctg   547
Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val Lys Met Arg Val Leu
    135                 140                 145

act gga aac aac gat ctc acc cca gct cac cgc ctc gat cgc ctg act   595
Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg Leu Asp Arg Leu Thr
150                 155                 160                 165

tcc ggt gtg tta gtc atg gtg aaa aaa cca gaa ctc cgt ggc gct tac   643
Ser Gly Val Leu Val Met Val Lys Lys Pro Glu Leu Arg Gly Ala Tyr
                170                 175                 180

caa acc ttg ttt gcc cga cgt gag gcg tcc aaa acc tat gag           685
Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys Thr Tyr Glu
            185                 190                 195
```

09550565.090505

<210> 1874
<211> 195
<212> PRT
<213> Corynebacterium glutamicum

<400> 1874

```
Met Ile Ala Leu Lys Ser Met Ser Asn Arg Val Val Gln Lys Pro Lys
  1               5                  10                  15

Met Lys Ala Pro Leu Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val
             20                  25                  30

Arg Leu Pro Leu Asp Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu
         35                  40                  45

Tyr Leu Ile Ser Thr Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu
     50                  55                  60

Ala Leu Gln Ala Arg Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly
 65                  70                  75                  80
```

```
Glu Pro Tyr Ala Pro Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp
                 85                  90                  95

Phe Tyr Arg Met Pro Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His
            100                 105                 110

Val Ile His Glu Asp Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr
        115                 120                 125

Leu Ala Thr Met Pro Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val
    130                 135                 140

Lys Met Arg Val Leu Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg
145                 150                 155                 160

Leu Asp Arg Leu Thr Ser Gly Val Leu Val Met Val Lys Lys Pro Glu
                165                 170                 175

Leu Arg Gly Ala Tyr Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys
            180                 185                 190

Thr Tyr Glu
        195
```

<210> 1875
<211> 870
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(847)
<223> RXA00676

<400> 1875

```
ggtttgcgac ctccccggcg tgccgccagg ggaggaggcg ataaaacttt tttacctttc 60

gaatatcaaa atcataaaac agccttatat acttcaacgt atg gcg aag aat tct   115
                                            Met Ala Lys Asn Ser
                                              1               5

cga atc cga tac agc gcg tca atc aag cgt gcc gca gct gca atc ctc   163
Arg Ile Arg Tyr Ser Ala Ser Ile Lys Arg Ala Ala Ala Ala Ile Leu
                10                  15                  20

acc gca gct gct acc tca gtc gcg ttg atc gct gtg cca gca act gct   211
Thr Ala Ala Ala Thr Ser Val Ala Leu Ile Ala Val Pro Ala Thr Ala
            25                  30                  35

tca gca cag gac ctc gca acc ggc agc tcc cag atc cag act gat gct   259
Ser Ala Gln Asp Leu Ala Thr Gly Ser Ser Gln Ile Gln Thr Asp Ala
        40                  45                  50

cgt gaa ggt gcg tgg gca acc cgc aac acc atc caa gac caa ctt gcc   307
Arg Glu Gly Ala Trp Ala Thr Arg Asn Thr Ile Gln Asp Gln Leu Ala
    55                  60                  65

tcc att ggg cca gca gcc ctc cca gtc cgc gca gcg gta gac aat gcc   355
Ser Ile Gly Pro Ala Ala Leu Pro Val Arg Ala Ala Val Asp Asn Ala
70                  75                  80                  85
```

```
atc aac ggc atg ttc cca gga ctt gtt gat gaa aag gtt gca gca gag   403
Ile Asn Gly Met Phe Pro Gly Leu Val Asp Glu Lys Val Ala Ala Glu
                 90                  95                 100

cag gaa gct gca cgc gca gaa gct gag cgc gaa gca gca gct gca cgt   451
Gln Glu Ala Ala Arg Ala Glu Ala Glu Arg Glu Ala Ala Ala Ala Arg
            105                 110                 115

gaa gca gaa gca gcc cgc gta gcc gca gaa gaa gcc gca cgc ttt gac   499
Glu Ala Glu Ala Ala Arg Val Ala Ala Glu Glu Ala Ala Arg Phe Asp
        120                 125                 130

cgc ggc tct tgc cca gca atc gct gat gtc tgc gtg gac att gat ggt   547
Arg Gly Ser Cys Pro Ala Ile Ala Asp Val Cys Val Asp Ile Asp Gly
    135                 140                 145

gga cgt acc tgg ctg cag gaa aac ggt cag gtc acc tac ggt gca gtc   595
Gly Arg Thr Trp Leu Gln Glu Asn Gly Gln Val Thr Tyr Gly Ala Val
150                 155                 160                 165

cca gtt tcc tcc ggc gga gtt ggc cag gaa acc cct cgc gga acg ttc   643
Pro Val Ser Ser Gly Gly Val Gly Gln Glu Thr Pro Arg Gly Thr Phe
                170                 175                 180

tac atc aac cgc aag gtc aag gat gaa atc tct tac gag ttc ggt aac   691
Tyr Ile Asn Arg Lys Val Lys Asp Glu Ile Ser Tyr Glu Phe Gly Asn
            185                 190                 195

gcc cca atg ccg tac gcc atg tac ttc acc tac aac ggc cac gca ttc   739
Ala Pro Met Pro Tyr Ala Met Tyr Phe Thr Tyr Asn Gly His Ala Phe
        200                 205                 210

cac cag ggc aat gtt gcg act act tcc gct ggt tgt gtt cgc cta aac   787
His Gln Gly Asn Val Ala Thr Thr Ser Ala Gly Cys Val Arg Leu Asn
    215                 220                 225

act caa gat gcc atc tac tac ttc aac aac gtt ggc atc ggc gac atg   835
Thr Gln Asp Ala Ile Tyr Tyr Phe Asn Asn Val Gly Ile Gly Asp Met
230                 235                 240                 245

gtg tac atc tac taaaactcac cgttgctagc agg                        870
Val Tyr Ile Tyr
```

<210> 1876
<211> 249
<212> PRT
<213> Corynebacterium glutamicum

<400> 1876

```
Met Ala Lys Asn Ser Arg Ile Arg Tyr Ser Ala Ser Ile Lys Arg Ala
  1               5                  10                  15

Ala Ala Ala Ile Leu Thr Ala Ala Ala Thr Ser Val Ala Leu Ile Ala
             20                  25                  30

Val Pro Ala Thr Ala Ser Ala Gln Asp Leu Ala Thr Gly Ser Ser Gln
         35                  40                  45
```

```
Ile Gln Thr Asp Ala Arg Glu Gly Ala Trp Ala Thr Arg Asn Thr Ile
     50                  55                  60

Gln Asp Gln Leu Ala Ser Ile Gly Pro Ala Ala Leu Pro Val Arg Ala
 65                  70                  75                  80

Ala Val Asp Asn Ala Ile Asn Gly Met Phe Pro Gly Leu Val Asp Glu
                 85                  90                  95

Lys Val Ala Ala Glu Gln Glu Ala Ala Arg Ala Glu Ala Glu Arg Glu
            100                 105                 110

Ala Ala Ala Ala Arg Glu Ala Glu Ala Ala Arg Val Ala Ala Glu Glu
        115                 120                 125

Ala Ala Arg Phe Asp Arg Gly Ser Cys Pro Ala Ile Ala Asp Val Cys
    130                 135                 140

Val Asp Ile Asp Gly Gly Arg Thr Trp Leu Gln Glu Asn Gly Gln Val
145                 150                 155                 160

Thr Tyr Gly Ala Val Pro Val Ser Ser Gly Gly Val Gly Gln Glu Thr
                165                 170                 175

Pro Arg Gly Thr Phe Tyr Ile Asn Arg Lys Val Lys Asp Glu Ile Ser
            180                 185                 190

Tyr Glu Phe Gly Asn Ala Pro Met Pro Tyr Ala Met Tyr Phe Thr Tyr
        195                 200                 205

Asn Gly His Ala Phe His Gln Gly Asn Val Ala Thr Thr Ser Ala Gly
    210                 215                 220

Cys Val Arg Leu Asn Thr Gln Asp Ala Ile Tyr Tyr Phe Asn Asn Val
225                 230                 235                 240

Gly Ile Gly Asp Met Val Tyr Ile Tyr
                245
```

<210> 1877
<211> 858
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(835)
<223> RXA00678

<400> 1877

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tgcgcagtgc actttccagg aaccaaaata tccccgccga ccttgctgca gatatttcgc 60

agccgctgaa aaaactagcc gttgacctgg aggttacccg atg act cgc agt aat   115
                                              Met Thr Arg Ser Asn
                                                1               5

tta ccc gct tgg gag caa gca gac ccc agc gtc cac gcc tct gat ccc   163
Leu Pro Ala Trp Glu Gln Ala Asp Pro Ser Val His Ala Ser Asp Pro
                10                  15                  20
```

```
cgc gcc atc act ttt gcg gag gat ttt ggg att cgt ccc atc ccg gcc   211
Arg Ala Ile Thr Phe Ala Glu Asp Phe Gly Ile Arg Pro Ile Pro Ala
             25                  30                  35

gta ggt cca att gat acc acc gct atc tgt gca aca cct tca aat gga   259
Val Gly Pro Ile Asp Thr Thr Ala Ile Cys Ala Thr Pro Ser Asn Gly
         40                  45                  50

ttt gag caa tta tgg aaa gcc att gag ccg gaa acc cgc acc cgc gcc   307
Phe Glu Gln Leu Trp Lys Ala Ile Glu Pro Glu Thr Arg Thr Arg Ala
     55                  60                  65

aac gac att cat ctt ccc atc gtc gtg gcg tac gct gaa cgt ctc tgc   355
Asn Asp Ile His Leu Pro Ile Val Val Ala Tyr Ala Glu Arg Leu Cys
 70                  75                  80                  85

gac gct tac cca ctg gca gat aga gaa ttg gtt ctc gta gcc gca atc   403
Asp Ala Tyr Pro Leu Ala Asp Arg Glu Leu Val Leu Val Ala Ala Ile
                 90                  95                 100

ctc cac gac acg ggc tgg gca cat gtc gat gag agc cga atc atc tcc   451
Leu His Asp Thr Gly Trp Ala His Val Asp Glu Ser Arg Ile Ile Ser
             105                 110                 115

gaa gga ttc tcc gga aac tgg cgc aaa gca gca atc cgc ttc gaa cac   499
Glu Gly Phe Ser Gly Asn Trp Arg Lys Ala Ala Ile Arg Phe Glu His
         120                 125                 130

gaa aca gaa ggc tgc act gtg gcc cgc cga gtg ctt cca tcc ctc gga   547
Glu Thr Glu Gly Cys Thr Val Ala Arg Arg Val Leu Pro Ser Leu Gly
     135                 140                 145

tat act gtc gat ttt gtc gag cat gtc tgc gac atc atc gac gga cac   595
Tyr Thr Val Asp Phe Val Glu His Val Cys Asp Ile Ile Asp Gly His
150                 155                 160                 165

gac acc cgc caa gtg gcc tac tca cta gaa gac gct ctt gtt cgc gat   643
Asp Thr Arg Gln Val Ala Tyr Ser Leu Glu Asp Ala Leu Val Arg Asp
                170                 175                 180

tgc gac cga ctc tgg cgt ttc gac cgc gcc ggg atc acg gct tct agc   691
Cys Asp Arg Leu Trp Arg Phe Asp Arg Ala Gly Ile Thr Ala Ser Ser
             185                 190                 195

tca tgg ttc ggg atg cca gtc tca gat tat gtc gac cgc ctg cac agg   739
Ser Trp Phe Gly Met Pro Val Ser Asp Tyr Val Asp Arg Leu His Arg
         200                 205                 210

gaa atc ctc cca gaa tta atc acc gaa gct gca cac cag atg gct act   787
Glu Ile Leu Pro Glu Leu Ile Thr Glu Ala Ala His Gln Met Ala Thr
     215                 220                 225

gca gac ctc aat cgt gca aag gcc ctg tta aga acg gat gcg atc cga   835
Ala Asp Leu Asn Arg Ala Lys Ala Leu Leu Arg Thr Asp Ala Ile Arg
230                 235                 240                 245

tgaatgctgc aaccaggcgt gct                                        858
```

<210> 1878
<211> 245

<212> PRT
<213> Corynebacterium glutamicum

<400> 1878

```
Met Thr Arg Ser Asn Leu Pro Ala Trp Glu Gln Ala Asp Pro Ser Val
  1               5                  10                  15

His Ala Ser Asp Pro Arg Ala Ile Thr Phe Ala Glu Asp Phe Gly Ile
             20                  25                  30

Arg Pro Ile Pro Ala Val Gly Pro Ile Asp Thr Thr Ala Ile Cys Ala
         35                  40                  45

Thr Pro Ser Asn Gly Phe Glu Gln Leu Trp Lys Ala Ile Glu Pro Glu
     50                  55                  60

Thr Arg Thr Arg Ala Asn Asp Ile His Leu Pro Ile Val Val Ala Tyr
 65                  70                  75                  80

Ala Glu Arg Leu Cys Asp Ala Tyr Pro Leu Ala Asp Arg Glu Leu Val
                 85                  90                  95

Leu Val Ala Ala Ile Leu His Asp Thr Gly Trp Ala His Val Asp Glu
            100                 105                 110

Ser Arg Ile Ile Ser Glu Gly Phe Ser Gly Asn Trp Arg Lys Ala Ala
        115                 120                 125

Ile Arg Phe Glu His Glu Thr Glu Gly Cys Thr Val Ala Arg Arg Val
    130                 135                 140

Leu Pro Ser Leu Gly Tyr Thr Val Asp Phe Val Glu His Val Cys Asp
145                 150                 155                 160

Ile Ile Asp Gly His Asp Thr Arg Gln Val Ala Tyr Ser Leu Glu Asp
                165                 170                 175

Ala Leu Val Arg Asp Cys Asp Arg Leu Trp Arg Phe Asp Arg Ala Gly
            180                 185                 190

Ile Thr Ala Ser Ser Ser Trp Phe Gly Met Pro Val Ser Asp Tyr Val
        195                 200                 205

Asp Arg Leu His Arg Glu Ile Leu Pro Glu Leu Ile Thr Glu Ala Ala
    210                 215                 220

His Gln Met Ala Thr Ala Asp Leu Asn Arg Ala Lys Ala Leu Leu Arg
225                 230                 235                 240

Thr Asp Ala Ile Arg
                245
```

<210> 1879
<211> 1053
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1030)

<223> RXA00691

<400> 1879

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tgcagctgca gtcgcactat ggattgttct tgccatatcg ccatgggttc cttctgcgca 60

cgccttgacc acgccttgtg aagacgacca agtgacagtg atg gtt gag ggc aac   115
                                            Met Val Glu Gly Asn
                                              1               5

acc atc ggc tgt gct gac gcc ggc gga aat ggc tat caa acg ctt ctt   163
Thr Ile Gly Cys Ala Asp Ala Gly Gly Asn Gly Tyr Gln Thr Leu Leu
                 10                  15                  20

gat gcc gga ttt gat gtg gaa acc acc gtt cag ttt cca gaa ttc ttg   211
Asp Ala Gly Phe Asp Val Glu Thr Thr Val Gln Phe Pro Glu Phe Leu
             25                  30                  35

tgc cga atc aat gat ttc cca ggt cct gat gtg gac gat tgc atg acc   259
Cys Arg Ile Asn Asp Phe Pro Gly Pro Asp Val Asp Asp Cys Met Thr
         40                  45                  50

gca tca cct gct gaa gct tat tgg tct tat tgg cat gct ccc ctc ggc   307
Ala Ser Pro Ala Glu Ala Tyr Trp Ser Tyr Trp His Ala Pro Leu Gly
     55                  60                  65

gga gat gaa tgg gaa tac agc aac ctt gga gct ttc ctc tac tac ccc   355
Gly Asp Glu Trp Glu Tyr Ser Asn Leu Gly Ala Phe Leu Tyr Tyr Pro
 70                  75                  80                  85

aaa ccc ggc act gtt gaa gcg tgg tat tgg gga gat act gat cgt ccc   403
Lys Pro Gly Thr Val Glu Ala Trp Tyr Trp Gly Asp Thr Asp Arg Pro
                 90                  95                 100

ggc gcg atc ccg gtg agt aaa tct cag gcg gag ttg ggg tta gac tcc   451
Gly Ala Ile Pro Val Ser Lys Ser Gln Ala Glu Leu Gly Leu Asp Ser
            105                 110                 115

gcg gat ccg gat tac aaa att gat ttt gat cca aat gat ttc atc acc   499
Ala Asp Pro Asp Tyr Lys Ile Asp Phe Asp Pro Asn Asp Phe Ile Thr
        120                 125                 130

aca acc cca acc tcc gag tcc cct atc gcc gat tta ggg ggt gac gaa   547
Thr Thr Pro Thr Ser Glu Ser Pro Ile Ala Asp Leu Gly Gly Asp Glu
    135                 140                 145

gag ccc act gaa act act gaa gct cct atc gca ggg gct gga gct ggt   595
Glu Pro Thr Glu Thr Thr Glu Ala Pro Ile Ala Gly Ala Gly Ala Gly
150                 155                 160                 165

tcg gca aga gga caa gca gct gaa ccc act gtt gag gta aac cct gag   643
Ser Ala Arg Gly Gln Ala Ala Glu Pro Thr Val Glu Val Asn Pro Glu
                170                 175                 180

aac cct aat gag gta ttg gtg tat cag gat tct gaa gga aac tcg att   691
Asn Pro Asn Glu Val Leu Val Tyr Gln Asp Ser Glu Gly Asn Ser Ile
            185                 190                 195

act aaa ggt cag tac gag aac ttg gtt gct gca gca gcc gct aag acc   739
Thr Lys Gly Gln Tyr Glu Asn Leu Val Ala Ala Ala Ala Ala Lys Thr
        200                 205                 210
```

```
act gct gct gtc caa gcc cca gct ggg gct ggt gaa gca aat agc caa   787
Thr Ala Ala Val Gln Ala Pro Ala Gly Ala Gly Glu Ala Asn Ser Gln
    215                 220                 225

ccg cag gca aca gcg gtg gca gaa gct cct gaa gtt gat ccg atg acc   835
Pro Gln Ala Thr Ala Val Ala Glu Ala Pro Glu Val Asp Pro Met Thr
230                 235                 240                 245

acg cag gtt ctt atg gcg cct gcg ggc caa gat gga gac gtc atg gct   883
Thr Gln Val Leu Met Ala Pro Ala Gly Gln Asp Gly Asp Val Met Ala
                250                 255                 260

gag ggt tcg acg cag cag acg tac gcc aca ggc acg gtg gat tct tct   931
Glu Gly Ser Thr Gln Gln Thr Tyr Ala Thr Gly Thr Val Asp Ser Ser
            265                 270                 275

gct cag gga tgg atc att gga ctc aca ctg gct gtc att tcc ttg gtt   979
Ala Gln Gly Trp Ile Ile Gly Leu Thr Leu Ala Val Ile Ser Leu Val
        280                 285                 290

tca gcg tct gct gtg gcg gcg tgg gcg att cgt cgt tca gag gtc cag   1027
Ser Ala Ser Ala Val Ala Ala Trp Ala Ile Arg Arg Ser Glu Val Gln
    295                 300                 305

ggt taaagcttcg tgaaatggat tga                                    1053
Gly
310
```

<210> 1880
<211> 310
<212> PRT
<213> Corynebacterium glutamicum

<400> 1880

```
Met Val Glu Gly Asn Thr Ile Gly Cys Ala Asp Ala Gly Gly Asn Gly
  1               5                  10                  15

Tyr Gln Thr Leu Leu Asp Ala Gly Phe Asp Val Glu Thr Thr Val Gln
            20                  25                  30

Phe Pro Glu Phe Leu Cys Arg Ile Asn Asp Phe Pro Gly Pro Asp Val
        35                  40                  45

Asp Asp Cys Met Thr Ala Ser Pro Ala Glu Ala Tyr Trp Ser Tyr Trp
    50                  55                  60

His Ala Pro Leu Gly Gly Asp Glu Trp Glu Tyr Ser Asn Leu Gly Ala
65                  70                  75                  80

Phe Leu Tyr Tyr Pro Lys Pro Gly Thr Val Glu Ala Trp Tyr Trp Gly
                85                  90                  95

Asp Thr Asp Arg Pro Gly Ala Ile Pro Val Ser Lys Ser Gln Ala Glu
            100                 105                 110

Leu Gly Leu Asp Ser Ala Asp Pro Asp Tyr Lys Ile Asp Phe Asp Pro
        115                 120                 125

Asn Asp Phe Ile Thr Thr Thr Pro Thr Ser Glu Ser Pro Ile Ala Asp
    130                 135                 140
```

```
Leu Gly Gly Asp Glu Glu Pro Thr Glu Thr Thr Glu Ala Pro Ile Ala
145                 150                 155                 160

Gly Ala Gly Ala Gly Ser Ala Arg Gly Gln Ala Ala Glu Pro Thr Val
                165                 170                 175

Glu Val Asn Pro Glu Asn Pro Asn Glu Val Leu Val Tyr Gln Asp Ser
            180                 185                 190

Glu Gly Asn Ser Ile Thr Lys Gly Gln Tyr Glu Asn Leu Val Ala Ala
        195                 200                 205

Ala Ala Ala Lys Thr Thr Ala Ala Val Gln Ala Pro Ala Gly Ala Gly
    210                 215                 220

Glu Ala Asn Ser Gln Pro Gln Ala Thr Ala Val Ala Glu Ala Pro Glu
225                 230                 235                 240

Val Asp Pro Met Thr Thr Gln Val Leu Met Ala Pro Ala Gly Gln Asp
                245                 250                 255

Gly Asp Val Met Ala Glu Gly Ser Thr Gln Gln Thr Tyr Ala Thr Gly
            260                 265                 270

Thr Val Asp Ser Ser Ala Gln Gly Trp Ile Ile Gly Leu Thr Leu Ala
        275                 280                 285

Val Ile Ser Leu Val Ser Ala Ser Ala Val Ala Ala Trp Ala Ile Arg
    290                 295                 300

Arg Ser Glu Val Gln Gly
305                 310


<210> 1881
<211> 1257
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1234)
<223> RXA00692

<400> 1881
ccttaaagcg gggtcagaac atttctccaa ttcattttaa ggacatgttt tcatggctca 60

tctacgtggg aagagaacca ttcgctggtc tgctgcaacc gtg gct tta gca acc   115
                                              Val Ala Leu Ala Thr
                                                1               5

ggt gtt tcc ctg ttg gct cca cag gtc gtt gct gca cag gat gca tca   163
Gly Val Ser Leu Leu Ala Pro Gln Val Val Ala Ala Gln Asp Ala Ser
                10                  15                  20

tcg gat att caa tta gct acc caa ttc atc gaa aaa gaa ttt gca acg   211
Ser Asp Ile Gln Leu Ala Thr Gln Phe Ile Glu Lys Glu Phe Ala Thr
            25                  30                  35

aat ggc ctc atc cct ggg cct gta ggt act cca gat att ggg ctc aat   259
```

```
Asn Gly Leu Ile Pro Gly Pro Val Gly Thr Pro Asp Ile Gly Leu Asn
          40                  45                  50

cag gat ctg ttg ctg tcc cta aat gcg ctt gcc cct gat tct cca gag   307
Gln Asp Leu Leu Leu Ser Leu Asn Ala Leu Ala Pro Asp Ser Pro Glu
     55                  60                  65

atc gac gct gca tat gct gca att gct ccg gag ctc gag ggc tat gtc   355
Ile Asp Ala Ala Tyr Ala Ala Ile Ala Pro Glu Leu Glu Gly Tyr Val
 70                  75                  80                  85

tca gtt tct gac tac atc ttc agc gat cgt cta gcc aag acc gta gct   403
Ser Val Ser Asp Tyr Ile Phe Ser Asp Arg Leu Ala Lys Thr Val Ala
                 90                  95                 100

ttc caa gat gcc ctc ggc gtc aga gat gct gat ttt atc gcg caa ctt   451
Phe Gln Asp Ala Leu Gly Val Arg Asp Ala Asp Phe Ile Ala Gln Leu
            105                 110                 115

gtc agc gct gtt caa gaa aac ggt cag atc aaa aac tta gat aat ggt   499
Val Ser Ala Val Gln Glu Asn Gly Gln Ile Lys Asn Leu Asp Asn Gly
        120                 125                 130

gaa gcc aca act gca att aat aac ttc agc cag gcc tgg ggc gtt cta   547
Glu Ala Thr Thr Ala Ile Asn Asn Phe Ser Gln Ala Trp Gly Val Leu
    135                 140                 145

gct ctg cac cgc gtc ggt gaa acc gaa gca gcc gag cgc gca aca gaa   595
Ala Leu His Arg Val Gly Glu Thr Glu Ala Ala Glu Arg Ala Thr Glu
150                 155                 160                 165

ttc ctt aaa act caa gtg tgc tcc gac ggt ggt gtc caa tta gcc tca   643
Phe Leu Lys Thr Gln Val Cys Ser Asp Gly Gly Val Gln Leu Ala Ser
                170                 175                 180

gca atc gaa cct aca tgc aaa acc acg gat tcc gat gtc act gca atg   691
Ala Ile Glu Pro Thr Cys Lys Thr Thr Asp Ser Asp Val Thr Ala Met
            185                 190                 195

gct gca cag gct ttg act ctg gca aat ggt gcg cag gat cca acc aca   739
Ala Ala Gln Ala Leu Thr Leu Ala Asn Gly Ala Gln Asp Pro Thr Thr
        200                 205                 210

caa gcc act ctc gat tac ctc gtc acc acg atg gat gag acc ggt ggt   787
Gln Ala Thr Leu Asp Tyr Leu Val Thr Thr Met Asp Glu Thr Gly Gly
    215                 220                 225

gtc aaa aat act tgg acc ggt gtg aat tcc aac tcc acg gga att gtc   835
Val Lys Asn Thr Trp Thr Gly Val Asn Ser Asn Ser Thr Gly Ile Val
230                 235                 240                 245

gga tcc gct ttt gct ctt gcg ggc gat gag gaa aac tac ctc aag gct   883
Gly Ser Ala Phe Ala Leu Ala Gly Asp Glu Glu Asn Tyr Leu Lys Ala
                250                 255                 260

cgt gaa tac ctg gca tct gtt caa ttt ggc gaa gat gca gac cca tcg   931
Arg Glu Tyr Leu Ala Ser Val Gln Phe Gly Glu Asp Ala Asp Pro Ser
            265                 270                 275

att cag ggt ggc ttt gct ttc acc gtg aag gct aag gaa acc aac act   979
Ile Gln Gly Gly Phe Ala Phe Thr Val Lys Ala Lys Glu Thr Asn Thr
```

```
        280                 285                 290

gcg att agc gat cag att cga cgc gca act ggc caa gca gca tta ggt   1027
Ala Ile Ser Asp Gln Ile Arg Arg Ala Thr Gly Gln Ala Ala Leu Gly
    295                 300                 305

ttt gca ggc ggt aac tac gcc aac gat aaa ctg atc acc att gcg aac   1075
Phe Ala Gly Gly Asn Tyr Ala Asn Asp Lys Leu Ile Thr Ile Ala Asn
310                 315                 320                 325

cca gta gat cca act cca gat cca gaa att cca act ccc cca gct gat   1123
Pro Val Asp Pro Thr Pro Asp Pro Glu Ile Pro Thr Pro Pro Ala Asp
                330                 335                 340

tca gag gga tcc acc ggt gga att ggc ggc gct gga att atc atc gcc   1171
Ser Glu Gly Ser Thr Gly Gly Ile Gly Gly Ala Gly Ile Ile Ile Ala
            345                 350                 355

atc ttg gcc atc ctt gcc gcc atc gct ggt gtc atg gga cca atg atg   1219
Ile Leu Ala Ile Leu Ala Ala Ile Ala Gly Val Met Gly Pro Met Met
        360                 365                 370

gct aac ctg cag ttt taacatctga gagaagtaca gtg                    1257
Ala Asn Leu Gln Phe
    375


<210> 1882
<211> 378
<212> PRT
<213> Corynebacterium glutamicum

<400> 1882
Val Ala Leu Ala Thr Gly Val Ser Leu Leu Ala Pro Gln Val Val Ala
  1               5                  10                  15

Ala Gln Asp Ala Ser Ser Asp Ile Gln Leu Ala Thr Gln Phe Ile Glu
             20                  25                  30

Lys Glu Phe Ala Thr Asn Gly Leu Ile Pro Gly Pro Val Gly Thr Pro
         35                  40                  45

Asp Ile Gly Leu Asn Gln Asp Leu Leu Leu Ser Leu Asn Ala Leu Ala
     50                  55                  60

Pro Asp Ser Pro Glu Ile Asp Ala Ala Tyr Ala Ala Ile Ala Pro Glu
 65                  70                  75                  80

Leu Glu Gly Tyr Val Ser Val Ser Asp Tyr Ile Phe Ser Asp Arg Leu
                 85                  90                  95

Ala Lys Thr Val Ala Phe Gln Asp Ala Leu Gly Val Arg Asp Ala Asp
            100                 105                 110

Phe Ile Ala Gln Leu Val Ser Ala Val Gln Glu Asn Gly Gln Ile Lys
        115                 120                 125

Asn Leu Asp Asn Gly Glu Ala Thr Thr Ala Ile Asn Asn Phe Ser Gln
    130                 135                 140

Ala Trp Gly Val Leu Ala Leu His Arg Val Gly Glu Thr Glu Ala Ala
```

```
145                 150                 155                 160

Glu Arg Ala Thr Glu Phe Leu Lys Thr Gln Val Cys Ser Asp Gly Gly
                165                 170                 175

Val Gln Leu Ala Ser Ala Ile Glu Pro Thr Cys Lys Thr Thr Asp Ser
            180                 185                 190

Asp Val Thr Ala Met Ala Ala Gln Ala Leu Thr Leu Ala Asn Gly Ala
        195                 200                 205

Gln Asp Pro Thr Thr Gln Ala Thr Leu Asp Tyr Leu Val Thr Thr Met
    210                 215                 220

Asp Glu Thr Gly Gly Val Lys Asn Thr Trp Thr Gly Val Asn Ser Asn
225                 230                 235                 240

Ser Thr Gly Ile Val Gly Ser Ala Phe Ala Leu Ala Gly Asp Glu Glu
                245                 250                 255

Asn Tyr Leu Lys Ala Arg Glu Tyr Leu Ala Ser Val Gln Phe Gly Glu
            260                 265                 270

Asp Ala Asp Pro Ser Ile Gln Gly Gly Phe Ala Phe Thr Val Lys Ala
        275                 280                 285

Lys Glu Thr Asn Thr Ala Ile Ser Asp Gln Ile Arg Arg Ala Thr Gly
    290                 295                 300

Gln Ala Ala Leu Gly Phe Ala Gly Gly Asn Tyr Ala Asn Asp Lys Leu
305                 310                 315                 320

Ile Thr Ile Ala Asn Pro Val Asp Pro Thr Pro Asp Pro Glu Ile Pro
                325                 330                 335

Thr Pro Pro Ala Asp Ser Glu Gly Ser Thr Gly Gly Ile Gly Gly Ala
            340                 345                 350

Gly Ile Ile Ile Ala Ile Leu Ala Ile Leu Ala Ala Ile Ala Gly Val
        355                 360                 365

Met Gly Pro Met Met Ala Asn Leu Gln Phe
    370                 375


<210> 1883
<211> 606
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(583)
<223> RXA00693

<400> 1883
tccatcagcc ctccccgcg tgccccacgc ggggcacggt tagcgctgct aacctggccc 60

gatgtacaaa ttaatctcac cgcatttgtc aggccacgcc atg tgg aaa gag gct   115
                                               Met Trp Lys Glu Ala
                                                 1               5
```

```
ttg gaa gaa ttc gga tca ggc ccc atc cac ggc tcg ggt tat ttc gag   163
Leu Glu Glu Phe Gly Ser Gly Pro Ile His Gly Ser Gly Tyr Phe Glu
                 10                  15                  20

aac tat ctt ccc atc gac tat tcc gaa gca gga ttt cac cac tac ctc   211
Asn Tyr Leu Pro Ile Asp Tyr Ser Glu Ala Gly Phe His His Tyr Leu
             25                  30                  35

aag gag cgc act gac gcg gcc gat cct tcg gtt cca cca ccg gaa ggt   259
Lys Glu Arg Thr Asp Ala Ala Asp Pro Ser Val Pro Pro Pro Glu Gly
         40                  45                  50

ttt gtg cac tgc agc tat ttc tgg atc gtt gat gat gac gat gtt ctt   307
Phe Val His Cys Ser Tyr Phe Trp Ile Val Asp Asp Asp Asp Val Leu
     55                  60                  65

gtc gga ttc tta gct tta agg cac gag ctg aac caa cat ctc ctg gaa   355
Val Gly Phe Leu Ala Leu Arg His Glu Leu Asn Gln His Leu Leu Glu
 70                  75                  80                  85

gtc gcg ggc cac att ggt tac ggc gtg cgc ccg tct gcg cgt cga aaa   403
Val Ala Gly His Ile Gly Tyr Gly Val Arg Pro Ser Ala Arg Arg Lys
                 90                  95                 100

ggt gct gca acc gca gcg ctg aaa ctc ggt gtt cat gaa gct cag gcc   451
Gly Ala Ala Thr Ala Ala Leu Lys Leu Gly Val His Glu Ala Gln Ala
             105                 110                 115

ttg ggc atc gac aag gtt ttg ctg tgc gtc gca gga gat aac gaa gcg   499
Leu Gly Ile Asp Lys Val Leu Leu Cys Val Ala Gly Asp Asn Glu Ala
         120                 125                 130

tcc agg aac gtc atc gaa aag tgc ggt gga gtt tat gaa tcc acg atc   547
Ser Arg Asn Val Ile Glu Lys Cys Gly Gly Val Tyr Glu Ser Thr Ile
     135                 140                 145

cgt gga atg cga cgc tat tgg ata gcc aca gat tct taaaaaatct        593
Arg Gly Met Arg Arg Tyr Trp Ile Ala Thr Asp Ser
150                 155                 160

tcgcaagaac tta                                                   606


<210> 1884
<211> 161
<212> PRT
<213> Corynebacterium glutamicum

<400> 1884
Met Trp Lys Glu Ala Leu Glu Glu Phe Gly Ser Gly Pro Ile His Gly
  1               5                  10                  15

Ser Gly Tyr Phe Glu Asn Tyr Leu Pro Ile Asp Tyr Ser Glu Ala Gly
             20                  25                  30

Phe His His Tyr Leu Lys Glu Arg Thr Asp Ala Ala Asp Pro Ser Val
         35                  40                  45

Pro Pro Pro Glu Gly Phe Val His Cys Ser Tyr Phe Trp Ile Val Asp
     50                  55                  60
```

```
Asp Asp Asp Val Leu Val Gly Phe Leu Ala Leu Arg His Glu Leu Asn
 65                  70                  75                  80

Gln His Leu Leu Glu Val Ala Gly His Ile Gly Tyr Gly Val Arg Pro
                 85                  90                  95

Ser Ala Arg Arg Lys Gly Ala Ala Thr Ala Ala Leu Lys Leu Gly Val
            100                 105                 110

His Glu Ala Gln Ala Leu Gly Ile Asp Lys Val Leu Leu Cys Val Ala
        115                 120                 125

Gly Asp Asn Glu Ala Ser Arg Asn Val Ile Glu Lys Cys Gly Gly Val
    130                 135                 140

Tyr Glu Ser Thr Ile Arg Gly Met Arg Arg Tyr Trp Ile Ala Thr Asp
145                 150                 155                 160

Ser
```

US20030148473A1

```
<210> 1885
<211> 498
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(475)
<223> RXA00701

<400> 1885
aagagacgat ggcgtatagg acgatgatga gcatttcctt tttgccgcgt acttgggggga 60

gtaggccggc gccgaagctg acccaggcgg ctgcgagcat ttg gta ggg gag cca   115
                                              Leu Val Gly Glu Pro
                                                1               5

cgg tcc gat tcc tgc ggt gag cag cgc gga tgc gaa cag tcc ggt gtt   163
Arg Ser Asp Ser Cys Gly Glu Gln Arg Gly Cys Glu Gln Ser Gly Val
                 10                  15                  20

gcc gag gat gaa tcc gaa gcc ggg tcc gaa ggc tcg tcc gcc gag gat   211
Ala Glu Asp Glu Ser Glu Ala Gly Ser Glu Gly Ser Ser Ala Glu Asp
             25                  30                  35

gag gac aaa gaa gac tgc ttc aaa gcc tgc tgc gcc ggc acc gaa tgg   259
Glu Asp Lys Glu Asp Cys Phe Lys Ala Cys Cys Ala Gly Thr Glu Trp
         40                  45                  50

tcg gac tac ggc aac cat ggc ggt gag gac gcc gag cat ggc tac ggc   307
Ser Asp Tyr Gly Asn His Gly Gly Glu Asp Ala Glu His Gly Tyr Gly
     55                  60                  65

ttt aac gtc gaa tcc gtt ttc act gat ttc ggc gat gac agc ggc cag   355
Phe Asn Val Glu Ser Val Phe Thr Asp Phe Gly Asp Asp Ser Gly Gln
 70                  75                  80                  85

cac gag ggg aat gac gat cgc gat gta gag ggg cgc ttg ggc ttt gtc   403
```

```
His Glu Gly Asn Asp Asp Arg Asp Val Glu Gly Arg Leu Gly Phe Val
                  90                  95                 100

gga cag gaa gga ttc cgg gtt gac gat cag cgg cca gaa gaa aat cac   451
Gly Gln Glu Gly Phe Arg Val Asp Asp Gln Arg Pro Glu Glu Asn His
            105                 110                 115

gat gct caa aac cgc aag gaa gct taaggtgagg aaggttttgg gct         498
Asp Ala Gln Asn Arg Lys Glu Ala
        120                 125
```

<210> 1886
<211> 125
<212> PRT
<213> Corynebacterium glutamicum

<400> 1886

```
Leu Val Gly Glu Pro Arg Ser Asp Ser Cys Gly Glu Gln Arg Gly Cys
  1               5                  10                  15

Glu Gln Ser Gly Val Ala Glu Asp Glu Ser Glu Ala Gly Ser Glu Gly
             20                  25                  30

Ser Ser Ala Glu Asp Glu Asp Lys Glu Asp Cys Phe Lys Ala Cys Cys
         35                  40                  45

Ala Gly Thr Glu Trp Ser Asp Tyr Gly Asn His Gly Gly Glu Asp Ala
     50                  55                  60

Glu His Gly Tyr Gly Phe Asn Val Glu Ser Val Phe Thr Asp Phe Gly
 65                  70                  75                  80

Asp Asp Ser Gly Gln His Glu Gly Asn Asp Asp Arg Asp Val Glu Gly
                 85                  90                  95

Arg Leu Gly Phe Val Gly Gln Glu Gly Phe Arg Val Asp Asp Gln Arg
            100                 105                 110

Pro Glu Glu Asn His Asp Ala Gln Asn Arg Lys Glu Ala
        115                 120                 125
```

<210> 1887
<211> 1095
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1072)
<223> RXA00707

<400> 1887

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tagttaaaag cacttacctt aactggtagg tgctttttc atgtctacgc agtgggtaac 60

tttcagagga aaattaccca accaaaacaa aggaactttc atg aac gtg caa cgc   115
                                            Met Asn Val Gln Arg
                                              1               5

aaa ctg ctg gcg atc gta ggg gct ttc atg gca ggg tct tta gcc ttg   163
```

```
Lys Leu Leu Ala Ile Val Gly Ala Phe Met Ala Gly Ser Leu Ala Leu
                 10                  15                  20

gga aca cca act gca cag gcc caa agc att ggc agc agt gcc tca cag   211
Gly Thr Pro Thr Ala Gln Ala Gln Ser Ile Gly Ser Ser Ala Ser Gln
             25                  30                  35

aga act gaa gtc tta cgt ggg ctg acc tca tct gcc gga ata cca gat   259
Arg Thr Glu Val Leu Arg Gly Leu Thr Ser Ser Ala Gly Ile Pro Asp
         40                  45                  50

gcc aca gcg ccg gaa ggc ggg gca aaa gtc gtg gtc ttt gga gat tca   307
Ala Thr Ala Pro Glu Gly Gly Ala Lys Val Val Val Phe Gly Asp Ser
     55                  60                  65

cat gca tca gga acc aat gca cca ttt gat gtg gat gaa cgc ggc tgc   355
His Ala Ser Gly Thr Asn Ala Pro Phe Asp Val Asp Glu Arg Gly Cys
 70                  75                  80                  85

ctc aag ggg aac caa tcg tgg cct gat caa ttg caa gca caa caa gga   403
Leu Lys Gly Asn Gln Ser Trp Pro Asp Gln Leu Gln Ala Gln Gln Gly
                 90                  95                 100

ttg cag cag ggg gag ctc att gac ctt tcc tgc aac ggc gcc tcc atc   451
Leu Gln Gln Gly Glu Leu Ile Asp Leu Ser Cys Asn Gly Ala Ser Ile
             105                 110                 115

aac tcg acg ggt ttc cac ttt tcc gat gaa gtt cgg cat gca gaa gca   499
Asn Ser Thr Gly Phe His Phe Ser Asp Glu Val Arg His Ala Glu Ala
         120                 125                 130

cta ggg gcc att gga cca aat acc gag aac atc ttc atc caa ttt ggc   547
Leu Gly Ala Ile Gly Pro Asn Thr Glu Asn Ile Phe Ile Gln Phe Gly
     135                 140                 145

aag aat gat cag tgg gga cac tca cca atc aat ttg cgc tat tcc gtg   595
Lys Asn Asp Gln Trp Gly His Ser Pro Ile Asn Leu Arg Tyr Ser Val
150                 155                 160                 165

atc aac tgc ctt ttt gat gcg gcc aac gga tgc ggt gag aaa gct gta   643
Ile Asn Cys Leu Phe Asp Ala Ala Asn Gly Cys Gly Glu Lys Ala Val
                 170                 175                 180

gcg gct gga acc atg cag gat ccc tcc tcg gtc acc ggc gaa aac tat   691
Ala Ala Gly Thr Met Gln Asp Pro Ser Ser Val Thr Gly Glu Asn Tyr
             185                 190                 195

gct cag cgg atg aaa cct gtc atc gac tac ctc aag tac tac gct cca   739
Ala Gln Arg Met Lys Pro Val Ile Asp Tyr Leu Lys Tyr Tyr Ala Pro
         200                 205                 210

aat gcg cag atc acg ttg ctg gga tac cag gaa tac acc cca cga agc   787
Asn Ala Gln Ile Thr Leu Leu Gly Tyr Gln Glu Tyr Thr Pro Arg Ser
     215                 220                 225

gga agc gag att tgt gtc cgc gtg gga ggt acg gaa cta agg aaa cca   835
Gly Ser Glu Ile Cys Val Arg Val Gly Gly Thr Glu Leu Arg Lys Pro
230                 235                 240                 245

gac gcc acc aac ctg gtg tcc tat atg aac aat ctt gag tcg gcc att   883
Asp Ala Thr Asn Leu Val Ser Tyr Met Asn Asn Leu Glu Ser Ala Ile
```

```
                250                 255                 260

ttt gaa gcc tct gag att ctt gac gtc cag cat gcc aat ctc cgt gag   931
Phe Glu Ala Ser Glu Ile Leu Asp Val Gln His Ala Asn Leu Arg Glu
            265                 270                 275

gcc act gca gga cac agc agc tgc tca gct gaa ccg tgg gtc aac gga   979
Ala Thr Ala Gly His Ser Ser Cys Ser Ala Glu Pro Trp Val Asn Gly
        280                 285                 290

gtg ctg gat atg cgg gta aac gct gta gga ggc acc tgg cac cca tct   1027
Val Leu Asp Met Arg Val Asn Ala Val Gly Gly Thr Trp His Pro Ser
    295                 300                 305

cca aag gga gat gaa gtg acc gcg ggc ctc ctc gga acc ttg atg       1072
Pro Lys Gly Asp Glu Val Thr Ala Gly Leu Leu Gly Thr Leu Met
310                 315                 320

taactatcta gaattcttca tag                                        1095
```

09/20/2005 09:50:50

<210> 1888
<211> 324
<212> PRT
<213> Corynebacterium glutamicum

<400> 1888

```
Met Asn Val Gln Arg Lys Leu Leu Ala Ile Val Gly Ala Phe Met Ala
  1               5                  10                  15

Gly Ser Leu Ala Leu Gly Thr Pro Thr Ala Gln Ala Gln Ser Ile Gly
             20                  25                  30

Ser Ser Ala Ser Gln Arg Thr Glu Val Leu Arg Gly Leu Thr Ser Ser
         35                  40                  45

Ala Gly Ile Pro Asp Ala Thr Ala Pro Glu Gly Gly Ala Lys Val Val
     50                  55                  60

Val Phe Gly Asp Ser His Ala Ser Gly Thr Asn Ala Pro Phe Asp Val
 65                  70                  75                  80

Asp Glu Arg Gly Cys Leu Lys Gly Asn Gln Ser Trp Pro Asp Gln Leu
                 85                  90                  95

Gln Ala Gln Gln Gly Leu Gln Gln Gly Glu Leu Ile Asp Leu Ser Cys
            100                 105                 110

Asn Gly Ala Ser Ile Asn Ser Thr Gly Phe His Phe Ser Asp Glu Val
        115                 120                 125

Arg His Ala Glu Ala Leu Gly Ala Ile Gly Pro Asn Thr Glu Asn Ile
    130                 135                 140

Phe Ile Gln Phe Gly Lys Asn Asp Gln Trp Gly His Ser Pro Ile Asn
145                 150                 155                 160

Leu Arg Tyr Ser Val Ile Asn Cys Leu Phe Asp Ala Ala Asn Gly Cys
                165                 170                 175

Gly Glu Lys Ala Val Ala Ala Gly Thr Met Gln Asp Pro Ser Ser Val
```

```
            180                 185                 190

Thr Gly Glu Asn Tyr Ala Gln Arg Met Lys Pro Val Ile Asp Tyr Leu
        195                 200                 205

Lys Tyr Tyr Ala Pro Asn Ala Gln Ile Thr Leu Leu Gly Tyr Gln Glu
    210                 215                 220

Tyr Thr Pro Arg Ser Gly Ser Glu Ile Cys Val Arg Val Gly Gly Thr
225                 230                 235                 240

Glu Leu Arg Lys Pro Asp Ala Thr Asn Leu Val Ser Tyr Met Asn Asn
                245                 250                 255

Leu Glu Ser Ala Ile Phe Glu Ala Ser Glu Ile Leu Asp Val Gln His
            260                 265                 270

Ala Asn Leu Arg Glu Ala Thr Ala Gly His Ser Ser Cys Ser Ala Glu
        275                 280                 285

Pro Trp Val Asn Gly Val Leu Asp Met Arg Val Asn Ala Val Gly Gly
    290                 295                 300

Thr Trp His Pro Ser Pro Lys Gly Asp Glu Val Thr Ala Gly Leu Leu
305                 310                 315                 320

Gly Thr Leu Met
```

Sequence Listing

<210> 1889
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (71)..(1033)
<223> RXA00713

<400> 1889

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aaccacgcct ccttgtgcgg gcctgtcagt aactgttatc gcaggttcat gcgttaaggt 60

gtggaagacc atg aca aaa gta gcg gag ctg gac caa gag tgg tcc gaa    109
           Met Thr Lys Val Ala Glu Leu Asp Gln Glu Trp Ser Glu
             1               5                   10

gta gat gac gcg gaa tta gac gcg caa agc gct ggc act tct gat agt   157
Val Asp Asp Ala Glu Leu Asp Ala Gln Ser Ala Gly Thr Ser Asp Ser
     15                  20                  25

tcc agc aca gac gac ttc gct gac gca gaa aac act tct gaa aat ctg   205
Ser Ser Thr Asp Asp Phe Ala Asp Ala Glu Asn Thr Ser Glu Asn Leu
 30                  35                  40                  45

gga ccc atc ggc cca gaa cca ctc cct gaa cca gat ggg gat gtt ccg   253
Gly Pro Ile Gly Pro Glu Pro Leu Pro Glu Pro Asp Gly Asp Val Pro
                 50                  55                  60

gca tcg ggt ttc caa gtg cag ctc gat aat ttt gaa ggt cct ttt gac   301
Ala Ser Gly Phe Gln Val Gln Leu Asp Asn Phe Glu Gly Pro Phe Asp
```

```
            65                  70                  75

ctt ctc ctg cag ctg att acc aag aag aaa ctt gat gtc act gaa gtt   349
Leu Leu Leu Gln Leu Ile Thr Lys Lys Lys Leu Asp Val Thr Glu Val
         80                  85                  90

gcc ttg gcc cag gtg acc gac gag ttt att gct tac acc cga aaa ctg   397
Ala Leu Ala Gln Val Thr Asp Glu Phe Ile Ala Tyr Thr Arg Lys Leu
     95                 100                 105

ggc gaa acc agc gat ttg gat gag acc aca gag ttc tta gtg gtg gcc   445
Gly Glu Thr Ser Asp Leu Asp Glu Thr Thr Glu Phe Leu Val Val Ala
110                 115                 120                 125

gca acg ctg ttg gat ctt aaa aca gct cgc ctg ctc ccg cgt ggt gaa   493
Ala Thr Leu Leu Asp Leu Lys Thr Ala Arg Leu Leu Pro Arg Gly Glu
                130                 135                 140

gtc gac gat gaa gat gat ctc gaa ttg ctc gaa ata aag gat ctc ctt   541
Val Asp Asp Glu Asp Asp Leu Glu Leu Leu Glu Ile Lys Asp Leu Leu
            145                 150                 155

ttc gcc agg ttg ttg cag tat cgc gct tac aag caa gtt gcg gaa atg   589
Phe Ala Arg Leu Leu Gln Tyr Arg Ala Tyr Lys Gln Val Ala Glu Met
        160                 165                 170

ttt gcg caa tgg cag cga gat gct cga cgc agg tac ccg cgc gct gtc   637
Phe Ala Gln Trp Gln Arg Asp Ala Arg Arg Arg Tyr Pro Arg Ala Val
    175                 180                 185

tca tta gaa act cag ttt gcc aac ctc ttg ccg ccc gtt tcc ttg ggt   685
Ser Leu Glu Thr Gln Phe Ala Asn Leu Leu Pro Pro Val Ser Leu Gly
190                 195                 200                 205

cat tcc tta aaa agt ttc agc gag ttg gct gct gtg gtg ttt cgt ccg   733
His Ser Leu Lys Ser Phe Ser Glu Leu Ala Ala Val Val Phe Arg Pro
                210                 215                 220

aaa ccc cca gag acg gtg aaa aca gat cac gtg cac caa gtt gcg gtg   781
Lys Pro Pro Glu Thr Val Lys Thr Asp His Val His Gln Val Ala Val
            225                 230                 235

tca gtt cca gag caa gcg ggc agg att ctt aac acg ttg aaa ctt gcc   829
Ser Val Pro Glu Gln Ala Gly Arg Ile Leu Asn Thr Leu Lys Leu Ala
        240                 245                 250

gga att gat cat tat ttg agc ttt cag ctg ctc aca cgt gat tgt acc   877
Gly Ile Asp His Tyr Leu Ser Phe Gln Leu Leu Thr Arg Asp Cys Thr
    255                 260                 265

gcg tca atg gaa gtg att ggc cgc ttc ctt gcc ttg ctg gaa ttg tat   925
Ala Ser Met Glu Val Ile Gly Arg Phe Leu Ala Leu Leu Glu Leu Tyr
270                 275                 280                 285

aag gca cgc gct att gaa acc ttg caa gaa gag cca ctc ggc gag ctt   973
Lys Ala Arg Ala Ile Glu Thr Leu Gln Glu Glu Pro Leu Gly Glu Leu
                290                 295                 300

aaa gtt tcg tgg act ggc att gat gtc gat cca gca gtc gtc gcg gcg   1021
Lys Val Ser Trp Thr Gly Ile Asp Val Asp Pro Ala Val Val Ala Ala
            305                 310                 315
```

agt gac tgg gag taatcagttt ttcttaagga aac 1056
Ser Asp Trp Glu
320

<210> 1890
<211> 321
<212> PRT
<213> Corynebacterium glutamicum

<400> 1890
Met Thr Lys Val Ala Glu Leu Asp Gln Glu Trp Ser Glu Val Asp Asp
1 5 10 15

Ala Glu Leu Asp Ala Gln Ser Ala Gly Thr Ser Asp Ser Ser Ser Thr
20 25 30

Asp Asp Phe Ala Asp Ala Glu Asn Thr Ser Glu Asn Leu Gly Pro Ile
35 40 45

Gly Pro Glu Pro Leu Pro Glu Pro Asp Gly Asp Val Pro Ala Ser Gly
50 55 60

Phe Gln Val Gln Leu Asp Asn Phe Glu Gly Pro Phe Asp Leu Leu Leu
65 70 75 80

Gln Leu Ile Thr Lys Lys Lys Leu Asp Val Thr Glu Val Ala Leu Ala
85 90 95

Gln Val Thr Asp Glu Phe Ile Ala Tyr Thr Arg Lys Leu Gly Glu Thr
100 105 110

Ser Asp Leu Asp Glu Thr Thr Glu Phe Leu Val Val Ala Ala Thr Leu
115 120 125

Leu Asp Leu Lys Thr Ala Arg Leu Leu Pro Arg Gly Glu Val Asp Asp
130 135 140

Glu Asp Asp Leu Glu Leu Leu Glu Ile Lys Asp Leu Leu Phe Ala Arg
145 150 155 160

Leu Leu Gln Tyr Arg Ala Tyr Lys Gln Val Ala Glu Met Phe Ala Gln
165 170 175

Trp Gln Arg Asp Ala Arg Arg Arg Tyr Pro Arg Ala Val Ser Leu Glu
180 185 190

Thr Gln Phe Ala Asn Leu Leu Pro Pro Val Ser Leu Gly His Ser Leu
195 200 205

Lys Ser Phe Ser Glu Leu Ala Ala Val Val Phe Arg Pro Lys Pro Pro
210 215 220

Glu Thr Val Lys Thr Asp His Val His Gln Val Ala Val Ser Val Pro
225 230 235 240

Glu Gln Ala Gly Arg Ile Leu Asn Thr Leu Lys Leu Ala Gly Ile Asp
245 250 255

His Tyr Leu Ser Phe Gln Leu Leu Thr Arg Asp Cys Thr Ala Ser Met

```
            260                 265                 270

Glu Val Ile Gly Arg Phe Leu Ala Leu Leu Glu Leu Tyr Lys Ala Arg
        275                 280                 285

Ala Ile Glu Thr Leu Gln Glu Glu Pro Leu Gly Glu Leu Lys Val Ser
    290                 295                 300

Trp Thr Gly Ile Asp Val Asp Pro Ala Val Val Ala Ala Ser Asp Trp
305                 310                 315                 320

Glu
```

<210> 1891
<211> 684
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(661)
<223> RXA00714

<400> 1891

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cgtcaatcaa gctgtcaaaa aaaatacaag ttaggtcaca aaatgatttc agtcgtgaga 60

accatcacat ataagacatc tcatgatcta acatttcttc atg gct acg att aca   115
                                            Met Ala Thr Ile Thr
                                              1               5

cgc acc gac aga ctg atc ctc gta ccg ctc act gtt gag ctc gaa gac   163
Arg Thr Asp Arg Leu Ile Leu Val Pro Leu Thr Val Glu Leu Glu Asp
                  10                  15                  20

gag gcc cac cag att tac tct gat tct cga atc tgg gaa cac cgc ccc   211
Glu Ala His Gln Ile Tyr Ser Asp Ser Arg Ile Trp Glu His Arg Pro
              25                  30                  35

cag gcg cgt cac acc aac gtg cgt gtc acg cgc gac atc atc aag cgc   259
Gln Ala Arg His Thr Asn Val Arg Val Thr Arg Asp Ile Ile Lys Arg
          40                  45                  50

acc aat gaa agc tgg ggc aag aaa gac ctt ggc ccc tgg ggt gtt tac   307
Thr Asn Glu Ser Trp Gly Lys Lys Asp Leu Gly Pro Trp Gly Val Tyr
      55                  60                  65

ctc cgt gac cgc cca tcg gaa ttc gtt ggc gtt ggt ggc gtt gaa ctc   355
Leu Arg Asp Arg Pro Ser Glu Phe Val Gly Val Gly Gly Val Glu Leu
  70                  75                  80                  85

atc gac gga aaa gta tgg gac ctc aag tac cgc ctc cgc ccc gac cta   403
Ile Asp Gly Lys Val Trp Asp Leu Lys Tyr Arg Leu Arg Pro Asp Leu
                  90                  95                 100

tgg ggc aat gga tac gcc acg gaa atc tcc aac gcc gca aca ctg gcc   451
Trp Gly Asn Gly Tyr Ala Thr Glu Ile Ser Asn Ala Ala Thr Leu Ala
             105                 110                 115

acc aag cgt atc gac gac agc ctc cca ctc acg gcc agg gtg act acc   499
```

```
Thr Lys Arg Ile Asp Asp Ser Leu Pro Leu Thr Ala Arg Val Thr Thr
        120                 125                 130

aac cac cct gcc tca ttc cgt att ttg gaa aaa ctg gga ctc acc ccc   547
Asn His Pro Ala Ser Phe Arg Ile Leu Glu Lys Leu Gly Leu Thr Pro
    135                 140                 145

gta tgg gaa ggc cga cga gtc gga acg gaa gat gac ccc aac gag cct   595
Val Trp Glu Gly Arg Arg Val Gly Thr Glu Asp Asp Pro Asn Glu Pro
150                 155                 160                 165

gat gtg aga att tat tct gac cgt ccg cta tcg gat gaa att ctt gaa   643
Asp Val Arg Ile Tyr Ser Asp Arg Pro Leu Ser Asp Glu Ile Leu Glu
                170                 175                 180

atg ctc aag caa cga cca tagaccagaa aatctcaccc ctt                684
Met Leu Lys Gln Arg Pro
            185
```

<210> 1892
<211> 187
<212> PRT
<213> Corynebacterium glutamicum

<400> 1892

```
Met Ala Thr Ile Thr Arg Thr Asp Arg Leu Ile Leu Val Pro Leu Thr
  1               5                  10                  15

Val Glu Leu Glu Asp Glu Ala His Gln Ile Tyr Ser Asp Ser Arg Ile
             20                  25                  30

Trp Glu His Arg Pro Gln Ala Arg His Thr Asn Val Arg Val Thr Arg
         35                  40                  45

Asp Ile Ile Lys Arg Thr Asn Glu Ser Trp Gly Lys Lys Asp Leu Gly
     50                  55                  60

Pro Trp Gly Val Tyr Leu Arg Asp Arg Pro Ser Glu Phe Val Gly Val
 65                  70                  75                  80

Gly Gly Val Glu Leu Ile Asp Gly Lys Val Trp Asp Leu Lys Tyr Arg
                 85                  90                  95

Leu Arg Pro Asp Leu Trp Gly Asn Gly Tyr Ala Thr Glu Ile Ser Asn
            100                 105                 110

Ala Ala Thr Leu Ala Thr Lys Arg Ile Asp Asp Ser Leu Pro Leu Thr
        115                 120                 125

Ala Arg Val Thr Thr Asn His Pro Ala Ser Phe Arg Ile Leu Glu Lys
    130                 135                 140

Leu Gly Leu Thr Pro Val Trp Glu Gly Arg Arg Val Gly Thr Glu Asp
145                 150                 155                 160

Asp Pro Asn Glu Pro Asp Val Arg Ile Tyr Ser Asp Arg Pro Leu Ser
                165                 170                 175

Asp Glu Ile Leu Glu Met Leu Lys Gln Arg Pro
            180                 185
```

<210> 1893
<211> 636
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(613)
<223> RXA00716

<400> 1893
aaagccgatt gcttaacgcc cgctatgata accactcatg aatgatttcg atccagcatt 60

gatttccgcg atgagcctta tccctcagac gaggtctcgg atg gaa tca atc ttg 115
Met Glu Ser Ile Leu
1 5

ttg gtg gtc gat acc cca gtt tca gca cgc acg ctg gct ggg gtg ttg 163
Leu Val Val Asp Thr Pro Val Ser Ala Arg Thr Leu Ala Gly Val Leu
10 15 20

ggc att gac gtg cct gca aca gag gca att ttg aag gaa atg gcc ttt 211
Gly Ile Asp Val Pro Ala Thr Glu Ala Ile Leu Lys Glu Met Ala Phe
25 30 35

gag ctt tct gaa cgg ggc agc ggc att gat ctg cgg gaa acg gca gaa 259
Glu Leu Ser Glu Arg Gly Ser Gly Ile Asp Leu Arg Glu Thr Ala Glu
40 45 50

gga tgg cgc tat tac acc cgc ccg gaa aat gcg gac atc gtc gag caa 307
Gly Trp Arg Tyr Tyr Thr Arg Pro Glu Asn Ala Asp Ile Val Glu Gln
55 60 65

ttc ctc ctc gat gga aac caa acc aga ctg tcc cgt gca gca ttg gaa 355
Phe Leu Leu Asp Gly Asn Gln Thr Arg Leu Ser Arg Ala Ala Leu Glu
70 75 80 85

aca ctc gcg gtg gtg gca tat cgg cag ccg gtc aca cgc tcc cag att 403
Thr Leu Ala Val Val Ala Tyr Arg Gln Pro Val Thr Arg Ser Gln Ile
90 95 100

tca gca gtg cgc gga gta aat gtc gac ggc gtc atg aga acc ttg cag 451
Ser Ala Val Arg Gly Val Asn Val Asp Gly Val Met Arg Thr Leu Gln
105 110 115

ctt cga ggc cta gtc aaa gaa gtc gat gtg gac gaa tca acg ggc gca 499
Leu Arg Gly Leu Val Lys Glu Val Asp Val Asp Glu Ser Thr Gly Ala
120 125 130

cac cgc tat ggc aca acg gaa ttg ctg ctt gag ctg ttg ggt att gat 547
His Arg Tyr Gly Thr Thr Glu Leu Leu Leu Glu Leu Leu Gly Ile Asp
135 140 145

tct ttg gat aaa tta cca gat cta gca ccg ctt ttg ccg gat gtt gac 595
Ser Leu Asp Lys Leu Pro Asp Leu Ala Pro Leu Leu Pro Asp Val Asp
150 155 160 165

tcc att gat gaa gac ttc taaagcatca gttaaagccc cga 636
Ser Ile Asp Glu Asp Phe

170

<210> 1894
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 1894

```
Met Glu Ser Ile Leu Leu Val Val Asp Thr Pro Val Ser Ala Arg Thr
  1               5                  10                  15

Leu Ala Gly Val Leu Gly Ile Asp Val Pro Ala Thr Glu Ala Ile Leu
            20                  25                  30

Lys Glu Met Ala Phe Glu Leu Ser Glu Arg Gly Ser Gly Ile Asp Leu
         35                  40                  45

Arg Glu Thr Ala Glu Gly Trp Arg Tyr Tyr Thr Arg Pro Glu Asn Ala
     50                  55                  60

Asp Ile Val Glu Gln Phe Leu Leu Asp Gly Asn Gln Thr Arg Leu Ser
 65                  70                  75                  80

Arg Ala Ala Leu Glu Thr Leu Ala Val Val Ala Tyr Arg Gln Pro Val
                85                  90                  95

Thr Arg Ser Gln Ile Ser Ala Val Arg Gly Val Asn Val Asp Gly Val
            100                 105                 110

Met Arg Thr Leu Gln Leu Arg Gly Leu Val Lys Glu Val Asp Val Asp
        115                 120                 125

Glu Ser Thr Gly Ala His Arg Tyr Gly Thr Thr Glu Leu Leu Leu Glu
    130                 135                 140

Leu Leu Gly Ile Asp Ser Leu Asp Lys Leu Pro Asp Leu Ala Pro Leu
145                 150                 155                 160

Leu Pro Asp Val Asp Ser Ile Asp Glu Asp Phe
                165                 170
```

<210> 1895
<211> 1752
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1729)
<223> RXA00719

<400> 1895

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cagatgatgc acacatcgtg gacacctctg atatgaccat ggatcaagta cttgatcacc 60

tcatccacct agtggaagcc tccgctgaaa ggagcaacca gtg act gat aaa cac   115
                                              Val Thr Asp Lys His
                                                1               5

acc atg cct ggt gaa gag gac gac acc gta ttc gtc tac cac acc cac   163
```

```
Thr Met Pro Gly Glu Glu Asp Asp Thr Val Phe Val Tyr His Thr His
                 10                  15                  20

aaa ggc gaa atg gac gtc gaa ggt gcg ttt gct gac gaa gaa gaa cta   211
Lys Gly Glu Met Asp Val Glu Gly Ala Phe Ala Asp Glu Glu Glu Leu
            25                  30                  35

gca cca cac ggc ggt tgg gct tcc gca gat ttc gac cca gca gaa ttc   259
Ala Pro His Gly Gly Trp Ala Ser Ala Asp Phe Asp Pro Ala Glu Phe
        40                  45                  50

ggc tac gaa gac tct gac gat gac ttc gat gca gag gac ttt gac gaa   307
Gly Tyr Glu Asp Ser Asp Asp Asp Phe Asp Ala Glu Asp Phe Asp Glu
    55                  60                  65

aca gag ttc tcc aac cct gat ttc ggc gaa gac tac tct gat gaa gac   355
Thr Glu Phe Ser Asn Pro Asp Phe Gly Glu Asp Tyr Ser Asp Glu Asp
70                  75                  80                  85

tgg gaa gaa atc gag acc gca ttc gga ttc gac cca agc cac ctt gaa   403
Trp Glu Glu Ile Glu Thr Ala Phe Gly Phe Asp Pro Ser His Leu Glu
                90                  95                 100

gaa gct ctc tgc acg gtc gct atc gtc gga cgc cca aat gtt ggt aaa   451
Glu Ala Leu Cys Thr Val Ala Ile Val Gly Arg Pro Asn Val Gly Lys
            105                 110                 115

tca acc ttg gtg aac cgc ttt att gga cgt cga gaa gca gtc gtg gaa   499
Ser Thr Leu Val Asn Arg Phe Ile Gly Arg Arg Glu Ala Val Val Glu
        120                 125                 130

gat ttc ccc ggc gta acc cgt gac cgc atc tcc tac atc tct gac tgg   547
Asp Phe Pro Gly Val Thr Arg Asp Arg Ile Ser Tyr Ile Ser Asp Trp
    135                 140                 145

ggt gga cac cgt ttc tgg gtt cag gac aca ggc gga tgg gat cct aac   595
Gly Gly His Arg Phe Trp Val Gln Asp Thr Gly Gly Trp Asp Pro Asn
150                 155                 160                 165

gtc aag ggc atc cac gca tcg atc gca cag caa gca gaa gtt gct atg   643
Val Lys Gly Ile His Ala Ser Ile Ala Gln Gln Ala Glu Val Ala Met
                170                 175                 180

agc act gcc gat gtc atc gta ttc gtc gtg gac acc aag gtg ggc atc   691
Ser Thr Ala Asp Val Ile Val Phe Val Val Asp Thr Lys Val Gly Ile
            185                 190                 195

acc gaa act gac tca gtg atg gca gca aaa ctg ttg cgc tcg gaa gtg   739
Thr Glu Thr Asp Ser Val Met Ala Ala Lys Leu Leu Arg Ser Glu Val
        200                 205                 210

cca gtg atc ttg gtt gcg aac aaa ttc gac tcc gac agc cag tgg gct   787
Pro Val Ile Leu Val Ala Asn Lys Phe Asp Ser Asp Ser Gln Trp Ala
    215                 220                 225

gac atg gct gag ttc tac agc ctc ggc ctt ggc gat cca tac cca gtt   835
Asp Met Ala Glu Phe Tyr Ser Leu Gly Leu Gly Asp Pro Tyr Pro Val
230                 235                 240                 245

tca gcc cag cat gga cgt ggt ggc gct gac gtt ttg gac aaa gtc ctt   883
Ser Ala Gln His Gly Arg Gly Gly Ala Asp Val Leu Asp Lys Val Leu
```

```
                250                 255                 260

gaa ctc ttc cca gaa gag cct cgc tcc aag tcc atc gtg gaa ggc cct   931
Glu Leu Phe Pro Glu Glu Pro Arg Ser Lys Ser Ile Val Glu Gly Pro
            265                 270                 275

cgt cgt gtc gcc ctt gtg ggt aag cca aac gtg ggt aag tct tca ctg   979
Arg Arg Val Ala Leu Val Gly Lys Pro Asn Val Gly Lys Ser Ser Leu
        280                 285                 290

ctc aac aag ttt gct ggc gag acc cgc tct gtc gtg gac aat gtt gca   1027
Leu Asn Lys Phe Ala Gly Glu Thr Arg Ser Val Val Asp Asn Val Ala
    295                 300                 305

gga acc acc gtt gac ccc gtt gac tcc ctg att cag ctg gat caa aaa   1075
Gly Thr Thr Val Asp Pro Val Asp Ser Leu Ile Gln Leu Asp Gln Lys
310                 315                 320                 325

ctg tgg aaa ttc gtg gat act gct ggt ctt cgc aaa aag gtc aag act   1123
Leu Trp Lys Phe Val Asp Thr Ala Gly Leu Arg Lys Lys Val Lys Thr
                330                 335                 340

gca tct ggc cac gag tac tac gca tca ctg cgt acc cac ggt gcc atc   1171
Ala Ser Gly His Glu Tyr Tyr Ala Ser Leu Arg Thr His Gly Ala Ile
            345                 350                 355

gat gca gct gag ctg tgt gtt ttg ctt atc gat tcc tcc gaa ccc atc   1219
Asp Ala Ala Glu Leu Cys Val Leu Leu Ile Asp Ser Ser Glu Pro Ile
        360                 365                 370

acc gag cag gat cag cgc gtg ctc gca atg atc acc gat gcc ggt aag   1267
Thr Glu Gln Asp Gln Arg Val Leu Ala Met Ile Thr Asp Ala Gly Lys
    375                 380                 385

gca ctg gtt att gcg ttc aac aag tgg gat ctc atg gat gaa gat cgc   1315
Ala Leu Val Ile Ala Phe Asn Lys Trp Asp Leu Met Asp Glu Asp Arg
390                 395                 400                 405

cgc atc gat ttg gat cgc gaa ctt gat ctc cag ttg gca cac gtg cct   1363
Arg Ile Asp Leu Asp Arg Glu Leu Asp Leu Gln Leu Ala His Val Pro
                410                 415                 420

tgg gca aag cgc atc aac atc tcc gcc aaa acc ggt cgt gca ctg cag   1411
Trp Ala Lys Arg Ile Asn Ile Ser Ala Lys Thr Gly Arg Ala Leu Gln
            425                 430                 435

cgc ctc gag cca gca atg ttg gaa gcg ctc gac aac tgg gat cgc cgt   1459
Arg Leu Glu Pro Ala Met Leu Glu Ala Leu Asp Asn Trp Asp Arg Arg
        440                 445                 450

atc tcc act ggt cag ctg aac acc tgg ctg cgt gaa gca att gct gcg   1507
Ile Ser Thr Gly Gln Leu Asn Thr Trp Leu Arg Glu Ala Ile Ala Ala
    455                 460                 465

aac cca cca cca atg cgt ggc gga cgt ttg cct cga gtg ctg ttt gcc   1555
Asn Pro Pro Pro Met Arg Gly Gly Arg Leu Pro Arg Val Leu Phe Ala
470                 475                 480                 485

acc cag gca tct act cag cca cca gtg atc gta ctg ttc acc acc ggc   1603
Thr Gln Ala Ser Thr Gln Pro Pro Val Ile Val Leu Phe Thr Thr Gly
                490                 495                 500
```

```
ttc ctc gaa gca ggt tac cga cga tac ctg gag cgc aag ttc cgt gaa   1651
Phe Leu Glu Ala Gly Tyr Arg Arg Tyr Leu Glu Arg Lys Phe Arg Glu
            505                 510                 515

cgt ttc ggc ttt gaa ggc act cca gtg cga atc gct gtg cgt gtt cgc   1699
Arg Phe Gly Phe Glu Gly Thr Pro Val Arg Ile Ala Val Arg Val Arg
        520                 525                 530

gag cgc cgc ggc aag ggc gga aac aag cag taaagcttga ttttccctaa    1749
Glu Arg Arg Gly Lys Gly Gly Asn Lys Gln
    535                 540

aag                                                              1752
```

<210> 1896
<211> 543
<212> PRT
<213> Corynebacterium glutamicum

<400> 1896

```
Val Thr Asp Lys His Thr Met Pro Gly Glu Glu Asp Asp Thr Val Phe
  1               5                  10                  15

Val Tyr His Thr His Lys Gly Glu Met Asp Val Glu Gly Ala Phe Ala
             20                  25                  30

Asp Glu Glu Glu Leu Ala Pro His Gly Gly Trp Ala Ser Ala Asp Phe
         35                  40                  45

Asp Pro Ala Glu Phe Gly Tyr Glu Asp Ser Asp Asp Asp Phe Asp Ala
     50                  55                  60

Glu Asp Phe Asp Glu Thr Glu Phe Ser Asn Pro Asp Phe Gly Glu Asp
 65                  70                  75                  80

Tyr Ser Asp Glu Asp Trp Glu Glu Ile Glu Thr Ala Phe Gly Phe Asp
                 85                  90                  95

Pro Ser His Leu Glu Glu Ala Leu Cys Thr Val Ala Ile Val Gly Arg
            100                 105                 110

Pro Asn Val Gly Lys Ser Thr Leu Val Asn Arg Phe Ile Gly Arg Arg
        115                 120                 125

Glu Ala Val Val Glu Asp Phe Pro Gly Val Thr Arg Asp Arg Ile Ser
    130                 135                 140

Tyr Ile Ser Asp Trp Gly Gly His Arg Phe Trp Val Gln Asp Thr Gly
145                 150                 155                 160

Gly Trp Asp Pro Asn Val Lys Gly Ile His Ala Ser Ile Ala Gln Gln
                165                 170                 175

Ala Glu Val Ala Met Ser Thr Ala Asp Val Ile Val Phe Val Val Asp
            180                 185                 190

Thr Lys Val Gly Ile Thr Glu Thr Asp Ser Val Met Ala Ala Lys Leu
        195                 200                 205
```

```
Leu Arg Ser Glu Val Pro Val Ile Leu Val Ala Asn Lys Phe Asp Ser
    210                 215                 220

Asp Ser Gln Trp Ala Asp Met Ala Glu Phe Tyr Ser Leu Gly Leu Gly
225                 230                 235                 240

Asp Pro Tyr Pro Val Ser Ala Gln His Gly Arg Gly Gly Ala Asp Val
                245                 250                 255

Leu Asp Lys Val Leu Glu Leu Phe Pro Glu Glu Pro Arg Ser Lys Ser
            260                 265                 270

Ile Val Glu Gly Pro Arg Arg Val Ala Leu Val Gly Lys Pro Asn Val
        275                 280                 285

Gly Lys Ser Ser Leu Leu Asn Lys Phe Ala Gly Glu Thr Arg Ser Val
    290                 295                 300

Val Asp Asn Val Ala Gly Thr Thr Val Asp Pro Val Asp Ser Leu Ile
305                 310                 315                 320

Gln Leu Asp Gln Lys Leu Trp Lys Phe Val Asp Thr Ala Gly Leu Arg
                325                 330                 335

Lys Lys Val Lys Thr Ala Ser Gly His Glu Tyr Tyr Ala Ser Leu Arg
            340                 345                 350

Thr His Gly Ala Ile Asp Ala Ala Glu Leu Cys Val Leu Leu Ile Asp
        355                 360                 365

Ser Ser Glu Pro Ile Thr Glu Gln Asp Gln Arg Val Leu Ala Met Ile
    370                 375                 380

Thr Asp Ala Gly Lys Ala Leu Val Ile Ala Phe Asn Lys Trp Asp Leu
385                 390                 395                 400

Met Asp Glu Asp Arg Arg Ile Asp Leu Asp Arg Glu Leu Asp Leu Gln
                405                 410                 415

Leu Ala His Val Pro Trp Ala Lys Arg Ile Asn Ile Ser Ala Lys Thr
            420                 425                 430

Gly Arg Ala Leu Gln Arg Leu Glu Pro Ala Met Leu Glu Ala Leu Asp
        435                 440                 445

Asn Trp Asp Arg Arg Ile Ser Thr Gly Gln Leu Asn Thr Trp Leu Arg
    450                 455                 460

Glu Ala Ile Ala Ala Asn Pro Pro Pro Met Arg Gly Gly Arg Leu Pro
465                 470                 475                 480

Arg Val Leu Phe Ala Thr Gln Ala Ser Thr Gln Pro Pro Val Ile Val
                485                 490                 495

Leu Phe Thr Thr Gly Phe Leu Glu Ala Gly Tyr Arg Arg Tyr Leu Glu
            500                 505                 510

Arg Lys Phe Arg Glu Arg Phe Gly Phe Glu Gly Thr Pro Val Arg Ile
        515                 520                 525

Ala Val Arg Val Arg Glu Arg Arg Gly Lys Gly Gly Asn Lys Gln
```

```
    530                 535                 540

<210> 1897
<211> 671
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(648)
<223> RXA00724

<400> 1897
atc ggt gag gaa gtc ctc gcc gga cgc caa gcc tat gtg gtg tgt ccg   48
Ile Gly Glu Glu Val Leu Ala Gly Arg Gln Ala Tyr Val Val Cys Pro
  1               5                  10                  15

cgc att gaa ggc gaa ggc ggc gtg ctg gaa atc cac gcc tat ctt tcc   96
Arg Ile Glu Gly Glu Gly Gly Val Leu Glu Ile His Ala Tyr Leu Ser
             20                  25                  30

gaa cag gta tat cca gga ttg aat gtt gga atg ctg cac ggt cgc atg   144
Glu Gln Val Tyr Pro Gly Leu Asn Val Gly Met Leu His Gly Arg Met
         35                  40                  45

gac acg gat ctc aaa gat tcg gtc atg cag gaa ttc gcc caa ggt gag   192
Asp Thr Asp Leu Lys Asp Ser Val Met Gln Glu Phe Ala Gln Gly Glu
     50                  55                  60

atc gat att ttg gtc gcc acc acg gtc att gag gtc ggt att gac gtt   240
Ile Asp Ile Leu Val Ala Thr Thr Val Ile Glu Val Gly Ile Asp Val
 65                  70                  75                  80

gcc aac gcc acc gtc atg ctc atc cgc gag gcg gaa cgc ttc ggc gtt   288
Ala Asn Ala Thr Val Met Leu Ile Arg Glu Ala Glu Arg Phe Gly Val
                 85                  90                  95

tcc cag atc cac cag ctg cgc ggc cgt gtt ggc cgt ggg cag cac gat   336
Ser Gln Ile His Gln Leu Arg Gly Arg Val Gly Arg Gly Gln His Asp
            100                 105                 110

tcc ctc tgc ctg ctg cac acc acc ttc gac gag gac tcc cca caa ggc   384
Ser Leu Cys Leu Leu His Thr Thr Phe Asp Glu Asp Ser Pro Gln Gly
        115                 120                 125

caa cgc ctc gcc gca att tcc acc aca acc gac ggt ttt caa ctc tct   432
Gln Arg Leu Ala Ala Ile Ser Thr Thr Thr Asp Gly Phe Gln Leu Ser
    130                 135                 140

gaa ctt gat ttg cag gta cgc caa gaa ggc gac gtg ttg ggc acc cgc   480
Glu Leu Asp Leu Gln Val Arg Gln Glu Gly Asp Val Leu Gly Thr Arg
145                 150                 155                 160

cag tcc ggc agc gac acc aaa ctc cgt cac ctc tcg ttt atc agc gac   528
Gln Ser Gly Ser Asp Thr Lys Leu Arg His Leu Ser Phe Ile Ser Asp
                165                 170                 175

caa aaa atc atc gag cgt gcg ctt atc gac gcc acc gag ctg gtt gcc   576
Gln Lys Ile Ile Glu Arg Ala Leu Ile Asp Ala Thr Glu Leu Val Ala
            180                 185                 190
```

```
gcc agc cgt tcc agg gcg ctt gag ctg gtc agc gac atc gca atg atc   624
Ala Ser Arg Ser Arg Ala Leu Glu Leu Val Ser Asp Ile Ala Met Ile
        195                 200                 205

aac cag gaa tac ctg gaa aag agc tgatattgat agggtttaag tca         671
Asn Gln Glu Tyr Leu Glu Lys Ser
    210                 215


<210> 1898
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 1898
Ile Gly Glu Glu Val Leu Ala Gly Arg Gln Ala Tyr Val Val Cys Pro
  1               5                  10                  15

Arg Ile Glu Gly Glu Gly Gly Val Leu Glu Ile His Ala Tyr Leu Ser
             20                  25                  30

Glu Gln Val Tyr Pro Gly Leu Asn Val Gly Met Leu His Gly Arg Met
         35                  40                  45

Asp Thr Asp Leu Lys Asp Ser Val Met Gln Glu Phe Ala Gln Gly Glu
     50                  55                  60

Ile Asp Ile Leu Val Ala Thr Thr Val Ile Glu Val Gly Ile Asp Val
 65                  70                  75                  80

Ala Asn Ala Thr Val Met Leu Ile Arg Glu Ala Glu Arg Phe Gly Val
                 85                  90                  95

Ser Gln Ile His Gln Leu Arg Gly Arg Val Gly Arg Gly Gln His Asp
            100                 105                 110

Ser Leu Cys Leu Leu His Thr Thr Phe Asp Glu Asp Ser Pro Gln Gly
        115                 120                 125

Gln Arg Leu Ala Ala Ile Ser Thr Thr Thr Asp Gly Phe Gln Leu Ser
    130                 135                 140

Glu Leu Asp Leu Gln Val Arg Gln Glu Gly Asp Val Leu Gly Thr Arg
145                 150                 155                 160

Gln Ser Gly Ser Asp Thr Lys Leu Arg His Leu Ser Phe Ile Ser Asp
                165                 170                 175

Gln Lys Ile Ile Glu Arg Ala Leu Ile Asp Ala Thr Glu Leu Val Ala
            180                 185                 190

Ala Ser Arg Ser Arg Ala Leu Glu Leu Val Ser Asp Ile Ala Met Ile
        195                 200                 205

Asn Gln Glu Tyr Leu Glu Lys Ser
    210                 215


<210> 1899
<211> 164
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(141)
<223> RXA00726

<400> 1899
cac gaa atg ggc ttc gcc cac gaa gtc gcc gac cag gtc gtg ttc atg 48
His Glu Met Gly Phe Ala His Glu Val Ala Asp Gln Val Val Phe Met
1 5 10 15

gcc gat gga gtt gtc gtt gaa gcc gga acc ccc gaa caa gtt ctg gac 96
Ala Asp Gly Val Val Val Glu Ala Gly Thr Pro Glu Gln Val Leu Asp
20 25 30

aat cca aag gaa cag cgc acc aaa gac ttc ctg tct tct ctg ctc 141
Asn Pro Lys Glu Gln Arg Thr Lys Asp Phe Leu Ser Ser Leu Leu
35 40 45

taacctttc gggtcttaaa aaa 164

<210> 1900
<211> 47
<212> PRT
<213> Corynebacterium glutamicum

<400> 1900
His Glu Met Gly Phe Ala His Glu Val Ala Asp Gln Val Val Phe Met
1 5 10 15

Ala Asp Gly Val Val Val Glu Ala Gly Thr Pro Glu Gln Val Leu Asp
20 25 30

Asn Pro Lys Glu Gln Arg Thr Lys Asp Phe Leu Ser Ser Leu Leu
35 40 45

<210> 1901
<211> 702
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(679)
<223> RXA00740

<400> 1901
gttataaata ttaaagtacg ctaaccatgg gtgcaggggg agacttctac agcagtcatg 60

gtccacacca cgactgctgt atatattaag gacgtaactc atg ttg aag aat aaa 115
Met Leu Lys Asn Lys
1 5

act ctt gcg ctg ctg gct gtc agt acg ctg atg ttt ggc tta tct gct 163
Thr Leu Ala Leu Leu Ala Val Ser Thr Leu Met Phe Gly Leu Ser Ala
10 15 20

```
tgc tct agt gat gct gac ggc ccg gac agt agc ggt gct agt agt agc   211
Cys Ser Ser Asp Ala Asp Gly Pro Asp Ser Ser Gly Ala Ser Ser Ser
            25                  30                  35

agt act ggc tca tct tct gca tcg gct gac aca aca gat tct gca gct   259
Ser Thr Gly Ser Ser Ser Ala Ser Ala Asp Thr Thr Asp Ser Ala Ala
        40                  45                  50

gtt gat aag gat gct caa tta gac acc ttt atg cgt tct gct gtg gct   307
Val Asp Lys Asp Ala Gln Leu Asp Thr Phe Met Arg Ser Ala Val Ala
    55                  60                  65

gat gga tca tct gct gct gtg gct gtg gac aac gct gta ggt aag ggc   355
Asp Gly Ser Ser Ala Ala Val Ala Val Asp Asn Ala Val Gly Lys Gly
70                  75                  80                  85

ttt gat aaa gct gat gcg cag gcg gct gcg gag cgc ttg ggt gat ggt   403
Phe Asp Lys Ala Asp Ala Gln Ala Ala Ala Glu Arg Leu Gly Asp Gly
                90                  95                  100

ttc caa ttc gct gcg gat tac cag gct gtt ggc tat ttg gaa tct tgg   451
Phe Gln Phe Ala Ala Asp Tyr Gln Ala Val Gly Tyr Leu Glu Ser Trp
            105                 110                 115

tac ttt ggt ggc gcg cga agc gag aag ctt gac gag gtg cgt agt gat   499
Tyr Phe Gly Gly Ala Arg Ser Glu Lys Leu Asp Glu Val Arg Ser Asp
        120                 125                 130

gtc atc gct cat ttg tct gaa ttg gga ttt aca gat tta gag gct gaa   547
Val Ile Ala His Leu Ser Glu Leu Gly Phe Thr Asp Leu Glu Ala Glu
    135                 140                 145

tcc tcg gca tct cgt att aca tta ggt gat tac tgt gat ggg gtc cct   595
Ser Ser Ala Ser Arg Ile Thr Leu Gly Asp Tyr Cys Asp Gly Val Pro
150                 155                 160                 165

gag tat tgt gag ttg ttt ttt gat ggc gaa tct cct gac ttg tat gac   643
Glu Tyr Cys Glu Leu Phe Phe Asp Gly Glu Ser Pro Asp Leu Tyr Asp
                170                 175                 180

atg ggt acg gag ctt gac tcg tat aag ccc act gaa taaagctatt        689
Met Gly Thr Glu Leu Asp Ser Tyr Lys Pro Thr Glu
            185                 190

tcacttaaag cac                                                   702
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<210> 1902
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 1902

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Met Leu Lys Asn Lys Thr Leu Ala Leu Leu Ala Val Ser Thr Leu Met
  1               5                  10                  15

Phe Gly Leu Ser Ala Cys Ser Ser Asp Ala Asp Gly Pro Asp Ser Ser
            20                  25                  30

Gly Ala Ser Ser Ser Ser Thr Gly Ser Ser Ser Ala Ser Ala Asp Thr
        35                  40                  45
```

```
Thr Asp Ser Ala Ala Val Asp Lys Asp Ala Gln Leu Asp Thr Phe Met
     50                  55                  60

Arg Ser Ala Val Ala Asp Gly Ser Ser Ala Ala Val Ala Val Asp Asn
 65                  70                  75                  80

Ala Val Gly Lys Gly Phe Asp Lys Ala Asp Ala Gln Ala Ala Ala Glu
                 85                  90                  95

Arg Leu Gly Asp Gly Phe Gln Phe Ala Ala Asp Tyr Gln Ala Val Gly
            100                 105                 110

Tyr Leu Glu Ser Trp Tyr Phe Gly Gly Ala Arg Ser Glu Lys Leu Asp
        115                 120                 125

Glu Val Arg Ser Asp Val Ile Ala His Leu Ser Glu Leu Gly Phe Thr
    130                 135                 140

Asp Leu Glu Ala Glu Ser Ser Ala Ser Arg Ile Thr Leu Gly Asp Tyr
145                 150                 155                 160

Cys Asp Gly Val Pro Glu Tyr Cys Glu Leu Phe Phe Asp Gly Glu Ser
                165                 170                 175

Pro Asp Leu Tyr Asp Met Gly Thr Glu Leu Asp Ser Tyr Lys Pro Thr
            180                 185                 190

Glu
```

US 60/445,550

<210> 1903
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1033)
<223> RXA00741

<400> 1903
tggtgatcac taggtccacc tcgtcttgca tggtggtcac ctcagtccag aacgcattga 60

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ttgacaccga tcaaatgttt gatggattat gatatttagc atg act gat tct ctg   115
                                            Met Thr Asp Ser Leu
                                              1               5

ctt gta tcc atc aga aaa ggc tta ata gaa gag cgt cca tta acg gag   163
Leu Val Ser Ile Arg Lys Gly Leu Ile Glu Glu Arg Pro Leu Thr Glu
                 10                  15                  20

ctt ctt cgg gcg tgt atc ttc ctt gga agt gat act aac tcg gac tct   211
Leu Leu Arg Ala Cys Ile Phe Leu Gly Ser Asp Thr Asn Ser Asp Ser
             25                  30                  35

tta caa gag tgg gcg aaa aat gaa tta aat ggt tat ggc tcc att gat   259
Leu Gln Glu Trp Ala Lys Asn Glu Leu Asn Gly Tyr Gly Ser Ile Asp
         40                  45                  50
```

```
ggt att ccg gaa tat cgc aaa ttg aaa gga cct cct gta ttc gcg aaa   307
Gly Ile Pro Glu Tyr Arg Lys Leu Lys Gly Pro Pro Val Phe Ala Lys
     55                  60                  65

att caa gct ggt aat tca ata atg tct aat atg gta ctg ggg cca cat   355
Ile Gln Ala Gly Asn Ser Ile Met Ser Asn Met Val Leu Gly Pro His
 70                  75                  80                  85

aat gtt cct gaa aga gct cgt aag tat ttc cct gaa gag ctg cat ttt   403
Asn Val Pro Glu Arg Ala Arg Lys Tyr Phe Pro Glu Glu Leu His Phe
                 90                  95                 100

gat cag ccg att caa acg cta att gaa tgg tcg act agg cag gat ggg   451
Asp Gln Pro Ile Gln Thr Leu Ile Glu Trp Ser Thr Arg Gln Asp Gly
            105                 110                 115

att aat tta tcg ccc ccg aat tta ctt cgg gtc cgc gat ctt cat aat   499
Ile Asn Leu Ser Pro Pro Asn Leu Leu Arg Val Arg Asp Leu His Asn
        120                 125                 130

gat cag tac gcg cca tta aat caa att ttg aat tta aat gtt tac tta   547
Asp Gln Tyr Ala Pro Leu Asn Gln Ile Leu Asn Leu Asn Val Tyr Leu
    135                 140                 145

gat aac tct tat ttt tcg gga att gtg gac cgc atc cga act cta atg   595
Asp Asn Ser Tyr Phe Ser Gly Ile Val Asp Arg Ile Arg Thr Leu Met
150                 155                 160                 165

act tcc atg att gcc gac ctc aca cac gca act cct ctg gat gaa cta   643
Thr Ser Met Ile Ala Asp Leu Thr His Ala Thr Pro Leu Asp Glu Leu
                170                 175                 180

cca agc agc gaa aag gtt aat gcc acg gtc atg aag cac att gaa aat   691
Pro Ser Ser Glu Lys Val Asn Ala Thr Val Met Lys His Ile Glu Asn
            185                 190                 195

aac tac gaa act aca atc act caa gcc aat gga gct gta gcc att ggt   739
Asn Tyr Glu Thr Thr Ile Thr Gln Ala Asn Gly Ala Val Ala Ile Gly
        200                 205                 210

aac agc gct aaa gct gtg cag aag gga ttg tcc gtg gat gac cta ctg   787
Asn Ser Ala Lys Ala Val Gln Lys Gly Leu Ser Val Asp Asp Leu Leu
    215                 220                 225

aag att atg cag acc att aat cct gaa aag ttc gac tta ggg gaa gct   835
Lys Ile Met Gln Thr Ile Asn Pro Glu Lys Phe Asp Leu Gly Glu Ala
230                 235                 240                 245

aga gct gaa gcc gaa gaa agc att caa tcc atc gcg gat gag ttg aag   883
Arg Ala Glu Ala Glu Glu Ser Ile Gln Ser Ile Ala Asp Glu Leu Lys
                250                 255                 260

aag gag tct ccg aat aaa ggt ttt atc cag aat gct ttt gaa aag ttg   931
Lys Glu Ser Pro Asn Lys Gly Phe Ile Gln Asn Ala Phe Glu Lys Leu
            265                 270                 275

aag gaa ctc agc ata aaa gcc ggc gat aaa gcc ttc act aca atg tta   979
Lys Glu Leu Ser Ile Lys Ala Gly Asp Lys Ala Phe Thr Thr Met Leu
        280                 285                 290

aat ctt gta ggt aaa cag ata atc gaa aac atc cca caa ctg gtt tca   1027
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Asn Leu Val Gly Lys Gln Ile Ile Glu Asn Ile Pro Gln Leu Val Ser
295 300 305

ggt ggc tagagaaatt caaggccgtc agc 1056
Gly Gly
310

<210> 1904
<211> 311
<212> PRT
<213> Corynebacterium glutamicum

<400> 1904
Met Thr Asp Ser Leu Leu Val Ser Ile Arg Lys Gly Leu Ile Glu Glu
1 5 10 15

Arg Pro Leu Thr Glu Leu Leu Arg Ala Cys Ile Phe Leu Gly Ser Asp
20 25 30

Thr Asn Ser Asp Ser Leu Gln Glu Trp Ala Lys Asn Glu Leu Asn Gly
35 40 45

Tyr Gly Ser Ile Asp Gly Ile Pro Glu Tyr Arg Lys Leu Lys Gly Pro
50 55 60

Pro Val Phe Ala Lys Ile Gln Ala Gly Asn Ser Ile Met Ser Asn Met
65 70 75 80

Val Leu Gly Pro His Asn Val Pro Glu Arg Ala Arg Lys Tyr Phe Pro
85 90 95

Glu Glu Leu His Phe Asp Gln Pro Ile Gln Thr Leu Ile Glu Trp Ser
100 105 110

Thr Arg Gln Asp Gly Ile Asn Leu Ser Pro Pro Asn Leu Leu Arg Val
115 120 125

Arg Asp Leu His Asn Asp Gln Tyr Ala Pro Leu Asn Gln Ile Leu Asn
130 135 140

Leu Asn Val Tyr Leu Asp Asn Ser Tyr Phe Ser Gly Ile Val Asp Arg
145 150 155 160

Ile Arg Thr Leu Met Thr Ser Met Ile Ala Asp Leu Thr His Ala Thr
165 170 175

Pro Leu Asp Glu Leu Pro Ser Ser Glu Lys Val Asn Ala Thr Val Met
180 185 190

Lys His Ile Glu Asn Asn Tyr Glu Thr Thr Ile Thr Gln Ala Asn Gly
195 200 205

Ala Val Ala Ile Gly Asn Ser Ala Lys Ala Val Gln Lys Gly Leu Ser
210 215 220

Val Asp Asp Leu Leu Lys Ile Met Gln Thr Ile Asn Pro Glu Lys Phe
225 230 235 240

Asp Leu Gly Glu Ala Arg Ala Glu Ala Glu Glu Ser Ile Gln Ser Ile
245 250 255

```
Ala Asp Glu Leu Lys Lys Glu Ser Pro Asn Lys Gly Phe Ile Gln Asn
            260                 265                 270

Ala Phe Glu Lys Leu Lys Glu Leu Ser Ile Lys Ala Gly Asp Lys Ala
        275                 280                 285

Phe Thr Thr Met Leu Asn Leu Val Gly Lys Gln Ile Ile Glu Asn Ile
    290                 295                 300

Pro Gln Leu Val Ser Gly Gly
305                 310


<210> 1905
<211> 1773
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1750)
<223> RXA00742

<400> 1905
agaggggttt tttagtgaaa atgataaaac cacttttaca gatggacaca tagatattag 60

taatgatgct tctggagcta agcgtagctt tgggggtcgg gtg aat gtt cag att   115
                                          Val Asn Val Gln Ile
                                            1               5

aaa ggg cga aag gtt aat gcc aag gct gcc gac tta aat agc tat ccg   163
Lys Gly Arg Lys Val Asn Ala Lys Ala Ala Asp Leu Asn Ser Tyr Pro
                  10                  15                  20

gtc tca gta gtt gat cta cga ggc ttc gtg aca ctg gct ggt ctc tta   211
Val Ser Val Val Asp Leu Arg Gly Phe Val Thr Leu Ala Gly Leu Leu
              25                  30                  35

ttt ttt gtg gtt gat att gat aag aaa tca aat aag aaa tat cca aag   259
Phe Phe Val Val Asp Ile Asp Lys Lys Ser Asn Lys Lys Tyr Pro Lys
          40                  45                  50

tat gtt ctt ttg aaa ccg ttt tat att cat gat cta ctg agt aaa gcg   307
Tyr Val Leu Leu Lys Pro Phe Tyr Ile His Asp Leu Leu Ser Lys Ala
      55                  60                  65

aag ccg ggc caa aag aca att agc gtc cgc tta aaa cgg tta cca tct   355
Lys Pro Gly Gln Lys Thr Ile Ser Val Arg Leu Lys Arg Leu Pro Ser
  70                  75                  80                  85

gat gaa gat cga atg gaa gcc ata atc gca tta gcg ctc gca tcg agg   403
Asp Glu Asp Arg Met Glu Ala Ile Ile Ala Leu Ala Leu Ala Ser Arg
                  90                  95                 100

caa gaa aag ata gtc gag aac ccc agt aac tat ctc tat gaa aat atg   451
Gln Glu Lys Ile Val Glu Asn Pro Ser Asn Tyr Leu Tyr Glu Asn Met
              105                 110                 115

gaa tca att act gtt aaa tcg gct gaa ccc ctt aat agg gat aag ctg   499
Glu Ser Ile Thr Val Lys Ser Ala Glu Pro Leu Asn Arg Asp Lys Leu
```

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        120                 125                 130

gct gta tat gat ggt agt tcg cca gac cat tcg atc att att cgt act   547
Ala Val Tyr Asp Gly Ser Ser Pro Asp His Ser Ile Ile Ile Arg Thr
    135                 140                 145

ggg gat gga att gaa cag ttc gtc aat gcc acc gta gaa ata ata ccc   595
Gly Asp Gly Ile Glu Gln Phe Val Asn Ala Thr Val Glu Ile Ile Pro
150                 155                 160                 165

ccg aat atg cag ttt cat caa gcc aat tat aat gtt tcg tgt aat ggg   643
Pro Asn Met Gln Phe His Gln Ala Asn Tyr Asn Val Ser Cys Asn Gly
                170                 175                 180

gtc gtc tat gac aat gtt ttg cat cga aac att gat gat gag cac att   691
Val Val Tyr Asp Asn Val Leu His Arg Asn Ile Asp Asp Glu His Ile
            185                 190                 195

gaa ttg aaa atc gga aag ggg att act ctc cgc cta caa aag ctc gcc   739
Glu Leu Lys Ile Gly Lys Gly Ile Thr Leu Arg Leu Gln Lys Leu Ala
        200                 205                 210

att gat gct ccg ggg agc gtt acg gtt gag ttt caa gat agt ctt cct   787
Ile Asp Ala Pro Gly Ser Val Thr Val Glu Phe Gln Asp Ser Leu Pro
    215                 220                 225

gaa cgg tta aaa gac att gag ttc ttc cta gga gtg ctt cag gcg aat   835
Glu Arg Leu Lys Asp Ile Glu Phe Phe Leu Gly Val Leu Gln Ala Asn
230                 235                 240                 245

acg ttt ttt att aat gaa gaa cct gtt gtg ttg aag att aac tcg aac   883
Thr Phe Phe Ile Asn Glu Glu Pro Val Val Leu Lys Ile Asn Ser Asn
                250                 255                 260

cgg act gtg gct gac ctt aag gat gaa gcg ggt gtt ctt cgt cag ttg   931
Arg Thr Val Ala Asp Leu Lys Asp Glu Ala Gly Val Leu Arg Gln Leu
            265                 270                 275

gta gaa ata gct aac cat ttc aat att gat ccg tcc ctt att cga att   979
Val Glu Ile Ala Asn His Phe Asn Ile Asp Pro Ser Leu Ile Arg Ile
        280                 285                 290

ggt gag att aca gaa aaa cag ttc tgg cag ttg gat att gtg tat cga   1027
Gly Glu Ile Thr Glu Lys Gln Phe Trp Gln Leu Asp Ile Val Tyr Arg
    295                 300                 305

aca gcc gtt aag gga gaa tac gta aag aat tta gag gtt aaa gat gag   1075
Thr Ala Val Lys Gly Glu Tyr Val Lys Asn Leu Glu Val Lys Asp Glu
310                 315                 320                 325

act aga ctt ata ttg cag cct ttt ggt cgt tgg aat ctt gcg ttg ata   1123
Thr Arg Leu Ile Leu Gln Pro Phe Gly Arg Trp Asn Leu Ala Leu Ile
                330                 335                 340

gct cac cct ggt gat gtt gca ggg gag tgg act tat cat gaa gta att   1171
Ala His Pro Gly Asp Val Ala Gly Glu Trp Thr Tyr His Glu Val Ile
            345                 350                 355

tcc aag cgt cat cat ttt gct atg aca cct tca acg gat cgg agc gac   1219
Ser Lys Arg His His Phe Ala Met Thr Pro Ser Thr Asp Arg Ser Asp
        360                 365                 370
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```
tcc tca atc gag cga gtg acg ccg tac gag ctc att gat aat cga tgg   1267
Ser Ser Ile Glu Arg Val Thr Pro Tyr Glu Leu Ile Asp Asn Arg Trp
    375                 380                 385

ctt cca tca gta ttg aat ctg cat ttg gat aag ctt gtt gat ttc tat   1315
Leu Pro Ser Val Leu Asn Leu His Leu Asp Lys Leu Val Asp Phe Tyr
390                 395                 400                 405

tca gcg ctt gaa gaa act gtt gat gtt gat aat ctc gcc aca tgg atg   1363
Ser Ala Leu Glu Glu Thr Val Asp Val Asp Asn Leu Ala Thr Trp Met
                410                 415                 420

gtg ctt cgc cta att aag gca gct gat tct gag cag agc agg aaa act   1411
Val Leu Arg Leu Ile Lys Ala Ala Asp Ser Glu Gln Ser Arg Lys Thr
            425                 430                 435

gca ttt ctt ata gca gct caa gct ctc aat gat tgg ctc gtg gaa cga   1459
Ala Phe Leu Ile Ala Ala Gln Ala Leu Asn Asp Trp Leu Val Glu Arg
        440                 445                 450

gat cga gaa gag tcg cca att tac agg ctt aat ggt tgg caa att ttg   1507
Asp Arg Glu Glu Ser Pro Ile Tyr Arg Leu Asn Gly Trp Gln Ile Leu
    455                 460                 465

tat cgc caa act gga tta ctg gat tca caa aga aca gaa att cga tct   1555
Tyr Arg Gln Thr Gly Leu Leu Asp Ser Gln Arg Thr Glu Ile Arg Ser
470                 475                 480                 485

ttt agg cat aat ctt gat caa aca atg cac cca gac aac tat agc gag   1603
Phe Arg His Asn Leu Asp Gln Thr Met His Pro Asp Asn Tyr Ser Glu
                490                 495                 500

att atg att ggt tgc gct ttg ctt ctt gac gat aga gaa gag gcg aat   1651
Ile Met Ile Gly Cys Ala Leu Leu Leu Asp Asp Arg Glu Glu Ala Asn
            505                 510                 515

ttt ttg ctt act cag ctt tcg gtt gat cga cgc gca gtt ttt aat gaa   1699
Phe Leu Leu Thr Gln Leu Ser Val Asp Arg Arg Ala Val Phe Asn Glu
        520                 525                 530

tgg ccg ata gct caa ttg atg acg ggt gcc cta aaa gaa gag att gaa   1747
Trp Pro Ile Ala Gln Leu Met Thr Gly Ala Leu Lys Glu Glu Ile Glu
    535                 540                 545

aaa tgagttctga gatcttgatt taa                                    1773
Lys
550
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US20050059102A1

<210> 1906
<211> 550
<212> PRT
<213> Corynebacterium glutamicum

<400> 1906

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Val Asn Val Gln Ile Lys Gly Arg Lys Val Asn Ala Lys Ala Ala Asp
  1               5                  10                  15

Leu Asn Ser Tyr Pro Val Ser Val Val Asp Leu Arg Gly Phe Val Thr
             20                  25                  30
```

```
Leu Ala Gly Leu Leu Phe Phe Val Val Asp Ile Asp Lys Lys Ser Asn
          35                  40                  45

Lys Lys Tyr Pro Lys Tyr Val Leu Leu Lys Pro Phe Tyr Ile His Asp
      50                  55                  60

Leu Leu Ser Lys Ala Lys Pro Gly Gln Lys Thr Ile Ser Val Arg Leu
 65                  70                  75                  80

Lys Arg Leu Pro Ser Asp Glu Asp Arg Met Glu Ala Ile Ile Ala Leu
                 85                  90                  95

Ala Leu Ala Ser Arg Gln Glu Lys Ile Val Glu Asn Pro Ser Asn Tyr
            100                 105                 110

Leu Tyr Glu Asn Met Glu Ser Ile Thr Val Lys Ser Ala Glu Pro Leu
        115                 120                 125

Asn Arg Asp Lys Leu Ala Val Tyr Asp Gly Ser Ser Pro Asp His Ser
    130                 135                 140

Ile Ile Ile Arg Thr Gly Asp Gly Ile Glu Gln Phe Val Asn Ala Thr
145                 150                 155                 160

Val Glu Ile Ile Pro Pro Asn Met Gln Phe His Gln Ala Asn Tyr Asn
                165                 170                 175

Val Ser Cys Asn Gly Val Val Tyr Asp Asn Val Leu His Arg Asn Ile
            180                 185                 190

Asp Asp Glu His Ile Glu Leu Lys Ile Gly Lys Gly Ile Thr Leu Arg
        195                 200                 205

Leu Gln Lys Leu Ala Ile Asp Ala Pro Gly Ser Val Thr Val Glu Phe
    210                 215                 220

Gln Asp Ser Leu Pro Glu Arg Leu Lys Asp Ile Glu Phe Phe Leu Gly
225                 230                 235                 240

Val Leu Gln Ala Asn Thr Phe Phe Ile Asn Glu Glu Pro Val Val Leu
                245                 250                 255

Lys Ile Asn Ser Asn Arg Thr Val Ala Asp Leu Lys Asp Glu Ala Gly
            260                 265                 270

Val Leu Arg Gln Leu Val Glu Ile Ala Asn His Phe Asn Ile Asp Pro
        275                 280                 285

Ser Leu Ile Arg Ile Gly Glu Ile Thr Glu Lys Gln Phe Trp Gln Leu
    290                 295                 300

Asp Ile Val Tyr Arg Thr Ala Val Lys Gly Glu Tyr Val Lys Asn Leu
305                 310                 315                 320

Glu Val Lys Asp Glu Thr Arg Leu Ile Leu Gln Pro Phe Gly Arg Trp
                325                 330                 335

Asn Leu Ala Leu Ile Ala His Pro Gly Asp Val Ala Gly Glu Trp Thr
            340                 345                 350
```

```
Tyr His Glu Val Ile Ser Lys Arg His His Phe Ala Met Thr Pro Ser
        355                 360                 365

Thr Asp Arg Ser Asp Ser Ser Ile Glu Arg Val Thr Pro Tyr Glu Leu
    370                 375                 380

Ile Asp Asn Arg Trp Leu Pro Ser Val Leu Asn Leu His Leu Asp Lys
385                 390                 395                 400

Leu Val Asp Phe Tyr Ser Ala Leu Glu Glu Thr Val Asp Val Asp Asn
                405                 410                 415

Leu Ala Thr Trp Met Val Leu Arg Leu Ile Lys Ala Ala Asp Ser Glu
            420                 425                 430

Gln Ser Arg Lys Thr Ala Phe Leu Ile Ala Ala Gln Ala Leu Asn Asp
        435                 440                 445

Trp Leu Val Glu Arg Asp Arg Glu Glu Ser Pro Ile Tyr Arg Leu Asn
    450                 455                 460

Gly Trp Gln Ile Leu Tyr Arg Gln Thr Gly Leu Leu Asp Ser Gln Arg
465                 470                 475                 480

Thr Glu Ile Arg Ser Phe Arg His Asn Leu Asp Gln Thr Met His Pro
                485                 490                 495

Asp Asn Tyr Ser Glu Ile Met Ile Gly Cys Ala Leu Leu Leu Asp Asp
            500                 505                 510

Arg Glu Glu Ala Asn Phe Leu Leu Thr Gln Leu Ser Val Asp Arg Arg
        515                 520                 525

Ala Val Phe Asn Glu Trp Pro Ile Ala Gln Leu Met Thr Gly Ala Leu
    530                 535                 540

Lys Glu Glu Ile Glu Lys
545                 550
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<210> 1907
<211> 546
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(523)
<223> RXA00743

<400> 1907

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attttggcgt agtgtttcgg gttttatagg ttgagattga ataccaaga caaggatgga 60

catcatgtca gcgcatctac cttctcatca tgatgagtta gtg cag cac tta gtt   115
                                              Val Gln His Leu Val
                                                1               5

ctt gcg gat gta aag tat cgg gag ctc agt gcg tta tcg gtc aaa att   163
Leu Ala Asp Val Lys Tyr Arg Glu Leu Ser Ala Leu Ser Val Lys Ile
                10                  15                  20
```

```
gag gaa cca tca gat cgt cct gag ttt aaa ctt gga gtt act gtt aac   211
Glu Glu Pro Ser Asp Arg Pro Glu Phe Lys Leu Gly Val Thr Val Asn
            25                  30                  35

gac aag agt aaa gac gaa gaa ggt gtg ccg cga atc att gag gtt tca   259
Asp Lys Ser Lys Asp Glu Glu Gly Val Pro Arg Ile Ile Glu Val Ser
        40                  45                  50

ttg agg gtg tcc atc gag gtt ccc gac gga aag ata acg gta gag cct   307
Leu Arg Val Ser Ile Glu Val Pro Asp Gly Lys Ile Thr Val Glu Pro
    55                  60                  65

gaa gca atc tat ttg att cct gag aat aag gtt tat tta acg gaa tct   355
Glu Ala Ile Tyr Leu Ile Pro Glu Asn Lys Val Tyr Leu Thr Glu Ser
70                  75                  80                  85

gat gca atg gtg gat tat ttt aac aac cat gcg att ttt act ctg gtg   403
Asp Ala Met Val Asp Tyr Phe Asn Asn His Ala Ile Phe Thr Leu Val
                90                  95                  100

cca tat gca cga cag gcc gtg tct gat tta ggg cag cgt gca ttc cac   451
Pro Tyr Ala Arg Gln Ala Val Ser Asp Leu Gly Gln Arg Ala Phe His
            105                 110                 115

acg cag atc ctc atg cct gcg tta ggt cct ggt gat ttg gtt ttt agt   499
Thr Gln Ile Leu Met Pro Ala Leu Gly Pro Gly Asp Leu Val Phe Ser
        120                 125                 130

aaa tcg acg gcc tca cga gaa tgg tagagaatta cctgatagtt gca         546
Lys Ser Thr Ala Ser Arg Glu Trp
    135                 140
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<210> 1908
<211> 141
<212> PRT
<213> Corynebacterium glutamicum

<400> 1908

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Val Gln His Leu Val Leu Ala Asp Val Lys Tyr Arg Glu Leu Ser Ala
  1               5                  10                  15

Leu Ser Val Lys Ile Glu Glu Pro Ser Asp Arg Pro Glu Phe Lys Leu
            20                  25                  30

Gly Val Thr Val Asn Asp Lys Ser Lys Asp Glu Glu Gly Val Pro Arg
        35                  40                  45

Ile Ile Glu Val Ser Leu Arg Val Ser Ile Glu Val Pro Asp Gly Lys
    50                  55                  60

Ile Thr Val Glu Pro Glu Ala Ile Tyr Leu Ile Pro Glu Asn Lys Val
65                  70                  75                  80

Tyr Leu Thr Glu Ser Asp Ala Met Val Asp Tyr Phe Asn Asn His Ala
                85                  90                  95

Ile Phe Thr Leu Val Pro Tyr Ala Arg Gln Ala Val Ser Asp Leu Gly
            100                 105                 110

Gln Arg Ala Phe His Thr Gln Ile Leu Met Pro Ala Leu Gly Pro Gly
```

```
        115                 120                 125

Asp Leu Val Phe Ser Lys Ser Thr Ala Ser Arg Glu Trp
    130                 135                 140


<210> 1909
<211> 657
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(634)
<223> RXA00745

<400> 1909
tttgacgtgg gatggccaca ccggtgacgg ggtcaatgtg cagaatctgt gcagtggtga 60

gttcagcatt gttttccgca tcagataacg cggtgggcga gtg gct tat ctg tac   115
                                              Val Ala Tyr Leu Tyr
                                                1               5

gga tct gcc gat ggg atg ctt aat aca gat ggt ttt aat atg ttt ccg   163
Gly Ser Ala Asp Gly Met Leu Asn Thr Asp Gly Phe Asn Met Phe Pro
                  10                  15                  20

cgt gcg tcg tac acc att ctt ggc cct atg gat gct gac gcg gtc ggt   211
Arg Ala Ser Tyr Thr Ile Leu Gly Pro Met Asp Ala Asp Ala Val Gly
              25                  30                  35

gtg tac caa cag cta ctg aac agc acg att ccc atg gat ttg gca cgt   259
Val Tyr Gln Gln Leu Leu Asn Ser Thr Ile Pro Met Asp Leu Ala Arg
          40                  45                  50

ctt gta acc acg cat aat tcc ggt gca agt tat ctt cgc cgc ggt gct   307
Leu Val Thr Thr His Asn Ser Gly Ala Ser Tyr Leu Arg Arg Gly Ala
      55                  60                  65

acc aac gta gtt ttt gaa acg aat ctt gcc ctc ggt gtg aat ccg tat   355
Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val Asn Pro Tyr
  70                  75                  80                  85

atg aag aaa cgc cga gca aca gaa gca caa cgt ggt aag aag cgt ttt   403
Met Lys Lys Arg Arg Ala Thr Glu Ala Gln Arg Gly Lys Lys Arg Phe
                  90                  95                 100

aaa cga gac agt cat tac ggc ggt ggc act gtg acc aca ggt act gct   451
Lys Arg Asp Ser His Tyr Gly Gly Gly Thr Val Thr Thr Gly Thr Ala
             105                 110                 115

gat ttg gat gtg gtg gcg atg cag gcg cgg gca gag cac cgg gaa gaa   499
Asp Leu Asp Val Val Ala Met Gln Ala Arg Ala Glu His Arg Glu Glu
         120                 125                 130

agg ttg gga gaa aaa tct acc cgc aag aaa gag gag ctt gct gca gta   547
Arg Leu Gly Glu Lys Ser Thr Arg Lys Lys Glu Glu Leu Ala Ala Val
     135                 140                 145

gag gcg aaa gag tta gct gcg aag aag ggt ccg cag act gtg gaa gaa   595
Glu Ala Lys Glu Leu Ala Ala Lys Lys Gly Pro Gln Thr Val Glu Glu
```

```
150                 155                 160                 165

ggt ctt gct gcg gtg gag aag aaa cac ctg gcg aag cgg taggcgacgt    644
Gly Leu Ala Ala Val Glu Lys Lys His Leu Ala Lys Arg
                170                 175

ggttggcggt ggg                                                   657


<210> 1910
<211> 178
<212> PRT
<213> Corynebacterium glutamicum

<400> 1910
Val Ala Tyr Leu Tyr Gly Ser Ala Asp Gly Met Leu Asn Thr Asp Gly
  1               5                  10                  15

Phe Asn Met Phe Pro Arg Ala Ser Tyr Thr Ile Leu Gly Pro Met Asp
            20                  25                  30

Ala Asp Ala Val Gly Val Tyr Gln Gln Leu Leu Asn Ser Thr Ile Pro
          35                  40                  45

Met Asp Leu Ala Arg Leu Val Thr Thr His Asn Ser Gly Ala Ser Tyr
     50                  55                  60

Leu Arg Arg Gly Ala Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu
 65                  70                  75                  80

Gly Val Asn Pro Tyr Met Lys Lys Arg Arg Ala Thr Glu Ala Gln Arg
                85                  90                  95

Gly Lys Lys Arg Phe Lys Arg Asp Ser His Tyr Gly Gly Gly Thr Val
            100                 105                 110

Thr Thr Gly Thr Ala Asp Leu Asp Val Val Ala Met Gln Ala Arg Ala
        115                 120                 125

Glu His Arg Glu Glu Arg Leu Gly Glu Lys Ser Thr Arg Lys Lys Glu
    130                 135                 140

Glu Leu Ala Ala Val Glu Ala Lys Glu Leu Ala Ala Lys Lys Gly Pro
145                 150                 155                 160

Gln Thr Val Glu Glu Gly Leu Ala Ala Val Glu Lys Lys His Leu Ala
                165                 170                 175

Lys Arg


<210> 1911
<211> 1314
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1291)
<223> RXA00746
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<400> 1911
aaactacgtt ggtagcaccg cggcgaagat aacttgcacc ggaattatgc gtggttacaa 60

```
gacgtgccaa atccatggga atcgtgctgt tcagtagctg ttg gta cac acc gac   115
                                            Leu Val His Thr Asp
                                              1               5

cgc gtc agc atc cat agg gcc aag aat ggt gta cga cgc acg cgg aaa   163
Arg Val Ser Ile His Arg Ala Lys Asn Gly Val Arg Arg Thr Arg Lys
                  10                  15                  20

cat att aaa acc atc tgt att aag cat ccc atc ggc aga tcc gta cag   211
His Ile Lys Thr Ile Cys Ile Lys His Pro Ile Gly Arg Ser Val Gln
              25                  30                  35

ata agc cac tcg ccc acc gcg tta tct gat gcg gaa aac aat gct gaa   259
Ile Ser His Ser Pro Thr Ala Leu Ser Asp Ala Glu Asn Asn Ala Glu
          40                  45                  50

ctc acc act gca cag att ctg cac att gac ccc gtc acc ggt gtg gcc   307
Leu Thr Thr Ala Gln Ile Leu His Ile Asp Pro Val Thr Gly Val Ala
      55                  60                  65

atc cca cgt caa aac att ctg ctg ggt gag gat ttt cag act atg gcc   355
Ile Pro Arg Gln Asn Ile Leu Leu Gly Glu Asp Phe Gln Thr Met Ala
  70                  75                  80                  85

agc tct ttt agt caa atc cgc cat gga tgg ggt atc acc cag ctc atc   403
Ser Ser Phe Ser Gln Ile Arg His Gly Trp Gly Ile Thr Gln Leu Ile
                  90                  95                 100

gga caa gac ccc aac aga aac caa cca atc cgc tct gct gat acg tgg   451
Gly Gln Asp Pro Asn Arg Asn Gln Pro Ile Arg Ser Ala Asp Thr Trp
              105                 110                 115

aca gtg act gga tcg act gga ctc acc ggc ttt aat act gct acg cat   499
Thr Val Thr Gly Ser Thr Gly Leu Thr Gly Phe Asn Thr Ala Thr His
          120                 125                 130

aat aca gat gac aca gac gcc act gcc gca tat acc atg ccg gca agc   547
Asn Thr Asp Asp Thr Asp Ala Thr Ala Ala Tyr Thr Met Pro Ala Ser
      135                 140                 145

gat cct gcc gta gga cta tgc gca ctg gaa tcc aac aaa gac gca ccg   595
Asp Pro Ala Val Gly Leu Cys Ala Leu Glu Ser Asn Lys Asp Ala Pro
150                 155                 160                 165

gtg gat gaa ttt cgc gat ctc agc ctc agt gct tta cgt acc gct acg   643
Val Asp Glu Phe Arg Asp Leu Ser Leu Ser Ala Leu Arg Thr Ala Thr
                  170                 175                 180

gtc atg tca agc tct ggc tcc gcc gtg att act atg cat gat cct atg   691
Val Met Ser Ser Ser Gly Ser Ala Val Ile Thr Met His Asp Pro Met
              185                 190                 195

gtc atg agc acc act ggc gca ttg gaa gca cgt gca tac gtt gac ggc   739
Val Met Ser Thr Thr Gly Ala Leu Glu Ala Arg Ala Tyr Val Asp Gly
          200                 205                 210

gaa gtc atc aac cag cac gat ctt gac tca ctg cgt gac cag cta ggt   787
```

```
Glu Val Ile Asn Gln His Asp Leu Asp Ser Leu Arg Asp Gln Leu Gly
    215                 220                 225

att act aca gac agc gca gat acc acc cct gcc cta cct gct gat ccc   835
Ile Thr Thr Asp Ser Ala Asp Thr Thr Pro Ala Leu Pro Ala Asp Pro
230                 235                 240                 245

ttg gca gca ttg ggc ttg agc aca cca act aca tca gct ctt gtc cca   883
Leu Ala Ala Leu Gly Leu Ser Thr Pro Thr Thr Ser Ala Leu Val Pro
                250                 255                 260

ggt ctt gcc gag ctg gac tgc ctc aac act gat caa gct cgc acc tgg   931
Gly Leu Ala Glu Leu Asp Cys Leu Asn Thr Asp Gln Ala Arg Thr Trp
            265                 270                 275

cat gac cgt gac aac agc att ggc act ggt aaa cca gct att ctt gcc   979
His Asp Arg Asp Asn Ser Ile Gly Thr Gly Lys Pro Ala Ile Leu Ala
        280                 285                 290

gtg att aac gcc gag ctc gct gat gat tac acc ctg cag atc ctc aaa   1027
Val Ile Asn Ala Glu Leu Ala Asp Asp Tyr Thr Leu Gln Ile Leu Lys
    295                 300                 305

aat agc act gcg acc ccc acc gac tcc acc gac tcc agc gat act gct   1075
Asn Ser Thr Ala Thr Pro Thr Asp Ser Thr Asp Ser Ser Asp Thr Ala
310                 315                 320                 325

gaa cgc ttc gta gcg cag cta cct gcg gaa aca gcc ttt gtg ctt att   1123
Glu Arg Phe Val Ala Gln Leu Pro Ala Glu Thr Ala Phe Val Leu Ile
                330                 335                 340

gat ccg gac atc ggc gct gtg acc gat ctg ttc ttt atc aac agc ata   1171
Asp Pro Asp Ile Gly Ala Val Thr Asp Leu Phe Phe Ile Asn Ser Ile
            345                 350                 355

aat cag gat ctc ccc gca ccg aca acc cag atc aac tca gta gcg gta   1219
Asn Gln Asp Leu Pro Ala Pro Thr Thr Gln Ile Asn Ser Val Ala Val
        360                 365                 370

gat caa cgt gac ccc aac atc atc tac gcg acc ttt gcc aat gat gac   1267
Asp Gln Arg Asp Pro Asn Ile Ile Tyr Ala Thr Phe Ala Asn Asp Asp
    375                 380                 385

cgc gtg tac cag ctc atg ctg ggt taaccgcgac ccgtttttat ctg        1314
Arg Val Tyr Gln Leu Met Leu Gly
390                 395
```

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<210> 1912
<211> 397
<212> PRT
<213> Corynebacterium glutamicum

<400> 1912

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Leu Val His Thr Asp Arg Val Ser Ile His Arg Ala Lys Asn Gly Val
  1               5                  10                  15

Arg Arg Thr Arg Lys His Ile Lys Thr Ile Cys Ile Lys His Pro Ile
             20                  25                  30

Gly Arg Ser Val Gln Ile Ser His Ser Pro Thr Ala Leu Ser Asp Ala
```

```
         35                  40                  45

Glu Asn Asn Ala Glu Leu Thr Thr Ala Gln Ile Leu His Ile Asp Pro
     50                  55                  60

Val Thr Gly Val Ala Ile Pro Arg Gln Asn Ile Leu Leu Gly Glu Asp
 65                  70                  75                  80

Phe Gln Thr Met Ala Ser Ser Phe Ser Gln Ile Arg His Gly Trp Gly
                 85                  90                  95

Ile Thr Gln Leu Ile Gly Gln Asp Pro Asn Arg Asn Gln Pro Ile Arg
            100                 105                 110

Ser Ala Asp Thr Trp Thr Val Thr Gly Ser Thr Gly Leu Thr Gly Phe
        115                 120                 125

Asn Thr Ala Thr His Asn Thr Asp Asp Thr Asp Ala Thr Ala Ala Tyr
    130                 135                 140

Thr Met Pro Ala Ser Asp Pro Ala Val Gly Leu Cys Ala Leu Glu Ser
145                 150                 155                 160

Asn Lys Asp Ala Pro Val Asp Glu Phe Arg Asp Leu Ser Leu Ser Ala
                165                 170                 175

Leu Arg Thr Ala Thr Val Met Ser Ser Ser Gly Ser Ala Val Ile Thr
            180                 185                 190

Met His Asp Pro Met Val Met Ser Thr Thr Gly Ala Leu Glu Ala Arg
        195                 200                 205

Ala Tyr Val Asp Gly Glu Val Ile Asn Gln His Asp Leu Asp Ser Leu
    210                 215                 220

Arg Asp Gln Leu Gly Ile Thr Thr Asp Ser Ala Asp Thr Thr Pro Ala
225                 230                 235                 240

Leu Pro Ala Asp Pro Leu Ala Ala Leu Gly Leu Ser Thr Pro Thr Thr
                245                 250                 255

Ser Ala Leu Val Pro Gly Leu Ala Glu Leu Asp Cys Leu Asn Thr Asp
            260                 265                 270

Gln Ala Arg Thr Trp His Asp Arg Asp Asn Ser Ile Gly Thr Gly Lys
        275                 280                 285

Pro Ala Ile Leu Ala Val Ile Asn Ala Glu Leu Ala Asp Asp Tyr Thr
    290                 295                 300

Leu Gln Ile Leu Lys Asn Ser Thr Ala Thr Pro Thr Asp Ser Thr Asp
305                 310                 315                 320

Ser Ser Asp Thr Ala Glu Arg Phe Val Ala Gln Leu Pro Ala Glu Thr
                325                 330                 335

Ala Phe Val Leu Ile Asp Pro Asp Ile Gly Ala Val Thr Asp Leu Phe
            340                 345                 350

Phe Ile Asn Ser Ile Asn Gln Asp Leu Pro Ala Pro Thr Thr Gln Ile
        355                 360                 365
```

```
Asn Ser Val Ala Val Asp Gln Arg Asp Pro Asn Ile Ile Tyr Ala Thr
    370                 375                 380

Phe Ala Asn Asp Asp Arg Val Tyr Gln Leu Met Leu Gly
385                 390                 395

<210> 1913
<211> 711
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(688)
<223> RXA00747

<400> 1913
tgtgctgatc cgcgccgtgc caactcgcac tgggtcgcac tgggtcgcac aaccgcatac 60

acatacacac aattaatcac cctcaacacg aagatttatc atg aca ttt ttg cac   115
                                        Met Thr Phe Leu His
                                          1               5

cgt tcc gcc agt ttc cac cct cgt acc cac gat cac ctc agc gag ctc   163
Arg Ser Ala Ser Phe His Pro Arg Thr His Asp His Leu Ser Glu Leu
                 10                  15                  20

ggt ctt gat cct tat aag ctc tct caa gac atc ccc act gtt att tat   211
Gly Leu Asp Pro Tyr Lys Leu Ser Gln Asp Ile Pro Thr Val Ile Tyr
             25                  30                  35

gaa gtc cag ccg cac agt gtg ttc att tta aaa ttc aac act gcc gat   259
Glu Val Gln Pro His Ser Val Phe Ile Leu Lys Phe Asn Thr Ala Asp
         40                  45                  50

gtt cgg gtc tat cag gaa cac tcc gat ctc ttt gtg cga cat gct gtg   307
Val Arg Val Tyr Gln Glu His Ser Asp Leu Phe Val Arg His Ala Val
     55                  60                  65

ctt gtt gat cca gaa cag cgt aaa cat gag cat gac cag ctc ctt aaa   355
Leu Val Asp Pro Glu Gln Arg Lys His Glu His Asp Gln Leu Leu Lys
 70                  75                  80                  85

gag att ctc gac ctc gat gcc cct cgt gtc aac gat gat att agt ggt   403
Glu Ile Leu Asp Leu Asp Ala Pro Arg Val Asn Asp Asp Ile Ser Gly
                 90                  95                 100

cgc acg aca gtg ttt ctc cac gat aaa aca gtt gtt acg cac agt ggt   451
Arg Thr Thr Val Phe Leu His Asp Lys Thr Val Val Thr His Ser Gly
            105                 110                 115

ggc ccc att gcg att att ccg cac aat ccc gat gtc gcc agc gcc gct   499
Gly Pro Ile Ala Ile Ile Pro His Asn Pro Asp Val Ala Ser Ala Ala
        120                 125                 130

gcg tca gct aat aaa cac aaa caa tct gtg atg aca aca tcc agg cat   547
Ala Ser Ala Asn Lys His Lys Gln Ser Val Met Thr Thr Ser Arg His
    135                 140                 145
```

```
cct tat gcg cag atg tct ctc agc gac atg ctg aaa caa ggc ttc acg   595
Pro Tyr Ala Gln Met Ser Leu Ser Asp Met Leu Lys Gln Gly Phe Thr
150                 155                 160                 165

ctc aca cct cta gag ttc ccc tac tgc gct gtt gat gac ccc gac agc   643
Leu Thr Pro Leu Glu Phe Pro Tyr Cys Ala Val Asp Asp Pro Asp Ser
                170                 175                 180

tca cgc cac aca atg cac gtc atc aac gtt cga gat cat aca gtg       688
Ser Arg His Thr Met His Val Ile Asn Val Arg Asp His Thr Val
            185                 190                 195

tgaactaccg cgccgctaga gat                                        711
```

<210> 1914
<211> 196
<212> PRT
<213> Corynebacterium glutamicum

<400> 1914

```
Met Thr Phe Leu His Arg Ser Ala Ser Phe His Pro Arg Thr His Asp
  1               5                  10                  15

His Leu Ser Glu Leu Gly Leu Asp Pro Tyr Lys Leu Ser Gln Asp Ile
            20                  25                  30

Pro Thr Val Ile Tyr Glu Val Gln Pro His Ser Val Phe Ile Leu Lys
        35                  40                  45

Phe Asn Thr Ala Asp Val Arg Val Tyr Gln Glu His Ser Asp Leu Phe
    50                  55                  60

Val Arg His Ala Val Leu Val Asp Pro Glu Gln Arg Lys His Glu His
65                  70                  75                  80

Asp Gln Leu Leu Lys Glu Ile Leu Asp Leu Asp Ala Pro Arg Val Asn
                85                  90                  95

Asp Asp Ile Ser Gly Arg Thr Thr Val Phe Leu His Asp Lys Thr Val
            100                 105                 110

Val Thr His Ser Gly Gly Pro Ile Ala Ile Ile Pro His Asn Pro Asp
        115                 120                 125

Val Ala Ser Ala Ala Ala Ser Ala Asn Lys His Lys Gln Ser Val Met
    130                 135                 140

Thr Thr Ser Arg His Pro Tyr Ala Gln Met Ser Leu Ser Asp Met Leu
145                 150                 155                 160

Lys Gln Gly Phe Thr Leu Thr Pro Leu Glu Phe Pro Tyr Cys Ala Val
                165                 170                 175

Asp Asp Pro Asp Ser Ser Arg His Thr Met His Val Ile Asn Val Arg
            180                 185                 190

Asp His Thr Val
        195
```

<210> 1915
<211> 567
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(544)
<223> RXA00748

<400> 1915
aagccttatt ctcctcttaa ctaccatgag gtaaccatct aaagtagatg gttgcaacaa 60

cttttcatta catcaacatg tttaaaaaag gacactgatt atg act tac ttc gca 115
Met Thr Tyr Phe Ala
1 5

ctc gtt gct cgc aat tac gct gag aca ggt gtc tct gtt gaa ttc cat 163
Leu Val Ala Arg Asn Tyr Ala Glu Thr Gly Val Ser Val Glu Phe His
10 15 20

gag gtc gat gat gac gca gat aac tca aat ggc ccc aac aac aca agc 211
Glu Val Asp Asp Asp Ala Asp Asn Ser Asn Gly Pro Asn Asn Thr Ser
25 30 35

aat tta cct cta aaa ctt ctt cga gat cac tct ttt gat gcc act gtt 259
Asn Leu Pro Leu Lys Leu Leu Arg Asp His Ser Phe Asp Ala Thr Val
40 45 50

gtc tat ggt gac ctg gtg ctt cac acc tca gca cat ctc aga gat acg 307
Val Tyr Gly Asp Leu Val Leu His Thr Ser Ala His Leu Arg Asp Thr
55 60 65

gct atc gcc aac tca gac aac cgt ccg cga gta gtg acc aca gct caa 355
Ala Ile Ala Asn Ser Asp Asn Arg Pro Arg Val Val Thr Thr Ala Gln
70 75 80 85

aaa ttc ttt gat tac atc cgc tta gcc acc aga cac ggt gct atc cac 403
Lys Phe Phe Asp Tyr Ile Arg Leu Ala Thr Arg His Gly Ala Ile His
90 95 100

gac atg atc aat aac gcg cca gat acc ggc act gac atc gtt gtt att 451
Asp Met Ile Asn Asn Ala Pro Asp Thr Gly Thr Asp Ile Val Val Ile
105 110 115

acg gcc act aat gat gct ctt att agt gat gaa tca gaa tac tat gac 499
Thr Ala Thr Asn Asp Ala Leu Ile Ser Asp Glu Ser Glu Tyr Tyr Asp
120 125 130

gag ctt ttt cat att ctc gaa tcc gca cag ggt gtg att ctt aaa 544
Glu Leu Phe His Ile Leu Glu Ser Ala Gln Gly Val Ile Leu Lys
135 140 145

tgattgatta attgatatga tta 567

<210> 1916
<211> 148
<212> PRT
<213> Corynebacterium glutamicum

<400> 1916
Met Thr Tyr Phe Ala Leu Val Ala Arg Asn Tyr Ala Glu Thr Gly Val
1 5 10 15

Ser Val Glu Phe His Glu Val Asp Asp Asp Ala Asp Asn Ser Asn Gly
20 25 30

Pro Asn Asn Thr Ser Asn Leu Pro Leu Lys Leu Leu Arg Asp His Ser
35 40 45

Phe Asp Ala Thr Val Val Tyr Gly Asp Leu Val Leu His Thr Ser Ala
50 55 60

His Leu Arg Asp Thr Ala Ile Ala Asn Ser Asp Asn Arg Pro Arg Val
65 70 75 80

Val Thr Thr Ala Gln Lys Phe Phe Asp Tyr Ile Arg Leu Ala Thr Arg
85 90 95

His Gly Ala Ile His Asp Met Ile Asn Asn Ala Pro Asp Thr Gly Thr
100 105 110

Asp Ile Val Val Ile Thr Ala Thr Asn Asp Ala Leu Ile Ser Asp Glu
115 120 125

Ser Glu Tyr Tyr Asp Glu Leu Phe His Ile Leu Glu Ser Ala Gln Gly
130 135 140

Val Ile Leu Lys
145

<210> 1917
<211> 822
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(799)
<223> RXA00749

<400> 1917
cgtttcgatc atttgtaaca ttcttattac aagactggaa ataaaggtga gtcaatcata 60

cagtcagatg tggtcatcgg caaaacagaa aggaatcccg atg tta cga aaa aca 115
Met Leu Arg Lys Thr
1 5

gtt acc ggt gga att gtt gct ctt att gcg act gcc act ctc atg aat 163
Val Thr Gly Gly Ile Val Ala Leu Ile Ala Thr Ala Thr Leu Met Asn
10 15 20

tct gtc tct tct gct gaa gag gta tcc gga gat gtc tca gca gta gat 211
Ser Val Ser Ser Ala Glu Glu Val Ser Gly Asp Val Ser Ala Val Asp
25 30 35

ctc gca ttt gca gaa ttc gaa cgt aca act gca gag gac gtg gcc aat 259
Leu Ala Phe Ala Glu Phe Glu Arg Thr Thr Ala Glu Asp Val Ala Asn
40 45 50

```
gga gtg cca gag gct ata gct aat gca gaa aaa att tcc aat ttc act   307
Gly Val Pro Glu Ala Ile Ala Asn Ala Glu Lys Ile Ser Asn Phe Thr
     55                  60                  65

ccg agc gaa cta gag ggc ttc aag agt ctt tta gct agt gat gca gtg   355
Pro Ser Glu Leu Glu Gly Phe Lys Ser Leu Leu Ala Ser Asp Ala Val
 70                  75                  80                  85

ctg agg tcg gtc tct gga gaa gaa att ctc cca gat aat gtt gaa gtg   403
Leu Arg Ser Val Ser Gly Glu Glu Ile Leu Pro Asp Asn Val Glu Val
                 90                  95                 100

gtt cag acg gac aac gta ggc gac gaa gat cca aat gtc att tct cca   451
Val Gln Thr Asp Asn Val Gly Asp Glu Asp Pro Asn Val Ile Ser Pro
            105                 110                 115

gca gcc tgg cag ggt tct gat tat att gag ggg tgt tta acg aat act   499
Ala Ala Trp Gln Gly Ser Asp Tyr Ile Glu Gly Cys Leu Thr Asn Thr
        120                 125                 130

ctc tac gga att gaa gtc cta aag gtt tgt act ggt gga acc tac tac   547
Leu Tyr Gly Ile Glu Val Leu Lys Val Cys Thr Gly Gly Thr Tyr Tyr
    135                 140                 145

tcc aat gta gga atc gct act tct gtc agc aat cct cgc agt tac gta   595
Ser Asn Val Gly Ile Ala Thr Ser Val Ser Asn Pro Arg Ser Tyr Val
150                 155                 160                 165

aag tat aac agt gct cca gga ttg gca gtg acg aca agc aat cca cgt   643
Lys Tyr Asn Ser Ala Pro Gly Leu Ala Val Thr Thr Ser Asn Pro Arg
                170                 175                 180

gga ggt ata gag ggt ggt ctt gcg gcc ttc tat ggt gat gtt aac ctt   691
Gly Gly Ile Glu Gly Gly Leu Ala Ala Phe Tyr Gly Asp Val Asn Leu
            185                 190                 195

gtt gct ttt cca aat att cca tgg gtg gga cca att agt tct tct gca   739
Val Ala Phe Pro Asn Ile Pro Trp Val Gly Pro Ile Ser Ser Ser Ala
        200                 205                 210

gga act cac cgc gtt gtc gct aga tca ttt ccg aat tca gtg gtg ctt   787
Gly Thr His Arg Val Val Ala Arg Ser Phe Pro Asn Ser Val Val Leu
    215                 220                 225

aac gtc tac tac taatcgtttt ttagtttgaa aca                        822
Asn Val Tyr Tyr
230
```

<210> 1918
<211> 233
<212> PRT
<213> Corynebacterium glutamicum

<400> 1918

```
Met Leu Arg Lys Thr Val Thr Gly Gly Ile Val Ala Leu Ile Ala Thr
  1               5                  10                  15

Ala Thr Leu Met Asn Ser Val Ser Ser Ala Glu Glu Val Ser Gly Asp
             20                  25                  30
```

```
Val Ser Ala Val Asp Leu Ala Phe Ala Glu Phe Glu Arg Thr Thr Ala
          35                  40                  45

Glu Asp Val Ala Asn Gly Val Pro Glu Ala Ile Ala Asn Ala Glu Lys
     50                  55                  60

Ile Ser Asn Phe Thr Pro Ser Glu Leu Glu Gly Phe Lys Ser Leu Leu
 65                  70                  75                  80

Ala Ser Asp Ala Val Leu Arg Ser Val Ser Gly Glu Glu Ile Leu Pro
                 85                  90                  95

Asp Asn Val Glu Val Val Gln Thr Asp Asn Val Gly Asp Glu Asp Pro
            100                 105                 110

Asn Val Ile Ser Pro Ala Ala Trp Gln Gly Ser Asp Tyr Ile Glu Gly
        115                 120                 125

Cys Leu Thr Asn Thr Leu Tyr Gly Ile Glu Val Leu Lys Val Cys Thr
    130                 135                 140

Gly Gly Thr Tyr Tyr Ser Asn Val Gly Ile Ala Thr Ser Val Ser Asn
145                 150                 155                 160

Pro Arg Ser Tyr Val Lys Tyr Asn Ser Ala Pro Gly Leu Ala Val Thr
                165                 170                 175

Thr Ser Asn Pro Arg Gly Gly Ile Glu Gly Gly Leu Ala Ala Phe Tyr
            180                 185                 190

Gly Asp Val Asn Leu Val Ala Phe Pro Asn Ile Pro Trp Val Gly Pro
        195                 200                 205

Ile Ser Ser Ser Ala Gly Thr His Arg Val Val Ala Arg Ser Phe Pro
    210                 215                 220

Asn Ser Val Val Leu Asn Val Tyr Tyr
225                 230
```

<210> 1919
<211> 951
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(928)
<223> RXA00751

<400> 1919

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cgcagcaacc ccgtccatga gggcagggaa cgccacacat cctgtaccta tactgtgagg 60

tggcatagag tatctctaat ttagaaagtg gtgtagaagt atg ttg gta cgt tca   115
                                              Met Leu Val Arg Ser
                                                1               5

cgc acg ttg gtt acc gct gca ctg tca tgt tca ctg ttg ttc gga gca   163
Arg Thr Leu Val Thr Ala Ala Leu Ser Cys Ser Leu Leu Phe Gly Ala
                10                  15                  20
```

```
acg gta aat ggc acg ggt gtt gcg att gca tat gaa aat gtg tct atg   211
Thr Val Asn Gly Thr Gly Val Ala Ile Ala Tyr Glu Asn Val Ser Met
            25                  30                  35

gct gct cag tat gaa cca cgg tat gaa tcc tta gaa acg cgt ctc ggt   259
Ala Ala Gln Tyr Glu Pro Arg Tyr Glu Ser Leu Glu Thr Arg Leu Gly
        40                  45                  50

tct agt gga gtc ttt ccc aag tcg gtt gaa cag tct gtt gaa aac ctt   307
Ser Ser Gly Val Phe Pro Lys Ser Val Glu Gln Ser Val Glu Asn Leu
    55                  60                  65

gct gaa tta cca gag gag act cga ttt tta ctt gag ggt gat tcg ttt   355
Ala Glu Leu Pro Glu Glu Thr Arg Phe Leu Leu Glu Gly Asp Ser Phe
70                  75                  80                  85

tca att att att gat gat ggt ctg ctc gct tct cga ttg gac cca aat   403
Ser Ile Ile Ile Asp Asp Gly Leu Leu Ala Ser Arg Leu Asp Pro Asn
                90                  95                  100

aca ggg gag att cga cat act ctt ggg gct tcg ggg atc agc tac acc   451
Thr Gly Glu Ile Arg His Thr Leu Gly Ala Ser Gly Ile Ser Tyr Thr
            105                 110                 115

cct ggt gaa atg aaa cga tct tat aca gat cga gtg act gtc aag gtg   499
Pro Gly Glu Met Lys Arg Ser Tyr Thr Asp Arg Val Thr Val Lys Val
        120                 125                 130

gtc tac cct gat ggg tca ttt gat aga gtg aca ccc cat tca gtg gtt   547
Val Tyr Pro Asp Gly Ser Phe Asp Arg Val Thr Pro His Ser Val Val
    135                 140                 145

tat gtg gct gac agt att tac tac ggc att gaa agc acg ggt tat cct   595
Tyr Val Ala Asp Ser Ile Tyr Tyr Gly Ile Glu Ser Thr Gly Tyr Pro
150                 155                 160                 165

aaa gtc cgc aat ggt cag act gtc aag atc cca ttg agg gtg acg gat   643
Lys Val Arg Asn Gly Gln Thr Val Lys Ile Pro Leu Arg Val Thr Asp
                170                 175                 180

ggt ggt aca gga gcg gtt ggt ggg gtc cca cag gga tcg aag gtg gtc   691
Gly Gly Thr Gly Ala Val Gly Gly Val Pro Gln Gly Ser Lys Val Val
            185                 190                 195

cga gat cgt tac ggc tca att gag aat gcg gag ttg atg ggt gca atc   739
Arg Asp Arg Tyr Gly Ser Ile Glu Asn Ala Glu Leu Met Gly Ala Ile
        200                 205                 210

att ctc ata gat gag aag act ggc gat ctc acc ttc acg gcg cct gat   787
Ile Leu Ile Asp Glu Lys Thr Gly Asp Leu Thr Phe Thr Ala Pro Asp
    215                 220                 225

gat cga acc ggt caa ctg tgg ttt cgt aca gaa gtg act ttc ccg gat   835
Asp Arg Thr Gly Gln Leu Trp Phe Arg Thr Glu Val Thr Phe Pro Asp
230                 235                 240                 245

ggt tcg gac tca gag gtt caa tat gtg atc gag gtg acg gat cag cct   883
Gly Ser Asp Ser Glu Val Gln Tyr Val Ile Glu Val Thr Asp Gln Pro
                250                 255                 260

gaa cct gtg gat gtc att cgt cct gcc gga tcg tct ctg agt tct       928
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Glu Pro Val Asp Val Ile Arg Pro Ala Gly Ser Ser Leu Ser Ser
265 270 275

tgatttatgc ctgagactta agc 951

<210> 1920
<211> 276
<212> PRT
<213> Corynebacterium glutamicum

<400> 1920
Met Leu Val Arg Ser Arg Thr Leu Val Thr Ala Ala Leu Ser Cys Ser
1 5 10 15

Leu Leu Phe Gly Ala Thr Val Asn Gly Thr Gly Val Ala Ile Ala Tyr
20 25 30

Glu Asn Val Ser Met Ala Ala Gln Tyr Glu Pro Arg Tyr Glu Ser Leu
35 40 45

Glu Thr Arg Leu Gly Ser Ser Gly Val Phe Pro Lys Ser Val Glu Gln
50 55 60

Ser Val Glu Asn Leu Ala Glu Leu Pro Glu Glu Thr Arg Phe Leu Leu
65 70 75 80

Glu Gly Asp Ser Phe Ser Ile Ile Ile Asp Asp Gly Leu Leu Ala Ser
85 90 95

Arg Leu Asp Pro Asn Thr Gly Glu Ile Arg His Thr Leu Gly Ala Ser
100 105 110

Gly Ile Ser Tyr Thr Pro Gly Glu Met Lys Arg Ser Tyr Thr Asp Arg
115 120 125

Val Thr Val Lys Val Val Tyr Pro Asp Gly Ser Phe Asp Arg Val Thr
130 135 140

Pro His Ser Val Val Tyr Val Ala Asp Ser Ile Tyr Tyr Gly Ile Glu
145 150 155 160

Ser Thr Gly Tyr Pro Lys Val Arg Asn Gly Gln Thr Val Lys Ile Pro
165 170 175

Leu Arg Val Thr Asp Gly Gly Thr Gly Ala Val Gly Gly Val Pro Gln
180 185 190

Gly Ser Lys Val Val Arg Asp Arg Tyr Gly Ser Ile Glu Asn Ala Glu
195 200 205

Leu Met Gly Ala Ile Ile Leu Ile Asp Glu Lys Thr Gly Asp Leu Thr
210 215 220

Phe Thr Ala Pro Asp Asp Arg Thr Gly Gln Leu Trp Phe Arg Thr Glu
225 230 235 240

Val Thr Phe Pro Asp Gly Ser Asp Ser Glu Val Gln Tyr Val Ile Glu
245 250 255

Val Thr Asp Gln Pro Glu Pro Val Asp Val Ile Arg Pro Ala Gly Ser

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            260                 265                 270

Ser Leu Ser Ser
        275


<210> 1921
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> RXA00752

<400> 1921
aaggtcagcc gtatttcggt cagtcagcaa ctaactacgc ttatcttccg tgtacgatag 60

accgtagtta acataaggaa tggaatagga gaattgcggc atg tat tcc gac aag   115
                                            Met Tyr Ser Asp Lys
                                              1               5

ctg att ctc ttg ttc ctt tct gag cag gat tca agc tat gaa tgc tgc   163
Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser Ser Tyr Glu Cys Cys
                  10                  15                  20

gta ggt tta tta gat ggc tca gat gga ctt gat tat att gaa aag ctt   211
Val Gly Leu Leu Asp Gly Ser Asp Gly Leu Asp Tyr Ile Glu Lys Leu
              25                  30                  35

ctg aag ggt agg aag ctg aag aac cat ttt ctt gaa tgg gaa gat att   259
Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu Glu Trp Glu Asp Ile
          40                  45                  50

aac aag gct gat gtt gct cgt gaa gaa ata tat aaa ggg caa ttg gtg   307
Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr Lys Gly Gln Leu Val
      55                  60                  65

cat ctg gtg ttt gtg acg gct ctt tcc acg cct ggt gaa att tct ttt   355
His Leu Val Phe Val Thr Ala Leu Ser Thr Pro Gly Glu Ile Ser Phe
  70                  75                  80                  85

gtt ttt cca ggt caa tct ctt atg agt gca aca ctc gaa gaa gac ttt   403
Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr Leu Glu Glu Asp Phe
                  90                  95                 100

gct gcg ctt gtg ctc gaa gag gag cgc aca tca ttt aga cct gaa ctg   451
Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser Phe Arg Pro Glu Leu
              105                 110                 115

tct cac ctg tgg tca ctc ccc gta ggg tgg gta gct ccg ggg ctt gag   499
Ser His Leu Trp Ser Leu Pro Val Gly Trp Val Ala Pro Gly Leu Glu
          120                 125                 130

ggt ttc gtg gag cgt aat tcc gag gca gct tgaaccaccg ctttctgagc     549
Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
      135                 140

cgg                                                              552
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<210> 1922
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 1922
Met Tyr Ser Asp Lys Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser
1 5 10 15

Ser Tyr Glu Cys Cys Val Gly Leu Leu Asp Gly Ser Asp Gly Leu Asp
20 25 30

Tyr Ile Glu Lys Leu Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu
35 40 45

Glu Trp Glu Asp Ile Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr
50 55 60

Lys Gly Gln Leu Val His Leu Val Phe Val Thr Ala Leu Ser Thr Pro
65 70 75 80

Gly Glu Ile Ser Phe Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr
85 90 95

Leu Glu Glu Asp Phe Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser
100 105 110

Phe Arg Pro Glu Leu Ser His Leu Trp Ser Leu Pro Val Gly Trp Val
115 120 125

Ala Pro Gly Leu Glu Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
130 135 140

<210> 1923
<211> 1377
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1354)
<223> RXA00757

<400> 1923
caggtttagc gaattcaatt tctaccactg ctcgagggga atgtgctaat tcaagggttg 60

tgacctcgag caacttttta ttccgctcga tcaaaacaac gtg agt ttc ggc gtc 115
Val Ser Phe Gly Val
1 5

gtt aag cgc ccc gat gcg tgc tac gcg ctt ttt gcc atc ctg atc aag 163
Val Lys Arg Pro Asp Ala Cys Tyr Ala Leu Phe Ala Ile Leu Ile Lys
10 15 20

cgc aac cag gcg acc gcg gtt tct gcg cca atg gcg cgg cag cgt cag 211
Arg Asn Gln Ala Thr Ala Val Ser Ala Pro Met Ala Arg Gln Arg Gln
25 30 35

tgg gtt gtc cac gcc cgg cgt gga cac ttc gag cgt gta acc cgc tcc 259

```
Trp Val Val His Ala Arg Arg Gly His Phe Glu Arg Val Thr Arg Ser
          40                  45                  50

gaa gtt gag ctc tcc gcg ctg ctc ggc ggc gtc gaa aag ctc tcc gat   307
Glu Val Glu Leu Ser Ala Leu Leu Gly Gly Val Glu Lys Leu Ser Asp
     55                  60                  65

ttc ttg gct gaa tac ttc cag ctg gtc gag atc ggg gcg gga atc cga   355
Phe Leu Ala Glu Tyr Phe Gln Leu Val Glu Ile Gly Ala Gly Ile Arg
 70                  75                  80                  85

atc tac ctt gat ggc gac ggc gga ttt tgg acc tgc ttt ggt cac ttt   403
Ile Tyr Leu Asp Gly Asp Gly Gly Phe Trp Thr Cys Phe Gly His Phe
                 90                  95                 100

cag gcc ctc gag gtc gaa ttt gtg gga tgc ggc gag cgg ctc gat gag   451
Gln Ala Leu Glu Val Glu Phe Val Gly Cys Gly Glu Arg Leu Asp Glu
            105                 110                 115

cgc aga cag aat ttc agt ggt tgg aaa agc cat aaa gac aag gat aac   499
Arg Arg Gln Asn Phe Ser Gly Trp Lys Ser His Lys Asp Lys Asp Asn
        120                 125                 130

ctg ccg gca aaa atc atc ggg cta tta cac tgt gaa gcc atg cgt agg   547
Leu Pro Ala Lys Ile Ile Gly Leu Leu His Cys Glu Ala Met Arg Arg
    135                 140                 145

cgt atc ccc tct gtc ctt ggt gtt tct ctt ctg gct gcc ttt ttg gtg   595
Arg Ile Pro Ser Val Leu Gly Val Ser Leu Leu Ala Ala Phe Leu Val
150                 155                 160                 165

gcg tgc acc ccc tcc ccc aat ccg aat gcg gcg ttg gcc cag atg tat   643
Ala Cys Thr Pro Ser Pro Asn Pro Asn Ala Ala Leu Ala Gln Met Tyr
                170                 175                 180

cag gat gcg ctt ttt gat tcc cag gcg atg tca gag gcc gag cct gag   691
Gln Asp Ala Leu Phe Asp Ser Gln Ala Met Ser Glu Ala Glu Pro Glu
            185                 190                 195

ctt gcc act ttg cgc agt cag cac gca gat gaa tta ttg gcc gag att   739
Leu Ala Thr Leu Arg Ser Gln His Ala Asp Glu Leu Leu Ala Glu Ile
        200                 205                 210

cgg cgt att tgt ggc ttt gat gaa ggc cag gtt ccg gaa tcg tgc cag   787
Arg Arg Ile Cys Gly Phe Asp Glu Gly Gln Val Pro Glu Ser Cys Gln
    215                 220                 225

gta acg gtt cct gcg atc gct att ctg ccc acc gat gat cca gag aag   835
Val Thr Val Pro Ala Ile Ala Ile Leu Pro Thr Asp Asp Pro Glu Lys
230                 235                 240                 245

tat gtc aac gac agt cag gcg ttg atc ctt gat aat ttg gat gac att   883
Tyr Val Asn Asp Ser Gln Ala Leu Ile Leu Asp Asn Leu Asp Asp Ile
                250                 255                 260

ccg gaa gat tcc gtg gct tta gtg gtt gag caa tac atc gcg cag gcg   931
Pro Glu Asp Ser Val Ala Leu Val Val Glu Gln Tyr Ile Ala Gln Ala
            265                 270                 275

gaa ttt gct gaa gga tct gag gtg tcc gtt cct gtt gat ttg gag ctc   979
Glu Phe Ala Glu Gly Ser Glu Val Ser Val Pro Val Asp Leu Glu Leu
```

```
        280                 285                 290

acc gag gca gaa tta gct gct gcg aag gac ttg gcg gac cgc gag ttt   1027
Thr Glu Ala Glu Leu Ala Ala Ala Lys Asp Leu Ala Asp Arg Glu Phe
    295                 300                 305

tcc gcc gcg tgg tct ttg ggc gtg gct ttg gct cag ctt ccg gaa acc   1075
Ser Ala Ala Trp Ser Leu Gly Val Ala Leu Ala Gln Leu Pro Glu Thr
310                 315                 320                 325

gac cgc gag gag gtg gaa acg gcg atc agc aac cac cat gac cgc gcg   1123
Asp Arg Glu Glu Val Glu Thr Ala Ile Ser Asn His His Asp Arg Ala
                330                 335                 340

tcg cag ctg caa att att acc tcc ggc act acc cca gcg cca ggt tac   1171
Ser Gln Leu Gln Ile Ile Thr Ser Gly Thr Thr Pro Ala Pro Gly Tyr
            345                 350                 355

gtg agc gag ctg ccc gac ccc acc gac gag act tca gcg cga agc aac   1219
Val Ser Glu Leu Pro Asp Pro Thr Asp Glu Thr Ser Ala Arg Ser Asn
        360                 365                 370

att gaa acc gtc gaa aac aac gtc acc cag gcc tgg cat gca gct gca   1267
Ile Glu Thr Val Glu Asn Asn Val Thr Gln Ala Trp His Ala Ala Ala
    375                 380                 385

agc gcc gca acc acc gac gcc tgg cgt gtc ttc tgc gcg cac atc gcc   1315
Ser Ala Ala Thr Thr Asp Ala Trp Arg Val Phe Cys Ala His Ile Ala
390                 395                 400                 405

ggc gat acc gca cgc gaa tta acg ctt atc gac gtc tcc tagcagtttc    1364
Gly Asp Thr Ala Arg Glu Leu Thr Leu Ile Asp Val Ser
                410                 415

actgccaatt ttt                                                   1377
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Sequence Listing Page 2191 of 2200

<210> 1924
<211> 418
<212> PRT
<213> Corynebacterium glutamicum

<400> 1924

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Val Ser Phe Gly Val Val Lys Arg Pro Asp Ala Cys Tyr Ala Leu Phe
  1               5                  10                  15

Ala Ile Leu Ile Lys Arg Asn Gln Ala Thr Ala Val Ser Ala Pro Met
            20                  25                  30

Ala Arg Gln Arg Gln Trp Val Val His Ala Arg Arg Gly His Phe Glu
        35                  40                  45

Arg Val Thr Arg Ser Glu Val Glu Leu Ser Ala Leu Leu Gly Gly Val
    50                  55                  60

Glu Lys Leu Ser Asp Phe Leu Ala Glu Tyr Phe Gln Leu Val Glu Ile
65                  70                  75                  80

Gly Ala Gly Ile Arg Ile Tyr Leu Asp Gly Asp Gly Gly Phe Trp Thr
                85                  90                  95
```

```
Cys Phe Gly His Phe Gln Ala Leu Glu Val Glu Phe Val Gly Cys Gly
            100                 105                 110

Glu Arg Leu Asp Glu Arg Arg Gln Asn Phe Ser Gly Trp Lys Ser His
        115                 120                 125

Lys Asp Lys Asp Asn Leu Pro Ala Lys Ile Ile Gly Leu Leu His Cys
    130                 135                 140

Glu Ala Met Arg Arg Arg Ile Pro Ser Val Leu Gly Val Ser Leu Leu
145                 150                 155                 160

Ala Ala Phe Leu Val Ala Cys Thr Pro Ser Pro Asn Pro Asn Ala Ala
                165                 170                 175

Leu Ala Gln Met Tyr Gln Asp Ala Leu Phe Asp Ser Gln Ala Met Ser
            180                 185                 190

Glu Ala Glu Pro Glu Leu Ala Thr Leu Arg Ser Gln His Ala Asp Glu
        195                 200                 205

Leu Leu Ala Glu Ile Arg Arg Ile Cys Gly Phe Asp Glu Gly Gln Val
    210                 215                 220

Pro Glu Ser Cys Gln Val Thr Val Pro Ala Ile Ala Ile Leu Pro Thr
225                 230                 235                 240

Asp Asp Pro Glu Lys Tyr Val Asn Asp Ser Gln Ala Leu Ile Leu Asp
                245                 250                 255

Asn Leu Asp Asp Ile Pro Glu Asp Ser Val Ala Leu Val Val Glu Gln
            260                 265                 270

Tyr Ile Ala Gln Ala Glu Phe Ala Glu Gly Ser Glu Val Ser Val Pro
        275                 280                 285

Val Asp Leu Glu Leu Thr Glu Ala Glu Leu Ala Ala Ala Lys Asp Leu
    290                 295                 300

Ala Asp Arg Glu Phe Ser Ala Ala Trp Ser Leu Gly Val Ala Leu Ala
305                 310                 315                 320

Gln Leu Pro Glu Thr Asp Arg Glu Glu Val Glu Thr Ala Ile Ser Asn
                325                 330                 335

His His Asp Arg Ala Ser Gln Leu Gln Ile Ile Thr Ser Gly Thr Thr
            340                 345                 350

Pro Ala Pro Gly Tyr Val Ser Glu Leu Pro Asp Pro Thr Asp Glu Thr
        355                 360                 365

Ser Ala Arg Ser Asn Ile Glu Thr Val Glu Asn Asn Val Thr Gln Ala
    370                 375                 380

Trp His Ala Ala Ala Ser Ala Ala Thr Thr Asp Ala Trp Arg Val Phe
385                 390                 395                 400

Cys Ala His Ile Ala Gly Asp Thr Ala Arg Glu Leu Thr Leu Ile Asp
                405                 410                 415

Val Ser
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<210> 1925
<211> 906
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(883)
<223> RXA00763

<400> 1925
agcgcgattt gagtgctttt aatacgatcg gaagtattca tgtccccagg ttagccccaa 60

gtttgaatct cttgcaggaa cgtggggtaa agatatagat gtg gaa aaa tcc aga 115
Val Glu Lys Ser Arg
1 5

aaa cga ctt gtg acc atc gca gca tcg aca att ggg gcc gtt gcg gtg 163
Lys Arg Leu Val Thr Ile Ala Ala Ser Thr Ile Gly Ala Val Ala Val
10 15 20

gct ggc ggc gct ttt tgg atc gtt gat gct tcc atc gct gcg cac gcg 211
Ala Gly Gly Ala Phe Trp Ile Val Asp Ala Ser Ile Ala Ala His Ala
25 30 35

gaa cgc aac ttg tct aaa gca gtt gcg gaa tcc gca gat ctt gaa aac 259
Glu Arg Asn Leu Ser Lys Ala Val Ala Glu Ser Ala Asp Leu Glu Asn
40 45 50

gac ccg cga gta ttc ctc ggc agc tcc att tac tcc acg gcg ttt ttt 307
Asp Pro Arg Val Phe Leu Gly Ser Ser Ile Tyr Ser Thr Ala Phe Phe
55 60 65

acc ggc aaa ctc gac tcc gta agc atc gac atg ctg gac gtg gaa atc 355
Thr Gly Lys Leu Asp Ser Val Ser Ile Asp Met Leu Asp Val Glu Ile
70 75 80 85

ccc ggc gtc ggc atg gtg aat gca cgc aca gag gta gaa agc gtg gaa 403
Pro Gly Val Gly Met Val Asn Ala Arg Thr Glu Val Glu Ser Val Glu
90 95 100

gtc tca cgg gat caa atc ctc tcc ggt gac ctc gac ggc acc act gcg 451
Val Ser Arg Asp Gln Ile Leu Ser Gly Asp Leu Asp Gly Thr Thr Ala
105 110 115

gaa acc ttc acg cgc aca tta cgc atg gac ggc gtc gca atc ggc gcg 499
Glu Thr Phe Thr Arg Thr Leu Arg Met Asp Gly Val Ala Ile Gly Ala
120 125 130

cag ctc gga atc acc gac ctc gac atc tcc cac ccc atc gac atc tcc 547
Gln Leu Gly Ile Thr Asp Leu Asp Ile Ser His Pro Ile Asp Ile Ser
135 140 145

ccc tcc ggc ggc atc acc tca gaa gcg ctc ctg aca gga acc cca cca 595
Pro Ser Gly Gly Ile Thr Ser Glu Ala Leu Leu Thr Gly Thr Pro Pro
150 155 160 165

gac atg gaa gac ccg gtc agt gtg ctg gtc acc ctt cgc cta gtc ggc 643

```
Asp Met Glu Asp Pro Val Ser Val Leu Val Thr Leu Arg Leu Val Gly
                170                 175                 180

tca gaa ttc cag atg ctg ccg tac gag ctt atc gac gca ccc tcc gga   691
Ser Glu Phe Gln Met Leu Pro Tyr Glu Leu Ile Asp Ala Pro Ser Gly
            185                 190                 195

ctc acc ctc gac gat gtc gcc ccc gac ttc acg tgg aaa atc gac acc   739
Leu Thr Leu Asp Asp Val Ala Pro Asp Phe Thr Trp Lys Ile Asp Thr
        200                 205                 210

ctg caa cta ccc ctc gca gat cgg gca atg gcg gtt tac cta tct ggt   787
Leu Gln Leu Pro Leu Ala Asp Arg Ala Met Ala Val Tyr Leu Ser Gly
    215                 220                 225

ggc tcc gtc cat ttc caa tct gaa gcc cgc aac gtc cag ctc acc acc   835
Gly Ser Val His Phe Gln Ser Glu Ala Arg Asn Val Gln Leu Thr Thr
230                 235                 240                 245

cgc gaa cta tca cca cta gct gca ccg gaa gaa aac tcc gat gaa tcc   883
Arg Glu Leu Ser Pro Leu Ala Ala Pro Glu Glu Asn Ser Asp Glu Ser
                250                 255                 260

tagatgccaa acgtgcgcac ccg                                        906
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Sequence Listing

<210> 1926
<211> 261
<212> PRT
<213> Corynebacterium glutamicum

<400> 1926

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Val Glu Lys Ser Arg Lys Arg Leu Val Thr Ile Ala Ala Ser Thr Ile
  1               5                  10                  15

Gly Ala Val Ala Val Ala Gly Gly Ala Phe Trp Ile Val Asp Ala Ser
            20                  25                  30

Ile Ala Ala His Ala Glu Arg Asn Leu Ser Lys Ala Val Ala Glu Ser
        35                  40                  45

Ala Asp Leu Glu Asn Asp Pro Arg Val Phe Leu Gly Ser Ser Ile Tyr
    50                  55                  60

Ser Thr Ala Phe Phe Thr Gly Lys Leu Asp Ser Val Ser Ile Asp Met
65                  70                  75                  80

Leu Asp Val Glu Ile Pro Gly Val Gly Met Val Asn Ala Arg Thr Glu
                85                  90                  95

Val Glu Ser Val Glu Val Ser Arg Asp Gln Ile Leu Ser Gly Asp Leu
            100                 105                 110

Asp Gly Thr Thr Ala Glu Thr Phe Thr Arg Thr Leu Arg Met Asp Gly
        115                 120                 125

Val Ala Ile Gly Ala Gln Leu Gly Ile Thr Asp Leu Asp Ile Ser His
    130                 135                 140

Pro Ile Asp Ile Ser Pro Ser Gly Gly Ile Thr Ser Glu Ala Leu Leu
145                 150                 155                 160
```

```
Thr Gly Thr Pro Pro Asp Met Glu Asp Pro Val Ser Val Leu Val Thr
                165                 170                 175

Leu Arg Leu Val Gly Ser Glu Phe Gln Met Leu Pro Tyr Glu Leu Ile
            180                 185                 190

Asp Ala Pro Ser Gly Leu Thr Leu Asp Asp Val Ala Pro Asp Phe Thr
        195                 200                 205

Trp Lys Ile Asp Thr Leu Gln Leu Pro Leu Ala Asp Arg Ala Met Ala
    210                 215                 220

Val Tyr Leu Ser Gly Gly Ser Val His Phe Gln Ser Glu Ala Arg Asn
225                 230                 235                 240

Val Gln Leu Thr Thr Arg Glu Leu Ser Pro Leu Ala Ala Pro Glu Glu
                245                 250                 255

Asn Ser Asp Glu Ser
            260
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09337360.090705

<210> 1927
<211> 810
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(787)
<223> RXA00765

<400> 1927

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acggaaaagt ttctgcgtct gcgtggtcga ctcaggattc gcaatcagaa gaacatgcac 60

gttatctaag agtagtgcca aaacgctagt cttgagtgtc atg agc gaa aat tcc   115
                                            Met Ser Glu Asn Ser
                                              1               5

acc cct aat aat cca gtc gtc cca ggt gca ggc gca gac ggc cca tca   163
Thr Pro Asn Asn Pro Val Val Pro Gly Ala Gly Ala Asp Gly Pro Ser
                 10                  15                  20

ctg tcc gat tct gca agc atc agc gga tcc gac gca gta aac ctc gct   211
Leu Ser Asp Ser Ala Ser Ile Ser Gly Ser Asp Ala Val Asn Leu Ala
             25                  30                  35

gcc gaa caa tcc aag agc acc gct cac cgc aac atc cca ggc cta ggt   259
Ala Glu Gln Ser Lys Ser Thr Ala His Arg Asn Ile Pro Gly Leu Gly
         40                  45                  50

gac ctt cct atc cct gac gac acc gct aac ctc cgc gaa ggc ccc aac   307
Asp Leu Pro Ile Pro Asp Asp Thr Ala Asn Leu Arg Glu Gly Pro Asn
     55                  60                  65

ctc cac gac gga ctc ctc gcg ctc ctc cct ctc gtc ggc gtc tgg cgc   355
Leu His Asp Gly Leu Leu Ala Leu Leu Pro Leu Val Gly Val Trp Arg
 70                  75                  80                  85

ggc gaa ggc caa gcc gac acc gca gaa gac gga caa tac gca ttc ggc   403
```

```
Gly Glu Gly Gln Ala Asp Thr Ala Glu Asp Gly Gln Tyr Ala Phe Gly
                 90                  95                 100

cag caa atc acc ttc gcc cac gac ggt gaa aac tac ctc tcc ttc gaa   451
Gln Gln Ile Thr Phe Ala His Asp Gly Glu Asn Tyr Leu Ser Phe Glu
            105                 110                 115

tcc cgc atg tgg aaa ctc gac gaa gaa gga aac ccc acc ggc gtc gac   499
Ser Arg Met Trp Lys Leu Asp Glu Glu Gly Asn Pro Thr Gly Val Asp
        120                 125                 130

cag cgc gaa tcc ggc ttc tgg cgc atc aat ctc aaa gat gaa atc gaa   547
Gln Arg Glu Ser Gly Phe Trp Arg Ile Asn Leu Lys Asp Glu Ile Glu
    135                 140                 145

ttc gtc tgc acc cac gcc ggc gga gtt gta gaa atc tac tac ggc cag   595
Phe Val Cys Thr His Ala Gly Gly Val Val Glu Ile Tyr Tyr Gly Gln
150                 155                 160                 165

cca ctc aat gag cgc gcc tgg cag ctt gaa tcc gca tct acc atg gtc   643
Pro Leu Asn Glu Arg Ala Trp Gln Leu Glu Ser Ala Ser Thr Met Val
                170                 175                 180

acc gcc acc ggc cca tcc acc ctt gga cca gga aag cgt ctc tac gga   691
Thr Ala Thr Gly Pro Ser Thr Leu Gly Pro Gly Lys Arg Leu Tyr Gly
            185                 190                 195

ctg ctt cca acc aac gaa ctc ggc tgg gtt gat gag cgt ctc gtt ggc   739
Leu Leu Pro Thr Asn Glu Leu Gly Trp Val Asp Glu Arg Leu Val Gly
        200                 205                 210

gac gcc ctc aag cca cgc atg tcc gca cag ctc acc cgc gtg atc ggc   787
Asp Ala Leu Lys Pro Arg Met Ser Ala Gln Leu Thr Arg Val Ile Gly
    215                 220                 225

tagttttttc tagttcaccg tca                                        810


<210> 1928
<211> 229
<212> PRT
<213> Corynebacterium glutamicum

<400> 1928
Met Ser Glu Asn Ser Thr Pro Asn Asn Pro Val Val Pro Gly Ala Gly
  1               5                  10                  15

Ala Asp Gly Pro Ser Leu Ser Asp Ser Ala Ser Ile Ser Gly Ser Asp
             20                  25                  30

Ala Val Asn Leu Ala Ala Glu Gln Ser Lys Ser Thr Ala His Arg Asn
         35                  40                  45

Ile Pro Gly Leu Gly Asp Leu Pro Ile Pro Asp Asp Thr Ala Asn Leu
     50                  55                  60

Arg Glu Gly Pro Asn Leu His Asp Gly Leu Leu Ala Leu Leu Pro Leu
 65                  70                  75                  80

Val Gly Val Trp Arg Gly Glu Gly Gln Ala Asp Thr Ala Glu Asp Gly
                 85                  90                  95
```

```
Gln Tyr Ala Phe Gly Gln Gln Ile Thr Phe Ala His Asp Gly Glu Asn
            100                 105                 110

Tyr Leu Ser Phe Glu Ser Arg Met Trp Lys Leu Asp Glu Glu Gly Asn
        115                 120                 125

Pro Thr Gly Val Asp Gln Arg Glu Ser Gly Phe Trp Arg Ile Asn Leu
    130                 135                 140

Lys Asp Glu Ile Glu Phe Val Cys Thr His Ala Gly Gly Val Val Glu
145                 150                 155                 160

Ile Tyr Tyr Gly Gln Pro Leu Asn Glu Arg Ala Trp Gln Leu Glu Ser
                165                 170                 175

Ala Ser Thr Met Val Thr Ala Thr Gly Pro Ser Thr Leu Gly Pro Gly
            180                 185                 190

Lys Arg Leu Tyr Gly Leu Leu Pro Thr Asn Glu Leu Gly Trp Val Asp
        195                 200                 205

Glu Arg Leu Val Gly Asp Ala Leu Lys Pro Arg Met Ser Ala Gln Leu
    210                 215                 220

Thr Arg Val Ile Gly
225
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<210> 1929
<211> 411
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(388)
<223> RXA00781

<400> 1929

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cggttaattc caccgggatg agataccgag gagaacgcac atg agc gag aac aaa   115
                                              Met Ser Glu Asn Lys
                                                1               5

aac att gag att gtc cac aat gaa gga cag aag cgc ttt gtt atc agc   163
Asn Ile Glu Ile Val His Asn Glu Gly Gln Lys Arg Phe Val Ile Ser
                 10                  15                  20

gtt gat gga acg cca gct gga ttt gcc agc tat tta gac ggc ccg gat   211
Val Asp Gly Thr Pro Ala Gly Phe Ala Ser Tyr Leu Asp Gly Pro Asp
             25                  30                  35

atc cgc aac ttc aac cac act gtt att aag cct gaa ttc cgt gga cag   259
Ile Arg Asn Phe Asn His Thr Val Ile Lys Pro Glu Phe Arg Gly Gln
         40                  45                  50

gga ctg tct gcg cca ttg atc aag ttt gct ttg gat gat gca cgt gag   307
Gly Leu Ser Ala Pro Leu Ile Lys Phe Ala Leu Asp Asp Ala Arg Glu
     55                  60                  65
```

```
tcc ggt atc cgt att cat gat gct tgc tct gca gtc gct ggc ttc att   355
Ser Gly Ile Arg Ile His Asp Ala Cys Ser Ala Val Ala Gly Phe Ile
 70                  75                  80                  85

cag aag aac cct gag tat aag gat cta aag aac tagctggcac agggggtgg 408
Gln Lys Asn Pro Glu Tyr Lys Asp Leu Lys Asn
                90                  95

ttc                                                               411
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<210> 1930
<211> 96
<212> PRT
<213> Corynebacterium glutamicum

<400> 1930

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Met Ser Glu Asn Lys Asn Ile Glu Ile Val His Asn Glu Gly Gln Lys
  1               5                  10                  15

Arg Phe Val Ile Ser Val Asp Gly Thr Pro Ala Gly Phe Ala Ser Tyr
             20                  25                  30

Leu Asp Gly Pro Asp Ile Arg Asn Phe Asn His Thr Val Ile Lys Pro
         35                  40                  45

Glu Phe Arg Gly Gln Gly Leu Ser Ala Pro Leu Ile Lys Phe Ala Leu
     50                  55                  60

Asp Asp Ala Arg Glu Ser Gly Ile Arg Ile His Asp Ala Cys Ser Ala
 65                  70                  75                  80

Val Ala Gly Phe Ile Gln Lys Asn Pro Glu Tyr Lys Asp Leu Lys Asn
                85                  90                  95
```

<210> 1931
<211> 348
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(325)
<223> RXA00788

<400> 1931

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cgcatccctc tagttttcca tcacctcaat gaacggcgct aactccggtt cattgcgcaa 60

ttgatccagc actgcttgca gtgaggcctc attagttggc atg gcc tcc tcc atc   115
                                            Met Ala Ser Ser Ile
                                              1               5

aac atc gga gtg ttc aac ctt gga aat gct gtt gct gcc tgg ctt gct   163
Asn Ile Gly Val Phe Asn Leu Gly Asn Ala Val Ala Ala Trp Leu Ala
                10                  15                  20
```

```
ggt gca acc atc acc act tcc ctt gga ctc aca tca gcc gga tta gtt   211
Gly Ala Thr Ile Thr Thr Ser Leu Gly Leu Thr Ser Ala Gly Leu Val
             25                  30                  35

ggc ggt ttg atg acg tcc ctc gga cta gtg ttg gcc atc gtg gct gtg   259
Gly Gly Leu Met Thr Ser Leu Gly Leu Val Leu Ala Ile Val Ala Val
         40                  45                  50

gtt ttg cgt cga aaa gcg caa ggc acc caa gcg acc atc agc gtt gtg   307
Val Leu Arg Arg Lys Ala Gln Gly Thr Gln Ala Thr Ile Ser Val Val
     55                  60                  65

gag cac cag ccc gcc caa taaataattt ctctcttcta att               348
Glu His Gln Pro Ala Gln
 70                  75
```

<210> 1932
<211> 75
<212> PRT
<213> Corynebacterium glutamicum

<400> 1932

```
Met Ala Ser Ser Ile Asn Ile Gly Val Phe Asn Leu Gly Asn Ala Val
  1               5                  10                  15

Ala Ala Trp Leu Ala Gly Ala Thr Ile Thr Thr Ser Leu Gly Leu Thr
             20                  25                  30

Ser Ala Gly Leu Val Gly Gly Leu Met Thr Ser Leu Gly Leu Val Leu
         35                  40                  45

Ala Ile Val Ala Val Val Leu Arg Arg Lys Ala Gln Gly Thr Gln Ala
     50                  55                  60

Thr Ile Ser Val Val Glu His Gln Pro Ala Gln
 65                  70                  75
```

<210> 1933
<211> 567
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(544)
<223> RXA00804

<400> 1933

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aatctagtgc aagttccagc gaaaaccttc caaaactgac caagtttaag aagattcgct 60

accctatgaa tcagttgtag gagtaagagg ggagttagag atg aag atc aga agt   115
                                              Met Lys Ile Arg Ser
                                                1               5

gca cgt gaa atc gcg gag tgg ttc gtt gcc tgg gga gat gaa ctc gat   163
Ala Arg Glu Ile Ala Glu Trp Phe Val Ala Trp Gly Asp Glu Leu Asp
                10                  15                  20

gct gaa gtc tcc cct ttg aaa ttg cag aag ctc ctt tat tac tcc cag   211
```

```
Ala Glu Val Ser Pro Leu Lys Leu Gln Lys Leu Leu Tyr Tyr Ser Gln
             25                  30                  35

ggt gag cat ata gct gca aca ggg cga aaa ctt ttc tcg gat aag att   259
Gly Glu His Ile Ala Ala Thr Gly Arg Lys Leu Phe Ser Asp Lys Ile
         40                  45                  50

ctg gcg tgg cag cac gga cct gtc act ccg ggc gtt tat tca gat aca   307
Leu Ala Trp Gln His Gly Pro Val Thr Pro Gly Val Tyr Ser Asp Thr
     55                  60                  65

aaa tca tac ggc cga aac cca att gat cct gat gag ttt gtg tca gat   355
Lys Ser Tyr Gly Arg Asn Pro Ile Asp Pro Asp Glu Phe Val Ser Asp
 70                  75                  80                  85

gaa ttt aac tgg gat gac tac tca gat gtg tca gat gag ctt gta acc   403
Glu Phe Asn Trp Asp Asp Tyr Ser Asp Val Ser Asp Glu Leu Val Thr
                 90                  95                 100

gta tgg cga aaa tac ggc atc tat tcg gcg tgg gca ctg agg gaa aaa   451
Val Trp Arg Lys Tyr Gly Ile Tyr Ser Ala Trp Ala Leu Arg Glu Lys
            105                 110                 115

act cac agt gaa tcg ccg tgg ctc gat gcc tgg gca caa ggg caa aat   499
Thr His Ser Glu Ser Pro Trp Leu Asp Ala Trp Ala Gln Gly Gln Asn
        120                 125                 130

att gaa att aca gat gct gcg ctg aaa gat ttc ttc ttg gtg cat       544
Ile Glu Ile Thr Asp Ala Ala Leu Lys Asp Phe Phe Leu Val His
    135                 140                 145

tagaaatttg aaaaagaaac gaa                                        567


<210> 1934
<211> 148
<212> PRT
<213> Corynebacterium glutamicum

<400> 1934
Met Lys Ile Arg Ser Ala Arg Glu Ile Ala Glu Trp Phe Val Ala Trp
  1               5                  10                  15

Gly Asp Glu Leu Asp Ala Glu Val Ser Pro Leu Lys Leu Gln Lys Leu
             20                  25                  30

Leu Tyr Tyr Ser Gln Gly Glu His Ile Ala Ala Thr Gly Arg Lys Leu
         35                  40                  45

Phe Ser Asp Lys Ile Leu Ala Trp Gln His Gly Pro Val Thr Pro Gly
     50                  55                  60

Val Tyr Ser Asp Thr Lys Ser Tyr Gly Arg Asn Pro Ile Asp Pro Asp
 65                  70                  75                  80

Glu Phe Val Ser Asp Glu Phe Asn Trp Asp Asp Tyr Ser Asp Val Ser
                 85                  90                  95

Asp Glu Leu Val Thr Val Trp Arg Lys Tyr Gly Ile Tyr Ser Ala Trp
            100                 105                 110
```

```
Ala Leu Arg Glu Lys Thr His Ser Glu Ser Pro Trp Leu Asp Ala Trp
        115                 120                 125

Ala Gln Gly Gln Asn Ile Glu Ile Thr Asp Ala Ala Leu Lys Asp Phe
    130                 135                 140

Phe Leu Val His
145
```

<210> 1935
<211> 1005
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(982)
<223> RXA00805

<400> 1935

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tgctccgctg acagtggtgc gcctgagcag cccaaaagag acaaagcgct ggttgagggc 60

atatggggaa agcgtgaaac tctgataggg tgccatatcc atg gca gaa agt ttt   115
                                            Met Ala Glu Ser Phe
                                              1               5

ata gag gtc tcg gcg ggg cat gcg gat cgg cgg ata gat aag ttt ttg   163
Ile Glu Val Ser Ala Gly His Ala Asp Arg Arg Ile Asp Lys Phe Leu
                  10                  15                  20

cgg gca cag cta aag ggc gtg ccc gcg tcg ttg att ttc cgt caa atg   211
Arg Ala Gln Leu Lys Gly Val Pro Ala Ser Leu Ile Phe Arg Gln Met
              25                  30                  35

cgt aaa ggc gac att cgg gtg aat ggt cgt aaa gtg gat ccg aat tac   259
Arg Lys Gly Asp Ile Arg Val Asn Gly Arg Lys Val Asp Pro Asn Tyr
          40                  45                  50

cgg ttg caa gaa ggc gac cga att cga atg tgg cag atg gat ttg ctg   307
Arg Leu Gln Glu Gly Asp Arg Ile Arg Met Trp Gln Met Asp Leu Leu
      55                  60                  65

gca gat ttg ccg cca ccg gtc gtc gat aag cat att ttt aag gct gtc   355
Ala Asp Leu Pro Pro Pro Val Val Asp Lys His Ile Phe Lys Ala Val
  70                  75                  80                  85

gca gac agc gtg ctt ttt gag gac gcc gaa tta ctg gtg atc aat aag   403
Ala Asp Ser Val Leu Phe Glu Asp Ala Glu Leu Leu Val Ile Asn Lys
                  90                  95                 100

cca gct gga att cct gtg cac ggt ggc acg ggg cac ggc ggt ggc gtg   451
Pro Ala Gly Ile Pro Val His Gly Gly Thr Gly His Gly Gly Gly Val
              105                 110                 115

att gag gcg ctg cgg cag aag ttt ccg cag gaa cgc gac ctg gaa ttg   499
Ile Glu Ala Leu Arg Gln Lys Phe Pro Gln Glu Arg Asp Leu Glu Leu
          120                 125                 130

gtg cat cgt ttg gat cgg gac acc tca ggt ttg ttg ctg gtt tct aaa   547
Val His Arg Leu Asp Arg Asp Thr Ser Gly Leu Leu Leu Val Ser Lys
```

```
    135                 140                 145

acg aca tct gtg ttg cgc gag ttg cag gaa att ttg cga gac cgc gaa   595
Thr Thr Ser Val Leu Arg Glu Leu Gln Glu Ile Leu Arg Asp Arg Glu
150                 155                 160                 165

gag gag att ttt cgg ggg tat tta ctc aag gtc gag ggg gct tgg cct   643
Glu Glu Ile Phe Arg Gly Tyr Leu Leu Lys Val Glu Gly Ala Trp Pro
                170                 175                 180

ggc gat ttg cga caa att gat gtg ccg ttg aag cgg acg gag aca act   691
Gly Asp Leu Arg Gln Ile Asp Val Pro Leu Lys Arg Thr Glu Thr Thr
            185                 190                 195

gtt gtg cca cat tcg gat ggt ttg cgg gcg cgg acg tat ttt gag gtt   739
Val Val Pro His Ser Asp Gly Leu Arg Ala Arg Thr Tyr Phe Glu Val
        200                 205                 210

gta aag cgt ttg ccg ggt gcg acc ttg gtg aag gcg cag ttg gcg acc   787
Val Lys Arg Leu Pro Gly Ala Thr Leu Val Lys Ala Gln Leu Ala Thr
    215                 220                 225

ggg cgg aaa cat cag att cgg gtc cat gcg cag tat gcg ggt cac cct   835
Gly Arg Lys His Gln Ile Arg Val His Ala Gln Tyr Ala Gly His Pro
230                 235                 240                 245

att gtt ggc gat cca cga tac ggg tcg cgt ggg ggc aga gct gcg acg   883
Ile Val Gly Asp Pro Arg Tyr Gly Ser Arg Gly Gly Arg Ala Ala Thr
                250                 255                 260

atg cat ttg cat gcg gcg gaa ttg gtg gcg cct cgt ggg gcg ggg aag   931
Met His Leu His Ala Ala Glu Leu Val Ala Pro Arg Gly Ala Gly Lys
            265                 270                 275

cgt cag aaa ttc act gca ccg ttg ccg aag gag tgg ggt atg gga cgg   979
Arg Gln Lys Phe Thr Ala Pro Leu Pro Lys Glu Trp Gly Met Gly Arg
        280                 285                 290

gtc tgagtcgggc cttcgtggaa tcg                                    1005
Val
```

Sequence Listing

<210> 1936
<211> 294
<212> PRT
<213> Corynebacterium glutamicum

<400> 1936

```
Met Ala Glu Ser Phe Ile Glu Val Ser Ala Gly His Ala Asp Arg Arg
  1               5                  10                  15

Ile Asp Lys Phe Leu Arg Ala Gln Leu Lys Gly Val Pro Ala Ser Leu
             20                  25                  30

Ile Phe Arg Gln Met Arg Lys Gly Asp Ile Arg Val Asn Gly Arg Lys
         35                  40                  45

Val Asp Pro Asn Tyr Arg Leu Gln Glu Gly Asp Arg Ile Arg Met Trp
     50                  55                  60
```

```
Gln Met Asp Leu Leu Ala Asp Leu Pro Pro Pro Val Val Asp Lys His
 65                  70                  75                  80

Ile Phe Lys Ala Val Ala Asp Ser Val Leu Phe Glu Asp Ala Glu Leu
                85                  90                  95

Leu Val Ile Asn Lys Pro Ala Gly Ile Pro Val His Gly Gly Thr Gly
            100                 105                 110

His Gly Gly Gly Val Ile Glu Ala Leu Arg Gln Lys Phe Pro Gln Glu
        115                 120                 125

Arg Asp Leu Glu Leu Val His Arg Leu Asp Arg Asp Thr Ser Gly Leu
    130                 135                 140

Leu Leu Val Ser Lys Thr Thr Ser Val Leu Arg Glu Leu Gln Glu Ile
145                 150                 155                 160

Leu Arg Asp Arg Glu Glu Glu Ile Phe Arg Gly Tyr Leu Leu Lys Val
                165                 170                 175

Glu Gly Ala Trp Pro Gly Asp Leu Arg Gln Ile Asp Val Pro Leu Lys
            180                 185                 190

Arg Thr Glu Thr Thr Val Val Pro His Ser Asp Gly Leu Arg Ala Arg
        195                 200                 205

Thr Tyr Phe Glu Val Val Lys Arg Leu Pro Gly Ala Thr Leu Val Lys
    210                 215                 220

Ala Gln Leu Ala Thr Gly Arg Lys His Gln Ile Arg Val His Ala Gln
225                 230                 235                 240

Tyr Ala Gly His Pro Ile Val Gly Asp Pro Arg Tyr Gly Ser Arg Gly
                245                 250                 255

Gly Arg Ala Ala Thr Met His Leu His Ala Ala Glu Leu Val Ala Pro
            260                 265                 270

Arg Gly Ala Gly Lys Arg Gln Lys Phe Thr Ala Pro Leu Pro Lys Glu
        275                 280                 285

Trp Gly Met Gly Arg Val
    290
```

<210> 1937
<211> 701
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(678)
<223> RXA00808

<400> 1937

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gct ggc ttc aat gag atg atg cgt ggc ctg cgt gaa cgt cag cgc gtc   48
Ala Gly Phe Asn Glu Met Met Arg Gly Leu Arg Glu Arg Gln Arg Val
  1               5                  10                  15
```

```
cgt gac ctt ttc ggt cgc tac gtg ggc gct gaa gtg gcc aag cgt gcg   96
Arg Asp Leu Phe Gly Arg Tyr Val Gly Ala Glu Val Ala Lys Arg Ala
             20                  25                  30

ctg gag gaa cgc ccc act ctg ggt ggc gag gac cgt aag gtt gcc gtg   144
Leu Glu Glu Arg Pro Thr Leu Gly Gly Glu Asp Arg Lys Val Ala Val
         35                  40                  45

ttg ttt gtc gat gtc atc ggc tcc act acc ttt gcc gtc aac cac act   192
Leu Phe Val Asp Val Ile Gly Ser Thr Thr Phe Ala Val Asn His Thr
     50                  55                  60

cct gaa gag gtt gtg gag gcg ctc aat gag ttc ttc gag cac gtc gtg   240
Pro Glu Glu Val Val Glu Ala Leu Asn Glu Phe Phe Glu His Val Val
 65                  70                  75                  80

gag gtt gtg cac cgc aac aag ggt gtt atc aac aag ttc cag ggt gac   288
Glu Val Val His Arg Asn Lys Gly Val Ile Asn Lys Phe Gln Gly Asp
                 85                  90                  95

gcg gcg ttg gcg att ttc ggc gct ccc ctg ccc ctg tct gat gcc acc   336
Ala Ala Leu Ala Ile Phe Gly Ala Pro Leu Pro Leu Ser Asp Ala Thr
            100                 105                 110

ggt cat gcg ctt gcg gct gcc cgt gag ctc cgc gca gag ctg aaa gat   384
Gly His Ala Leu Ala Ala Ala Arg Glu Leu Arg Ala Glu Leu Lys Asp
        115                 120                 125

ctc cag ctc aag gcc gga att ggt gtg gct gct ggc cat gtc gtt gct   432
Leu Gln Leu Lys Ala Gly Ile Gly Val Ala Ala Gly His Val Val Ala
    130                 135                 140

ggt cat atc ggc ggt cac gcg agg ttt gag tac act gtg atc ggc gac   480
Gly His Ile Gly Gly His Ala Arg Phe Glu Tyr Thr Val Ile Gly Asp
145                 150                 155                 160

gcg gtg aac cag gct gcg cgc ctg acg gag atc gcg aaa acg acc cca   528
Ala Val Asn Gln Ala Ala Arg Leu Thr Glu Ile Ala Lys Thr Thr Pro
                165                 170                 175

ggc cgc acc gtc acc aac gct tcc acg ctg cgt gag gcc aac gag gcg   576
Gly Arg Thr Val Thr Asn Ala Ser Thr Leu Arg Glu Ala Asn Glu Ala
            180                 185                 190

gag cag gct cgc tgg acg ctc atg aag tcc gtg gag ctg cgc gga cgt   624
Glu Gln Ala Arg Trp Thr Leu Met Lys Ser Val Glu Leu Arg Gly Arg
        195                 200                 205

agc cag atg acg cag att gcg cgg cct att cgg ccg acg ttg gcg gat   672
Ser Gln Met Thr Gln Ile Ala Arg Pro Ile Arg Pro Thr Leu Ala Asp
    210                 215                 220

agg tcc taatacgctt ttcgacgcaa aaa                                701
Arg Ser
225
```

<210> 1938
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 1938
Ala Gly Phe Asn Glu Met Met Arg Gly Leu Arg Glu Arg Gln Arg Val
1 5 10 15

Arg Asp Leu Phe Gly Arg Tyr Val Gly Ala Glu Val Ala Lys Arg Ala
20 25 30

Leu Glu Glu Arg Pro Thr Leu Gly Gly Glu Asp Arg Lys Val Ala Val
35 40 45

Leu Phe Val Asp Val Ile Gly Ser Thr Thr Phe Ala Val Asn His Thr
50 55 60

Pro Glu Glu Val Val Glu Ala Leu Asn Glu Phe Phe Glu His Val Val
65 70 75 80

Glu Val Val His Arg Asn Lys Gly Val Ile Asn Lys Phe Gln Gly Asp
85 90 95

Ala Ala Leu Ala Ile Phe Gly Ala Pro Leu Pro Leu Ser Asp Ala Thr
100 105 110

Gly His Ala Leu Ala Ala Ala Arg Glu Leu Arg Ala Glu Leu Lys Asp
115 120 125

Leu Gln Leu Lys Ala Gly Ile Gly Val Ala Ala Gly His Val Val Ala
130 135 140

Gly His Ile Gly Gly His Ala Arg Phe Glu Tyr Thr Val Ile Gly Asp
145 150 155 160

Ala Val Asn Gln Ala Ala Arg Leu Thr Glu Ile Ala Lys Thr Thr Pro
165 170 175

Gly Arg Thr Val Thr Asn Ala Ser Thr Leu Arg Glu Ala Asn Glu Ala
180 185 190

Glu Gln Ala Arg Trp Thr Leu Met Lys Ser Val Glu Leu Arg Gly Arg
195 200 205

Ser Gln Met Thr Gln Ile Ala Arg Pro Ile Arg Pro Thr Leu Ala Asp
210 215 220

Arg Ser
225

<210> 1939
<211> 1182
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1159)
<223> RXA00812

<400> 1939
ttcacaggtg agcgtatcgc gggcggttga gaggtgagtt atccacaggc cgcagagggg 60

```
gtcgttgaaa gcacgtaagc ctcaggccac agtaggtgcc atg aac acc atc aca   115
                                            Met Asn Thr Ile Thr
                                              1               5

cac caa gca att ctc atc gca gtg gaa gat ccg gtc ctg cac cca gag   163
His Gln Ala Ile Leu Ile Ala Val Glu Asp Pro Val Leu His Pro Glu
                 10                  15                  20

gcc atg cac gta gct gca gcc act ggt cgg ccg gtt att gaa aca aca   211
Ala Met His Val Ala Ala Ala Thr Gly Arg Pro Val Ile Glu Thr Thr
             25                  30                  35

aat ttg atg gac atc tcc agg cat ttt cac cgc aca tcg gca gtg ctc   259
Asn Leu Met Asp Ile Ser Arg His Phe His Arg Thr Ser Ala Val Leu
         40                  45                  50

att gat gcg tcg atg gcc tct caa tta tca cct ggg aaa cgc cgc gac   307
Ile Asp Ala Ser Met Ala Ser Gln Leu Ser Pro Gly Lys Arg Arg Asp
     55                  60                  65

agg gtg ttt ctt ctc gat tct gat cca ggg ccc tct gat tgg aaa acg   355
Arg Val Phe Leu Leu Asp Ser Asp Pro Gly Pro Ser Asp Trp Lys Thr
 70                  75                  80                  85

gcg atg aaa atc cac gct gag caa gcc atg ttg ctt ccc gct cag gca   403
Ala Met Lys Ile His Ala Glu Gln Ala Met Leu Leu Pro Ala Gln Ala
                 90                  95                 100

ggg gag ttg ctc agc gct tta ggc aga gat gac aaa caa ctg ccg gtg   451
Gly Glu Leu Leu Ser Ala Leu Gly Arg Asp Asp Lys Gln Leu Pro Val
             105                 110                 115

gct tcg ggc cat gtc atc ggt gtt gcc ggg gtg gtg gga gga aca ggc   499
Ala Ser Gly His Val Ile Gly Val Ala Gly Val Val Gly Gly Thr Gly
         120                 125                 130

gcg agc acg ttt gct gcg gcg ctc gca aag cgg cgt gcg gag tca gtc   547
Ala Ser Thr Phe Ala Ala Ala Leu Ala Lys Arg Arg Ala Glu Ser Val
     135                 140                 145

acc act gtg ctt atc gac gcc gac cct tcc tct ggc ggc atc gac ctg   595
Thr Thr Val Leu Ile Asp Ala Asp Pro Ser Ser Gly Gly Ile Asp Leu
150                 155                 160                 165

ttg cta gga atc gaa gat gtg ccc ggc gcg cgg tgg cct gat gtg ggg   643
Leu Leu Gly Ile Glu Asp Val Pro Gly Ala Arg Trp Pro Asp Val Gly
                 170                 175                 180

ttg cgt cgc gga act gtc cag gct gct gat gtg ttg aaa gcg ctg ccg   691
Leu Arg Arg Gly Thr Val Gln Ala Ala Asp Val Leu Lys Ala Leu Pro
             185                 190                 195

agc act cct gat gag gtc gtg gtg ttg tct acg gcg cgg tct aat att   739
Ser Thr Pro Asp Glu Val Val Val Leu Ser Thr Ala Arg Ser Asn Ile
         200                 205                 210

ctg gat cct ttt gca tta tcc gag tct gat gtt tca gcg gcg att gat   787
Leu Asp Pro Phe Ala Leu Ser Glu Ser Asp Val Ser Ala Ala Ile Asp
     215                 220                 225

tgt ttc tta agc gcc gat agg tcg gtg gat gtg gtg gtg gat ctg cct   835
```

```
Cys Phe Leu Ser Ala Asp Arg Ser Val Asp Val Val Val Asp Leu Pro
230                 235                 240                 245

cat gcg aga gtg cat cca gat att gcg gag cgc tta tcc cac ctg gtg   883
His Ala Arg Val His Pro Asp Ile Ala Glu Arg Leu Ser His Leu Val
                250                 255                 260

tta gtc atc cct gca gag gtc cga gcg gtg gct gct gcc agg gct cgg   931
Leu Val Ile Pro Ala Glu Val Arg Ala Val Ala Ala Ala Arg Ala Arg
            265                 270                 275

tgt ctg gaa tta caa caa ttg cat gta tcc atc acg tgc gtg ttg agg   979
Cys Leu Glu Leu Gln Gln Leu His Val Ser Ile Thr Cys Val Leu Arg
        280                 285                 290

cat cgc ggg tgg tca ggt ttg gat gtt gca gaa gtg gaa gag att tta   1027
His Arg Gly Trp Ser Gly Leu Asp Val Ala Glu Val Glu Glu Ile Leu
    295                 300                 305

ggt gcg gat att acc gcg gag gtt ggc tcg atc cag cgg ctg gct aag   1075
Gly Ala Asp Ile Thr Ala Glu Val Gly Ser Ile Gln Arg Leu Ala Lys
310                 315                 320                 325

tcc gtg gag atg cat ggg ctg acc ggt tct ttg ccg agg gtt tta agc   1123
Ser Val Glu Met His Gly Leu Thr Gly Ser Leu Pro Arg Val Leu Ser
                330                 335                 340

tca gca tgc gac gcg gtc ctc ggg gag gtg gcg gca tgactgacat        1169
Ser Ala Cys Asp Ala Val Leu Gly Glu Val Ala Ala
            345                 350

tgatctggtg gtg                                                   1182


<210> 1940
<211> 353
<212> PRT
<213> Corynebacterium glutamicum

<400> 1940
Met Asn Thr Ile Thr His Gln Ala Ile Leu Ile Ala Val Glu Asp Pro
  1               5                  10                  15

Val Leu His Pro Glu Ala Met His Val Ala Ala Ala Thr Gly Arg Pro
            20                  25                  30

Val Ile Glu Thr Thr Asn Leu Met Asp Ile Ser Arg His Phe His Arg
        35                  40                  45

Thr Ser Ala Val Leu Ile Asp Ala Ser Met Ala Ser Gln Leu Ser Pro
    50                  55                  60

Gly Lys Arg Arg Asp Arg Val Phe Leu Leu Asp Ser Asp Pro Gly Pro
65                  70                  75                  80

Ser Asp Trp Lys Thr Ala Met Lys Ile His Ala Glu Gln Ala Met Leu
                85                  90                  95

Leu Pro Ala Gln Ala Gly Glu Leu Leu Ser Ala Leu Gly Arg Asp Asp
            100                 105                 110
```

```
Lys Gln Leu Pro Val Ala Ser Gly His Val Ile Gly Val Ala Gly Val
        115                 120                 125

Val Gly Gly Thr Gly Ala Ser Thr Phe Ala Ala Ala Leu Ala Lys Arg
    130                 135                 140

Arg Ala Glu Ser Val Thr Thr Val Leu Ile Asp Ala Asp Pro Ser Ser
145                 150                 155                 160

Gly Gly Ile Asp Leu Leu Leu Gly Ile Glu Asp Val Pro Gly Ala Arg
                165                 170                 175

Trp Pro Asp Val Gly Leu Arg Arg Gly Thr Val Gln Ala Ala Asp Val
            180                 185                 190

Leu Lys Ala Leu Pro Ser Thr Pro Asp Glu Val Val Val Leu Ser Thr
        195                 200                 205

Ala Arg Ser Asn Ile Leu Asp Pro Phe Ala Leu Ser Glu Ser Asp Val
    210                 215                 220

Ser Ala Ala Ile Asp Cys Phe Leu Ser Ala Asp Arg Ser Val Asp Val
225                 230                 235                 240

Val Val Asp Leu Pro His Ala Arg Val His Pro Asp Ile Ala Glu Arg
                245                 250                 255

Leu Ser His Leu Val Leu Val Ile Pro Ala Glu Val Arg Ala Val Ala
            260                 265                 270

Ala Ala Arg Ala Arg Cys Leu Glu Leu Gln Gln Leu His Val Ser Ile
        275                 280                 285

Thr Cys Val Leu Arg His Arg Gly Trp Ser Gly Leu Asp Val Ala Glu
    290                 295                 300

Val Glu Glu Ile Leu Gly Ala Asp Ile Thr Ala Glu Val Gly Ser Ile
305                 310                 315                 320

Gln Arg Leu Ala Lys Ser Val Glu Met His Gly Leu Thr Gly Ser Leu
                325                 330                 335

Pro Arg Val Leu Ser Ser Ala Cys Asp Ala Val Leu Gly Glu Val Ala
            340                 345                 350

Ala
```

<210> 1941
<211> 897
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> RXA00814

<400> 1941
gccgcaggct agctcaactc ggggtgctcc gcggaaatcc tgtgaccacg caggtggtgt 60

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gggatttgga ccacggcatg cacgaaggga gcgaagaggc atg gtt tat gcc cta   115
                                              Met Val Tyr Ala Leu
                                                1               5

ggc ctt ctt agc gtg gcg gtg ttg atc tct ggt tca agg ggc ccc ggc   163
Gly Leu Leu Ser Val Ala Val Leu Ile Ser Gly Ser Arg Gly Pro Gly
                   10                  15                  20

gcg cgt acc agg cca cca aca cct ggg aat ggc gtc cat cta ttc gcc   211
Ala Arg Thr Arg Pro Pro Thr Pro Gly Asn Gly Val His Leu Phe Ala
               25                  30                  35

cta att gca cta ttt tgc ctg gcc aca gtg cta ttt atc gtc gtt gac   259
Leu Ile Ala Leu Phe Cys Leu Ala Thr Val Leu Phe Ile Val Val Asp
           40                  45                  50

gcc tac acg atg atc gcc ggc atc atc atc gcc aca act cta ttc tgg   307
Ala Tyr Thr Met Ile Ala Gly Ile Ile Ile Ala Thr Thr Leu Phe Trp
       55                  60                  65

tat ctc cgc cag aca cac gcc gca gcc caa cgc acc aaa caa tcc ctc   355
Tyr Leu Arg Gln Thr His Ala Ala Ala Gln Arg Thr Lys Gln Ser Leu
   70                  75                  80                  85

caa tta gcc agc ttc tta agc ctc tgc gca ggc aat tta cgc gcc ggg   403
Gln Leu Ala Ser Phe Leu Ser Leu Cys Ala Gly Asn Leu Arg Ala Gly
                   90                  95                 100

gtc acc atg gtc gac gcc atg gac tac gcg ctc gac aac acc acg ccg   451
Val Thr Met Val Asp Ala Met Asp Tyr Ala Leu Asp Asn Thr Thr Pro
               105                 110                 115

gac aaa ttc tta agc ccc acg ttg cag acc gca gcc agg cag gcg cgc   499
Asp Lys Phe Leu Ser Pro Thr Leu Gln Thr Ala Ala Arg Gln Ala Arg
           120                 125                 130

tcg ggc ggc agc ggg ccg cga gtg ctt atc gac gcc tcc ctc ccc gat   547
Ser Gly Gly Ser Gly Pro Arg Val Leu Ile Asp Ala Ser Leu Pro Asp
       135                 140                 145

ctt caa cgc ctc ggc cat ttg tgg gaa aca tca gaa cga cac ggc atc   595
Leu Gln Arg Leu Gly His Leu Trp Glu Thr Ser Glu Arg His Gly Ile
150                 155                 160                 165

ccg ctg gtc gcc ctc att gat caa atg agg tcc cgg att tca tcg aag   643
Pro Leu Val Ala Leu Ile Asp Gln Met Arg Ser Arg Ile Ser Ser Lys
                   170                 175                 180

caa cgc cac ggc gaa tcc acc cga gct gca ctc caa gga ccg caa gca   691
Gln Arg His Gly Glu Ser Thr Arg Ala Ala Leu Gln Gly Pro Gln Ala
               185                 190                 195

acc gca gtg atc ctt acc gtg ttg cca cta gca gga atg ctc atg ggc   739
Thr Ala Val Ile Leu Thr Val Leu Pro Leu Ala Gly Met Leu Met Gly
           200                 205                 210

aca gcc atg gga gca aac ccc ctt ggg cta ctc acc ggt ggt ggg atc   787
Thr Ala Met Gly Ala Asn Pro Leu Gly Leu Leu Thr Gly Gly Gly Ile
       215                 220                 225
```

```
ggt ggg ttc ctg ctt gtc atc ggt gtg ggc ctc gat gct gca ggg ttt   835
Gly Gly Phe Leu Leu Val Ile Gly Val Gly Leu Asp Ala Ala Gly Phe
230                 235                 240                 245

gtg ctc acc cac aaa att ctc cag agc gcg agc ccc tca tgattacagc   884
Val Leu Thr His Lys Ile Leu Gln Ser Ala Ser Pro Ser
                250                 255

actagttctt gca                                                   897
```

<210> 1942
<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 1942

```
Met Val Tyr Ala Leu Gly Leu Leu Ser Val Ala Val Leu Ile Ser Gly
  1               5                  10                  15

Ser Arg Gly Pro Gly Ala Arg Thr Arg Pro Pro Thr Pro Gly Asn Gly
             20                  25                  30

Val His Leu Phe Ala Leu Ile Ala Leu Phe Cys Leu Ala Thr Val Leu
         35                  40                  45

Phe Ile Val Val Asp Ala Tyr Thr Met Ile Ala Gly Ile Ile Ile Ala
     50                  55                  60

Thr Thr Leu Phe Trp Tyr Leu Arg Gln Thr His Ala Ala Ala Gln Arg
 65                  70                  75                  80

Thr Lys Gln Ser Leu Gln Leu Ala Ser Phe Leu Ser Leu Cys Ala Gly
                 85                  90                  95

Asn Leu Arg Ala Gly Val Thr Met Val Asp Ala Met Asp Tyr Ala Leu
            100                 105                 110

Asp Asn Thr Thr Pro Asp Lys Phe Leu Ser Pro Thr Leu Gln Thr Ala
        115                 120                 125

Ala Arg Gln Ala Arg Ser Gly Gly Ser Gly Pro Arg Val Leu Ile Asp
    130                 135                 140

Ala Ser Leu Pro Asp Leu Gln Arg Leu Gly His Leu Trp Glu Thr Ser
145                 150                 155                 160

Glu Arg His Gly Ile Pro Leu Val Ala Leu Ile Asp Gln Met Arg Ser
                165                 170                 175

Arg Ile Ser Ser Lys Gln Arg His Gly Glu Ser Thr Arg Ala Ala Leu
            180                 185                 190

Gln Gly Pro Gln Ala Thr Ala Val Ile Leu Thr Val Leu Pro Leu Ala
        195                 200                 205

Gly Met Leu Met Gly Thr Ala Met Gly Ala Asn Pro Leu Gly Leu Leu
    210                 215                 220

Thr Gly Gly Gly Ile Gly Gly Phe Leu Leu Val Ile Gly Val Gly Leu
225                 230                 235                 240
```

```
Asp Ala Ala Gly Phe Val Leu Thr His Lys Ile Leu Gln Ser Ala Ser
                245                 250                 255

Pro Ser



<210> 1943
<211> 696
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(673)
<223> RXA00815

<400> 1943
ccggtggtgg gatcggtggg ttcctgcttg tcatcggtgt gggcctcgat gctgcagggt 60

ttgtgctcac ccacaaaatt ctccagagcg cgagcccctc atg att aca gca cta   115
                                            Met Ile Thr Ala Leu
                                              1               5

gtt ctt gca gca gtg gcc atg ttc ctc ggt tca ccc aac cct gga gtt   163
Val Leu Ala Ala Val Ala Met Phe Leu Gly Ser Pro Asn Pro Gly Val
                 10                  15                  20

cgc ggt gga ttg ata agc ccc aaa tcc ggt aaa agc ctg cgt atc cga   211
Arg Gly Gly Leu Ile Ser Pro Lys Ser Gly Lys Ser Leu Arg Ile Arg
             25                  30                  35

gct ggc cca aaa aag ctg ggc aac gct gac cca gtg gat gtc tct gca   259
Ala Gly Pro Lys Lys Leu Gly Asn Ala Asp Pro Val Asp Val Ser Ala
         40                  45                  50

gat atc gaa ctg ttt tca gcg tgt ttg gat gcg ggt tta aac aca cgt   307
Asp Ile Glu Leu Phe Ser Ala Cys Leu Asp Ala Gly Leu Asn Thr Arg
     55                  60                  65

gat gca gcg cag gtg gtg gct cat gtt gca gcc att acg cac cgc gaa   355
Asp Ala Ala Gln Val Val Ala His Val Ala Ala Ile Thr His Arg Glu
 70                  75                  80                  85

ctg tgg aca cat gtg gtg gca ttg cta tcg att gga gtg agt gcc cct   403
Leu Trp Thr His Val Val Ala Leu Leu Ser Ile Gly Val Ser Ala Pro
                 90                  95                 100

caa gca ttc gcc ctg atg gca gga gtt gat ggg ctg gat gaa cta gcc   451
Gln Ala Phe Ala Leu Met Ala Gly Val Asp Gly Leu Asp Glu Leu Ala
            105                 110                 115

aat tta gcc acc gtg tcg cac agg tcg ggc agt gca tta agt gat ggg   499
Asn Leu Ala Thr Val Ser His Arg Ser Gly Ser Ala Leu Ser Asp Gly
        120                 125                 130

tgc agg aac att tcc acc tcg ttg ttg gcc tct gct ggt gac aag cgc   547
Cys Arg Asn Ile Ser Thr Ser Leu Leu Ala Ser Ala Gly Asp Lys Arg
    135                 140                 145
```

```
acc gcc gca gca gaa cgc gca gga gtg ttc atc gcc ctg cca ctt gct   595
Thr Ala Ala Ala Glu Arg Ala Gly Val Phe Ile Ala Leu Pro Leu Ala
150                 155                 160                 165

ctg tgt ttc ctc ccc gca ttc atg att gtc ggg ctt gca cca gtg gtg   643
Leu Cys Phe Leu Pro Ala Phe Met Ile Val Gly Leu Ala Pro Val Val
                170                 175                 180

ctc agc ttg ggt acg caa ctt atc aat ttc tagaaaacac acacaggaga     693
Leu Ser Leu Gly Thr Gln Leu Ile Asn Phe
            185                 190

aaa                                                               696
```

<210> 1944
<211> 191
<212> PRT
<213> Corynebacterium glutamicum

<400> 1944

```
Met Ile Thr Ala Leu Val Leu Ala Ala Val Ala Met Phe Leu Gly Ser
  1               5                  10                  15

Pro Asn Pro Gly Val Arg Gly Gly Leu Ile Ser Pro Lys Ser Gly Lys
             20                  25                  30

Ser Leu Arg Ile Arg Ala Gly Pro Lys Lys Leu Gly Asn Ala Asp Pro
         35                  40                  45

Val Asp Val Ser Ala Asp Ile Glu Leu Phe Ser Ala Cys Leu Asp Ala
     50                  55                  60

Gly Leu Asn Thr Arg Asp Ala Ala Gln Val Val Ala His Val Ala Ala
 65                  70                  75                  80

Ile Thr His Arg Glu Leu Trp Thr His Val Val Ala Leu Leu Ser Ile
                 85                  90                  95

Gly Val Ser Ala Pro Gln Ala Phe Ala Leu Met Ala Gly Val Asp Gly
            100                 105                 110

Leu Asp Glu Leu Ala Asn Leu Ala Thr Val Ser His Arg Ser Gly Ser
        115                 120                 125

Ala Leu Ser Asp Gly Cys Arg Asn Ile Ser Thr Ser Leu Leu Ala Ser
    130                 135                 140

Ala Gly Asp Lys Arg Thr Ala Ala Ala Glu Arg Ala Gly Val Phe Ile
145                 150                 155                 160

Ala Leu Pro Leu Ala Leu Cys Phe Leu Pro Ala Phe Met Ile Val Gly
                165                 170                 175

Leu Ala Pro Val Val Leu Ser Leu Gly Thr Gln Leu Ile Asn Phe
            180                 185                 190
```

<210> 1945
<211> 420
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(397)
<223> RXA00816

<400> 1945
atgctcaccg caacagccac tatcccggca ccgattgggc aggtgagcgc gagtgcggtg 60

ttcccggtgg aaaactagct gtgcaaatga cgaaggctac atg acc atc gcc agc 115
Met Thr Ile Ala Ser
1 5

gct ggt gtc gcc tcc atc ctc att agc ctg ctg gtg gtg ctg gcc tgg 163
Ala Gly Val Ala Ser Ile Leu Ile Ser Leu Leu Val Val Leu Ala Trp
10 15 20

cag gcg gga aac ctc gtg gcc agg gaa caa gca cag gta gcg gcc gat 211
Gln Ala Gly Asn Leu Val Ala Arg Glu Gln Ala Gln Val Ala Ala Asp
25 30 35

gtt tca gct gtt gcc gga gcc tac gcc ttt gcc cgc ggg gaa cta ccc 259
Val Ser Ala Val Ala Gly Ala Tyr Ala Phe Ala Arg Gly Glu Leu Pro
40 45 50

gac gct gcc tgc gcc acc gcg aaa cac aca gcc gaa gca aac aac gca 307
Asp Ala Ala Cys Ala Thr Ala Lys His Thr Ala Glu Ala Asn Asn Ala
55 60 65

caa cta gaa aac tgc gca aca gaa ggg gag gat ctc acg ctc acc gtc 355
Gln Leu Glu Asn Cys Ala Thr Glu Gly Glu Asp Leu Thr Leu Thr Val
70 75 80 85

acc gtt cgt gga caa gaa gcc cac gca aaa gca gga cct tta 397
Thr Val Arg Gly Gln Glu Ala His Ala Lys Ala Gly Pro Leu
90 95

tgaggttccc aacaaggtca cca 420

<210> 1946
<211> 99
<212> PRT
<213> Corynebacterium glutamicum

<400> 1946
Met Thr Ile Ala Ser Ala Gly Val Ala Ser Ile Leu Ile Ser Leu Leu
1 5 10 15

Val Val Leu Ala Trp Gln Ala Gly Asn Leu Val Ala Arg Glu Gln Ala
20 25 30

Gln Val Ala Ala Asp Val Ser Ala Val Ala Gly Ala Tyr Ala Phe Ala
35 40 45

Arg Gly Glu Leu Pro Asp Ala Ala Cys Ala Thr Ala Lys His Thr Ala
50 55 60

Glu Ala Asn Asn Ala Gln Leu Glu Asn Cys Ala Thr Glu Gly Glu Asp
65 70 75 80

```
Leu Thr Leu Thr Val Thr Val Arg Gly Gln Glu Ala His Ala Lys Ala
                  85                  90                  95

Gly Pro Leu
```

<210> 1947
<211> 654
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(631)
<223> RXA00826

<400> 1947

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tcggcgcgcg cgatctggtg ctcatcttgg tgtgtgctgc catttccgcg atcgctctaa 60

ccgtgtccat tcagactggt ttctttaagt tcttgggcac atg atc aca gtt tta   115
                                              Met Ile Thr Val Leu
                                                1               5

att gat gga caa tcc ggt gcg ggc aaa acc acc ttg gcg ggt gag tta   163
Ile Asp Gly Gln Ser Gly Ala Gly Lys Thr Thr Leu Ala Gly Glu Leu
                  10                  15                  20

gct gcc cgc acc ggg ttt cag ttg gtt cat ttg gat gac ttt tat cct   211
Ala Ala Arg Thr Gly Phe Gln Leu Val His Leu Asp Asp Phe Tyr Pro
              25                  30                  35

ggt tgg act ggc ctt gaa gcg gca tcg gag att gtt gca cgc cat gtt   259
Gly Trp Thr Gly Leu Glu Ala Ala Ser Glu Ile Val Ala Arg His Val
          40                  45                  50

ttg gac gcg gac aac ccc ggt ttc ttc acg tgg gat tgg cac aac aat   307
Leu Asp Ala Asp Asn Pro Gly Phe Phe Thr Trp Asp Trp His Asn Asn
      55                  60                  65

tgc caa ggc gat tgg atc aag ttg gag cct ggt cga agt ctc att atc   355
Cys Gln Gly Asp Trp Ile Lys Leu Glu Pro Gly Arg Ser Leu Ile Ile
  70                  75                  80                  85

gaa ggc tct gga tca atc act gct gca aca aaa cgc aag gca tcg ctg   403
Glu Gly Ser Gly Ser Ile Thr Ala Ala Thr Lys Arg Lys Ala Ser Leu
                  90                  95                 100

ttg ggc gag ctg gtg acc gtt cgt atc act ggt cct gag gct tta aga   451
Leu Gly Glu Leu Val Thr Val Arg Ile Thr Gly Pro Glu Ala Leu Arg
             105                 110                 115

aaa cag cgc gcc ctc aac cgc gat cct gat tac gca cca ttt tgg aaa   499
Lys Gln Arg Ala Leu Asn Arg Asp Pro Asp Tyr Ala Pro Phe Trp Lys
         120                 125                 130

gtg tgg gcg cag cag gag caa cgc cat ttc tct tta ggc gtt gag gtg   547
Val Trp Ala Gln Gln Glu Gln Arg His Phe Ser Leu Gly Val Glu Val
     135                 140                 145
```

```
gat cat gag att gtg cta ggt tct gat gag gct tcg gga cga ccc gaa   595
Asp His Glu Ile Val Leu Gly Ser Asp Glu Ala Ser Gly Arg Pro Glu
150                 155                 160                 165

gaa atc tat gac agc ctg gga acg gcc cag agt tct taagaaagtt        641
Glu Ile Tyr Asp Ser Leu Gly Thr Ala Gln Ser Ser
                170                 175

tgactagaga aca                                                   654
```

<210> 1948
<211> 177
<212> PRT
<213> Corynebacterium glutamicum

<400> 1948

```
Met Ile Thr Val Leu Ile Asp Gly Gln Ser Gly Ala Gly Lys Thr Thr
  1               5                  10                  15

Leu Ala Gly Glu Leu Ala Ala Arg Thr Gly Phe Gln Leu Val His Leu
            20                  25                  30

Asp Asp Phe Tyr Pro Gly Trp Thr Gly Leu Glu Ala Ala Ser Glu Ile
        35                  40                  45

Val Ala Arg His Val Leu Asp Ala Asp Asn Pro Gly Phe Phe Thr Trp
    50                  55                  60

Asp Trp His Asn Asn Cys Gln Gly Asp Trp Ile Lys Leu Glu Pro Gly
65                  70                  75                  80

Arg Ser Leu Ile Ile Glu Gly Ser Gly Ser Ile Thr Ala Ala Thr Lys
                85                  90                  95

Arg Lys Ala Ser Leu Leu Gly Glu Leu Val Thr Val Arg Ile Thr Gly
            100                 105                 110

Pro Glu Ala Leu Arg Lys Gln Arg Ala Leu Asn Arg Asp Pro Asp Tyr
        115                 120                 125

Ala Pro Phe Trp Lys Val Trp Ala Gln Gln Glu Gln Arg His Phe Ser
    130                 135                 140

Leu Gly Val Glu Val Asp His Glu Ile Val Leu Gly Ser Asp Glu Ala
145                 150                 155                 160

Ser Gly Arg Pro Glu Glu Ile Tyr Asp Ser Leu Gly Thr Ala Gln Ser
                165                 170                 175

Ser
```

<210> 1949
<211> 846
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(823)
<223> RXA00830

<400> 1949
tgatggtggc tcgattgtat tcgagggcag ccccgcggaa ctcatcaaaa ctgatactcc 60

aacaggacgc caccttaaag cttatgtaga ttagtttctt atg gaa aac cct ggt 115
Met Glu Asn Pro Gly
1 5

gat ctc ggc gct atg cca cag tac ggt ttt gag cat att tcg atg ctc 163
Asp Leu Gly Ala Met Pro Gln Tyr Gly Phe Glu His Ile Ser Met Leu
10 15 20

atc acc gct gtg gtt tta gcg att ctt gtc gtc ccc att gct cgt cga 211
Ile Thr Ala Val Val Leu Ala Ile Leu Val Val Pro Ile Ala Arg Arg
25 30 35

ttc aac ttc gca ccg gca ttt ggc tgg gtg cta ctc atc gca aca ctt 259
Phe Asn Phe Ala Pro Ala Phe Gly Trp Val Leu Leu Ile Ala Thr Leu
40 45 50

ctg tcg aac ctg tgg aat ttt atg ccc ggc tat tac acg ctg gac caa 307
Leu Ser Asn Leu Trp Asn Phe Met Pro Gly Tyr Tyr Thr Leu Asp Gln
55 60 65

tct tgg cca ttc cac ttc tca gat gca ttg cgc att att gct gcc atc 355
Ser Trp Pro Phe His Phe Ser Asp Ala Leu Arg Ile Ile Ala Ala Ile
70 75 80 85

gca ttg att aat cgc gcg cgg tgg gca gtt tca gtg act att ttg tgg 403
Ala Leu Ile Asn Arg Ala Arg Trp Ala Val Ser Val Thr Ile Leu Trp
90 95 100

ggc acc acg atc aac ctg atg tca ctg ctc act cca gat gtt cag tat 451
Gly Thr Thr Ile Asn Leu Met Ser Leu Leu Thr Pro Asp Val Gln Tyr
105 110 115

tta cag gtt ccc tgg ctg gag ttt tta atg tac tgg ttt atg cac att 499
Leu Gln Val Pro Trp Leu Glu Phe Leu Met Tyr Trp Phe Met His Ile
120 125 130

tct gtg ttc cta gca gct ata att ctc att ttc gct ttt gga gaa aag 547
Ser Val Phe Leu Ala Ala Ile Ile Leu Ile Phe Ala Phe Gly Glu Lys
135 140 145

cca ggg ctg tcc gga gtg gtt atg tcc gtt gca gtg gcg att agc tgg 595
Pro Gly Leu Ser Gly Val Val Met Ser Val Ala Val Ala Ile Ser Trp
150 155 160 165

ggc atc atg tgc ctc atg gtc aac gca ttt ttg gga acc aac tac ggg 643
Gly Ile Met Cys Leu Met Val Asn Ala Phe Leu Gly Thr Asn Tyr Gly
170 175 180

tac ctc tcc aca gaa cca gaa tca gcg tca att ctg gat ttg ttg gga 691
Tyr Leu Ser Thr Glu Pro Glu Ser Ala Ser Ile Leu Asp Leu Leu Gly
185 190 195

gga tgg ccg ttc tac atc gtc gcg gaa gta tta ctc ctg tgt gca gtg 739
Gly Trp Pro Phe Tyr Ile Val Ala Glu Val Leu Leu Leu Cys Ala Val
200 205 210

```
tgg gct ttg tgg tct tat ctg att gat aag ctg cct atc acg tat cgc   787
Trp Ala Leu Trp Ser Tyr Leu Ile Asp Lys Leu Pro Ile Thr Tyr Arg
    215                 220                 225

cct gct tac cgt ccg aaa act cgg aag gcc gct gcg taaccgccct        833
Pro Ala Tyr Arg Pro Lys Thr Arg Lys Ala Ala Ala
230                 235                 240

ctacctcgag aaa                                                   846
```

<210> 1950
<211> 241
<212> PRT
<213> Corynebacterium glutamicum

<400> 1950

```
Met Glu Asn Pro Gly Asp Leu Gly Ala Met Pro Gln Tyr Gly Phe Glu
  1               5                  10                  15

His Ile Ser Met Leu Ile Thr Ala Val Val Leu Ala Ile Leu Val Val
             20                  25                  30

Pro Ile Ala Arg Arg Phe Asn Phe Ala Pro Ala Phe Gly Trp Val Leu
         35                  40                  45

Leu Ile Ala Thr Leu Leu Ser Asn Leu Trp Asn Phe Met Pro Gly Tyr
     50                  55                  60

Tyr Thr Leu Asp Gln Ser Trp Pro Phe His Phe Ser Asp Ala Leu Arg
 65                  70                  75                  80

Ile Ile Ala Ala Ile Ala Leu Ile Asn Arg Ala Arg Trp Ala Val Ser
                 85                  90                  95

Val Thr Ile Leu Trp Gly Thr Thr Ile Asn Leu Met Ser Leu Leu Thr
            100                 105                 110

Pro Asp Val Gln Tyr Leu Gln Val Pro Trp Leu Glu Phe Leu Met Tyr
        115                 120                 125

Trp Phe Met His Ile Ser Val Phe Leu Ala Ala Ile Ile Leu Ile Phe
    130                 135                 140

Ala Phe Gly Glu Lys Pro Gly Leu Ser Gly Val Val Met Ser Val Ala
145                 150                 155                 160

Val Ala Ile Ser Trp Gly Ile Met Cys Leu Met Val Asn Ala Phe Leu
                165                 170                 175

Gly Thr Asn Tyr Gly Tyr Leu Ser Thr Glu Pro Glu Ser Ala Ser Ile
            180                 185                 190

Leu Asp Leu Leu Gly Gly Trp Pro Phe Tyr Ile Val Ala Glu Val Leu
        195                 200                 205

Leu Leu Cys Ala Val Trp Ala Leu Trp Ser Tyr Leu Ile Asp Lys Leu
    210                 215                 220

Pro Ile Thr Tyr Arg Pro Ala Tyr Arg Pro Lys Thr Arg Lys Ala Ala
```

```
225                 230                 235                 240

Ala
```

<210> 1951
<211> 726
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> RXA00853

<400> 1951

```
ttggatccag ttgagaaatt tcagccccca tcccccacat gaacgctgtt caaaacatcc 60

agcttgcttg ttgaacactg ttcaggtgta tgatttttc atg cct aca tcc tct   115
                                          Met Pro Thr Ser Ser
                                            1               5

tct cct gca act gtg act ccg cta aag aag cag tct tca cgt aaa cag   163
Ser Pro Ala Thr Val Thr Pro Leu Lys Lys Gln Ser Ser Arg Lys Gln
                  10                  15                  20

ctc caa gac atc gcg ctt att gca gtt ttt gca gca ctg atc att gtg   211
Leu Gln Asp Ile Ala Leu Ile Ala Val Phe Ala Ala Leu Ile Ile Val
              25                  30                  35

ctt gct ttt gtt tcc atc cca gtt ggc aca gcg gga gtg cct att gtt   259
Leu Ala Phe Val Ser Ile Pro Val Gly Thr Ala Gly Val Pro Ile Val
          40                  45                  50

ttg cag aat gcc tcc atc gtt ttg gct ggc ctg att ctt ggt ggt cga   307
Leu Gln Asn Ala Ser Ile Val Leu Ala Gly Leu Ile Leu Gly Gly Arg
      55                  60                  65

cgt ggt ttt ctc act gct ttg ctg ttc ctg gca ctc ggc ctg att ggc   355
Arg Gly Phe Leu Thr Ala Leu Leu Phe Leu Ala Leu Gly Leu Ile Gly
  70                  75                  80                  85

ctg cct gtc ctt gca ggt ggt cgt acc act ttg gcc gca ctt gct ggc   403
Leu Pro Val Leu Ala Gly Gly Arg Thr Thr Leu Ala Ala Leu Ala Gly
                  90                  95                 100

cca aca gct ggc tac atc gtg ggt tac ctc att tcc cca ctt gtt gca   451
Pro Thr Ala Gly Tyr Ile Val Gly Tyr Leu Ile Ser Pro Leu Val Ala
              105                 110                 115

ggc atc atc gct tac ctc gca cct aaa aag cgt ggc gct gga atg ttc   499
Gly Ile Ile Ala Tyr Leu Ala Pro Lys Lys Arg Gly Ala Gly Met Phe
          120                 125                 130

atc gtt tta ggc ctg gcg ggt ctc gcg ggt ctg atc acc caa tac gct   547
Ile Val Leu Gly Leu Ala Gly Leu Ala Gly Leu Ile Thr Gln Tyr Ala
      135                 140                 145

tgc ggc atc gtg ggt ctc gtc ctt cgt gcg ggt cta agc ttg agt gaa   595
Cys Gly Ile Val Gly Leu Val Leu Arg Ala Gly Leu Ser Leu Ser Glu
```

```
150                 155                 160                 165

gca aca att gct caa ggt gcc ttt gtg ctg cca gat ttg gcc aag atc   643
Ala Thr Ile Ala Gln Gly Ala Phe Val Leu Pro Asp Leu Ala Lys Ile
                170                 175                 180

acc gtc atg gtc ata atc gcc gct gga gtt cat gca gca ttc cct gac   691
Thr Val Met Val Ile Ile Ala Ala Gly Val His Ala Ala Phe Pro Asp
            185                 190                 195

atc cgt aag aaa tagttccaac ccacttttcc tca                        726
Ile Arg Lys Lys
        200


<210> 1952
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 1952
Met Pro Thr Ser Ser Ser Pro Ala Thr Val Thr Pro Leu Lys Lys Gln
  1               5                  10                  15

Ser Ser Arg Lys Gln Leu Gln Asp Ile Ala Leu Ile Ala Val Phe Ala
             20                  25                  30

Ala Leu Ile Ile Val Leu Ala Phe Val Ser Ile Pro Val Gly Thr Ala
         35                  40                  45

Gly Val Pro Ile Val Leu Gln Asn Ala Ser Ile Val Leu Ala Gly Leu
     50                  55                  60

Ile Leu Gly Gly Arg Arg Gly Phe Leu Thr Ala Leu Leu Phe Leu Ala
 65                  70                  75                  80

Leu Gly Leu Ile Gly Leu Pro Val Leu Ala Gly Gly Arg Thr Thr Leu
                 85                  90                  95

Ala Ala Leu Ala Gly Pro Thr Ala Gly Tyr Ile Val Gly Tyr Leu Ile
            100                 105                 110

Ser Pro Leu Val Ala Gly Ile Ile Ala Tyr Leu Ala Pro Lys Lys Arg
        115                 120                 125

Gly Ala Gly Met Phe Ile Val Leu Gly Leu Ala Gly Leu Ala Gly Leu
    130                 135                 140

Ile Thr Gln Tyr Ala Cys Gly Ile Val Gly Leu Val Leu Arg Ala Gly
145                 150                 155                 160

Leu Ser Leu Ser Glu Ala Thr Ile Ala Gln Gly Ala Phe Val Leu Pro
                165                 170                 175

Asp Leu Ala Lys Ile Thr Val Met Val Ile Ile Ala Ala Gly Val His
            180                 185                 190

Ala Ala Phe Pro Asp Ile Arg Lys Lys
        195                 200
```

<210> 1953
<211> 426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(426)
<223> RXA00861

<400> 1953

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atg gct cct cac aag gtc atg ctg att acc act ggt act cag ggt gag   48
Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
  1               5                  10                  15

cct atg gct gcg ctg tct cgc atg gcg cgt cgt gag cac cga cag atc   96
Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
             20                  25                  30

act gtc cgt gat gga gac ttg att atc ctt tct tcc tcc ctg gtt cca   144
Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
         35                  40                  45

ggt aac gaa gaa gca gtg ttc ggt gtc atc aac atg ctg gct cag atc   192
Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
     50                  55                  60

ggt gca act gtt gtt acc ggt cgc gac gcc aag gtg cac acc tcg ggc   240
Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65                  70                  75                  80

cac ggc tac tcc gga gag ctg ttg ttc ttg tac aac gcc gct cgt ccg   288
His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
                 85                  90                  95

aag aac gct atg cct gtc cac ggc gag tgg cgc cac ctg cgc gcc aac   336
Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
            100                 105                 110

aag gaa ctg gct atc tcc act ggt gtt aac cgc gac aac gtt gtg ctt   384
Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
        115                 120                 125

gca caa aac ggt gtt gtg gtt gat atg gtc aac ggt cgc gca           426
Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
    130                 135                 140
```

<210> 1954
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 1954

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Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
  1               5                  10                  15

Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
             20                  25                  30

Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
```

```
         35                  40                  45

Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
     50                  55                  60

Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65                  70                  75                  80

His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
                 85                  90                  95

Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
            100                 105                 110

Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
        115                 120                 125

Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
    130                 135                 140
```

<210> 1955
<211> 680
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(664)
<223> RXA00862

<400> 1955

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aggtagttcc ttggcgcttg tggtttccgc ctctttactt ttaagtgctt gtgatggaag 60

cggctcaacg cctacaacct ctgctagtcc tgctccagtt gtg aca gaa act gaa   115
                                            Val Thr Glu Thr Glu
                                              1               5

acc gct aac ccg gtc acc aca act cgc acg cct tca gat gct gcc ccg   163
Thr Ala Asn Pro Val Thr Thr Thr Arg Thr Pro Ser Asp Ala Ala Pro
                 10                  15                  20

tcg cct acc act tca gag ccc act ggt tca gag tcc acc aac tcc cct   211
Ser Pro Thr Thr Ser Glu Pro Thr Gly Ser Glu Ser Thr Asn Ser Pro
             25                  30                  35

tcc ccc act gct ttg ccg ccg ttg ggt tcc ccg tcg atg gat cag aag   259
Ser Pro Thr Ala Leu Pro Pro Leu Gly Ser Pro Ser Met Asp Gln Lys
         40                  45                  50

cag cag gct caa gtt ggt gac tcc gat atg tcg atc gct ggc atc cgc   307
Gln Gln Ala Gln Val Gly Asp Ser Asp Met Ser Ile Ala Gly Ile Arg
     55                  60                  65

gtt gcc gag cac gaa acg ttc aca cga gtt gtt ttt gat atc gcc ggt   355
Val Ala Glu His Glu Thr Phe Thr Arg Val Val Phe Asp Ile Ala Gly
 70                  75                  80                  85

aat ggc caa cct ggt tgg tgg gtc gat tgg gcc act gat cca att cag   403
Asn Gly Gln Pro Gly Trp Trp Val Asp Trp Ala Thr Asp Pro Ile Gln
                 90                  95                 100
```

```
cag gcg tca ggt ctt cca gtt gag atg gct ggt gat tcc ttc ctc aac   451
Gln Ala Ser Gly Leu Pro Val Glu Met Ala Gly Asp Ser Phe Leu Asn
            105                 110                 115

gtc aat att caa ggc act gga tat cct gat cag gtt gtc gtt cca ggt   499
Val Asn Ile Gln Gly Thr Gly Tyr Pro Asp Gln Val Val Val Pro Gly
        120                 125                 130

atc gat acc gga tca tat cct ggt gca ggc att gtt gaa gac atc aac   547
Ile Asp Thr Gly Ser Tyr Pro Gly Ala Gly Ile Val Glu Asp Ile Asn
    135                 140                 145

ttc acc agt att ttt gaa gcc cgt tcc caa gtt ctc att ggt gta tct   595
Phe Thr Ser Ile Phe Glu Ala Arg Ser Gln Val Leu Ile Gly Val Ser
150                 155                 160                 165

ggt caa ccc cga aat tac tcg gtc tca ttg ctg cag gaa cca acc agg   643
Gly Gln Pro Arg Asn Tyr Ser Val Ser Leu Leu Gln Glu Pro Thr Arg
                170                 175                 180

ctt gtg gtg gac atc gtt cac tagcgctgga acgccg                    680
Leu Val Val Asp Ile Val His
            185


<210> 1956
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 1956
Val Thr Glu Thr Glu Thr Ala Asn Pro Val Thr Thr Thr Arg Thr Pro
  1               5                  10                  15

Ser Asp Ala Ala Pro Ser Pro Thr Thr Ser Glu Pro Thr Gly Ser Glu
             20                  25                  30

Ser Thr Asn Ser Pro Ser Pro Thr Ala Leu Pro Pro Leu Gly Ser Pro
         35                  40                  45

Ser Met Asp Gln Lys Gln Gln Ala Gln Val Gly Asp Ser Asp Met Ser
     50                  55                  60

Ile Ala Gly Ile Arg Val Ala Glu His Glu Thr Phe Thr Arg Val Val
 65                  70                  75                  80

Phe Asp Ile Ala Gly Asn Gly Gln Pro Gly Trp Trp Val Asp Trp Ala
                 85                  90                  95

Thr Asp Pro Ile Gln Gln Ala Ser Gly Leu Pro Val Glu Met Ala Gly
            100                 105                 110

Asp Ser Phe Leu Asn Val Asn Ile Gln Gly Thr Gly Tyr Pro Asp Gln
        115                 120                 125

Val Val Val Pro Gly Ile Asp Thr Gly Ser Tyr Pro Gly Ala Gly Ile
    130                 135                 140

Val Glu Asp Ile Asn Phe Thr Ser Ile Phe Glu Ala Arg Ser Gln Val
145                 150                 155                 160
```

```
Leu Ile Gly Val Ser Gly Gln Pro Arg Asn Tyr Ser Val Ser Leu Leu
                165                 170                 175

Gln Glu Pro Thr Arg Leu Val Val Asp Ile Val His
            180                 185


<210> 1957
<211> 1212
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1189)
<223> RXA00874

<400> 1957
agctgttccc taccattgct gaacgggagt ggattgtcac tttagcccct cacggattct 60

tctggtttga tctcaccgcc gatgaaaagg acgatatgga atg agc att ggc caa   115
                                          Met Ser Ile Gly Gln
                                            1               5

cac atc atc acc gag cgt ttc tac ggc gcc aag tcc cac acc atc gac   163
His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys Ser His Thr Ile Asp
                10                  15                  20

aac gta gat att gtg ttg tcc cgc gaa tgt ggc gag aac act ttg gct   211
Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly Glu Asn Thr Leu Ala
            25                  30                  35

gta gtg cgc atc aac aat gcg ctg tat cag ttg ttg gtc aat gat gat   259
Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu Leu Val Asn Asp Asp
        40                  45                  50

ggc aaa gat gtt ctc aac gac cac gta gaa gag gtc ggt gcg agt ttc   307
Gly Lys Asp Val Leu Asn Asp His Val Glu Glu Val Gly Ala Ser Phe
    55                  60                  65

gga gca tgg act ggc agc tct gct ttt ccc att ggc cct ttc act cca   355
Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile Gly Pro Phe Thr Pro
70                  75                  80                  85

ctc ggc aca gaa caa tcc aat agc tct ttc atc acc gcc gac aat aaa   403
Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile Thr Ala Asp Asn Lys
                90                  95                  100

gcg atc gtg aaa tac ttc cgc aaa tta gaa tcc ggg caa aac ccc gat   451
Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser Gly Gln Asn Pro Asp
            105                 110                 115

gtg gag cta att tct aaa att tcc tcc tgc ccc aac atc gcg ccc atc   499
Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro Asn Ile Ala Pro Ile
        120                 125                 130

ctg ggt ttt tcc tcc gct gag atc tcc ggg gct aac tac acc ctg gtc   547
Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala Asn Tyr Thr Leu Val
    135                 140                 145
```

```
atg gcg cag cag tac gtt cca ggt ttg gat ggc tgg tca cac gcg ctg   595
Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly Trp Ser His Ala Leu
150                 155                 160                 165

act act acc tct ggc agc ttt gca gag gat gca gaa aag atc ggc gaa   643
Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala Glu Lys Ile Gly Glu
                170                 175                 180

gcc acc cgc aat gtt cac act gct ctt gca tcg gcc ttc cct act cgg   691
Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser Ala Phe Pro Thr Arg
            185                 190                 195

gta gtt ccc gta gaa gca ctc gcc gat gcg ctc act acc cgc ctt aat   739
Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu Thr Thr Arg Leu Asn
        200                 205                 210

gaa cta atc tcc caa gca ccc gaa atc gcc cgc ttc aaa gaa gca gcc   787
Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg Phe Lys Glu Ala Ala
    215                 220                 225

atc gac ctc tac caa tcg ttg gaa ggc gaa gcc cac atc caa cgc atc   835
Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala His Ile Gln Arg Ile
230                 235                 240                 245

cac ggt gac ctc cac ttg ggg cag ctc atc aaa acc ccc gaa cgc tac   883
His Gly Asp Leu His Leu Gly Gln Leu Ile Lys Thr Pro Glu Arg Tyr
                250                 255                 260

atc ctc atc gat ttc gaa ggc gaa cct gcc cgc cca ctt aat caa cga   931
Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg Pro Leu Asn Gln Arg
            265                 270                 275

cgc ctc ccc gac tct ccc ctg aaa gat ctc gcc ggc atc atc aga tcc   979
Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala Gly Ile Ile Arg Ser
        280                 285                 290

atc gac tac gca gcc tac ttc gac ggc gaa cac acc caa tgg gcc aac   1027
Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His Thr Gln Trp Ala Asn
    295                 300                 305

gaa gcc acc gcg cta ttc ctc gac ggc tac gga tca att gaa gac caa   1075
Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly Ser Ile Glu Asp Gln
310                 315                 320                 325

gaa ctc ctc aat gcc tac att ctg gac aag gcg ttg tac gag gtt gcc   1123
Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala Leu Tyr Glu Val Ala
                330                 335                 340

tat gaa ata aac aac cgc ccc gac tgg gtg aaa atc cca ctc gag gcg   1171
Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys Ile Pro Leu Glu Ala
            345                 350                 355

gtc gaa agg ctt cta gac tagttagtta ctctgcgtca aac                1212
Val Glu Arg Leu Leu Asp
        360
```

Sequence Listing

<210> 1958
<211> 363
<212> PRT
<213> Corynebacterium glutamicum

<400> 1958

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Met Ser Ile Gly Gln His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys
  1               5                  10                  15

Ser His Thr Ile Asp Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly
            20                  25                  30

Glu Asn Thr Leu Ala Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu
        35                  40                  45

Leu Val Asn Asp Asp Gly Lys Asp Val Leu Asn Asp His Val Glu Glu
    50                  55                  60

Val Gly Ala Ser Phe Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile
65                  70                  75                  80

Gly Pro Phe Thr Pro Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile
                85                  90                  95

Thr Ala Asp Asn Lys Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser
            100                 105                 110

Gly Gln Asn Pro Asp Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro
        115                 120                 125

Asn Ile Ala Pro Ile Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala
    130                 135                 140

Asn Tyr Thr Leu Val Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly
145                 150                 155                 160

Trp Ser His Ala Leu Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala
                165                 170                 175

Glu Lys Ile Gly Glu Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser
            180                 185                 190

Ala Phe Pro Thr Arg Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu
        195                 200                 205

Thr Thr Arg Leu Asn Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg
    210                 215                 220

Phe Lys Glu Ala Ala Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala
225                 230                 235                 240

His Ile Gln Arg Ile His Gly Asp Leu His Leu Gly Gln Leu Ile Lys
                245                 250                 255

Thr Pro Glu Arg Tyr Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg
            260                 265                 270

Pro Leu Asn Gln Arg Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala
        275                 280                 285

Gly Ile Ile Arg Ser Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His
    290                 295                 300

Thr Gln Trp Ala Asn Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly
305                 310                 315                 320
```

```
Ser Ile Glu Asp Gln Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala
                325                 330                 335

Leu Tyr Glu Val Ala Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys
            340                 345                 350

Ile Pro Leu Glu Ala Val Glu Arg Leu Leu Asp
        355                 360


<210> 1959
<211> 1878
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1855)
<223> RXA00876

<400> 1959
ttgactatct cgaattaggt gagggctggg agccagaaat tttgtgctct gatgctgttg 60

aaattttaga aaatctcatc aaggaactaa ggggaattcc atg aca ttg aaa att   115
                                            Met Thr Leu Lys Ile
                                              1               5

gat ccc tcg tcc atc agt agt gct gtg tct cgc ttg aat gag ctt cag   163
Asp Pro Ser Ser Ile Ser Ser Ala Val Ser Arg Leu Asn Glu Leu Gln
                  10                  15                  20

cat caa gct att act gca tct caa gtg gga atg aaa tca aca att cta   211
His Gln Ala Ile Thr Ala Ser Gln Val Gly Met Lys Ser Thr Ile Leu
              25                  30                  35

tcc gcg ttt tcg ccc gtc tct gga ctc gat caa ttg ggt tcc ggt cac   259
Ser Ala Phe Ser Pro Val Ser Gly Leu Asp Gln Leu Gly Ser Gly His
          40                  45                  50

ggg aat gtg att aat ggt ggg gca ggc gca gca aac tct gtg ctg aat   307
Gly Asn Val Ile Asn Gly Gly Ala Gly Ala Ala Asn Ser Val Leu Asn
      55                  60                  65

tcc tat gcc gaa caa atc gag tgg ttg tct gcg gct ttg cag gct tct   355
Ser Tyr Ala Glu Gln Ile Glu Trp Leu Ser Ala Ala Leu Gln Ala Ser
  70                  75                  80                  85

ggt gcg gct ttg act ggc cag gat gaa tta ttc gct agg ggt atg gat   403
Gly Ala Ala Leu Thr Gly Gln Asp Glu Leu Phe Ala Arg Gly Met Asp
                  90                  95                 100

gta gcg gat acc ggt ggc agg gtt gta gaa gag tca gta atg ttc ccg   451
Val Ala Asp Thr Gly Gly Arg Val Val Glu Glu Ser Val Met Phe Pro
              105                 110                 115

gcg cgg ccg gca cct cgg ttt gag tct ttc gtt ttt aat cca cca gct   499
Ala Arg Pro Ala Pro Arg Phe Glu Ser Phe Val Phe Asn Pro Pro Ala
          120                 125                 130

gtt agt cct tcg ttg tcg ttg gat gcg ttg tgt agt cag ttt tcc gga   547
```

```
Val Ser Pro Ser Leu Ser Leu Asp Ala Leu Cys Ser Gln Phe Ser Gly
    135                 140                 145

acc aac tcg ggg gcg gtt ttg gag gcg cag ggg tct tgg ggc tct atg   595
Thr Asn Ser Gly Ala Val Leu Glu Ala Gln Gly Ser Trp Gly Ser Met
150                 155                 160                 165

gcg tcg gct att agc aat gtg tcg gct tcg ttg tcg tcg att gct ggt   643
Ala Ser Ala Ile Ser Asn Val Ser Ala Ser Leu Ser Ser Ile Ala Gly
                170                 175                 180

gag att ttg gcg gag aac tca ggc gaa acg ttt gag cag gct gct gct   691
Glu Ile Leu Ala Glu Asn Ser Gly Glu Thr Phe Glu Gln Ala Ala Ala
            185                 190                 195

cgg att aat gag gtg gcg gct gcg ggg gcg acg ttt gct gcg aat gcg   739
Arg Ile Asn Glu Val Ala Ala Ala Gly Ala Thr Phe Ala Ala Asn Ala
        200                 205                 210

aaa atg atg ggg gcg tcg gtg ggg acg ctg aat cgg att tat atg ggg   787
Lys Met Met Gly Ala Ser Val Gly Thr Leu Asn Arg Ile Tyr Met Gly
    215                 220                 225

cat cgc atg cag gtg ttt atg gct gcg acg tcg att aag gcg att ttg   835
His Arg Met Gln Val Phe Met Ala Ala Thr Ser Ile Lys Ala Ile Leu
230                 235                 240                 245

gat ccg gtg cag agg ctt gct gcg gag agg gcg ttt ttg gcg tcg ttt   883
Asp Pro Val Gln Arg Leu Ala Ala Glu Arg Ala Phe Leu Ala Ser Phe
                250                 255                 260

cag gct act ttt cag gcg gat gtg ttg acg ggt atg cct cct gtg agc   931
Gln Ala Thr Phe Gln Ala Asp Val Leu Thr Gly Met Pro Pro Val Ser
            265                 270                 275

aat ttg atg cag atg aag ggg gcg aat ggt tct gcg ggg gaa att gct   979
Asn Leu Met Gln Met Lys Gly Ala Asn Gly Ser Ala Gly Glu Ile Ala
        280                 285                 290

ctg ggg atg gat gag att gct ggc agt ggg cag gca tgg tct gcg gcg   1027
Leu Gly Met Asp Glu Ile Ala Gly Ser Gly Gln Ala Trp Ser Ala Ala
    295                 300                 305

ggg ttg act ccg tcg ggg gct gcg cag ggt ggt gtc gcc aat gcg ggc   1075
Gly Leu Thr Pro Ser Gly Ala Ala Gln Gly Gly Val Ala Asn Ala Gly
310                 315                 320                 325

agt atc gcg ccg gat gca gcg gtt caa ggt gct gcg ggg cag agt ggg   1123
Ser Ile Ala Pro Asp Ala Ala Val Gln Gly Ala Ala Gly Gln Ser Gly
                330                 335                 340

gtt gga agt ttt ggc act gtc act gat cag ttg gat ggc atc aat att   1171
Val Gly Ser Phe Gly Thr Val Thr Asp Gln Leu Asp Gly Ile Asn Ile
            345                 350                 355

ggg gat atg ttg acc tct gct gcc tca gct ggg cag agc ctt gcg aat   1219
Gly Asp Met Leu Thr Ser Ala Ala Ser Ala Gly Gln Ser Leu Ala Asn
        360                 365                 370

ggt ttg gcg atg cct act tct acg cct aat tcg gcg tcc ggt gcg att   1267
Gly Leu Ala Met Pro Thr Ser Thr Pro Asn Ser Ala Ser Gly Ala Ile
```

```
    375                 380                 385

cct tcc tcg atg tct gcg gca tcg ccg ctt ggt gcg ttt ggc agc ggt   1315
Pro Ser Ser Met Ser Ala Ala Ser Pro Leu Gly Ala Phe Gly Ser Gly
390                 395                 400                 405

gca ggg ttg ggc gca cag ggt ggc tcg att gga tct tcg gca cct gga   1363
Ala Gly Leu Gly Ala Gln Gly Gly Ser Ile Gly Ser Ser Ala Pro Gly
                410                 415                 420

gcg atc agt agt cga gcg gcc gga tcc gca ggt ggt tcg gta ccg gga   1411
Ala Ile Ser Ser Arg Ala Ala Gly Ser Ala Gly Gly Ser Val Pro Gly
            425                 430                 435

atg act ggt ggt cct ggc gcg ccg ggg att acc tcg gat tcg ttg atg   1459
Met Thr Gly Gly Pro Gly Ala Pro Gly Ile Thr Ser Asp Ser Leu Met
        440                 445                 450

gga gct cga act cat ggt gct tct tcc gcg gga gct gtc gct ccg atg   1507
Gly Ala Arg Thr His Gly Ala Ser Ser Ala Gly Ala Val Ala Pro Met
    455                 460                 465

atg ggt ggt gct ggc gga atg tct ggt ggc gtc gtt ggt gca ggt ggt   1555
Met Gly Gly Ala Gly Gly Met Ser Gly Gly Val Val Gly Ala Gly Gly
470                 475                 480                 485

act ggt tct cag agc aag tat gcg cgc cag act gga tcg tcg gtt gga   1603
Thr Gly Ser Gln Ser Lys Tyr Ala Arg Gln Thr Gly Ser Ser Val Gly
                490                 495                 500

tct agt tcg cag tcg ggt tct ggc ctg ggg atg gtg gga tca ggg agt   1651
Ser Ser Ser Gln Ser Gly Ser Gly Leu Gly Met Val Gly Ser Gly Ser
            505                 510                 515

ggg aag ccg tcg ata agc aat ttt ggg cgc ggc atg atg ccg atg atg   1699
Gly Lys Pro Ser Ile Ser Asn Phe Gly Arg Gly Met Met Pro Met Met
        520                 525                 530

ccc atg atg ccc atg gga ggc gcc ggc ggt ggg cag aag aat acc ggc   1747
Pro Met Met Pro Met Gly Gly Ala Gly Gly Gly Gln Lys Asn Thr Gly
    535                 540                 545

aag gtg aaa acg gtg acg tct gcg gtg gag gaa gac cgc aat ttg gcg   1795
Lys Val Lys Thr Val Thr Ser Ala Val Glu Glu Asp Arg Asn Leu Ala
550                 555                 560                 565

gcg ctg ctg ggt gat cgg ggg ccg gtt gtt ccg ggt gtg att ggt gac   1843
Ala Leu Leu Gly Asp Arg Gly Pro Val Val Pro Gly Val Ile Gly Asp
                570                 575                 580

tgg gtg agg ggc taacgcaaca atgtgtctaa gct                        1878
Trp Val Arg Gly
            585
```

<210> 1960
<211> 585
<212> PRT
<213> Corynebacterium glutamicum

<400> 1960

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Met Thr Leu Lys Ile Asp Pro Ser Ser Ile Ser Ser Ala Val Ser Arg
  1               5                  10                  15

Leu Asn Glu Leu Gln His Gln Ala Ile Thr Ala Ser Gln Val Gly Met
            20                  25                  30

Lys Ser Thr Ile Leu Ser Ala Phe Ser Pro Val Ser Gly Leu Asp Gln
        35                  40                  45

Leu Gly Ser Gly His Gly Asn Val Ile Asn Gly Gly Ala Gly Ala Ala
    50                  55                  60

Asn Ser Val Leu Asn Ser Tyr Ala Glu Gln Ile Glu Trp Leu Ser Ala
65                  70                  75                  80

Ala Leu Gln Ala Ser Gly Ala Ala Leu Thr Gly Gln Asp Glu Leu Phe
                85                  90                  95

Ala Arg Gly Met Asp Val Ala Asp Thr Gly Gly Arg Val Val Glu Glu
            100                 105                 110

Ser Val Met Phe Pro Ala Arg Pro Ala Pro Arg Phe Glu Ser Phe Val
        115                 120                 125

Phe Asn Pro Pro Ala Val Ser Pro Ser Leu Ser Leu Asp Ala Leu Cys
    130                 135                 140

Ser Gln Phe Ser Gly Thr Asn Ser Gly Ala Val Leu Glu Ala Gln Gly
145                 150                 155                 160

Ser Trp Gly Ser Met Ala Ser Ala Ile Ser Asn Val Ser Ala Ser Leu
                165                 170                 175

Ser Ser Ile Ala Gly Glu Ile Leu Ala Glu Asn Ser Gly Glu Thr Phe
            180                 185                 190

Glu Gln Ala Ala Ala Arg Ile Asn Glu Val Ala Ala Ala Gly Ala Thr
        195                 200                 205

Phe Ala Ala Asn Ala Lys Met Met Gly Ala Ser Val Gly Thr Leu Asn
    210                 215                 220

Arg Ile Tyr Met Gly His Arg Met Gln Val Phe Met Ala Ala Thr Ser
225                 230                 235                 240

Ile Lys Ala Ile Leu Asp Pro Val Gln Arg Leu Ala Ala Glu Arg Ala
                245                 250                 255

Phe Leu Ala Ser Phe Gln Ala Thr Phe Gln Ala Asp Val Leu Thr Gly
            260                 265                 270

Met Pro Pro Val Ser Asn Leu Met Gln Met Lys Gly Ala Asn Gly Ser
        275                 280                 285

Ala Gly Glu Ile Ala Leu Gly Met Asp Glu Ile Ala Gly Ser Gly Gln
    290                 295                 300

Ala Trp Ser Ala Ala Gly Leu Thr Pro Ser Gly Ala Ala Gln Gly Gly
305                 310                 315                 320

Val Ala Asn Ala Gly Ser Ile Ala Pro Asp Ala Ala Val Gln Gly Ala
```

```
                325                 330                 335

Ala Gly Gln Ser Gly Val Gly Ser Phe Gly Thr Val Thr Asp Gln Leu
            340                 345                 350

Asp Gly Ile Asn Ile Gly Asp Met Leu Thr Ser Ala Ala Ser Ala Gly
        355                 360                 365

Gln Ser Leu Ala Asn Gly Leu Ala Met Pro Thr Ser Thr Pro Asn Ser
    370                 375                 380

Ala Ser Gly Ala Ile Pro Ser Ser Met Ser Ala Ala Ser Pro Leu Gly
385                 390                 395                 400

Ala Phe Gly Ser Gly Ala Gly Leu Gly Ala Gln Gly Gly Ser Ile Gly
                405                 410                 415

Ser Ser Ala Pro Gly Ala Ile Ser Ser Arg Ala Ala Gly Ser Ala Gly
            420                 425                 430

Gly Ser Val Pro Gly Met Thr Gly Gly Pro Gly Ala Pro Gly Ile Thr
        435                 440                 445

Ser Asp Ser Leu Met Gly Ala Arg Thr His Gly Ala Ser Ser Ala Gly
    450                 455                 460

Ala Val Ala Pro Met Met Gly Gly Ala Gly Gly Met Ser Gly Gly Val
465                 470                 475                 480

Val Gly Ala Gly Gly Thr Gly Ser Gln Ser Lys Tyr Ala Arg Gln Thr
                485                 490                 495

Gly Ser Ser Val Gly Ser Ser Ser Gln Ser Gly Ser Gly Leu Gly Met
            500                 505                 510

Val Gly Ser Gly Ser Gly Lys Pro Ser Ile Ser Asn Phe Gly Arg Gly
        515                 520                 525

Met Met Pro Met Met Pro Met Met Pro Met Gly Gly Ala Gly Gly Gly
    530                 535                 540

Gln Lys Asn Thr Gly Lys Val Lys Thr Val Thr Ser Ala Val Glu Glu
545                 550                 555                 560

Asp Arg Asn Leu Ala Ala Leu Leu Gly Asp Arg Gly Pro Val Val Pro
                565                 570                 575

Gly Val Ile Gly Asp Trp Val Arg Gly
            580                 585


<210> 1961
<211> 501
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(478)
<223> RXA00881
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<400> 1961
acctgaccga ggaagccgac gagctgaccc caacgctgaa ggtcaagcgc aacgttgttg 60

ttcgccgtta cgcagacgcc atcgaccaca tctacaaccg atg agt aac aca gag 115
Met Ser Asn Thr Glu
1 5

acc caa ttt gat tgg gat gga tcg aca tgg acc cgc acc gaa gtc ggc 163
Thr Gln Phe Asp Trp Asp Gly Ser Thr Trp Thr Arg Thr Glu Val Gly
10 15 20

gaa gca cca aca cgc ttc gct gtg ggc gtg atg gag gat ttc gcc tac 211
Glu Ala Pro Thr Arg Phe Ala Val Gly Val Met Glu Asp Phe Ala Tyr
25 30 35

att gca gcc act ggc acg gac ggg gat gaa gag ttc ttt act ttg ggc 259
Ile Ala Ala Thr Gly Thr Asp Gly Asp Glu Glu Phe Phe Thr Leu Gly
40 45 50

tca aat ccg ggt ctg acg ttt ggt gat ccc gag tgg ctt ttc gct cag 307
Ser Asn Pro Gly Leu Thr Phe Gly Asp Pro Glu Trp Leu Phe Ala Gln
55 60 65

gat aat ccg cag tat gtg gtg gag tgc att ggc cag cag gga acc gag 355
Asp Asn Pro Gln Tyr Val Val Glu Cys Ile Gly Gln Gln Gly Thr Glu
70 75 80 85

ccg gca gcc ctg aag gtt gta gat aaa tat ttg tcg cga cta tct gat 403
Pro Ala Ala Leu Lys Val Val Asp Lys Tyr Leu Ser Arg Leu Ser Asp
90 95 100

gag gag tca cgt ggc gaa ccc acg cgg att ctc aat gaa ttg gtc tcg 451
Glu Glu Ser Arg Gly Glu Pro Thr Arg Ile Leu Asn Glu Leu Val Ser
105 110 115

gcg atg gag ttg ccg gca ttg ccg tgg tgatttttct cgggctttag 498
Ala Met Glu Leu Pro Ala Leu Pro Trp
120 125

tga 501

<210> 1962
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 1962
Met Ser Asn Thr Glu Thr Gln Phe Asp Trp Asp Gly Ser Thr Trp Thr
1 5 10 15

Arg Thr Glu Val Gly Glu Ala Pro Thr Arg Phe Ala Val Gly Val Met
20 25 30

Glu Asp Phe Ala Tyr Ile Ala Ala Thr Gly Thr Asp Gly Asp Glu Glu
35 40 45

Phe Phe Thr Leu Gly Ser Asn Pro Gly Leu Thr Phe Gly Asp Pro Glu
50 55 60

Trp Leu Phe Ala Gln Asp Asn Pro Gln Tyr Val Val Glu Cys Ile Gly

```
 65                  70                  75                  80

Gln Gln Gly Thr Glu Pro Ala Ala Leu Lys Val Val Asp Lys Tyr Leu
                 85                  90                  95

Ser Arg Leu Ser Asp Glu Glu Ser Arg Gly Glu Pro Thr Arg Ile Leu
            100                 105                 110

Asn Glu Leu Val Ser Ala Met Glu Leu Pro Ala Leu Pro Trp
        115                 120                 125


<210> 1963
<211> 801
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(778)
<223> RXA00882

<400> 1963
aaatagctga gaaattggct agaggacggc tagcaaaccg gatcaagacc ggctagaact 60

ttagctacga ggcaagaaaa ggaaggtgtg ttggaacgcg atg agc agt aca acc   115
                                              Met Ser Ser Thr Thr
                                                1               5

gca cag cta cgc cac cga gag ctg acc cag gag atc tac aac atc ggc   163
Ala Gln Leu Arg His Arg Glu Leu Thr Gln Glu Ile Tyr Asn Ile Gly
                 10                  15                  20

gac gag gtc gct gaa tac att gag cac atc atg gaa gca gtc tcc gac   211
Asp Glu Val Ala Glu Tyr Ile Glu His Ile Met Glu Ala Val Ser Asp
            25                  30                  35

tgg gat ctg gag ctc gtg gaa gat tgc ctc gct gaa ttc gat gag atc   259
Trp Asp Leu Glu Leu Val Glu Asp Cys Leu Ala Glu Phe Asp Glu Ile
        40                  45                  50

atc act gaa gcc cgc gat gac tcc cgc act gtt gtg gct gaa ctt tca   307
Ile Thr Glu Ala Arg Asp Asp Ser Arg Thr Val Val Ala Glu Leu Ser
    55                  60                  65

ggc ctg cgt cac gca cta acc act ggt atc cgt cag ggc acc gtg agc   355
Gly Leu Arg His Ala Leu Thr Thr Gly Ile Arg Gln Gly Thr Val Ser
70                  75                  80                  85

gct aga gcc acg gtg gag gtg gac gtc gat aag ccg gaa cgc ctg acc   403
Ala Arg Ala Thr Val Glu Val Asp Val Asp Lys Pro Glu Arg Leu Thr
                90                  95                 100

gcc tcc gag ctg gag cgc gac ttc gat att gat gcc ggc ctc gtt gat   451
Ala Ser Glu Leu Glu Arg Asp Phe Asp Ile Asp Ala Gly Leu Val Asp
            105                 110                 115

gta cgc gat ctg tcg acc gcg ctc aat gcg cgc aca gac gct gtg gtt   499
Val Arg Asp Leu Ser Thr Ala Leu Asn Ala Arg Thr Asp Ala Val Val
        120                 125                 130
```

```
aag cgc ctg gag gcc act gtg gag tgg gtg ctg gcg gaa act gac aag   547
Lys Arg Leu Glu Ala Thr Val Glu Trp Val Leu Ala Glu Thr Asp Lys
    135                 140                 145

gtg gcc aac gat ctg gat tcc ctg tct ctg cca ctg ctt tat ggc cgc   595
Val Ala Asn Asp Leu Asp Ser Leu Ser Leu Pro Leu Leu Tyr Gly Arg
150                 155                 160                 165

gtt gca gcg gtg atc gaa agc gcc acc agc gca tgg atc aac gca gtg   643
Val Ala Ala Val Ile Glu Ser Ala Thr Ser Ala Trp Ile Asn Ala Val
                170                 175                 180

ggc acc gcc aat ccg gcg tat gtg cgc acc atg cga ggc agc aac ccg   691
Gly Thr Ala Asn Pro Ala Tyr Val Arg Thr Met Arg Gly Ser Asn Pro
            185                 190                 195

cca cgt ttc ctg ctt gag cgt gcg cgt atc gac gct gtc gtg gcc cgg   739
Pro Arg Phe Leu Leu Glu Arg Ala Arg Ile Asp Ala Val Val Ala Arg
        200                 205                 210

gtt gca gac aag ctt gcg caa aag cgc aac gct gtt tcc tagaaatctc    788
Val Ala Asp Lys Leu Ala Gln Lys Arg Asn Ala Val Ser
    215                 220                 225

ggtgcagcaa aaa                                                   801


<210> 1964
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 1964
Met Ser Ser Thr Thr Ala Gln Leu Arg His Arg Glu Leu Thr Gln Glu
  1               5                  10                  15

Ile Tyr Asn Ile Gly Asp Glu Val Ala Glu Tyr Ile Glu His Ile Met
             20                  25                  30

Glu Ala Val Ser Asp Trp Asp Leu Glu Leu Val Glu Asp Cys Leu Ala
         35                  40                  45

Glu Phe Asp Glu Ile Ile Thr Glu Ala Arg Asp Asp Ser Arg Thr Val
     50                  55                  60

Val Ala Glu Leu Ser Gly Leu Arg His Ala Leu Thr Thr Gly Ile Arg
 65                  70                  75                  80

Gln Gly Thr Val Ser Ala Arg Ala Thr Val Glu Val Asp Val Asp Lys
                 85                  90                  95

Pro Glu Arg Leu Thr Ala Ser Glu Leu Glu Arg Asp Phe Asp Ile Asp
            100                 105                 110

Ala Gly Leu Val Asp Val Arg Asp Leu Ser Thr Ala Leu Asn Ala Arg
        115                 120                 125

Thr Asp Ala Val Val Lys Arg Leu Glu Ala Thr Val Glu Trp Val Leu
    130                 135                 140

Ala Glu Thr Asp Lys Val Ala Asn Asp Leu Asp Ser Leu Ser Leu Pro
```

```
145                 150                 155                 160

Leu Leu Tyr Gly Arg Val Ala Ala Val Ile Glu Ser Ala Thr Ser Ala
                165                 170                 175

Trp Ile Asn Ala Val Gly Thr Ala Asn Pro Ala Tyr Val Arg Thr Met
            180                 185                 190

Arg Gly Ser Asn Pro Pro Arg Phe Leu Leu Glu Arg Ala Arg Ile Asp
        195                 200                 205

Ala Val Val Ala Arg Val Ala Asp Lys Leu Ala Gln Lys Arg Asn Ala
    210                 215                 220

Val Ser
225
```

<210> 1965
<211> 642
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(619)
<223> RXA00883

<400> 1965

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aatatacaca ccaaaaactg acatgcccca agcctagtgc ctgcccccta tacatgatta 60

attgatgtta aacatagcga attcctaaga acagggtaga gtg cag ggt atg aaa   115
                                               Val Gln Gly Met Lys
                                                 1               5

cgg aag atg gtc gca gcg gcg ctg gca aca gcg ctt ctt ttt ggg gct   163
Arg Lys Met Val Ala Ala Ala Leu Ala Thr Ala Leu Leu Phe Gly Ala
                  10                  15                  20

gca cct gcg cac gct tcc gaa ttg gta gag ccc acc aca gtt gca gag   211
Ala Pro Ala His Ala Ser Glu Leu Val Glu Pro Thr Thr Val Ala Glu
             25                  30                  35

tca gtg gca ctc gat ccc aac aaa gca atc aat att ctc acc cca gat   259
Ser Val Ala Leu Asp Pro Asn Lys Ala Ile Asn Ile Leu Thr Pro Asp
         40                  45                  50

ctc tgg gaa gac att gag gca aaa cca ggc gat atc gtc cac atc ccc   307
Leu Trp Glu Asp Ile Glu Ala Lys Pro Gly Asp Ile Val His Ile Pro
     55                  60                  65

tac cag ggc acc cga aac tac gag gac ctc acc gta gaa gtc gcg aaa   355
Tyr Gln Gly Thr Arg Asn Tyr Glu Asp Leu Thr Val Glu Val Ala Lys
 70                  75                  80                  85

cct ttc gaa gat ttc caa atc ctc gtc gga ctc gac aac agc atc gtc   403
Pro Phe Glu Asp Phe Gln Ile Leu Val Gly Leu Asp Asn Ser Ile Val
                 90                  95                 100

atc gca gtg cca aag aac tta agt ggc gca gca tca gtc gcc cca gtt   451
Ile Ala Val Pro Lys Asn Leu Ser Gly Ala Ala Ser Val Ala Pro Val
```

```
            105                 110                 115

ttc act gtc tct gac aaa aac ggt gag atc gac tct ttc acc atc aaa   499
Phe Thr Val Ser Asp Lys Asn Gly Glu Ile Asp Ser Phe Thr Ile Lys
        120                 125                 130

gta agc gtc gag cca cgc cgc caa agc gac gaa gaa aag cgc tcc gca   547
Val Ser Val Glu Pro Arg Arg Gln Ser Asp Glu Glu Lys Arg Ser Ala
    135                 140                 145

cta ttt gat gtc atc tct gag ctt gcc tac cgc atg cct cat ctg cca   595
Leu Phe Asp Val Ile Ser Glu Leu Ala Tyr Arg Met Pro His Leu Pro
150                 155                 160                 165

ttc gtg tca gag ttg ctg aag tac tagaacagta acgagaaaac ccc         642
Phe Val Ser Glu Leu Leu Lys Tyr
                170
```

<210> 1966
<211> 173
<212> PRT
<213> Corynebacterium glutamicum

<400> 1966

```
Val Gln Gly Met Lys Arg Lys Met Val Ala Ala Ala Leu Ala Thr Ala
  1               5                  10                  15

Leu Leu Phe Gly Ala Ala Pro Ala His Ala Ser Glu Leu Val Glu Pro
             20                  25                  30

Thr Thr Val Ala Glu Ser Val Ala Leu Asp Pro Asn Lys Ala Ile Asn
         35                  40                  45

Ile Leu Thr Pro Asp Leu Trp Glu Asp Ile Glu Ala Lys Pro Gly Asp
     50                  55                  60

Ile Val His Ile Pro Tyr Gln Gly Thr Arg Asn Tyr Glu Asp Leu Thr
 65                  70                  75                  80

Val Glu Val Ala Lys Pro Phe Glu Asp Phe Gln Ile Leu Val Gly Leu
                 85                  90                  95

Asp Asn Ser Ile Val Ile Ala Val Pro Lys Asn Leu Ser Gly Ala Ala
            100                 105                 110

Ser Val Ala Pro Val Phe Thr Val Ser Asp Lys Asn Gly Glu Ile Asp
        115                 120                 125

Ser Phe Thr Ile Lys Val Ser Val Glu Pro Arg Arg Gln Ser Asp Glu
    130                 135                 140

Glu Lys Arg Ser Ala Leu Phe Asp Val Ile Ser Glu Leu Ala Tyr Arg
145                 150                 155                 160

Met Pro His Leu Pro Phe Val Ser Glu Leu Leu Lys Tyr
                165                 170
```

<210> 1967
<211> 846

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(823)
<223> RXA00887

<400> 1967
aagaaatccg caaccatcgc agcgacaacg cttccgtgca tcgcgaaggc ggagaagaat 60

ccggtttctt tgacaagctc cgaaacaagt tccgcaaata atg tca ctg cca gta 115
Met Ser Leu Pro Val
1 5

ttt atc tct gat tcc gca gcc gga cca ggc gaa acc att gag ctc gcc 163
Phe Ile Ser Asp Ser Ala Ala Gly Pro Gly Glu Thr Ile Glu Leu Ala
10 15 20

ggt ccg gaa ggc cgg cac gcc gtc acc gtc aaa cgg atc cag gta ggc 211
Gly Pro Glu Gly Arg His Ala Val Thr Val Lys Arg Ile Gln Val Gly
25 30 35

gaa aag att tcg ctt atc gac ggc cgg ggt aca gcg cgc acc tgc acg 259
Glu Lys Ile Ser Leu Ile Asp Gly Arg Gly Thr Ala Arg Thr Cys Thr
40 45 50

gtc acc gcc ttg cag ggc aaa gac cgc ctg aac gct gtg gtg gat ttg 307
Val Thr Ala Leu Gln Gly Lys Asp Arg Leu Asn Ala Val Val Asp Leu
55 60 65

gtc gag gaa atc ccc gca ccg aac cca cag gtc acc atc gtg cag gct 355
Val Glu Glu Ile Pro Ala Pro Asn Pro Gln Val Thr Ile Val Gln Ala
70 75 80 85

atc ccc aaa tca gag cgt tcc gag ctg acc atc gac ctg ctc acc caa 403
Ile Pro Lys Ser Glu Arg Ser Glu Leu Thr Ile Asp Leu Leu Thr Gln
90 95 100

gct ggc gcc gat cgg att gtt gcg tgg caa gca tcg cgc tgc gta gca 451
Ala Gly Ala Asp Arg Ile Val Ala Trp Gln Ala Ser Arg Cys Val Ala
105 110 115

aaa tgg ggc ggc aag gaa gca aaa tca ctg gct aaa tgg cag gtg gct 499
Lys Trp Gly Gly Lys Glu Ala Lys Ser Leu Ala Lys Trp Gln Val Ala
120 125 130

gcg gaa gca gcc gcc aag caa tcg cgg cgc gca acg atc cct gaa att 547
Ala Glu Ala Ala Ala Lys Gln Ser Arg Arg Ala Thr Ile Pro Glu Ile
135 140 145

ctt ggc gta gtg ggg gag gag ggc gtc gaa aag ctt atc gac gaa tcc 595
Leu Gly Val Val Gly Glu Glu Gly Val Glu Lys Leu Ile Asp Glu Ser
150 155 160 165

gac ctg gcc atc atc ctg cac gaa gaa gca acc gcc gcg atc cgt gaa 643
Asp Leu Ala Ile Ile Leu His Glu Glu Ala Thr Ala Ala Ile Arg Glu
170 175 180

ctg gaa ttt tcc ggc aac gtc gtg gtg atc atc gga ccc gaa ggt ggc 691
Leu Glu Phe Ser Gly Asn Val Val Val Ile Ile Gly Pro Glu Gly Gly

```
            185                 190                 195

gtc gcg cca tcg gaa att tca cgc ttc gtc gac gct ggc gca cac acc   739
Val Ala Pro Ser Glu Ile Ser Arg Phe Val Asp Ala Gly Ala His Thr
        200                 205                 210

gtg aaa cta ggc cct gag gtg ttg cgc act gcc tcc gca ggc atg gtg   787
Val Lys Leu Gly Pro Glu Val Leu Arg Thr Ala Ser Ala Gly Met Val
    215                 220                 225

gcg ctc gca gct atc ggc gtg ctg tct gac cgc tgg taacatttct        833
Ala Leu Ala Ala Ile Gly Val Leu Ser Asp Arg Trp
230                 235                 240

ctgacataac ctt                                                   846


<210> 1968
<211> 241
<212> PRT
<213> Corynebacterium glutamicum

<400> 1968
Met Ser Leu Pro Val Phe Ile Ser Asp Ser Ala Ala Gly Pro Gly Glu
  1               5                  10                  15

Thr Ile Glu Leu Ala Gly Pro Glu Gly Arg His Ala Val Thr Val Lys
             20                  25                  30

Arg Ile Gln Val Gly Glu Lys Ile Ser Leu Ile Asp Gly Arg Gly Thr
         35                  40                  45

Ala Arg Thr Cys Thr Val Thr Ala Leu Gln Gly Lys Asp Arg Leu Asn
     50                  55                  60

Ala Val Val Asp Leu Val Glu Glu Ile Pro Ala Pro Asn Pro Gln Val
 65                  70                  75                  80

Thr Ile Val Gln Ala Ile Pro Lys Ser Glu Arg Ser Glu Leu Thr Ile
                 85                  90                  95

Asp Leu Leu Thr Gln Ala Gly Ala Asp Arg Ile Val Ala Trp Gln Ala
            100                 105                 110

Ser Arg Cys Val Ala Lys Trp Gly Gly Lys Glu Ala Lys Ser Leu Ala
        115                 120                 125

Lys Trp Gln Val Ala Ala Glu Ala Ala Ala Lys Gln Ser Arg Arg Ala
    130                 135                 140

Thr Ile Pro Glu Ile Leu Gly Val Val Gly Glu Glu Gly Val Glu Lys
145                 150                 155                 160

Leu Ile Asp Glu Ser Asp Leu Ala Ile Ile Leu His Glu Glu Ala Thr
                165                 170                 175

Ala Ala Ile Arg Glu Leu Glu Phe Ser Gly Asn Val Val Val Ile Ile
            180                 185                 190

Gly Pro Glu Gly Gly Val Ala Pro Ser Glu Ile Ser Arg Phe Val Asp
        195                 200                 205
```

```
Ala Gly Ala His Thr Val Lys Leu Gly Pro Glu Val Leu Arg Thr Ala
    210                 215                 220

Ser Ala Gly Met Val Ala Leu Ala Ala Ile Gly Val Leu Ser Asp Arg
225                 230                 235                 240

Trp
```

<210> 1969
<211> 711
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(688)
<223> RXA00889

<400> 1969

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tggtccgcca ccaactggtt ggacacattg tggatgcata cgaagactat gaagaacgcg 60

aggcccgcga attgaaacgc aaacgccagg agacacggcc atg agc att gag gta   115
                                              Met Ser Ile Glu Val
                                                1               5

ttc aac gaa tca gga tac gac ggc gtc aat gaa gaa atg ctc att gat   163
Phe Asn Glu Ser Gly Tyr Asp Gly Val Asn Glu Glu Met Leu Ile Asp
                  10                  15                  20

gtc ctc tcc ttc gca ctc ggg gaa atg gac atc cac ccc gac gcc gaa   211
Val Leu Ser Phe Ala Leu Gly Glu Met Asp Ile His Pro Asp Ala Glu
              25                  30                  35

gca tcc atc cac atc gtc gac gtc gac acc atc gcc gat ctc cac gtg   259
Ala Ser Ile His Ile Val Asp Val Asp Thr Ile Ala Asp Leu His Val
          40                  45                  50

aaa tgg ctt gat ctt gaa ggc cca acc gac gtg atg agc ttc ccg atg   307
Lys Trp Leu Asp Leu Glu Gly Pro Thr Asp Val Met Ser Phe Pro Met
      55                  60                  65

gat gag ctc acc ccc ggc tac tcc cgc ccc gac ggc gcc acc ccc ggc   355
Asp Glu Leu Thr Pro Gly Tyr Ser Arg Pro Asp Gly Ala Thr Pro Gly
  70                  75                  80                  85

ccc gcc atg ctg ggc gac att gtg ctg tgc cca gag ttc gcg gca aag   403
Pro Ala Met Leu Gly Asp Ile Val Leu Cys Pro Glu Phe Ala Ala Lys
                  90                  95                 100

caa gcg acc aaa gca ggc cac gac tta gcc cac gag cta gct ttg ctg   451
Gln Ala Thr Lys Ala Gly His Asp Leu Ala His Glu Leu Ala Leu Leu
             105                 110                 115

acc gtg cac ggc agc ctg cac ctg ctt ggc tac gac cac gtc gat cca   499
Thr Val His Gly Ser Leu His Leu Leu Gly Tyr Asp His Val Asp Pro
         120                 125                 130

gcc gaa gag cgt gaa atg ttc gcc ctt caa aac gag ctg ctt gcc gat   547
```

```
Ala Glu Glu Arg Glu Met Phe Ala Leu Gln Asn Glu Leu Leu Ala Asp
    135                 140                 145

tgg tac gac aac gtc gaa gcc cgt ggc gtc acc tac cag cca aaa cca   595
Trp Tyr Asp Asn Val Glu Ala Arg Gly Val Thr Tyr Gln Pro Lys Pro
150                 155                 160                 165

tcc ggc gcc ggt gca ttc ccc acc gct gct gat cgt ctg gaa ttg gac   643
Ser Gly Ala Gly Ala Phe Pro Thr Ala Ala Asp Arg Leu Glu Leu Asp
                170                 175                 180

gaa aag atg gaa gcg gat gac tct ggc ttt gga ggc gtt gag tcc       688
Glu Lys Met Glu Ala Asp Asp Ser Gly Phe Gly Gly Val Glu Ser
            185                 190                 195

taggtggaat cctcagttat atg                                        711


<210> 1970
<211> 196
<212> PRT
<213> Corynebacterium glutamicum

<400> 1970
Met Ser Ile Glu Val Phe Asn Glu Ser Gly Tyr Asp Gly Val Asn Glu
  1               5                  10                  15

Glu Met Leu Ile Asp Val Leu Ser Phe Ala Leu Gly Glu Met Asp Ile
             20                  25                  30

His Pro Asp Ala Glu Ala Ser Ile His Ile Val Asp Val Asp Thr Ile
         35                  40                  45

Ala Asp Leu His Val Lys Trp Leu Asp Leu Glu Gly Pro Thr Asp Val
     50                  55                  60

Met Ser Phe Pro Met Asp Glu Leu Thr Pro Gly Tyr Ser Arg Pro Asp
 65                  70                  75                  80

Gly Ala Thr Pro Gly Pro Ala Met Leu Gly Asp Ile Val Leu Cys Pro
                 85                  90                  95

Glu Phe Ala Ala Lys Gln Ala Thr Lys Ala Gly His Asp Leu Ala His
            100                 105                 110

Glu Leu Ala Leu Leu Thr Val His Gly Ser Leu His Leu Leu Gly Tyr
        115                 120                 125

Asp His Val Asp Pro Ala Glu Glu Arg Glu Met Phe Ala Leu Gln Asn
    130                 135                 140

Glu Leu Leu Ala Asp Trp Tyr Asp Asn Val Glu Ala Arg Gly Val Thr
145                 150                 155                 160

Tyr Gln Pro Lys Pro Ser Gly Ala Gly Ala Phe Pro Thr Ala Ala Asp
                165                 170                 175

Arg Leu Glu Leu Asp Glu Lys Met Glu Ala Asp Asp Ser Gly Phe Gly
            180                 185                 190

Gly Val Glu Ser
```

195

<210> 1971
<211> 720
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(697)
<223> RXA00893

<400> 1971
acgccaacgc agagtgttta aagaaactgg cagttggaaa gctgcagttg atttagcctg 60

cgacgaactc aacgacctca aagcactgga ctaaatagct atg gtg gaa tcc caa 115
Met Val Glu Ser Gln
1 5

cac atc att ttc atc ccg gaa tcc caa caa aca ccc gac gag ttt acc 163
His Ile Ile Phe Ile Pro Glu Ser Gln Gln Thr Pro Asp Glu Phe Thr
10 15 20

gag gta gtc aac gag att ccc gcc gga atc aaa cca cgg atc gta ccg 211
Glu Val Val Asn Glu Ile Pro Ala Gly Ile Lys Pro Arg Ile Val Pro
25 30 35

tgg agc ggt agt gtt tcc gca ggt gtg cag gct gtg gaa tcc atc ctc 259
Trp Ser Gly Ser Val Ser Ala Gly Val Gln Ala Val Glu Ser Ile Leu
40 45 50

gac cgt gaa gaa atc cgg cgc gtc atc ctg gtc ggc gct gga acc gga 307
Asp Arg Glu Glu Ile Arg Arg Val Ile Leu Val Gly Ala Gly Thr Gly
55 60 65

gct gga gtg gcg ttg gaa att gcc aag aac caa ccc cgc cgc gtg gaa 355
Ala Gly Val Ala Leu Glu Ile Ala Lys Asn Gln Pro Arg Arg Val Glu
70 75 80 85

cgc ctc gtg ctg gat tca ccg ttg gtg acc ttt gat gag aaa caa ctc 403
Arg Leu Val Leu Asp Ser Pro Leu Val Thr Phe Asp Glu Lys Gln Leu
90 95 100

aaa ggc atg agc acc gca ctg aaa atg atg cca gga ttc ttc ttc cga 451
Lys Gly Met Ser Thr Ala Leu Lys Met Met Pro Gly Phe Phe Phe Arg
105 110 115

aag aag aac aag aaa gac ctc ctg cag cag gta gaa gaa gcc cgt act 499
Lys Lys Asn Lys Lys Asp Leu Leu Gln Gln Val Glu Glu Ala Arg Thr
120 125 130

gca gtt ccg atg gga ttt tcc gag att acc atg ccg acg tta atc atc 547
Ala Val Pro Met Gly Phe Ser Glu Ile Thr Met Pro Thr Leu Ile Ile
135 140 145

cga ggc tcc gct gcg aag gct gga att gat tct gac ttg gaa aaa caa 595
Arg Gly Ser Ala Ala Lys Ala Gly Ile Asp Ser Asp Leu Glu Lys Gln
150 155 160 165

atc ccg agc gct cgg gct acc acc att att ggt gcc aat tgg ctg act 643

```
Ile Pro Ser Ala Arg Ala Thr Thr Ile Ile Gly Ala Asn Trp Leu Thr
                170                 175                 180

tac aca acg cat gga cgc caa act ggt gct gcg att gcg gaa ttc ctc   691
Tyr Thr Thr His Gly Arg Gln Thr Gly Ala Ala Ile Ala Glu Phe Leu
            185                 190                 195

gcc caa tagaagggca cgcctaaacg cca                                 720
Ala Gln
```

<210> 1972
<211> 199
<212> PRT
<213> Corynebacterium glutamicum

<400> 1972

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Met Val Glu Ser Gln His Ile Ile Phe Ile Pro Glu Ser Gln Gln Thr
  1               5                  10                  15

Pro Asp Glu Phe Thr Glu Val Val Asn Glu Ile Pro Ala Gly Ile Lys
             20                  25                  30

Pro Arg Ile Val Pro Trp Ser Gly Ser Val Ser Ala Gly Val Gln Ala
         35                  40                  45

Val Glu Ser Ile Leu Asp Arg Glu Glu Ile Arg Arg Val Ile Leu Val
     50                  55                  60

Gly Ala Gly Thr Gly Ala Gly Val Ala Leu Glu Ile Ala Lys Asn Gln
 65                  70                  75                  80

Pro Arg Arg Val Glu Arg Leu Val Leu Asp Ser Pro Leu Val Thr Phe
                 85                  90                  95

Asp Glu Lys Gln Leu Lys Gly Met Ser Thr Ala Leu Lys Met Met Pro
            100                 105                 110

Gly Phe Phe Phe Arg Lys Lys Asn Lys Lys Asp Leu Leu Gln Gln Val
        115                 120                 125

Glu Glu Ala Arg Thr Ala Val Pro Met Gly Phe Ser Glu Ile Thr Met
    130                 135                 140

Pro Thr Leu Ile Ile Arg Gly Ser Ala Ala Lys Ala Gly Ile Asp Ser
145                 150                 155                 160

Asp Leu Glu Lys Gln Ile Pro Ser Ala Arg Ala Thr Thr Ile Ile Gly
                165                 170                 175

Ala Asn Trp Leu Thr Tyr Thr Thr His Gly Arg Gln Thr Gly Ala Ala
            180                 185                 190

Ile Ala Glu Phe Leu Ala Gln
        195
```

<210> 1973
<211> 714
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(691)
<223> RXA00895

<400> 1973
gtcgcgccgg aaagatagac taagccacat gacttcggac atgcagaatt ctccacagca 60

ctcggccacg ccttcagaag aaaaacaagg cggactgccc atg cgc ggt ttg gcc 115
Met Arg Gly Leu Ala
1 5

atg att ttg atc gcc gtg gcc gta ttg ctc gca gcg tgg gca ctg tgg 163
Met Ile Leu Ile Ala Val Ala Val Leu Leu Ala Ala Trp Ala Leu Trp
10 15 20

tca atg cag ggc aaa gac gac acc tcc acc acc agc gcc gga caa acc 211
Ser Met Gln Gly Lys Asp Asp Thr Ser Thr Thr Ser Ala Gly Gln Thr
25 30 35

cag tcc acg gaa acc aac gcg gga act att gct gaa tct tct ggc tct 259
Gln Ser Thr Glu Thr Asn Ala Gly Thr Ile Ala Glu Ser Ser Gly Ser
40 45 50

tcg gat tcc gag cag gca tca gca gaa cct gga acc tcc gaa gaa acc 307
Ser Asp Ser Glu Gln Ala Ser Ala Glu Pro Gly Thr Ser Glu Glu Thr
55 60 65

tct gct gag cag cca gct gca gat ggc gaa gcc gct aat gct gct ggg 355
Ser Ala Glu Gln Pro Ala Ala Asp Gly Glu Ala Ala Asn Ala Ala Gly
70 75 80 85

gcc gct gct gct ggt ggc gct agt tcg gct aac ggc aac tcc acc cca 403
Ala Ala Ala Ala Gly Gly Ala Ser Ser Ala Asn Gly Asn Ser Thr Pro
90 95 100

gtg aac act ctg tac gtg ctc aac aac tcc acc gtc cca caa ctt gca 451
Val Asn Thr Leu Tyr Val Leu Asn Asn Ser Thr Val Pro Gln Leu Ala
105 110 115

gca cga gtg gca gac agc cta agc ggt gac tac caa aag gta gag tcc 499
Ala Arg Val Ala Asp Ser Leu Ser Gly Asp Tyr Gln Lys Val Glu Ser
120 125 130

gga aac ctt cca gac acc atc att ccg cag aac act gtg tac ttc acc 547
Gly Asn Leu Pro Asp Thr Ile Ile Pro Gln Asn Thr Val Tyr Phe Thr
135 140 145

gct gga aac acc gaa gct gaa aag gct gca cgt gaa ctc gct gac cgc 595
Ala Gly Asn Thr Glu Ala Glu Lys Ala Ala Arg Glu Leu Ala Asp Arg
150 155 160 165

gtc agt ggc gta gca atg gaa cgc agc gat gca ctg cca acc gaa aca 643
Val Ser Gly Val Ala Met Glu Arg Ser Asp Ala Leu Pro Thr Glu Thr
170 175 180

gaa ggc aaa gat gcc ctc gtt ttg gtg ctg gtc caa gac gta gcg ctg 691
Glu Gly Lys Asp Ala Leu Val Leu Val Leu Val Gln Asp Val Ala Leu
185 190 195

tagttttctc ggatttgttg gaa 714

<210> 1974
<211> 197
<212> PRT
<213> Corynebacterium glutamicum

<400> 1974

```
Met Arg Gly Leu Ala Met Ile Leu Ile Ala Val Ala Val Leu Leu Ala
  1               5                  10                  15

Ala Trp Ala Leu Trp Ser Met Gln Gly Lys Asp Asp Thr Ser Thr Thr
             20                  25                  30

Ser Ala Gly Gln Thr Gln Ser Thr Glu Thr Asn Ala Gly Thr Ile Ala
         35                  40                  45

Glu Ser Ser Gly Ser Ser Asp Ser Glu Gln Ala Ser Ala Glu Pro Gly
     50                  55                  60

Thr Ser Glu Glu Thr Ser Ala Glu Gln Pro Ala Ala Asp Gly Glu Ala
 65                  70                  75                  80

Ala Asn Ala Ala Gly Ala Ala Ala Ala Gly Gly Ala Ser Ser Ala Asn
                 85                  90                  95

Gly Asn Ser Thr Pro Val Asn Thr Leu Tyr Val Leu Asn Asn Ser Thr
            100                 105                 110

Val Pro Gln Leu Ala Ala Arg Val Ala Asp Ser Leu Ser Gly Asp Tyr
        115                 120                 125

Gln Lys Val Glu Ser Gly Asn Leu Pro Asp Thr Ile Ile Pro Gln Asn
    130                 135                 140

Thr Val Tyr Phe Thr Ala Gly Asn Thr Glu Ala Glu Lys Ala Ala Arg
145                 150                 155                 160

Glu Leu Ala Asp Arg Val Ser Gly Val Ala Met Glu Arg Ser Asp Ala
                165                 170                 175

Leu Pro Thr Glu Thr Glu Gly Lys Asp Ala Leu Val Leu Val Leu Val
            180                 185                 190

Gln Asp Val Ala Leu
        195
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<210> 1975
<211> 815
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (37)..(792)
<223> RXA00904

<400> 1975

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aagcagtgca gtaccaggct ggaagtgtgg acaacaatg att aat acc atc cgc    54
                                        Met Ile Asn Thr Ile Arg
                                          1               5

tcc gaa tgg acc aaa ctt gtc acc acc aaa tcc ttc tgg tgg aca acc   102
Ser Glu Trp Thr Lys Leu Val Thr Thr Lys Ser Phe Trp Trp Thr Thr
            10                  15                  20

gca cta att ctg gtc ttc agc ctg gga tac gca gcg ctc acc gga tca   150
Ala Leu Ile Leu Val Phe Ser Leu Gly Tyr Ala Ala Leu Thr Gly Ser
        25                  30                  35

ctc gcc acc ggc gaa agc ttt gca tca ctg ttc ctt ctc gca ggc agc   198
Leu Ala Thr Gly Glu Ser Phe Ala Ser Leu Phe Leu Leu Ala Gly Ser
    40                  45                  50

aca gtc acc ggc ctt tac ctc ctt ggc ttc gtg gtg atc atg atc caa   246
Thr Val Thr Gly Leu Tyr Leu Leu Gly Phe Val Val Ile Met Ile Gln
55                  60                  65                  70

tcc atc atg atg ttc acc acc gaa ttt cga ttc ggc tac caa acc caa   294
Ser Ile Met Met Phe Thr Thr Glu Phe Arg Phe Gly Tyr Gln Thr Gln
                75                  80                  85

acc ttc ctc gcc aca cca aaa cgc tgg gtt gtc gcc gtt tcc aaa tgg   342
Thr Phe Leu Ala Thr Pro Lys Arg Trp Val Val Ala Val Ser Lys Trp
            90                  95                  100

ttg ctg tac ctc gtg ttc gcc gta gtg ttg acc ttc atc acc gtg att   390
Leu Leu Tyr Leu Val Phe Ala Val Val Leu Thr Phe Ile Thr Val Ile
        105                 110                 115

ctg tgc ttc tat cta gcc aaa gcc ctg gca tca gac act gca agc tcc   438
Leu Cys Phe Tyr Leu Ala Lys Ala Leu Ala Ser Asp Thr Ala Ser Ser
    120                 125                 130

acc ctg gtg gtg tgg gaa gat acg caa gca cga cga atc atg tgg caa   486
Thr Leu Val Val Trp Glu Asp Thr Gln Ala Arg Arg Ile Met Trp Gln
135                 140                 145                 150

tac cca ctg gca gca gca cta ttg gta act ttc tgt tcc gga att gcg   534
Tyr Pro Leu Ala Ala Ala Leu Leu Val Thr Phe Cys Ser Gly Ile Ala
                155                 160                 165

ctc ctg ctg cgt caa act gca gga gca gtg gca ctg gtg ctt atg tgg   582
Leu Leu Leu Arg Gln Thr Ala Gly Ala Val Ala Leu Val Leu Met Trp
            170                 175                 180

cac ttc gct atc gaa aac ctc ctg tct ttc ttg cca cgc atc ggc gaa   630
His Phe Ala Ile Glu Asn Leu Leu Ser Phe Leu Pro Arg Ile Gly Glu
        185                 190                 195

tac gtc ggc aag tat ggt ccc ttc acc aac ctc tac gca ttc atc acc   678
Tyr Val Gly Lys Tyr Gly Pro Phe Thr Asn Leu Tyr Ala Phe Ile Thr
    200                 205                 210

gac tat caa tca att gat cca gga tgg tcc acc acc atg gga gcg gtg   726
Asp Tyr Gln Ser Ile Asp Pro Gly Trp Ser Thr Thr Met Gly Ala Val
215                 220                 225                 230

tac ttc gga gcg tgg gca ttc gtg ctg ttc gca ctc gga atc gtc gtc   774
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```
Tyr Phe Gly Ala Trp Ala Phe Val Leu Phe Ala Leu Gly Ile Val Val
                235                 240                 245

cta gaa aag aaa gac gcc taaaatgccc tctaaaatat cgc                  815
Leu Glu Lys Lys Asp Ala
            250
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<210> 1976
<211> 252
<212> PRT
<213> Corynebacterium glutamicum

<400> 1976

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Met Ile Asn Thr Ile Arg Ser Glu Trp Thr Lys Leu Val Thr Thr Lys
  1               5                  10                  15

Ser Phe Trp Trp Thr Thr Ala Leu Ile Leu Val Phe Ser Leu Gly Tyr
             20                  25                  30

Ala Ala Leu Thr Gly Ser Leu Ala Thr Gly Glu Ser Phe Ala Ser Leu
         35                  40                  45

Phe Leu Leu Ala Gly Ser Thr Val Thr Gly Leu Tyr Leu Leu Gly Phe
     50                  55                  60

Val Val Ile Met Ile Gln Ser Ile Met Met Phe Thr Thr Glu Phe Arg
 65                  70                  75                  80

Phe Gly Tyr Gln Thr Gln Thr Phe Leu Ala Thr Pro Lys Arg Trp Val
                 85                  90                  95

Val Ala Val Ser Lys Trp Leu Leu Tyr Leu Val Phe Ala Val Val Leu
            100                 105                 110

Thr Phe Ile Thr Val Ile Leu Cys Phe Tyr Leu Ala Lys Ala Leu Ala
        115                 120                 125

Ser Asp Thr Ala Ser Ser Thr Leu Val Val Trp Glu Asp Thr Gln Ala
    130                 135                 140

Arg Arg Ile Met Trp Gln Tyr Pro Leu Ala Ala Ala Leu Leu Val Thr
145                 150                 155                 160

Phe Cys Ser Gly Ile Ala Leu Leu Leu Arg Gln Thr Ala Gly Ala Val
                165                 170                 175

Ala Leu Val Leu Met Trp His Phe Ala Ile Glu Asn Leu Leu Ser Phe
            180                 185                 190

Leu Pro Arg Ile Gly Glu Tyr Val Gly Lys Tyr Gly Pro Phe Thr Asn
        195                 200                 205

Leu Tyr Ala Phe Ile Thr Asp Tyr Gln Ser Ile Asp Pro Gly Trp Ser
    210                 215                 220

Thr Thr Met Gly Ala Val Tyr Phe Gly Ala Trp Ala Phe Val Leu Phe
225                 230                 235                 240

Ala Leu Gly Ile Val Val Leu Glu Lys Lys Asp Ala
                245                 250
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<210> 1977
<211> 681
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(658)
<223> RXA00908

<400> 1977
tcggtcctcc acctaacagg atccttcaca cccttctttt caatatctag aaaagaccga 60

tccgcccaac atctttttca tgacgcaaag gaccgtgtca atg tct ctc tac acc 115
Met Ser Leu Tyr Thr
1 5

cgt act caa aat acc cgt cac tcc acc atc atc gag ttc cgc cgc gag 163
Arg Thr Gln Asn Thr Arg His Ser Thr Ile Ile Glu Phe Arg Arg Glu
10 15 20

cag act cgt aat cac acg atg gag cca atc cag tcc gag cca cgg atc 211
Gln Thr Arg Asn His Thr Met Glu Pro Ile Gln Ser Glu Pro Arg Ile
25 30 35

tac gct gac gat cct ttc cgt gca cgc ttc gga cac caa ctc ccc cgc 259
Tyr Ala Asp Asp Pro Phe Arg Ala Arg Phe Gly His Gln Leu Pro Arg
40 45 50

gga ctt cgc gaa gaa gca cgc ggc atg gaa tgg cgc acc ttc acc aac 307
Gly Leu Arg Glu Glu Ala Arg Gly Met Glu Trp Arg Thr Phe Thr Asn
55 60 65

acc tac gca cca acc ggc aac ctg cgc atc agc aac ctc gag tcc gag 355
Thr Tyr Ala Pro Thr Gly Asn Leu Arg Ile Ser Asn Leu Glu Ser Glu
70 75 80 85

gca cgc cgc gga gga atg ttc cac ttc aac gca acc ctg atc aac aac 403
Ala Arg Arg Gly Gly Met Phe His Phe Asn Ala Thr Leu Ile Asn Asn
90 95 100

tgc cag ggc gag cgc acc acc acc gac gct cac atc atg gca acc ggc 451
Cys Gln Gly Glu Arg Thr Thr Thr Asp Ala His Ile Met Ala Thr Gly
105 110 115

cca gtt tcc gca tgc acc aac ttg ctt gcc gac gcc ggc cgt cgc gtt 499
Pro Val Ser Ala Cys Thr Asn Leu Leu Ala Asp Ala Gly Arg Arg Val
120 125 130

gaa atc ctc gaa ttc cac caa ttc gac atc ttt gaa gca acc gtc acc 547
Glu Ile Leu Glu Phe His Gln Phe Asp Ile Phe Glu Ala Thr Val Thr
135 140 145

ttc atc tac acc tgc aac aac gtt tcc cgc acc tgg gca atg ggc ttc 595
Phe Ile Tyr Thr Cys Asn Asn Val Ser Arg Thr Trp Ala Met Gly Phe
150 155 160 165

ggc ggt acc cct gag cag tcc gct gct tcc gca atg agc tcc gca gct 643
Gly Gly Thr Pro Glu Gln Ser Ala Ala Ser Ala Met Ser Ser Ala Ala

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                170                 175                 180

cac ttg ctc tac gga taggttgcaa taacattcat tcc                    681
His Leu Leu Tyr Gly
            185


<210> 1978
<211> 186
<212> PRT
<213> Corynebacterium glutamicum

<400> 1978
Met Ser Leu Tyr Thr Arg Thr Gln Asn Thr Arg His Ser Thr Ile Ile
  1               5                  10                  15

Glu Phe Arg Arg Glu Gln Thr Arg Asn His Thr Met Glu Pro Ile Gln
             20                  25                  30

Ser Glu Pro Arg Ile Tyr Ala Asp Asp Pro Phe Arg Ala Arg Phe Gly
         35                  40                  45

His Gln Leu Pro Arg Gly Leu Arg Glu Glu Ala Arg Gly Met Glu Trp
     50                  55                  60

Arg Thr Phe Thr Asn Thr Tyr Ala Pro Thr Gly Asn Leu Arg Ile Ser
 65                  70                  75                  80

Asn Leu Glu Ser Glu Ala Arg Arg Gly Gly Met Phe His Phe Asn Ala
                 85                  90                  95

Thr Leu Ile Asn Asn Cys Gln Gly Glu Arg Thr Thr Thr Asp Ala His
            100                 105                 110

Ile Met Ala Thr Gly Pro Val Ser Ala Cys Thr Asn Leu Leu Ala Asp
        115                 120                 125

Ala Gly Arg Arg Val Glu Ile Leu Glu Phe His Gln Phe Asp Ile Phe
    130                 135                 140

Glu Ala Thr Val Thr Phe Ile Tyr Thr Cys Asn Asn Val Ser Arg Thr
145                 150                 155                 160

Trp Ala Met Gly Phe Gly Gly Thr Pro Glu Gln Ser Ala Ala Ser Ala
                165                 170                 175

Met Ser Ser Ala Ala His Leu Leu Tyr Gly
            180                 185


<210> 1979
<211> 3714
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(3691)
<223> RXA00916

<400> 1979
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agcggatcca acgacacaaa tggtggattt ggttccagcg gcggcttcgg cgcgcgataa 60

cctgtaactt gcgattaaaa actaacttaa ggatttacac atg aag aaa gtt ctc   115
                                            Met Lys Lys Val Leu
                                              1               5

gtt gtc ggc tgt ggt ggt tca ggt gcc aaa acg ctc gct tat atg atg   163
Val Val Gly Cys Gly Gly Ser Gly Ala Lys Thr Leu Ala Tyr Met Met
                 10                  15                  20

gac cag ctc aag acc acc ctg gcg gat agt ctt ccc gag cgt tac cca   211
Asp Gln Leu Lys Thr Thr Leu Ala Asp Ser Leu Pro Glu Arg Tyr Pro
             25                  30                  35

aat cca aag gaa gca aaa ctt cct ggt gcg tgg cag ttc gtg tcg gtg   259
Asn Pro Lys Glu Ala Lys Leu Pro Gly Ala Trp Gln Phe Val Ser Val
         40                  45                  50

gat gtt ccg acc tcc cca gaa agc ccc ggc ccg aac ctt ccg aat gtt   307
Asp Val Pro Thr Ser Pro Glu Ser Pro Gly Pro Asn Leu Pro Asn Val
     55                  60                  65

cca gaa gcc ggt gga cgt tat att tcc tgt ggt tcc tcg gat cgc tat   355
Pro Glu Ala Gly Gly Arg Tyr Ile Ser Cys Gly Ser Ser Asp Arg Tyr
 70                  75                  80                  85

gcc acc gtt gat act gcg gtg tcc aac cag ctc tcc tcc agg ggc gcg   403
Ala Thr Val Asp Thr Ala Val Ser Asn Gln Leu Ser Ser Arg Gly Ala
                 90                  95                 100

ttg ggt ggc gtt tct tca tgg gcg ctt cga aac cct gat tct gaa acc   451
Leu Gly Gly Val Ser Ser Trp Ala Leu Arg Asn Pro Asp Ser Glu Thr
            105                 110                 115

acc cca att agt aaa ggt gcg ggc cag tac cgc tcc att ggc cgt atg   499
Thr Pro Ile Ser Lys Gly Ala Gly Gln Tyr Arg Ser Ile Gly Arg Met
        120                 125                 130

ttg atc ctg agc cga ctt cag gaa att cag gct gaa tta cgt aaa tca   547
Leu Ile Leu Ser Arg Leu Gln Glu Ile Gln Ala Glu Leu Arg Lys Ser
    135                 140                 145

tgg gat gtg ttg ttc agc ggt gag act gaa cgt gag ctc gct gac ctt   595
Trp Asp Val Leu Phe Ser Gly Glu Thr Glu Arg Glu Leu Ala Asp Leu
150                 155                 160                 165

cgt tct gca ctg tat ggc acg tct gtt tcc agt ggt gaa acc tct aaa   643
Arg Ser Ala Leu Tyr Gly Thr Ser Val Ser Ser Gly Glu Thr Ser Lys
                170                 175                 180

gag cag cca att atc ttc ggt gtc tcc tcc atg gct ggt ggc gcc ggt   691
Glu Gln Pro Ile Ile Phe Gly Val Ser Ser Met Ala Gly Gly Ala Gly
            185                 190                 195

gct tcg atg gct cta gat atc tgc cgc ctg ctc acc ggt ctt gaa ggc   739
Ala Ser Met Ala Leu Asp Ile Cys Arg Leu Leu Thr Gly Leu Glu Gly
        200                 205                 210

aac gca gtg ggt ctg agc tca ctg ttt atg gtg acc ccg gat atc ttc   787
Asn Ala Val Gly Leu Ser Ser Leu Phe Met Val Thr Pro Asp Ile Phe
    215                 220                 225
```

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tcc cag ctt tcc cca gac cag gtt gcc gga act aac cca aac gcg ctg   835
Ser Gln Leu Ser Pro Asp Gln Val Ala Gly Thr Asn Pro Asn Ala Leu
230                 235                 240                 245

gcc atg ttt gcc gag ctc gca gca gca cag atg ggt gca gct tcc gaa   883
Ala Met Phe Ala Glu Leu Ala Ala Ala Gln Met Gly Ala Ala Ser Glu
                250                 255                 260

gaa gat gcc cga ctg ttt aac gct ttg ggt gtt tct gtt ggc gat gac   931
Glu Asp Ala Arg Leu Phe Asn Ala Leu Gly Val Ser Val Gly Asp Asp
            265                 270                 275

tcc atc cca gtt gga cgt atc ttc cca gtg ggt att cgc tcc ggt gaa   979
Ser Ile Pro Val Gly Arg Ile Phe Pro Val Gly Ile Arg Ser Gly Glu
        280                 285                 290

aac ggc gct ctg ctt ggt gat ggc aag cca gat acc gtc tac cgc gca   1027
Asn Gly Ala Leu Leu Gly Asp Gly Lys Pro Asp Thr Val Tyr Arg Ala
    295                 300                 305

ctc ggc cgt ggc ctt gca gct ctg atg gct gat gaa gtg tcc atg gac   1075
Leu Gly Arg Gly Leu Ala Ala Leu Met Ala Asp Glu Val Ser Met Asp
310                 315                 320                 325

aac ttc gag caa ttc acc ctc ggc aac cgt ggt ggc gga agt gcc gat   1123
Asn Phe Glu Gln Phe Thr Leu Gly Asn Arg Gly Gly Gly Ser Ala Asp
                330                 335                 340

cag agc aag tac gca tgg ggt gca cag gaa gct aag aac att ccg tgg   1171
Gln Ser Lys Tyr Ala Trp Gly Ala Gln Glu Ala Lys Asn Ile Pro Trp
            345                 350                 355

ggc agc tac ggc tac tca caa cta tcc atg ggt cgt gat cgc tac gca   1219
Gly Ser Tyr Gly Tyr Ser Gln Leu Ser Met Gly Arg Asp Arg Tyr Ala
        360                 365                 370

gaa tac gcc gcc cag cga ctg gca cgc tct gcc gtg gat cgt ctg ctc   1267
Glu Tyr Ala Ala Gln Arg Leu Ala Arg Ser Ala Val Asp Arg Leu Leu
    375                 380                 385

aag gga cac ttt gat cca agc aat gat gcg gcc tct gac cag cag ctt   1315
Lys Gly His Phe Asp Pro Ser Asn Asp Ala Ala Ser Asp Gln Gln Leu
390                 395                 400                 405

caa aag cga ctc gag aac aac cgt cca tcg ctg atg ggc aac ctc agc   1363
Gln Lys Arg Leu Glu Asn Asn Arg Pro Ser Leu Met Gly Asn Leu Ser
                410                 415                 420

gac gtt ttg ccc gtc aac gcg ccg gca ggg gac tgg att ttc cat agt   1411
Asp Val Leu Pro Val Asn Ala Pro Ala Gly Asp Trp Ile Phe His Ser
            425                 430                 435

ttc aac cag atg att gaa aac tgg acc cag cgt atg aaa gca atc atc   1459
Phe Asn Gln Met Ile Glu Asn Trp Thr Gln Arg Met Lys Ala Ile Ile
        440                 445                 450

aag agc caa att cct gca gct aat ggc cag cgc gga agt gaa tgg ctc   1507
Lys Ser Gln Ile Pro Ala Ala Asn Gly Gln Arg Gly Ser Glu Trp Leu
    455                 460                 465
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ggg gat gtc cag cgt gct ttc caa tca tcc agc cag atg att gat aat   1555
Gly Asp Val Gln Arg Ala Phe Gln Ser Ser Ser Gln Met Ile Asp Asn
470                 475                 480                 485

gac tcc cgc cat gag ctc tac atg ggt gtc gcc gac tgg gcc agt gct   1603
Asp Ser Arg His Glu Leu Tyr Met Gly Val Ala Asp Trp Ala Ser Ala
                490                 495                 500

gat gtg ttg cag cgc cga gta gtc gag ttg ctt cgt gat gag atc gca   1651
Asp Val Leu Gln Arg Arg Val Val Glu Leu Leu Arg Asp Glu Ile Ala
            505                 510                 515

aaa ctg ggc gtt cct tac ggc gtc agc gtg atc gaa tct ctc agc gcc   1699
Lys Leu Gly Val Pro Tyr Gly Val Ser Val Ile Glu Ser Leu Ser Ala
        520                 525                 530

aca atc caa aac caa ctc atc gga cag ctt tct gat ctg gca aac aac   1747
Thr Ile Gln Asn Gln Leu Ile Gly Gln Leu Ser Asp Leu Ala Asn Asn
    535                 540                 545

cgt gca cct gag gct gtt caa cta gac gat gtc agc cgc agt gaa ctg   1795
Arg Ala Pro Glu Ala Val Gln Leu Asp Asp Val Ser Arg Ser Glu Leu
550                 555                 560                 565

gac aac agc aag ggc agg atc gac gat tct gac agc tac atc cag gaa   1843
Asp Asn Ser Lys Gly Arg Ile Asp Asp Ser Asp Ser Tyr Ile Gln Glu
                570                 575                 580

atc gtg tca cga tcc act ggt caa cta cac acc cgc gca gtg caa tac   1891
Ile Val Ser Arg Ser Thr Gly Gln Leu His Thr Arg Ala Val Gln Tyr
            585                 590                 595

att gcg gac cac atg gct tcg gtt ctg gac gat ttc ctc aaa aat ttc   1939
Ile Ala Asp His Met Ala Ser Val Leu Asp Asp Phe Leu Lys Asn Phe
        600                 605                 610

atc tac cca ctt cag cgc acc atc caa cgt gag cac cac tcc cta gaa   1987
Ile Tyr Pro Leu Gln Arg Thr Ile Gln Arg Glu His His Ser Leu Glu
    615                 620                 625

aag gac tac cag ctc acc aac gat gtg aac ctg gga atc tcc cag ctg   2035
Lys Asp Tyr Gln Leu Thr Asn Asp Val Asn Leu Gly Ile Ser Gln Leu
630                 635                 640                 645

aaa acc aac gtt cca gca ctg tgg cca gat gaa tct caa act acc gtc   2083
Lys Thr Asn Val Pro Ala Leu Trp Pro Asp Glu Ser Gln Thr Thr Val
                650                 655                 660

ccg tca cgt ttc agt cag gca gcc aac gaa gtc ttc ctg acc gat gtc   2131
Pro Ser Arg Phe Ser Gln Ala Ala Asn Glu Val Phe Leu Thr Asp Val
            665                 670                 675

gcc tcc ttc ccg gag cag ttc caa gca cac gtc cgc tcg tcc acc gat   2179
Ala Ser Phe Pro Glu Gln Phe Gln Ala His Val Arg Ser Ser Thr Asp
        680                 685                 690

gac atc aac gaa caa aac gat tac tcg agc gcc ctg caa gag gcc tca   2227
Asp Ile Asn Glu Gln Asn Asp Tyr Ser Ser Ala Leu Gln Glu Ala Ser
    695                 700                 705

act cga gta gtc agc ggt gtg tgg gaa tcc aag tcc ggc tct gaa aaa   2275
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Thr Arg Val Val Ser Gly Val Trp Glu Ser Lys Ser Gly Ser Glu Lys
710                 715                 720                 725

gca cca cgc gat ctc atc cgc ctc atc gac gta tgg gtt gcc cgt gac   2323
Ala Pro Arg Asp Leu Ile Arg Leu Ile Asp Val Trp Val Ala Arg Asp
                730                 735                 740

ctg acc agg gat ccg tcc ggt tcg gga agc ctc cgc gac cct aag caa   2371
Leu Thr Arg Asp Pro Ser Gly Ser Gly Ser Leu Arg Asp Pro Lys Gln
            745                 750                 755

gca cgc ttt gag ctg aag att gat acc ggc gaa gta ctc gag cgc tcc   2419
Ala Arg Phe Glu Leu Lys Ile Asp Thr Gly Glu Val Leu Glu Arg Ser
        760                 765                 770

cgc cag tac atc cgc cgc cct ggt ttc tcc ttc cag cag ttc atc gcc   2467
Arg Gln Tyr Ile Arg Arg Pro Gly Phe Ser Phe Gln Gln Phe Ile Ala
    775                 780                 785

agc tca ctg cgt gaa ttc atc acc gcg ccg ggc ttg gca gac cac gag   2515
Ser Ser Leu Arg Glu Phe Ile Thr Ala Pro Gly Leu Ala Asp His Glu
790                 795                 800                 805

cgt cgc gcg cgc cgt cag cag gtg ctg agc aag ttc agt gag gca atg   2563
Arg Arg Ala Arg Arg Gln Gln Val Leu Ser Lys Phe Ser Glu Ala Met
                810                 815                 820

acc tac gcg ctt cca ttg gct cag atc aac cct caa ctg gtt cgt gcg   2611
Thr Tyr Ala Leu Pro Leu Ala Gln Ile Asn Pro Gln Leu Val Arg Ala
            825                 830                 835

ctt tac ggc gat gaa gtc cgc tac aac ttc aac ttc tct cgc atc cca   2659
Leu Tyr Gly Asp Glu Val Arg Tyr Asn Phe Asn Phe Ser Arg Ile Pro
        840                 845                 850

ttt gcc ggc gat gag ctt gga tcc agc ctg gaa cag gca gtt cgt gat   2707
Phe Ala Gly Asp Glu Leu Gly Ser Ser Leu Glu Gln Ala Val Arg Asp
    855                 860                 865

tac ccg aac cac cga cca gca gat att tcc aag cca ctg ggc aag gct   2755
Tyr Pro Asn His Arg Pro Ala Asp Ile Ser Lys Pro Leu Gly Lys Ala
870                 875                 880                 885

ttg gtc tcc caa ggt gaa gag cgt tcc att gat atc ttc ggc tct tac   2803
Leu Val Ser Gln Gly Glu Glu Arg Ser Ile Asp Ile Phe Gly Ser Tyr
                890                 895                 900

ccc aac tac gcg ccg atc gtg ttt gac tcc ctg ctg cct cca atc gag   2851
Pro Asn Tyr Ala Pro Ile Val Phe Asp Ser Leu Leu Pro Pro Ile Glu
            905                 910                 915

aag cag tgg cgt cag atc acc ggc gat cgc acg gaa ttc tgg cat ggc   2899
Lys Gln Trp Arg Gln Ile Thr Gly Asp Arg Thr Glu Phe Trp His Gly
        920                 925                 930

cgc cgt act cgt cct ttg act gct gca ctt cca atg aca gac cta gag   2947
Arg Arg Thr Arg Pro Leu Thr Ala Ala Leu Pro Met Thr Asp Leu Glu
    935                 940                 945

cgc aac gcc atg gtc aag ggt tgg tac atc ggt cgt ctg gtc gga cga   2995
Arg Asn Ala Met Val Lys Gly Trp Tyr Ile Gly Arg Leu Val Gly Arg
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950                 955                 960                 965

gta ttc ttc ccc gca act cta gac act gcg gat acc act cca gtg cag   3043
Val Phe Phe Pro Ala Thr Leu Asp Thr Ala Asp Thr Thr Pro Val Gln
                970                 975                 980

atc tac gat gag aag tct gat tcg tgg atc aac ttc tcc acc cca atg   3091
Ile Tyr Asp Glu Lys Ser Asp Ser Trp Ile Asn Phe Ser Thr Pro Met
            985                 990                 995

ctc acc cca gtg tcc cgt ttc cgt gga agc ctc gat tgg ctg cca aac   3139
Leu Thr Pro Val Ser Arg Phe Arg Gly Ser Leu Asp Trp Leu Pro Asn
        1000                1005                1010

ctt ctg gaa tca gca tca ttg gca tgg gca cgg gca ggc gag cgt cct   3187
Leu Leu Glu Ser Ala Ser Leu Ala Trp Ala Arg Ala Gly Glu Arg Pro
    1015                1020                1025

gtc ttt gaa tcc gtc gag cct tac atc cag ctc cgc caa ctg tgg gat   3235
Val Phe Glu Ser Val Glu Pro Tyr Ile Gln Leu Arg Gln Leu Trp Asp
1030                1035                1040                1045

gat gct gcg agc cca tcc ttg cca gga cgc acc acc cgc ggt gag aag   3283
Asp Ala Ala Ser Pro Ser Leu Pro Gly Arg Thr Thr Arg Gly Glu Lys
                1050                1055                1060

ctg ctg cac gat tgg ctt ttc gac ggc aac cgc atg gct gga aac gtc   3331
Leu Leu His Asp Trp Leu Phe Asp Gly Asn Arg Met Ala Gly Asn Val
            1065                1070                1075

ctc cag atc cca gga acc gaa gct ggt gtc acc cca gct gca cgt ttt   3379
Leu Gln Ile Pro Gly Thr Glu Ala Gly Val Thr Pro Ala Ala Arg Phe
        1080                1085                1090

gag gct gcg aag aac ttc ctg cag cgc cag aac gag atc tcg caa aat   3427
Glu Ala Ala Lys Asn Phe Leu Gln Arg Gln Asn Glu Ile Ser Gln Asn
    1095                1100                1105

tac gtc cca agc gac aag ctt cgc caa ggc cgt ctg ttc acc acc gct   3475
Tyr Val Pro Ser Asp Lys Leu Arg Gln Gly Arg Leu Phe Thr Thr Ala
1110                1115                1120                1125

gat cgt cca ttt ggc gac gtc aag gat cgt gaa cta gca gca cag att   3523
Asp Arg Pro Phe Gly Asp Val Lys Asp Arg Glu Leu Ala Ala Gln Ile
                1130                1135                1140

cca gtg ttt gct gac ctt gca gcc gat gtt ttt gat ggc acc caa gaa   3571
Pro Val Phe Ala Asp Leu Ala Ala Asp Val Phe Asp Gly Thr Gln Glu
            1145                1150                1155

atc atc gac atc ctg gaa aag tgc ttg gct gca ggt cca cca tca gca   3619
Ile Ile Asp Ile Leu Glu Lys Cys Leu Ala Ala Gly Pro Pro Ser Ala
        1160                1165                1170

cag gtc ttt gac atg aac gta gct cgc cgc gac gtt tct tca gga cct   3667
Gln Val Phe Asp Met Asn Val Ala Arg Arg Asp Val Ser Ser Gly Pro
    1175                1180                1185

tct cta cct ggt gag ggt gag ttc taaatgtccg ccgcctattc gca         3714
Ser Leu Pro Gly Glu Gly Glu Phe
1190                1195
```

<210> 1980
<211> 1197
<212> PRT
<213> Corynebacterium glutamicum

<400> 1980

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Met Lys Lys Val Leu Val Val Gly Cys Gly Gly Ser Gly Ala Lys Thr
  1               5                  10                  15

Leu Ala Tyr Met Met Asp Gln Leu Lys Thr Thr Leu Ala Asp Ser Leu
             20                  25                  30

Pro Glu Arg Tyr Pro Asn Pro Lys Glu Ala Lys Leu Pro Gly Ala Trp
         35                  40                  45

Gln Phe Val Ser Val Asp Val Pro Thr Ser Pro Glu Ser Pro Gly Pro
     50                  55                  60

Asn Leu Pro Asn Val Pro Glu Ala Gly Gly Arg Tyr Ile Ser Cys Gly
 65                  70                  75                  80

Ser Ser Asp Arg Tyr Ala Thr Val Asp Thr Ala Val Ser Asn Gln Leu
                 85                  90                  95

Ser Ser Arg Gly Ala Leu Gly Gly Val Ser Ser Trp Ala Leu Arg Asn
            100                 105                 110

Pro Asp Ser Glu Thr Thr Pro Ile Ser Lys Gly Ala Gly Gln Tyr Arg
        115                 120                 125

Ser Ile Gly Arg Met Leu Ile Leu Ser Arg Leu Gln Glu Ile Gln Ala
    130                 135                 140

Glu Leu Arg Lys Ser Trp Asp Val Leu Phe Ser Gly Glu Thr Glu Arg
145                 150                 155                 160

Glu Leu Ala Asp Leu Arg Ser Ala Leu Tyr Gly Thr Ser Val Ser Ser
                165                 170                 175

Gly Glu Thr Ser Lys Glu Gln Pro Ile Ile Phe Gly Val Ser Ser Met
            180                 185                 190

Ala Gly Gly Ala Gly Ala Ser Met Ala Leu Asp Ile Cys Arg Leu Leu
        195                 200                 205

Thr Gly Leu Glu Gly Asn Ala Val Gly Leu Ser Ser Leu Phe Met Val
    210                 215                 220

Thr Pro Asp Ile Phe Ser Gln Leu Ser Pro Asp Gln Val Ala Gly Thr
225                 230                 235                 240

Asn Pro Asn Ala Leu Ala Met Phe Ala Glu Leu Ala Ala Ala Gln Met
                245                 250                 255

Gly Ala Ala Ser Glu Glu Asp Ala Arg Leu Phe Asn Ala Leu Gly Val
            260                 265                 270

Ser Val Gly Asp Asp Ser Ile Pro Val Gly Arg Ile Phe Pro Val Gly
        275                 280                 285
```

```
Ile Arg Ser Gly Glu Asn Gly Ala Leu Leu Gly Asp Gly Lys Pro Asp
    290                 295                 300

Thr Val Tyr Arg Ala Leu Gly Arg Gly Leu Ala Ala Leu Met Ala Asp
305                 310                 315                 320

Glu Val Ser Met Asp Asn Phe Glu Gln Phe Thr Leu Gly Asn Arg Gly
                325                 330                 335

Gly Gly Ser Ala Asp Gln Ser Lys Tyr Ala Trp Gly Ala Gln Glu Ala
            340                 345                 350

Lys Asn Ile Pro Trp Gly Ser Tyr Gly Tyr Ser Gln Leu Ser Met Gly
        355                 360                 365

Arg Asp Arg Tyr Ala Glu Tyr Ala Ala Gln Arg Leu Ala Arg Ser Ala
    370                 375                 380

Val Asp Arg Leu Leu Lys Gly His Phe Asp Pro Ser Asn Asp Ala Ala
385                 390                 395                 400

Ser Asp Gln Gln Leu Gln Lys Arg Leu Glu Asn Asn Arg Pro Ser Leu
                405                 410                 415

Met Gly Asn Leu Ser Asp Val Leu Pro Val Asn Ala Pro Ala Gly Asp
            420                 425                 430

Trp Ile Phe His Ser Phe Asn Gln Met Ile Glu Asn Trp Thr Gln Arg
        435                 440                 445

Met Lys Ala Ile Ile Lys Ser Gln Ile Pro Ala Ala Asn Gly Gln Arg
    450                 455                 460

Gly Ser Glu Trp Leu Gly Asp Val Gln Arg Ala Phe Gln Ser Ser Ser
465                 470                 475                 480

Gln Met Ile Asp Asn Asp Ser Arg His Glu Leu Tyr Met Gly Val Ala
                485                 490                 495

Asp Trp Ala Ser Ala Asp Val Leu Gln Arg Arg Val Val Glu Leu Leu
            500                 505                 510

Arg Asp Glu Ile Ala Lys Leu Gly Val Pro Tyr Gly Val Ser Val Ile
        515                 520                 525

Glu Ser Leu Ser Ala Thr Ile Gln Asn Gln Leu Ile Gly Gln Leu Ser
    530                 535                 540

Asp Leu Ala Asn Asn Arg Ala Pro Glu Ala Val Gln Leu Asp Asp Val
545                 550                 555                 560

Ser Arg Ser Glu Leu Asp Asn Ser Lys Gly Arg Ile Asp Asp Ser Asp
                565                 570                 575

Ser Tyr Ile Gln Glu Ile Val Ser Arg Ser Thr Gly Gln Leu His Thr
            580                 585                 590

Arg Ala Val Gln Tyr Ile Ala Asp His Met Ala Ser Val Leu Asp Asp
        595                 600                 605
```

```
Phe Leu Lys Asn Phe Ile Tyr Pro Leu Gln Arg Thr Ile Gln Arg Glu
    610                 615                 620

His His Ser Leu Glu Lys Asp Tyr Gln Leu Thr Asn Asp Val Asn Leu
625                 630                 635                 640

Gly Ile Ser Gln Leu Lys Thr Asn Val Pro Ala Leu Trp Pro Asp Glu
                645                 650                 655

Ser Gln Thr Thr Val Pro Ser Arg Phe Ser Gln Ala Ala Asn Glu Val
            660                 665                 670

Phe Leu Thr Asp Val Ala Ser Phe Pro Glu Gln Phe Gln Ala His Val
        675                 680                 685

Arg Ser Ser Thr Asp Asp Ile Asn Glu Gln Asn Asp Tyr Ser Ser Ala
    690                 695                 700

Leu Gln Glu Ala Ser Thr Arg Val Val Ser Gly Val Trp Glu Ser Lys
705                 710                 715                 720

Ser Gly Ser Glu Lys Ala Pro Arg Asp Leu Ile Arg Leu Ile Asp Val
                725                 730                 735

Trp Val Ala Arg Asp Leu Thr Arg Asp Pro Ser Gly Ser Gly Ser Leu
            740                 745                 750

Arg Asp Pro Lys Gln Ala Arg Phe Glu Leu Lys Ile Asp Thr Gly Glu
        755                 760                 765

Val Leu Glu Arg Ser Arg Gln Tyr Ile Arg Arg Pro Gly Phe Ser Phe
    770                 775                 780

Gln Gln Phe Ile Ala Ser Ser Leu Arg Glu Phe Ile Thr Ala Pro Gly
785                 790                 795                 800

Leu Ala Asp His Glu Arg Arg Ala Arg Arg Gln Gln Val Leu Ser Lys
                805                 810                 815

Phe Ser Glu Ala Met Thr Tyr Ala Leu Pro Leu Ala Gln Ile Asn Pro
            820                 825                 830

Gln Leu Val Arg Ala Leu Tyr Gly Asp Glu Val Arg Tyr Asn Phe Asn
        835                 840                 845

Phe Ser Arg Ile Pro Phe Ala Gly Asp Glu Leu Gly Ser Ser Leu Glu
    850                 855                 860

Gln Ala Val Arg Asp Tyr Pro Asn His Arg Pro Ala Asp Ile Ser Lys
865                 870                 875                 880

Pro Leu Gly Lys Ala Leu Val Ser Gln Gly Glu Glu Arg Ser Ile Asp
                885                 890                 895

Ile Phe Gly Ser Tyr Pro Asn Tyr Ala Pro Ile Val Phe Asp Ser Leu
            900                 905                 910

Leu Pro Pro Ile Glu Lys Gln Trp Arg Gln Ile Thr Gly Asp Arg Thr
        915                 920                 925

Glu Phe Trp His Gly Arg Arg Thr Arg Pro Leu Thr Ala Ala Leu Pro
```

930 935 940

Met Thr Asp Leu Glu Arg Asn Ala Met Val Lys Gly Trp Tyr Ile Gly
945 950 955 960

Arg Leu Val Gly Arg Val Phe Phe Pro Ala Thr Leu Asp Thr Ala Asp
965 970 975

Thr Thr Pro Val Gln Ile Tyr Asp Glu Lys Ser Asp Ser Trp Ile Asn
980 985 990

Phe Ser Thr Pro Met Leu Thr Pro Val Ser Arg Phe Arg Gly Ser Leu
995 1000 1005

Asp Trp Leu Pro Asn Leu Leu Glu Ser Ala Ser Leu Ala Trp Ala Arg
1010 1015 1020

Ala Gly Glu Arg Pro Val Phe Glu Ser Val Glu Pro Tyr Ile Gln Leu
1025 1030 1035 1040

Arg Gln Leu Trp Asp Asp Ala Ala Ser Pro Ser Leu Pro Gly Arg Thr
1045 1050 1055

Thr Arg Gly Glu Lys Leu Leu His Asp Trp Leu Phe Asp Gly Asn Arg
1060 1065 1070

Met Ala Gly Asn Val Leu Gln Ile Pro Gly Thr Glu Ala Gly Val Thr
1075 1080 1085

Pro Ala Ala Arg Phe Glu Ala Ala Lys Asn Phe Leu Gln Arg Gln Asn
1090 1095 1100

Glu Ile Ser Gln Asn Tyr Val Pro Ser Asp Lys Leu Arg Gln Gly Arg
1105 1110 1115 1120

Leu Phe Thr Thr Ala Asp Arg Pro Phe Gly Asp Val Lys Asp Arg Glu
1125 1130 1135

Leu Ala Ala Gln Ile Pro Val Phe Ala Asp Leu Ala Ala Asp Val Phe
1140 1145 1150

Asp Gly Thr Gln Glu Ile Ile Asp Ile Leu Glu Lys Cys Leu Ala Ala
1155 1160 1165

Gly Pro Pro Ser Ala Gln Val Phe Asp Met Asn Val Ala Arg Arg Asp
1170 1175 1180

Val Ser Ser Gly Pro Ser Leu Pro Gly Glu Gly Glu Phe
1185 1190 1195

<210> 1981
<211> 486
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(463)
<223> RXA00926

<400> 1981
atggagacac ctggggctgg aaccaccaga aggcaccatc ggcgattatt agccacctta 60

ggtggccagg atgttccatg gtctggcaaa ctaactaacc atg gac atc gtt ttc 115
Met Asp Ile Val Phe
1 5

ctc ata att ctt cta gcc att ttt atc gtt ccc act ttc ctc atg agc 163
Leu Ile Ile Leu Leu Ala Ile Phe Ile Val Pro Thr Phe Leu Met Ser
10 15 20

cgc cgc cag cgc gca cgg atg act gaa atc caa aag ctg cag gac tct 211
Arg Arg Gln Arg Ala Arg Met Thr Glu Ile Gln Lys Leu Gln Asp Ser
25 30 35

gtc gtc cca ggc gac cgc atc gtc acc acc gcg gga cag cac gca acg 259
Val Val Pro Gly Asp Arg Ile Val Thr Thr Ala Gly Gln His Ala Thr
40 45 50

gtc att tcc acc act gca gaa acc gtt gat cta gag atc gcg ccg ggt 307
Val Ile Ser Thr Thr Ala Glu Thr Val Asp Leu Glu Ile Ala Pro Gly
55 60 65

atg atc agc act ttt gaa aag ctt gct atc gtg cgt gtg ctg tcc aag 355
Met Ile Ser Thr Phe Glu Lys Leu Ala Ile Val Arg Val Leu Ser Lys
70 75 80 85

gcc aat gaa cct cag atg ttg gat gag ccg acg ctg ttt gat cag cca 403
Ala Asn Glu Pro Gln Met Leu Asp Glu Pro Thr Leu Phe Asp Gln Pro
90 95 100

gaa gac gat cag ccg aac gat ggt ttc gat gga cgc act gac gga cat 451
Glu Asp Asp Gln Pro Asn Asp Gly Phe Asp Gly Arg Thr Asp Gly His
105 110 115

cct gag aat cgt tagaaattaa taataattca gca 486
Pro Glu Asn Arg
120

<210> 1982
<211> 121
<212> PRT
<213> Corynebacterium glutamicum

<400> 1982
Met Asp Ile Val Phe Leu Ile Ile Leu Leu Ala Ile Phe Ile Val Pro
1 5 10 15

Thr Phe Leu Met Ser Arg Arg Gln Arg Ala Arg Met Thr Glu Ile Gln
20 25 30

Lys Leu Gln Asp Ser Val Val Pro Gly Asp Arg Ile Val Thr Thr Ala
35 40 45

Gly Gln His Ala Thr Val Ile Ser Thr Thr Ala Glu Thr Val Asp Leu
50 55 60

Glu Ile Ala Pro Gly Met Ile Ser Thr Phe Glu Lys Leu Ala Ile Val
65 70 75 80

```
Arg Val Leu Ser Lys Ala Asn Glu Pro Gln Met Leu Asp Glu Pro Thr
                 85                  90                  95

Leu Phe Asp Gln Pro Glu Asp Asp Gln Pro Asn Asp Gly Phe Asp Gly
            100                 105                 110

Arg Thr Asp Gly His Pro Glu Asn Arg
        115                 120
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<210> 1983
<211> 876
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(853)
<223> RXA00930

<400> 1983

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acggcgcacc acacatttgg tggtgtattg agctatctct gggctgcgtg agaaaccatt 60

ttccggtgga tgatggaagc tagacgacga aagggagcat atg tct ggc cac tca   115
                                            Met Ser Gly His Ser
                                              1               5

aaa tgg gcg act acc aag cac aag aag gct gct aac gac gcc aag cga   163
Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala Asn Asp Ala Lys Arg
                 10                  15                  20

ggc aag gaa ttt gcc aag ctg atc aag aac atc gaa gtt gcg gca cgt   211
Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile Glu Val Ala Ala Arg
             25                  30                  35

aca ggc ggt gga gat ccg tct gcg aac cca acg ctt gat gac atg atc   259
Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr Leu Asp Asp Met Ile
         40                  45                  50

aag aaa gcc aag aag gct tct gtg ccg aac gat aac atc gaa cgt gca   307
Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp Asn Ile Glu Arg Ala
     55                  60                  65

cgc aag cgt ggc tcc ggc gaa gaa gct ggt ggc gct gac tgg atg aac   355
Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly Ala Asp Trp Met Asn
 70                  75                  80                  85

atc atg tac gag gga tac ggc ccc aac ggc gtt gcc atg ctt atc gag   403
Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val Ala Met Leu Ile Glu
                 90                  95                 100

tgt ctg acc gac aac cgt aac cgc gca gct acc gaa gtt cgc acc gca   451
Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr Glu Val Arg Thr Ala
            105                 110                 115

atg acc aaa aac ggt ggc aac ttg ggc gag tcc ggt tcc gtg tcc tac   499
Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser Gly Ser Val Ser Tyr
        120                 125                 130

atg ttc acc cgc acc ggt gtc gtc acc gta caa aag ggc gat ctt agt   547
Met Phe Thr Arg Thr Gly Val Val Thr Val Gln Lys Gly Asp Leu Ser
```

```
    135                 140                 145

gaa gat gac gtg ctc atg gct gtt ctt gaa gct ggt gct gaa gaa gtc   595
Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala Gly Ala Glu Glu Val
150                 155                 160                 165

aac gac aac ggc gat ctg ttc gag gtt acc tgc gca cca act gac att   643
Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys Ala Pro Thr Asp Ile
                170                 175                 180

cag gct gtt cgc gac gca ctc gtg gaa gct ggc att gaa gta gaa gat   691
Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly Ile Glu Val Glu Asp
            185                 190                 195

tct gaa tca gac ttc cgg gca tct gtt cag gtc ccc ctg gac gct gac   739
Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val Pro Leu Asp Ala Asp
        200                 205                 210

ggt gca cgc aag atc ttc aag ctt gtg gac gcg ttg gaa gat tcc gac   787
Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala Leu Glu Asp Ser Asp
    215                 220                 225

gat gtg caa aac gtc tac acc aac atc gac ttg agc gat gag gtt ttg   835
Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu Ser Asp Glu Val Leu
230                 235                 240                 245

aca gag ctg gaa aac gac tagttcgtat tttccgcact ccg                 876
Thr Glu Leu Glu Asn Asp
                250
```

US09/470,202
US09/470,202

<210> 1984
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

<400> 1984

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Met Ser Gly His Ser Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala
  1               5                  10                  15

Asn Asp Ala Lys Arg Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile
            20                  25                  30

Glu Val Ala Ala Arg Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr
        35                  40                  45

Leu Asp Asp Met Ile Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp
    50                  55                  60

Asn Ile Glu Arg Ala Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly
65                  70                  75                  80

Ala Asp Trp Met Asn Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val
                85                  90                  95

Ala Met Leu Ile Glu Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr
            100                 105                 110

Glu Val Arg Thr Ala Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser
        115                 120                 125
```

```
Gly Ser Val Ser Tyr Met Phe Thr Arg Thr Gly Val Val Thr Val Gln
    130                 135                 140

Lys Gly Asp Leu Ser Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala
145                 150                 155                 160

Gly Ala Glu Glu Val Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys
                165                 170                 175

Ala Pro Thr Asp Ile Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly
            180                 185                 190

Ile Glu Val Glu Asp Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val
        195                 200                 205

Pro Leu Asp Ala Asp Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala
    210                 215                 220

Leu Glu Asp Ser Asp Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu
225                 230                 235                 240

Ser Asp Glu Val Leu Thr Glu Leu Glu Asn Asp
                245                 250
```

<210> 1985
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> RXA00932

<400> 1985

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cccaattaat ttatgcactt cggtgaggtt actcacaaag agtagcgtgc aaagcccagc 60

aataaggtga tgtttcaacg attaggttac ggtaggggcc atg acg cca cag aaa   115
                                              Met Thr Pro Gln Lys
                                                1               5

ctt cac cgt ttt gca gcc ctt tta gaa atg ggt acc tgg acc ctg ctg   163
Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly Thr Trp Thr Leu Leu
                  10                  15                  20

atc atc ggc atg atc tta aaa tac agt gga gtg aca gac gcc gta acc   211
Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val Thr Asp Ala Val Thr
              25                  30                  35

cct att gcc ggc ggt atc cac ggc ttt ggc ttc ctc tgt ttt gca gcc   259
Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe Leu Cys Phe Ala Ala
          40                  45                  50

atc acc atc acc gtg tgg atc aat aat aag tgg aca ttc ccg cag ggt   307
Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp Thr Phe Pro Gln Gly
      55                  60                  65

atc gca ggt ttg atc gtc tct gtt atc ccg tgg gct gca ttg cca ttt   355
Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp Ala Ala Leu Pro Phe
  70                  75                  80                  85
```

```
gca ttg tgg gca gac aag aag ggc ctc gtt gcc ggc gga tgg cgc ttt   403
Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala Gly Gly Trp Arg Phe
                 90                  95                 100

tca gat ccg tcc gaa aag cca cac act ttc ttt gac aag atc ttg gct   451
Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe Asp Lys Ile Leu Ala
            105                 110                 115

caa ttg gtc agg cac cca atc cga tcc att tta att ctg ctg gtg att   499
Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu Ile Leu Leu Val Ile
        120                 125                 130

atc gcc gtc gtc ttc tct atc ttg ctg gcg atg gga cca cct tat gat   547
Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met Gly Pro Pro Tyr Asp
    135                 140                 145

cca gat gcc atc gca aac act gtg gat taaacaacag cctccttcac         594
Pro Asp Ala Ile Ala Asn Thr Val Asp
150                 155

atg                                                               597
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<210> 1986
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 1986

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Met Thr Pro Gln Lys Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly
  1               5                  10                  15

Thr Trp Thr Leu Leu Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val
             20                  25                  30

Thr Asp Ala Val Thr Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe
         35                  40                  45

Leu Cys Phe Ala Ala Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp
     50                  55                  60

Thr Phe Pro Gln Gly Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp
 65                  70                  75                  80

Ala Ala Leu Pro Phe Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala
                 85                  90                  95

Gly Gly Trp Arg Phe Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe
            100                 105                 110

Asp Lys Ile Leu Ala Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu
        115                 120                 125

Ile Leu Leu Val Ile Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met
    130                 135                 140

Gly Pro Pro Tyr Asp Pro Asp Ala Ile Ala Asn Thr Val Asp
145                 150                 155
```

<210> 1987
<211> 585
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> RXA00933

<400> 1987
ccgcggggct aaagcgcgca aacgcctacg actggtcgac agtatccacc caggtcatgg 60

cagtctatga aaccattgcg atcgacaaag tgaggcttgg atg acc ctt gtt tac 115
Met Thr Leu Val Tyr
1 5

ctc ctc atc gct gtc gtt gtc acc gca act gtt ctg tgg gcg tat ttc 163
Leu Leu Ile Ala Val Val Val Thr Ala Thr Val Leu Trp Ala Tyr Phe
10 15 20

aca gca caa cgc ctc aac cgg ctc cac atc cgc acc gac tca gca aga 211
Thr Ala Gln Arg Leu Asn Arg Leu His Ile Arg Thr Asp Ser Ala Arg
25 30 35

caa gcc ctg caa gca gca ctg gat cgc cga gca gca cta gta ggt gcg 259
Gln Ala Leu Gln Ala Ala Leu Asp Arg Arg Ala Ala Leu Val Gly Ala
40 45 50

ttg ttg ccc gat gca gca gaa gcc tca aaa cgc gct gag gca att ccc 307
Leu Leu Pro Asp Ala Ala Glu Ala Ser Lys Arg Ala Glu Ala Ile Pro
55 60 65

ctg gaa tac tcc cgc ttc tcc caa cgc gcc cgc gcc gaa cga gaa atc 355
Leu Glu Tyr Ser Arg Phe Ser Gln Arg Ala Arg Ala Glu Arg Glu Ile
70 75 80 85

tct gaa ctc atc ttg aaa cag ggg aag acc ctt cca gat tcc atc gtg 403
Ser Glu Leu Ile Leu Lys Gln Gly Lys Thr Leu Pro Asp Ser Ile Val
90 95 100

gac gct gcc acc cgc gtg gaa tta gcc cac cgc ttc tac aac gaa gcc 451
Asp Ala Ala Thr Arg Val Glu Leu Ala His Arg Phe Tyr Asn Glu Ala
105 110 115

gtc agt gac acc cgc gat ctt cga acc cga ttg atg gtc aga tcc ttc 499
Val Ser Asp Thr Arg Asp Leu Arg Thr Arg Leu Met Val Arg Ser Phe
120 125 130

cga ctc ggc ggc acc gca ccc ttg ccg gag tac ttc gaa cta ctc gat 547
Arg Leu Gly Gly Thr Ala Pro Leu Pro Glu Tyr Phe Glu Leu Leu Asp
135 140 145

aca gat ctg ctg act taaatgtaaa aaagcctcct tca 585
Thr Asp Leu Leu Thr
150

<210> 1988
<211> 154
<212> PRT

<213> Corynebacterium glutamicum

<400> 1988

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Met Thr Leu Val Tyr Leu Leu Ile Ala Val Val Val Thr Ala Thr Val
  1               5                  10                  15

Leu Trp Ala Tyr Phe Thr Ala Gln Arg Leu Asn Arg Leu His Ile Arg
             20                  25                  30

Thr Asp Ser Ala Arg Gln Ala Leu Gln Ala Ala Leu Asp Arg Arg Ala
         35                  40                  45

Ala Leu Val Gly Ala Leu Leu Pro Asp Ala Ala Glu Ala Ser Lys Arg
     50                  55                  60

Ala Glu Ala Ile Pro Leu Glu Tyr Ser Arg Phe Ser Gln Arg Ala Arg
 65                  70                  75                  80

Ala Glu Arg Glu Ile Ser Glu Leu Ile Leu Lys Gln Gly Lys Thr Leu
                 85                  90                  95

Pro Asp Ser Ile Val Asp Ala Ala Thr Arg Val Glu Leu Ala His Arg
            100                 105                 110

Phe Tyr Asn Glu Ala Val Ser Asp Thr Arg Asp Leu Arg Thr Arg Leu
        115                 120                 125

Met Val Arg Ser Phe Arg Leu Gly Gly Thr Ala Pro Leu Pro Glu Tyr
    130                 135                 140

Phe Glu Leu Leu Asp Thr Asp Leu Leu Thr
145                 150
```

<210> 1989
<211> 519
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(496)
<223> RXA00940

<400> 1989

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tgctcaacgg cacgctgaag ggcacggaca tggacatcat cacggcaggc gacccggacg 60

tggtcgcggt ggacgtgctg gcagaggcga tctgcgcaat gtg att ttg gtg ctg   115
                                        Val Ile Leu Val Leu
                                          1               5

ctg gaa gct gag tca atg cgc ggc tac cag atc atc acc acc atc agt   163
Leu Glu Ala Glu Ser Met Arg Gly Tyr Gln Ile Ile Thr Thr Ile Ser
                 10                  15                  20

gag caa aca gaa ggt aac tgg act cca agc cca gga acc atc tat cca   211
Glu Gln Thr Glu Gly Asn Trp Thr Pro Ser Pro Gly Thr Ile Tyr Pro
             25                  30                  35

acc ttg tcc atg ctt gaa gat gaa ggc ctg att tcc atc tcc cat gaa   259
Thr Leu Ser Met Leu Glu Asp Glu Gly Leu Ile Ser Ile Ser His Glu
```

```
         40                  45                  50

atg ggc aga aaa atg gcg cgc ctt aca gaa gaa ggc gcg cag gaa gtg   307
Met Gly Arg Lys Met Ala Arg Leu Thr Glu Glu Gly Ala Gln Glu Val
     55                  60                  65

gca aag aac aag gat gcg tgg gga tca att ctg gag gct tat cgc aat   355
Ala Lys Asn Lys Asp Ala Trp Gly Ser Ile Leu Glu Ala Tyr Arg Asn
 70                  75                  80                  85

cca gaa tcc cga gag gtg cgg gtg ttt aac att cgc tct gag ttt cac   403
Pro Glu Ser Arg Glu Val Arg Val Phe Asn Ile Arg Ser Glu Phe His
                 90                  95                 100

aag gtc agg gaa gca gcg aaa gct gct ccc gac gat aaa gca gag caa   451
Lys Val Arg Glu Ala Ala Lys Ala Ala Pro Asp Asp Lys Ala Glu Gln
            105                 110                 115

ata atc gag att tta agg aga gca gca gat gac atc aag aga cta       496
Ile Ile Glu Ile Leu Arg Arg Ala Ala Asp Asp Ile Lys Arg Leu
        120                 125                 130

taaccccagt accatgcagc tgc                                        519


<210> 1990
<211> 132
<212> PRT
<213> Corynebacterium glutamicum

<400> 1990
Val Ile Leu Val Leu Leu Glu Ala Glu Ser Met Arg Gly Tyr Gln Ile
  1               5                  10                  15

Ile Thr Thr Ile Ser Glu Gln Thr Glu Gly Asn Trp Thr Pro Ser Pro
             20                  25                  30

Gly Thr Ile Tyr Pro Thr Leu Ser Met Leu Glu Asp Glu Gly Leu Ile
         35                  40                  45

Ser Ile Ser His Glu Met Gly Arg Lys Met Ala Arg Leu Thr Glu Glu
     50                  55                  60

Gly Ala Gln Glu Val Ala Lys Asn Lys Asp Ala Trp Gly Ser Ile Leu
 65                  70                  75                  80

Glu Ala Tyr Arg Asn Pro Glu Ser Arg Glu Val Arg Val Phe Asn Ile
                 85                  90                  95

Arg Ser Glu Phe His Lys Val Arg Glu Ala Ala Lys Ala Ala Pro Asp
            100                 105                 110

Asp Lys Ala Glu Gln Ile Ile Glu Ile Leu Arg Arg Ala Ala Asp Asp
        115                 120                 125

Ile Lys Arg Leu
    130


<210> 1991
<211> 771
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> RXA00949

<400> 1991
gctcaaggat ccttcctggg caaaccaagc agccctcgca ctaggtgcgg aacccaggta 60

tgttcaccaa tacgactacg tactttaaag gagagttgac atg aag gtt ttc atc 115
Met Lys Val Phe Ile
1 5

atc ggc gct gcg ggt ggc atc ggc aat cga ctt tcc agc ctg ctt cac 163
Ile Gly Ala Ala Gly Gly Ile Gly Asn Arg Leu Ser Ser Leu Leu His
10 15 20

gcc agg gga gat gca gtt agc ggc atg cac cgc aat ctt gag cag gcc 211
Ala Arg Gly Asp Ala Val Ser Gly Met His Arg Asn Leu Glu Gln Ala
25 30 35

tca aaa atc aca gac act ggg gca act gcc gta ctc ggg gat ctc atc 259
Ser Lys Ile Thr Asp Thr Gly Ala Thr Ala Val Leu Gly Asp Leu Ile
40 45 50

cac aac agc acg gag gag ctt gcg gag ctt ttc cgc ggt cac gat gcc 307
His Asn Ser Thr Glu Glu Leu Ala Glu Leu Phe Arg Gly His Asp Ala
55 60 65

atc gta ttt tct gca ggc gcc cac gga aca ggg caa gaa aat acc acg 355
Ile Val Phe Ser Ala Gly Ala His Gly Thr Gly Gln Glu Asn Thr Thr
70 75 80 85

ctt atc gac ggc gcc ggc ctc cgt aaa gcc gcc gac gct gcc agc gcg 403
Leu Ile Asp Gly Ala Gly Leu Arg Lys Ala Ala Asp Ala Ala Ser Ala
90 95 100

gcc aac gtt tca cgc ttc atc ttg gtc tct gcg ttt ccg gaa tcc tcc 451
Ala Asn Val Ser Arg Phe Ile Leu Val Ser Ala Phe Pro Glu Ser Ser
105 110 115

cgc ggg gag aac acc acc gag aac ttt gag cac tat atg aag gtg aag 499
Arg Gly Glu Asn Thr Thr Glu Asn Phe Glu His Tyr Met Lys Val Lys
120 125 130

aag tcc gcc gat gtc tac ctc agt cac act gac cta gac tgg gtt att 547
Lys Ser Ala Asp Val Tyr Leu Ser His Thr Asp Leu Asp Trp Val Ile
135 140 145

gtc cga cca ggc gtg ctt caa gat gag gca ggg gat ggt tta gtc act 595
Val Arg Pro Gly Val Leu Gln Asp Glu Ala Gly Asp Gly Leu Val Thr
150 155 160 165

gct ggc tta gcg att aat tac ggc aat gtt gct cgc gat aat gtc gca 643
Ala Gly Leu Ala Ile Asn Tyr Gly Asn Val Ala Arg Asp Asn Val Ala
170 175 180

gcg ttc att gat gaa gct ctg cat caa ccg cag ttg tca aag atc att 691
Ala Phe Ile Asp Glu Ala Leu His Gln Pro Gln Leu Ser Lys Ile Ile

```
            185                 190                 195

gtt gaa ctc acc gac ggt tca act ccg gtg gcg gaa gcc gta gaa cgc   739
Val Glu Leu Thr Asp Gly Ser Thr Pro Val Ala Glu Ala Val Glu Arg
        200                 205                 210

ctc atc aag taaagacgaa aagagggaga atg                             771
Leu Ile Lys
    215
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<210> 1992
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 1992

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Met Lys Val Phe Ile Ile Gly Ala Ala Gly Gly Ile Gly Asn Arg Leu
  1               5                  10                  15

Ser Ser Leu Leu His Ala Arg Gly Asp Ala Val Ser Gly Met His Arg
             20                  25                  30

Asn Leu Glu Gln Ala Ser Lys Ile Thr Asp Thr Gly Ala Thr Ala Val
         35                  40                  45

Leu Gly Asp Leu Ile His Asn Ser Thr Glu Glu Leu Ala Glu Leu Phe
     50                  55                  60

Arg Gly His Asp Ala Ile Val Phe Ser Ala Gly Ala His Gly Thr Gly
 65                  70                  75                  80

Gln Glu Asn Thr Thr Leu Ile Asp Gly Ala Gly Leu Arg Lys Ala Ala
                 85                  90                  95

Asp Ala Ala Ser Ala Ala Asn Val Ser Arg Phe Ile Leu Val Ser Ala
            100                 105                 110

Phe Pro Glu Ser Ser Arg Gly Glu Asn Thr Thr Glu Asn Phe Glu His
        115                 120                 125

Tyr Met Lys Val Lys Lys Ser Ala Asp Val Tyr Leu Ser His Thr Asp
    130                 135                 140

Leu Asp Trp Val Ile Val Arg Pro Gly Val Leu Gln Asp Glu Ala Gly
145                 150                 155                 160

Asp Gly Leu Val Thr Ala Gly Leu Ala Ile Asn Tyr Gly Asn Val Ala
                165                 170                 175

Arg Asp Asn Val Ala Ala Phe Ile Asp Glu Ala Leu His Gln Pro Gln
            180                 185                 190

Leu Ser Lys Ile Ile Val Glu Leu Thr Asp Gly Ser Thr Pro Val Ala
        195                 200                 205

Glu Ala Val Glu Arg Leu Ile Lys
    210                 215
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<210> 1993

<211> 170
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(147)
<223> RXA00969

<400> 1993
atc cga cag gaa gag cgc gat gat gat gca cgt ctg atc gtg gtc acc 48
Ile Arg Gln Glu Glu Arg Asp Asp Asp Ala Arg Leu Ile Val Val Thr
1 5 10 15

cac tct gcg ctg gaa tct gat ctt tcc cgc acc gtt gaa ctg ctg aag 96
His Ser Ala Leu Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys
20 25 30

gct aag cct gtt gtt aag gca atc aac agt gtg atc cgc ctc gaa agg 144
Ala Lys Pro Val Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg
35 40 45

gac taattttact gacatggcaa ttg 170
Asp

<210> 1994
<211> 49
<212> PRT
<213> Corynebacterium glutamicum

<400> 1994
Ile Arg Gln Glu Glu Arg Asp Asp Asp Ala Arg Leu Ile Val Val Thr
1 5 10 15

His Ser Ala Leu Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys
20 25 30

Ala Lys Pro Val Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg
35 40 45

Asp

<210> 1995
<211> 726
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> RXA00973

<400> 1995
ttgttggtgc aggccttaca gccattgcac tgagttccat gctgtcgcag ccagtacagg 60

ccttcaccat gaccattgag atggtgagtg tatttttcac atg aac cac tct gac 115
Met Asn His Ser Asp

```
                                                    1               5

gac gat cgc atg caa aag tgg ttc cag atc cgc cgc gaa ctg ggc aaa   163
Asp Asp Arg Met Gln Lys Trp Phe Gln Ile Arg Arg Glu Leu Gly Lys
                 10                  15                  20

gaa att gtg aaa cag ctt caa aag gat ctg ccc gca gtc gcc tct gac   211
Glu Ile Val Lys Gln Leu Gln Lys Asp Leu Pro Ala Val Ala Ser Asp
             25                  30                  35

atc ggc tcc atg gtg tat tcc tct gat caa gtt ccc ctc gga aac gcc   259
Ile Gly Ser Met Val Tyr Ser Ser Asp Gln Val Pro Leu Gly Asn Ala
         40                  45                  50

acg ctc act gca tac gga gac atc ggc aac cga gtc gct tcc gct gca   307
Thr Leu Thr Ala Tyr Gly Asp Ile Gly Asn Arg Val Ala Ser Ala Ala
     55                  60                  65

aca agt gcg aga tac aac gta gag gaa ctc ctg gac gca atc gaa aac   355
Thr Ser Ala Arg Tyr Asn Val Glu Glu Leu Leu Asp Ala Ile Glu Asn
 70                  75                  80                  85

gca cga ttt gcc atc tgg gtt cca aat tac gac aac tcc tac tac ctc   403
Ala Arg Phe Ala Ile Trp Val Pro Asn Tyr Asp Asn Ser Tyr Tyr Leu
                 90                  95                 100

tcc ggc gag gaa ggt gcc gac gaa ttc caa aca tac ctc atc aaa gat   451
Ser Gly Glu Glu Gly Ala Asp Glu Phe Gln Thr Tyr Leu Ile Lys Asp
             105                 110                 115

gcg tca aga ttt ctt gaa tcc tcc ggg aat act cca ccc gag aac ccg   499
Ala Ser Arg Phe Leu Glu Ser Ser Gly Asn Thr Pro Pro Glu Asn Pro
         120                 125                 130

cag tac agc gac tcc aaa tta acc ttt gct agc gaa cta ctc ccc ttc   547
Gln Tyr Ser Asp Ser Lys Leu Thr Phe Ala Ser Glu Leu Leu Pro Phe
     135                 140                 145

tac acc gca ttt aac aac tcg acc tac cca cta ctt cat gct tgt gtg   595
Tyr Thr Ala Phe Asn Asn Ser Thr Tyr Pro Leu Leu His Ala Cys Val
150                 155                 160                 165

caa ggt gaa cca act gaa gta gac ctc tac ttc tac gag ctc gag cag   643
Gln Gly Glu Pro Thr Glu Val Asp Leu Tyr Phe Tyr Glu Leu Glu Gln
                170                 175                 180

gca gaa ttg aag gaa aaa gag act gca cag ctc tcg agt gga tca agt   691
Ala Glu Leu Lys Glu Lys Glu Thr Ala Gln Leu Ser Ser Gly Ser Ser
             185                 190                 195

ttt ggc tcc agt tagtcagaat tctcctaaag ggc                        726
Phe Gly Ser Ser
         200
```

Sequence Listing

<210> 1996
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 1996

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Met Asn His Ser Asp Asp Asp Arg Met Gln Lys Trp Phe Gln Ile Arg
  1               5                  10                  15

Arg Glu Leu Gly Lys Glu Ile Val Lys Gln Leu Gln Lys Asp Leu Pro
             20                  25                  30

Ala Val Ala Ser Asp Ile Gly Ser Met Val Tyr Ser Ser Asp Gln Val
         35                  40                  45

Pro Leu Gly Asn Ala Thr Leu Thr Ala Tyr Gly Asp Ile Gly Asn Arg
     50                  55                  60

Val Ala Ser Ala Ala Thr Ser Ala Arg Tyr Asn Val Glu Glu Leu Leu
 65                  70                  75                  80

Asp Ala Ile Glu Asn Ala Arg Phe Ala Ile Trp Val Pro Asn Tyr Asp
                 85                  90                  95

Asn Ser Tyr Tyr Leu Ser Gly Glu Glu Gly Ala Asp Glu Phe Gln Thr
            100                 105                 110

Tyr Leu Ile Lys Asp Ala Ser Arg Phe Leu Glu Ser Ser Gly Asn Thr
        115                 120                 125

Pro Pro Glu Asn Pro Gln Tyr Ser Asp Ser Lys Leu Thr Phe Ala Ser
    130                 135                 140

Glu Leu Leu Pro Phe Tyr Thr Ala Phe Asn Asn Ser Thr Tyr Pro Leu
145                 150                 155                 160

Leu His Ala Cys Val Gln Gly Glu Pro Thr Glu Val Asp Leu Tyr Phe
                165                 170                 175

Tyr Glu Leu Glu Gln Ala Glu Leu Lys Glu Lys Glu Thr Ala Gln Leu
            180                 185                 190

Ser Ser Gly Ser Ser Phe Gly Ser Ser
        195                 200
```

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<210> 1997
<211> 738
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(715)
<223> RXA00978

<400> 1997
tcctgggtag catgggctta tgagcactga tagccaaaac cctgtaagaa aatcctgcgc 60

acagccacat tcttgttccc aagaggtgcg attgaaagcg atg tcc agg tca ccg 115
                                              Met Ser Arg Ser Pro
                                                1   5

ctt act aaa ggt cta aat caa ctt gaa cac ctc gag tta gat aag tca 163
Leu Thr Lys Gly Leu Asn Gln Leu Glu His Leu Glu Leu Asp Lys Ser
            10   15   20

```
cta act gcg tgg tcg tgg gca gaa gat gat cct ttg tac ctc gca ggt   211
Leu Thr Ala Trp Ser Trp Ala Glu Asp Asp Pro Leu Tyr Leu Ala Gly
             25                  30                  35

gag aac tta aac ggc agt tac ctc att gtc gca gga cga gtg cgg gtc   259
Glu Asn Leu Asn Gly Ser Tyr Leu Ile Val Ala Gly Arg Val Arg Val
         40                  45                  50

tct cgc gac acc atc gac ggg aaa gaa ctc acc gtt gat att gca acg   307
Ser Arg Asp Thr Ile Asp Gly Lys Glu Leu Thr Val Asp Ile Ala Thr
     55                  60                  65

ccc ggc gat gtt att ggt gcg ata gat aca gaa cct cag ccg gca gta   355
Pro Gly Asp Val Ile Gly Ala Ile Asp Thr Glu Pro Gln Pro Ala Val
 70                  75                  80                  85

gat tcc gct tgg gca ata gaa acc acc tgt gcg ctg ttt ctt cca gca   403
Asp Ser Ala Trp Ala Ile Glu Thr Thr Cys Ala Leu Phe Leu Pro Ala
                 90                  95                 100

acc gcg ttg gca act gtg att gaa cag cat cca agt ttt gct ttg gcg   451
Thr Ala Leu Ala Thr Val Ile Glu Gln His Pro Ser Phe Ala Leu Ala
            105                 110                 115

atg att cgg atg cag cag caa cgt ttg gct aca gcc aga gat cat gaa   499
Met Ile Arg Met Gln Gln Gln Arg Leu Ala Thr Ala Arg Asp His Glu
        120                 125                 130

att aac ctg act acg acc aca gtt gag caa cga gta gct att gca gtg   547
Ile Asn Leu Thr Thr Thr Thr Val Glu Gln Arg Val Ala Ile Ala Val
    135                 140                 145

aga act ctg gga cga aaa atc ggg caa cga cga ccc gat gga atc ttg   595
Arg Thr Leu Gly Arg Lys Ile Gly Gln Arg Arg Pro Asp Gly Ile Leu
150                 155                 160                 165

ctc att caa gtt cga atc cgg cgg gaa gat gtt gcg ggt tta gca ggc   643
Leu Ile Gln Val Arg Ile Arg Arg Glu Asp Val Ala Gly Leu Ala Gly
                170                 175                 180

acc acc gtg gaa tct act tct aga gtt ttg gcg cga tta cgt aaa gaa   691
Thr Thr Val Glu Ser Thr Ser Arg Val Leu Ala Arg Leu Arg Lys Glu
            185                 190                 195

ggg gtc att gat agc ggt agg gaa tgattgccgt ggtcgatgaa cgg        738
Gly Val Ile Asp Ser Gly Arg Glu
        200                 205
```

<210> 1998
<211> 205
<212> PRT
<213> Corynebacterium glutamicum

<400> 1998

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Met Ser Arg Ser Pro Leu Thr Lys Gly Leu Asn Gln Leu Glu His Leu
  1               5                  10                  15

Glu Leu Asp Lys Ser Leu Thr Ala Trp Ser Trp Ala Glu Asp Asp Pro
             20                  25                  30
```

```
Leu Tyr Leu Ala Gly Glu Asn Leu Asn Gly Ser Tyr Leu Ile Val Ala
          35                  40                  45

Gly Arg Val Arg Val Ser Arg Asp Thr Ile Asp Gly Lys Glu Leu Thr
      50                  55                  60

Val Asp Ile Ala Thr Pro Gly Asp Val Ile Gly Ala Ile Asp Thr Glu
 65                  70                  75                  80

Pro Gln Pro Ala Val Asp Ser Ala Trp Ala Ile Glu Thr Thr Cys Ala
                 85                  90                  95

Leu Phe Leu Pro Ala Thr Ala Leu Ala Thr Val Ile Glu Gln His Pro
            100                 105                 110

Ser Phe Ala Leu Ala Met Ile Arg Met Gln Gln Gln Arg Leu Ala Thr
        115                 120                 125

Ala Arg Asp His Glu Ile Asn Leu Thr Thr Thr Thr Val Glu Gln Arg
    130                 135                 140

Val Ala Ile Ala Val Arg Thr Leu Gly Arg Lys Ile Gly Gln Arg Arg
145                 150                 155                 160

Pro Asp Gly Ile Leu Leu Ile Gln Val Arg Ile Arg Arg Glu Asp Val
                165                 170                 175

Ala Gly Leu Ala Gly Thr Thr Val Glu Ser Thr Ser Arg Val Leu Ala
            180                 185                 190

Arg Leu Arg Lys Glu Gly Val Ile Asp Ser Gly Arg Glu
        195                 200                 205


<210> 1999
<211> 424
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (60)..(401)
<223> RXA00986

<400> 1999
ctactttgat aacaccgcca cccaagccaa gccggagtga tctccgtatc ctttaaggcatg 62
                                                                  Met
                                                                   1

act tta aaa gat aag tac gac act gaa gta gct gtt tct aat aat cag   110
Thr Leu Lys Asp Lys Tyr Asp Thr Glu Val Ala Val Ser Asn Asn Gln
              5                  10                  15

gac aag cac caa ttt gag gtc agt tac cct gaa gat gcc gtg act gct   158
Asp Lys His Gln Phe Glu Val Ser Tyr Pro Glu Asp Ala Val Thr Ala
          20                  25                  30

ggc ttt gct gca tac ctt gat aaa ggt gat tcg cgg atc ttc tat cac   206
Gly Phe Ala Ala Tyr Leu Asp Lys Gly Asp Ser Arg Ile Phe Tyr His
      35                  40                  45
```

```
acc gtt gtt ggc gat gaa ttc ggt ggc aag gga ctt gcg tca att ctt   254
Thr Val Val Gly Asp Glu Phe Gly Gly Lys Gly Leu Ala Ser Ile Leu
 50                  55                  60                  65

gtt tca gag gcg tta aaa gcc aca aaa gaa gct ggt ctt acc gtg gtt   302
Val Ser Glu Ala Leu Lys Ala Thr Lys Glu Ala Gly Leu Thr Val Val
                70                  75                  80

ccg gta tgt ccc ttt gtt aaa gga ttc gtg gaa aag aac gca ttc gag   350
Pro Val Cys Pro Phe Val Lys Gly Phe Val Glu Lys Asn Ala Phe Glu
            85                  90                  95

ggt tac cgc aaa cca aac cat gag gat atg gag ctg gtg aag agc cag   398
Gly Tyr Arg Lys Pro Asn His Glu Asp Met Glu Leu Val Lys Ser Gln
        100                 105                 110

atg tagaaactac tcaacttcca gaa                                    424
Met
```

<210> 2000
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 2000

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Met Thr Leu Lys Asp Lys Tyr Asp Thr Glu Val Ala Val Ser Asn Asn
  1               5                  10                  15

Gln Asp Lys His Gln Phe Glu Val Ser Tyr Pro Glu Asp Ala Val Thr
            20                  25                  30

Ala Gly Phe Ala Ala Tyr Leu Asp Lys Gly Asp Ser Arg Ile Phe Tyr
        35                  40                  45

His Thr Val Val Gly Asp Glu Phe Gly Gly Lys Gly Leu Ala Ser Ile
    50                  55                  60

Leu Val Ser Glu Ala Leu Lys Ala Thr Lys Glu Ala Gly Leu Thr Val
65                  70                  75                  80

Val Pro Val Cys Pro Phe Val Lys Gly Phe Val Glu Lys Asn Ala Phe
                85                  90                  95

Glu Gly Tyr Arg Lys Pro Asn His Glu Asp Met Glu Leu Val Lys Ser
            100                 105                 110

Gln Met
```

<210> 2001
<211> 588
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(565)
<223> RXA00987

<400> 2001
cgcgggctgc ttaccacgca gcacagctaa gctttaaggc cctccggggc ctttttgct 60

tttcgacgcc tacctccttc ggaggcgtat tctgtcgttc atg cct aaa tct ctg 115
Met Pro Lys Ser Leu
1 5

acc ttt gaa gac agc att aac atc gca gcg ccc atc aat cag gtc tac 163
Thr Phe Glu Asp Ser Ile Asn Ile Ala Ala Pro Ile Asn Gln Val Tyr
10 15 20

gca cta gtt tct gac atc act cga act gga gaa tgg tcg ccc gtg tgt 211
Ala Leu Val Ser Asp Ile Thr Arg Thr Gly Glu Trp Ser Pro Val Cys
25 30 35

gag aaa tgc tgg tgg gat gaa gac gaa ggc ccc gtc gtg ggt gcg cac 259
Glu Lys Cys Trp Trp Asp Glu Asp Glu Gly Pro Val Val Gly Ala His
40 45 50

ttt act ggc cga aac gtc aca cct gag cgc acc tgg gag aca cgg agc 307
Phe Thr Gly Arg Asn Val Thr Pro Glu Arg Thr Trp Glu Thr Arg Ser
55 60 65

gag gtt atc gtc gca gag cca aat cgt tgc ttt ggt tgg agc gtg act 355
Glu Val Ile Val Ala Glu Pro Asn Arg Cys Phe Gly Trp Ser Val Thr
70 75 80 85

gat gga aac gtc aag tgg att tat tcc atg gaa ccg tta gaa gaa ggc 403
Asp Gly Asn Val Lys Trp Ile Tyr Ser Met Glu Pro Leu Glu Glu Gly
90 95 100

aca gta ttg act gaa tca tgg gaa ttt acc ccc aaa ggt caa cga ttc 451
Thr Val Leu Thr Glu Ser Trp Glu Phe Thr Pro Lys Gly Gln Arg Phe
105 110 115

ttc cac gac aaa ttc ggc gac aaa tca att gaa gaa att gaa aag cga 499
Phe His Asp Lys Phe Gly Asp Lys Ser Ile Glu Glu Ile Glu Lys Arg
120 125 130

cgc ttg gca gct ata acc gga att cca gaa aca ctg gtt gcc att cag 547
Arg Leu Ala Ala Ile Thr Gly Ile Pro Glu Thr Leu Val Ala Ile Gln
135 140 145

cgc att ctg gaa gtt gag tagtttctac atctggctct tca 588
Arg Ile Leu Glu Val Glu
150 155

<210> 2002
<211> 155
<212> PRT
<213> Corynebacterium glutamicum

<400> 2002
Met Pro Lys Ser Leu Thr Phe Glu Asp Ser Ile Asn Ile Ala Ala Pro
1 5 10 15

Ile Asn Gln Val Tyr Ala Leu Val Ser Asp Ile Thr Arg Thr Gly Glu
20 25 30

```
Trp Ser Pro Val Cys Glu Lys Cys Trp Trp Asp Glu Asp Glu Gly Pro
          35                  40                  45

Val Val Gly Ala His Phe Thr Gly Arg Asn Val Thr Pro Glu Arg Thr
     50                  55                  60

Trp Glu Thr Arg Ser Glu Val Ile Val Ala Glu Pro Asn Arg Cys Phe
 65                  70                  75                  80

Gly Trp Ser Val Thr Asp Gly Asn Val Lys Trp Ile Tyr Ser Met Glu
                 85                  90                  95

Pro Leu Glu Glu Gly Thr Val Leu Thr Glu Ser Trp Glu Phe Thr Pro
            100                 105                 110

Lys Gly Gln Arg Phe Phe His Asp Lys Phe Gly Asp Lys Ser Ile Glu
        115                 120                 125

Glu Ile Glu Lys Arg Arg Leu Ala Ala Ile Thr Gly Ile Pro Glu Thr
    130                 135                 140

Leu Val Ala Ile Gln Arg Ile Leu Glu Val Glu
145                 150                 155


<210> 2003
<211> 546
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(523)
<223> RXA00988

<400> 2003
tagcagaaga caccgatgta cagtccggat caggtgttgt gatcaccggt tcaatcgtga 60

ccgccggcga tgcgcgcacg ctgtttggaa aggaacctgc atg agc aag cgt gaa   115
                                            Met Ser Lys Arg Glu
                                              1               5

gaa tca att gag tac gga cca tta ggc aaa ggc cac gat cca tta aag   163
Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly His Asp Pro Leu Lys
                 10                  15                  20

gat ccc atg aag ggt atc cga ggt gtc atg gcc ggc acc tta gtg atg   211
Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala Gly Thr Leu Val Met
             25                  30                  35

gaa gca atc acc tta ggt ctt gtt ctc acc gtg att ctg cgc gtg gac   259
Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val Ile Leu Arg Val Asp
         40                  45                  50

gac ggc atc tac tgg acc acc ttc aac tgg gtc tat gta tca gca gtc   307
Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val Tyr Val Ser Ala Val
     55                  60                  65

gcg atc gca cac ttt gtt gct gca ttt ctg caa agg ttt agt tgg tcc   355
Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln Arg Phe Ser Trp Ser
 70                  75                  80                  85
```

```
atc ccg atg aac atc gtg ctg cag gtt ctt gca ctt gcc ggt ttc ttt   403
Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala Leu Ala Gly Phe Phe
                 90                  95                 100

gtt cac ccc gcg atg ggc ttc gcc gcc atc atc ttc atc atc gcg tgg   451
Val His Pro Ala Met Gly Phe Ala Ala Ile Ile Phe Ile Ile Ala Trp
            105                 110                 115

gcg tac ctg ttc tac ctg cgc tct aat ctg att gat cgc atg aaa cgc   499
Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile Asp Arg Met Lys Arg
        120                 125                 130

ggg ctg ctt acc acg cag cac agc taagctttaa ggccctccgg ggc         546
Gly Leu Leu Thr Thr Gln His Ser
    135                 140
```

<210> 2004
<211> 141
<212> PRT
<213> Corynebacterium glutamicum

<400> 2004

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Met Ser Lys Arg Glu Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly
  1               5                  10                  15

His Asp Pro Leu Lys Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala
             20                  25                  30

Gly Thr Leu Val Met Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val
         35                  40                  45

Ile Leu Arg Val Asp Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val
     50                  55                  60

Tyr Val Ser Ala Val Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln
 65                  70                  75                  80

Arg Phe Ser Trp Ser Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala
                 85                  90                  95

Leu Ala Gly Phe Phe Val His Pro Ala Met Gly Phe Ala Ala Ile Ile
            100                 105                 110

Phe Ile Ile Ala Trp Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile
        115                 120                 125

Asp Arg Met Lys Arg Gly Leu Leu Thr Thr Gln His Ser
    130                 135                 140
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<210> 2005
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> RXA01005

<400> 2005
tgggcaccgt caacgattgg actcacgaaa gctccgacga ctagaaatag taactgtgtt 60

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ggacactttt cacctccgcg tattgagcga ggatgagtgg atg gaa cta gcc cgc   115
                                          Met Glu Leu Ala Arg
                                            1               5

gcc cac cac gcg cgg gct gat tca ttc acc aaa gac cac ttg aag cgt   163
Ala His His Ala Arg Ala Asp Ser Phe Thr Lys Asp His Leu Lys Arg
                  10                  15                  20

cga caa gcg cat atc aag cac ccc gtc ttc gac ttc ctc ttc gag tac   211
Arg Gln Ala His Ile Lys His Pro Val Phe Asp Phe Leu Phe Glu Tyr
              25                  30                  35

tac ccc gtg cgc gtc gcg cac cta aaa acc tgg cac ccc ggc atc ggc   259
Tyr Pro Val Arg Val Ala His Leu Lys Thr Trp His Pro Gly Ile Gly
          40                  45                  50

gtg ttt cta gaa ggc aca ccg ccg cat gcc acc atg cgc gat ttt ttg   307
Val Phe Leu Glu Gly Thr Pro Pro His Ala Thr Met Arg Asp Phe Leu
      55                  60                  65

ctt gtc gac gcc tcc ctc cat cac gca gcc ggc gtc cag ctt gac ctg   355
Leu Val Asp Ala Ser Leu His His Ala Ala Gly Val Gln Leu Asp Leu
  70                  75                  80                  85

gcc tcc tat atg caa cgc cgt ggg tcc tct gtg cgc tac atc cac gaa   403
Ala Ser Tyr Met Gln Arg Arg Gly Ser Ser Val Arg Tyr Ile His Glu
                  90                  95                 100

ctg ttg tcc gcc acc cgc gac aac cac gcc caa ttt gat tgt ttt ggt   451
Leu Leu Ser Ala Thr Arg Asp Asn His Ala Gln Phe Asp Cys Phe Gly
              105                 110                 115

ctg cac gaa tgg gca atg gtg tac aaa tca aac gat ctc cgc cat gac   499
Leu His Glu Trp Ala Met Val Tyr Lys Ser Asn Asp Leu Arg His Asp
          120                 125                 130

ctt ccc ctg cgc ctt acc cca tcg gaa acc gac cgt gtg gtg gaa agc   547
Leu Pro Leu Arg Leu Thr Pro Ser Glu Thr Asp Arg Val Val Glu Ser
      135                 140                 145

cac aac atc aaa tgc acc cac ttt gat gcc tac cga ttc ttc acc aca   595
His Asn Ile Lys Cys Thr His Phe Asp Ala Tyr Arg Phe Phe Thr Thr
150                 155                 160                 165

cca gcc atc ccg ttg aac ctc acg gtg tta acc cgc gaa gat cag cca   643
Pro Ala Ile Pro Leu Asn Leu Thr Val Leu Thr Arg Glu Asp Gln Pro
                  170                 175                 180

cgc aac gat caa tgt ggt tgt ctg cat gcc acg atg gat cta tac aaa   691
Arg Asn Asp Gln Cys Gly Cys Leu His Ala Thr Met Asp Leu Tyr Lys
              185                 190                 195

tgg tcc gca aag ctt ggc cct ctt gtg cca ggt gat ctt ttc ttg gac   739
Trp Ser Ala Lys Leu Gly Pro Leu Val Pro Gly Asp Leu Phe Leu Asp
          200                 205                 210

gcg ttt gaa cta gcc cgc gac acc cgc atc ttg gac atg gag gct tcg   787
```

```
Ala Phe Glu Leu Ala Arg Asp Thr Arg Ile Leu Asp Met Glu Ala Ser
    215                 220                 225

cct tac gac gtc cgc gga tac ggc ttt ggc tac gtc ccc att gag acc   835
Pro Tyr Asp Val Arg Gly Tyr Gly Phe Gly Tyr Val Pro Ile Glu Thr
230                 235                 240                 245

gcc gag ggc aaa gcc gaa tat gtc agt aga caa cgc gag ctg tct gaa   883
Ala Glu Gly Lys Ala Glu Tyr Val Ser Arg Gln Arg Glu Leu Ser Glu
                250                 255                 260

cga gca aaa ccc atc cgt gac cgg ctt gtc tcc att act aaa caa gct   931
Arg Ala Lys Pro Ile Arg Asp Arg Leu Val Ser Ile Thr Lys Gln Ala
            265                 270                 275

cta cag gct agt att tagaaaatta gacttgtcaa tgt                    969
Leu Gln Ala Ser Ile
        280
```

Sequence Listing

<210> 2006
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 2006

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Met Glu Leu Ala Arg Ala His His Ala Arg Ala Asp Ser Phe Thr Lys
  1               5                  10                  15

Asp His Leu Lys Arg Arg Gln Ala His Ile Lys His Pro Val Phe Asp
             20                  25                  30

Phe Leu Phe Glu Tyr Tyr Pro Val Arg Val Ala His Leu Lys Thr Trp
         35                  40                  45

His Pro Gly Ile Gly Val Phe Leu Glu Gly Thr Pro Pro His Ala Thr
     50                  55                  60

Met Arg Asp Phe Leu Leu Val Asp Ala Ser Leu His His Ala Ala Gly
 65                  70                  75                  80

Val Gln Leu Asp Leu Ala Ser Tyr Met Gln Arg Arg Gly Ser Ser Val
                 85                  90                  95

Arg Tyr Ile His Glu Leu Leu Ser Ala Thr Arg Asp Asn His Ala Gln
            100                 105                 110

Phe Asp Cys Phe Gly Leu His Glu Trp Ala Met Val Tyr Lys Ser Asn
        115                 120                 125

Asp Leu Arg His Asp Leu Pro Leu Arg Leu Thr Pro Ser Glu Thr Asp
    130                 135                 140

Arg Val Val Glu Ser His Asn Ile Lys Cys Thr His Phe Asp Ala Tyr
145                 150                 155                 160

Arg Phe Phe Thr Thr Pro Ala Ile Pro Leu Asn Leu Thr Val Leu Thr
                165                 170                 175

Arg Glu Asp Gln Pro Arg Asn Asp Gln Cys Gly Cys Leu His Ala Thr
            180                 185                 190
```

```
Met Asp Leu Tyr Lys Trp Ser Ala Lys Leu Gly Pro Leu Val Pro Gly
        195                 200                 205

Asp Leu Phe Leu Asp Ala Phe Glu Leu Ala Arg Asp Thr Arg Ile Leu
    210                 215                 220

Asp Met Glu Ala Ser Pro Tyr Asp Val Arg Gly Tyr Gly Phe Gly Tyr
225                 230                 235                 240

Val Pro Ile Glu Thr Ala Glu Gly Lys Ala Glu Tyr Val Ser Arg Gln
                245                 250                 255

Arg Glu Leu Ser Glu Arg Ala Lys Pro Ile Arg Asp Arg Leu Val Ser
            260                 265                 270

Ile Thr Lys Gln Ala Leu Gln Ala Ser Ile
        275                 280
```

<210> 2007
<211> 1830
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1807)
<223> RXA01007

<400> 2007

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tctgaaccaa tataccgatc agtctaaaag tgtgttaagt tctggaacat aaattagctg 60

acacgtaaag taacttaaag attcactgga ggtaagccta gtg ttt aaa aag cac   115
                                            Val Phe Lys Lys His
                                              1               5

aga cac ggt ctc ggc tcc ccc gaa acc aaa cca cgc tca ata acc cgc   163
Arg His Gly Leu Gly Ser Pro Glu Thr Lys Pro Arg Ser Ile Thr Arg
                 10                  15                  20

cgg ttt ttc acc gcg gcc gcc gct acg ctg gca gga ttg gca gtc ctg   211
Arg Phe Phe Thr Ala Ala Ala Ala Thr Leu Ala Gly Leu Ala Val Leu
             25                  30                  35

tcc ggc tgc aca gca caa ccc tca caa gca gaa gac aac acg ctc act   259
Ser Gly Cys Thr Ala Gln Pro Ser Gln Ala Glu Asp Asn Thr Leu Thr
         40                  45                  50

tac tta gag cca cag ttc ttc cgc acc ctg tac cca cca tca gcg ggc   307
Tyr Leu Glu Pro Gln Phe Phe Arg Thr Leu Tyr Pro Pro Ser Ala Gly
     55                  60                  65

ttt tac ccc aac ggc agt gtg gtg aac aac att gca gac cgc ttg ctc   355
Phe Tyr Pro Asn Gly Ser Val Val Asn Asn Ile Ala Asp Arg Leu Leu
 70                  75                  80                  85

tac cag gat cct gaa acc ttg gaa ctc aag ccg tgg atc gcc acc gaa   403
Tyr Gln Asp Pro Glu Thr Leu Glu Leu Lys Pro Trp Ile Ala Thr Glu
                 90                  95                 100
```

```
ctc cca gaa gta aac gaa gac gcc acg gaa ttt acc ttc aac atc cgc   451
Leu Pro Glu Val Asn Glu Asp Ala Thr Glu Phe Thr Phe Asn Ile Arg
            105                 110                 115

acc gat gtc acc tac tcc gat ggc acc ccg ctg acg gct gaa aac gtg   499
Thr Asp Val Thr Tyr Ser Asp Gly Thr Pro Leu Thr Ala Glu Asn Val
        120                 125                 130

gtg aaa aac ttc gat ctc tat ggc ctc ggc gat caa gat cga cgc ctc   547
Val Lys Asn Phe Asp Leu Tyr Gly Leu Gly Asp Gln Asp Arg Arg Leu
    135                 140                 145

acc atc tct gag cag atc acc aac tac gac cac ggc gaa gta gta gat   595
Thr Ile Ser Glu Gln Ile Thr Asn Tyr Asp His Gly Glu Val Val Asp
150                 155                 160                 165

gag gac acc gtc cga ttc cac ttc tct gag cct gca cct ggt ttt gct   643
Glu Asp Thr Val Arg Phe His Phe Ser Glu Pro Ala Pro Gly Phe Ala
                170                 175                 180

cag gcc acc agc tcc ttc aac gct ggc ctt tat gcc gat tcc acc ttg   691
Gln Ala Thr Ser Ser Phe Asn Ala Gly Leu Tyr Ala Asp Ser Thr Leu
            185                 190                 195

gag ttc gcc aat gag gat ttc gcg cca ggc aac gcc caa aac gtc atc   739
Glu Phe Ala Asn Glu Asp Phe Ala Pro Gly Asn Ala Gln Asn Val Ile
        200                 205                 210

ggc tcc ggt cct ttc gtg atc acc gat gaa acc cta ggc acc aac ctc   787
Gly Ser Gly Pro Phe Val Ile Thr Asp Glu Thr Leu Gly Thr Asn Leu
    215                 220                 225

acc ttg act gcg cgt gag gat tac gat tgg gca cca cca tca cgc gaa   835
Thr Leu Thr Ala Arg Glu Asp Tyr Asp Trp Ala Pro Pro Ser Arg Glu
230                 235                 240                 245

cat caa ggt cgc gcg aag ctt gac gcc gtc aat tat gtc ctc gcg ggt   883
His Gln Gly Arg Ala Lys Leu Asp Ala Val Asn Tyr Val Leu Ala Gly
                250                 255                 260

gaa gaa tcc gtc cgc atc gga gcc atc gtt gct ggc caa ggt gat atc   931
Glu Glu Ser Val Arg Ile Gly Ala Ile Val Ala Gly Gln Gly Asp Ile
            265                 270                 275

gcc cgc cag atc gaa gcg cca gtg gag gca cac ctg aag gat gca ggc   979
Ala Arg Gln Ile Glu Ala Pro Val Glu Ala His Leu Lys Asp Ala Gly
        280                 285                 290

atc ccg atc atc tcc gca gcc acc aac ggt gtg aac aac agc ttc aac   1027
Ile Pro Ile Ile Ser Ala Ala Thr Asn Gly Val Asn Asn Ser Phe Asn
    295                 300                 305

ttc cgc ttc aaa aac gag ctg ctc tca gac atc cgt gtt cgc caa gct   1075
Phe Arg Phe Lys Asn Glu Leu Leu Ser Asp Ile Arg Val Arg Gln Ala
310                 315                 320                 325

ctg atc cac gcg atc gac cgc gaa aag atc atg cgt gtg ctg ttt agt   1123
Leu Ile His Ala Ile Asp Arg Glu Lys Ile Met Arg Val Leu Phe Ser
                330                 335                 340

gat tcc tat ccg ctg gca act tct gtg ctt gcg caa aat gca ctg ggc   1171
```

```
Asp Ser Tyr Pro Leu Ala Thr Ser Val Leu Ala Gln Asn Ala Leu Gly
            345                 350                 355

tac aaa gaa caa gta gat gcc tat gtc tac gac cta gac aaa gca aca   1219
Tyr Lys Glu Gln Val Asp Ala Tyr Val Tyr Asp Leu Asp Lys Ala Thr
        360                 365                 370

gct ctg ctt gac gaa gcc ggc tgg acc ctt gat agc gac ggc atg cgt   1267
Ala Leu Leu Asp Glu Ala Gly Trp Thr Leu Asp Ser Asp Gly Met Arg
    375                 380                 385

cgc aag gac ggt gaa ctt cta gag ctc acc ttc aac gaa gcc ctc cca   1315
Arg Lys Asp Gly Glu Leu Leu Glu Leu Thr Phe Asn Glu Ala Leu Pro
390                 395                 400                 405

cag cct cgt tca cgc gaa gtt gtc acc atg gtc caa gaa cag ctc ggt   1363
Gln Pro Arg Ser Arg Glu Val Val Thr Met Val Gln Glu Gln Leu Gly
                410                 415                 420

gat ctg ggc atc aag gtc aac ctc aac cca ggt gac caa gca gcc cag   1411
Asp Leu Gly Ile Lys Val Asn Leu Asn Pro Gly Asp Gln Ala Ala Gln
            425                 430                 435

gac gct gac tcc aag gat ctc aac aag atc cag gtt cgc cac acc atg   1459
Asp Ala Asp Ser Lys Asp Leu Asn Lys Ile Gln Val Arg His Thr Met
        440                 445                 450

gtg ggt cgc gca gac tat gac gtg ctg aaa tcc cag ctg tac tcc acc   1507
Val Gly Arg Ala Asp Tyr Asp Val Leu Lys Ser Gln Leu Tyr Ser Thr
    455                 460                 465

aac cgc aac gag ctg ttg aac atg acc gtg gaa ggg gag acc gcc gat   1555
Asn Arg Asn Glu Leu Leu Asn Met Thr Val Glu Gly Glu Thr Ala Asp
470                 475                 480                 485

att ggc gat cct cat ttg gag gaa ctc ctc atg gct att gca tcc agc   1603
Ile Gly Asp Pro His Leu Glu Glu Leu Leu Met Ala Ile Ala Ser Ser
                490                 495                 500

cca cgc gaa gag gac cgt gca gca gca tct gcc gca gca cag gat tac   1651
Pro Arg Glu Glu Asp Arg Ala Ala Ala Ser Ala Ala Ala Gln Asp Tyr
            505                 510                 515

atc acc gag cag gca tat gtt ctt cca ctg ttt gaa gag cca gtt gtc   1699
Ile Thr Glu Gln Ala Tyr Val Leu Pro Leu Phe Glu Glu Pro Val Val
        520                 525                 530

tac ggc gtg cag cct tac gtg aag ggc ttt agc ccc gaa gtg atc ggc   1747
Tyr Gly Val Gln Pro Tyr Val Lys Gly Phe Ser Pro Glu Val Ile Gly
    535                 540                 545

cgc ccc agc ttc tat gag acc tac att gac cat tcc agc gac cat tcc   1795
Arg Pro Ser Phe Tyr Glu Thr Tyr Ile Asp His Ser Ser Asp His Ser
550                 555                 560                 565

agt gag gag gac taaatgacta cctcgcagat tct                        1830
Ser Glu Glu Asp
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<210> 2008

<211> 569
<212> PRT
<213> Corynebacterium glutamicum

<400> 2008

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Val Phe Lys Lys His Arg His Gly Leu Gly Ser Pro Glu Thr Lys Pro
  1               5                  10                  15

Arg Ser Ile Thr Arg Arg Phe Phe Thr Ala Ala Ala Ala Thr Leu Ala
             20                  25                  30

Gly Leu Ala Val Leu Ser Gly Cys Thr Ala Gln Pro Ser Gln Ala Glu
         35                  40                  45

Asp Asn Thr Leu Thr Tyr Leu Glu Pro Gln Phe Phe Arg Thr Leu Tyr
     50                  55                  60

Pro Pro Ser Ala Gly Phe Tyr Pro Asn Gly Ser Val Val Asn Asn Ile
 65                  70                  75                  80

Ala Asp Arg Leu Leu Tyr Gln Asp Pro Glu Thr Leu Glu Leu Lys Pro
                 85                  90                  95

Trp Ile Ala Thr Glu Leu Pro Glu Val Asn Glu Asp Ala Thr Glu Phe
            100                 105                 110

Thr Phe Asn Ile Arg Thr Asp Val Thr Tyr Ser Asp Gly Thr Pro Leu
        115                 120                 125

Thr Ala Glu Asn Val Val Lys Asn Phe Asp Leu Tyr Gly Leu Gly Asp
    130                 135                 140

Gln Asp Arg Arg Leu Thr Ile Ser Glu Gln Ile Thr Asn Tyr Asp His
145                 150                 155                 160

Gly Glu Val Val Asp Glu Asp Thr Val Arg Phe His Phe Ser Glu Pro
                165                 170                 175

Ala Pro Gly Phe Ala Gln Ala Thr Ser Ser Phe Asn Ala Gly Leu Tyr
            180                 185                 190

Ala Asp Ser Thr Leu Glu Phe Ala Asn Glu Asp Phe Ala Pro Gly Asn
        195                 200                 205

Ala Gln Asn Val Ile Gly Ser Gly Pro Phe Val Ile Thr Asp Glu Thr
    210                 215                 220

Leu Gly Thr Asn Leu Thr Leu Thr Ala Arg Glu Asp Tyr Asp Trp Ala
225                 230                 235                 240

Pro Pro Ser Arg Glu His Gln Gly Arg Ala Lys Leu Asp Ala Val Asn
                245                 250                 255

Tyr Val Leu Ala Gly Glu Glu Ser Val Arg Ile Gly Ala Ile Val Ala
            260                 265                 270

Gly Gln Gly Asp Ile Ala Arg Gln Ile Glu Ala Pro Val Glu Ala His
        275                 280                 285

Leu Lys Asp Ala Gly Ile Pro Ile Ile Ser Ala Ala Thr Asn Gly Val
    290                 295                 300
```

```
Asn Asn Ser Phe Asn Phe Arg Phe Lys Asn Glu Leu Leu Ser Asp Ile
305                 310                 315                 320

Arg Val Arg Gln Ala Leu Ile His Ala Ile Asp Arg Glu Lys Ile Met
                325                 330                 335

Arg Val Leu Phe Ser Asp Ser Tyr Pro Leu Ala Thr Ser Val Leu Ala
            340                 345                 350

Gln Asn Ala Leu Gly Tyr Lys Glu Gln Val Asp Ala Tyr Val Tyr Asp
        355                 360                 365

Leu Asp Lys Ala Thr Ala Leu Leu Asp Glu Ala Gly Trp Thr Leu Asp
    370                 375                 380

Ser Asp Gly Met Arg Arg Lys Asp Gly Glu Leu Leu Glu Leu Thr Phe
385                 390                 395                 400

Asn Glu Ala Leu Pro Gln Pro Arg Ser Arg Glu Val Val Thr Met Val
                405                 410                 415

Gln Glu Gln Leu Gly Asp Leu Gly Ile Lys Val Asn Leu Asn Pro Gly
            420                 425                 430

Asp Gln Ala Ala Gln Asp Ala Asp Ser Lys Asp Leu Asn Lys Ile Gln
        435                 440                 445

Val Arg His Thr Met Val Gly Arg Ala Asp Tyr Asp Val Leu Lys Ser
    450                 455                 460

Gln Leu Tyr Ser Thr Asn Arg Asn Glu Leu Leu Asn Met Thr Val Glu
465                 470                 475                 480

Gly Glu Thr Ala Asp Ile Gly Asp Pro His Leu Glu Glu Leu Leu Met
                485                 490                 495

Ala Ile Ala Ser Ser Pro Arg Glu Glu Asp Arg Ala Ala Ala Ser Ala
            500                 505                 510

Ala Ala Gln Asp Tyr Ile Thr Glu Gln Ala Tyr Val Leu Pro Leu Phe
        515                 520                 525

Glu Glu Pro Val Val Tyr Gly Val Gln Pro Tyr Val Lys Gly Phe Ser
    530                 535                 540

Pro Glu Val Ile Gly Arg Pro Ser Phe Tyr Glu Thr Tyr Ile Asp His
545                 550                 555                 560

Ser Ser Asp His Ser Ser Glu Glu Asp
                565
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<210> 2009
<211> 2064
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2041)

<223> RXA01008

<400> 2009

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atttatgttc cagaacttaa cacactttta gactgatcgg tatattggtt cagaccaacc 60

tgtctaattg gggtatttat tttaatgatc aggagttttc gtg agc aca acc gat   115
                                            Val Ser Thr Thr Asp
                                              1               5

aag cag gta gcc atc gtt gga gtt ggc ccc aga ggt att tcc ata ctc   163
Lys Gln Val Ala Ile Val Gly Val Gly Pro Arg Gly Ile Ser Ile Leu
                 10                  15                  20

gaa agg atc gca gca gct ctc aac aca gtt tcc cgc ccc aaa caa ggc   211
Glu Arg Ile Ala Ala Ala Leu Asn Thr Val Ser Arg Pro Lys Gln Gly
             25                  30                  35

ttg acc atc cac ctg att gag gat gcc cag atg ggt gca ggc aac gtg   259
Leu Thr Ile His Leu Ile Glu Asp Ala Gln Met Gly Ala Gly Asn Val
         40                  45                  50

tgg cgc act gat caa acc cgc acg ctg tgc atg aat act ctg gcc ggt   307
Trp Arg Thr Asp Gln Thr Arg Thr Leu Cys Met Asn Thr Leu Ala Gly
     55                  60                  65

gcg gtg aca tta ttc aca gag cca ggc tct acg gtg agc gct cca gtg   355
Ala Val Thr Leu Phe Thr Glu Pro Gly Ser Thr Val Ser Ala Pro Val
 70                  75                  80                  85

gtg gaa gga cca ctg caa ttt gat tgg att cgc ctg ctg cgc ggc gat   403
Val Glu Gly Pro Leu Gln Phe Asp Trp Ile Arg Leu Leu Arg Gly Asp
                 90                  95                 100

gag gat ttg agc ggc att cct aca aaa gcc atc gag ctg ttc cgc acc   451
Glu Asp Leu Ser Gly Ile Pro Thr Lys Ala Ile Glu Leu Phe Arg Thr
             105                 110                 115

tac ccc cca gct gca tcc gtg gcg gag gat ttc aag gaa gag cta gca   499
Tyr Pro Pro Ala Ala Ser Val Ala Glu Asp Phe Lys Glu Glu Leu Ala
         120                 125                 130

gcc act gtt atc cag tcc aat cct tcc cgt gct ctt tat ggc gca tat   547
Ala Thr Val Ile Gln Ser Asn Pro Ser Arg Ala Leu Tyr Gly Ala Tyr
     135                 140                 145

ctg cgg tgg gct ttc gat gtc gct ttg cag ctg ttg cca cag tgg gtc   595
Leu Arg Trp Ala Phe Asp Val Ala Leu Gln Leu Leu Pro Gln Trp Val
150                 155                 160                 165

aag gtc gag cag cac cat gcg cgc gcg att ggc atc cgc gaa gat ggt   643
Lys Val Glu Gln His His Ala Arg Ala Ile Gly Ile Arg Glu Asp Gly
                170                 175                 180

gac cgc gat gtg atc acc tta gat aat tct gag atg att tcc gcc gat   691
Asp Arg Asp Val Ile Thr Leu Asp Asn Ser Glu Met Ile Ser Ala Asp
            185                 190                 195

tcc act gtg ttg gct gtc ggc tgg caa acc ccc gcc ccc aat gcg gag   739
Ser Thr Val Leu Ala Val Gly Trp Gln Thr Pro Ala Pro Asn Ala Glu
        200                 205                 210
```

```
gag ctg tcc atc gcg gct gct ttg gag gag aac cct gat ctg gtg tgg   787
Glu Leu Ser Ile Ala Ala Ala Leu Glu Glu Asn Pro Asp Leu Val Trp
    215                 220                 225

gtc aag ccc ggc aac cct gtc gag cag gat gcc agc ctc att ccc gct   835
Val Lys Pro Gly Asn Pro Val Glu Gln Asp Ala Ser Leu Ile Pro Ala
230                 235                 240                 245

ggc gaa cag gtg ctt gtc cgc ggg ctg ggc atg gga ttt ttc gat atc   883
Gly Glu Gln Val Leu Val Arg Gly Leu Gly Met Gly Phe Phe Asp Ile
                250                 255                 260

atg gcg ctg acc acc atc gat cgt ggc ggc atc ttc cac gag gat ccc   931
Met Ala Leu Thr Thr Ile Asp Arg Gly Gly Ile Phe His Glu Asp Pro
            265                 270                 275

agc acc cgt tcc ggt ttg cgc tac gag gca tct ggt gag gaa cca cac   979
Ser Thr Arg Ser Gly Leu Arg Tyr Glu Ala Ser Gly Glu Glu Pro His
        280                 285                 290

ttt gtt att tcc tcc ggg cgc ggc tac ccc tac ctg cct aaa tcc gat   1027
Phe Val Ile Ser Ser Gly Arg Gly Tyr Pro Tyr Leu Pro Lys Ser Asp
    295                 300                 305

tac aaa tcg ctg cca cca ggg gca aag cta gcg cga ctc aag gct gtt   1075
Tyr Lys Ser Leu Pro Pro Gly Ala Lys Leu Ala Arg Leu Lys Ala Val
310                 315                 320                 325

atc gcg gcg atc aac gcg caa aat cgt ggt gtc gca tcc atc aac tat   1123
Ile Ala Ala Ile Asn Ala Gln Asn Arg Gly Val Ala Ser Ile Asn Tyr
                330                 335                 340

gat gcg gaa gtg tgg cca gct gtt gct cgc gac gcc tac gaa gcc tat   1171
Asp Ala Glu Val Trp Pro Ala Val Ala Arg Asp Ala Tyr Glu Ala Tyr
            345                 350                 355

tac gaa acc ctt gat cgc gta agc cca gaa tct atc cgg acc ggt ctg   1219
Tyr Glu Thr Leu Asp Arg Val Ser Pro Glu Ser Ile Arg Thr Gly Leu
        360                 365                 370

gat aaa att gtg gaa att att gat gag gtg gac gtc gat aag ctt cct   1267
Asp Lys Ile Val Glu Ile Ile Asp Glu Val Asp Val Asp Lys Leu Pro
    375                 380                 385

aaa gca ctc gcc gcg cac acc gat gac gtc ttt gac ctg cat gct tgg   1315
Lys Ala Leu Ala Ala His Thr Asp Asp Val Phe Asp Leu His Ala Trp
390                 395                 400                 405

gaa ttt ccg ctc gcg gga att aat gaa agc gtc gag gcg ctg acc gca   1363
Glu Phe Pro Leu Ala Gly Ile Asn Glu Ser Val Glu Ala Leu Thr Ala
                410                 415                 420

cgc atc gcg gac ggc atg gcc cgc gat att cgc cat gca gta acg gcc   1411
Arg Ile Ala Asp Gly Met Ala Arg Asp Ile Arg His Ala Val Thr Ala
            425                 430                 435

tgg gac agc ccg ctg aaa tcc gcg ctg tgg tcc att tcc gcc gcg cgc   1459
Trp Asp Ser Pro Leu Lys Ser Ala Leu Trp Ser Ile Ser Ala Ala Arg
        440                 445                 450

aaa ccc agc tcc atc ctg ggc gcg gaa ggc cgc ctg acc ttc gaa tcg   1507
```

```
Lys Pro Ser Ser Ile Leu Gly Ala Glu Gly Arg Leu Thr Phe Glu Ser
    455                 460                 465

cgc cgc aac cgc ttc gcc gcc gtc atg gcg atc ggc cag atg gtc ggc   1555
Arg Arg Asn Arg Phe Ala Ala Val Met Ala Ile Gly Gln Met Val Gly
470                 475                 480                 485

tcc ggc cca ccg ctt ttc cgc acc cgc gaa ctt ctt gcg ctt gtc gac   1603
Ser Gly Pro Pro Leu Phe Arg Thr Arg Glu Leu Leu Ala Leu Val Asp
                490                 495                 500

gcc ggc ctc gct cac ttc gcc ggc gcc cgc ccc cgc ctc agc gtg agc   1651
Ala Gly Leu Ala His Phe Ala Gly Ala Arg Pro Arg Leu Ser Val Ser
            505                 510                 515

gac ggt caa tgg cag atc tcc tcg ccc acc acc ggc gat acg ccg ctg   1699
Asp Gly Gln Trp Gln Ile Ser Ser Pro Thr Thr Gly Asp Thr Pro Leu
        520                 525                 530

aga tcg aaa gtg ctt gtc gac gcg tgg atg cac aac cca gat gtg cgt   1747
Arg Ser Lys Val Leu Val Asp Ala Trp Met His Asn Pro Asp Val Arg
    535                 540                 545

cgc aac gcc gac ccg cta gca ctg tct ttg gaa gat gcc gac cgg gta   1795
Arg Asn Ala Asp Pro Leu Ala Leu Ser Leu Glu Asp Ala Asp Arg Val
550                 555                 560                 565

cgc ccc ttc aac gac tat tcc gtc gac gga acc gct gcc ccc aca ggc   1843
Arg Pro Phe Asn Asp Tyr Ser Val Asp Gly Thr Ala Ala Pro Thr Gly
                570                 575                 580

tcc ccc gaa gtt gat ccg gca acc cga ctt ttg gtt cac ccc aac ggc   1891
Ser Pro Glu Val Asp Pro Ala Thr Arg Leu Leu Val His Pro Asn Gly
            585                 590                 595

aac ctc gat ccg cgc gtg cac ctg att ggc atc cca acc tat ggg cag   1939
Asn Leu Asp Pro Arg Val His Leu Ile Gly Ile Pro Thr Tyr Gly Gln
        600                 605                 610

ctg gcc gac acc acc atc tcg ccg atg cct gga acc aac ccg ctc atg   1987
Leu Ala Asp Thr Thr Ile Ser Pro Met Pro Gly Thr Asn Pro Leu Met
    615                 620                 625

ctg caa gaa acc gac aaa aca gcc gtt cac gtg cta aag cag ctc ggc   2035
Leu Gln Glu Thr Asp Lys Thr Ala Val His Val Leu Lys Gln Leu Gly
630                 635                 640                 645

ttg atc tagggtgagg tgagttattt aaa                                2064
Leu Ile
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<210> 2010
<211> 647
<212> PRT
<213> Corynebacterium glutamicum

<400> 2010

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Val Ser Thr Thr Asp Lys Gln Val Ala Ile Val Gly Val Gly Pro Arg
  1               5                  10                  15
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Gly Ile Ser Ile Leu Glu Arg Ile Ala Ala Ala Leu Asn Thr Val Ser
20 25 30

Arg Pro Lys Gln Gly Leu Thr Ile His Leu Ile Glu Asp Ala Gln Met
35 40 45

Gly Ala Gly Asn Val Trp Arg Thr Asp Gln Thr Arg Thr Leu Cys Met
50 55 60

Asn Thr Leu Ala Gly Ala Val Thr Leu Phe Thr Glu Pro Gly Ser Thr
65 70 75 80

Val Ser Ala Pro Val Val Glu Gly Pro Leu Gln Phe Asp Trp Ile Arg
85 90 95

Leu Leu Arg Gly Asp Glu Asp Leu Ser Gly Ile Pro Thr Lys Ala Ile
100 105 110

Glu Leu Phe Arg Thr Tyr Pro Pro Ala Ala Ser Val Ala Glu Asp Phe
115 120 125

Lys Glu Glu Leu Ala Ala Thr Val Ile Gln Ser Asn Pro Ser Arg Ala
130 135 140

Leu Tyr Gly Ala Tyr Leu Arg Trp Ala Phe Asp Val Ala Leu Gln Leu
145 150 155 160

Leu Pro Gln Trp Val Lys Val Glu Gln His His Ala Arg Ala Ile Gly
165 170 175

Ile Arg Glu Asp Gly Asp Arg Asp Val Ile Thr Leu Asp Asn Ser Glu
180 185 190

Met Ile Ser Ala Asp Ser Thr Val Leu Ala Val Gly Trp Gln Thr Pro
195 200 205

Ala Pro Asn Ala Glu Glu Leu Ser Ile Ala Ala Ala Leu Glu Glu Asn
210 215 220

Pro Asp Leu Val Trp Val Lys Pro Gly Asn Pro Val Glu Gln Asp Ala
225 230 235 240

Ser Leu Ile Pro Ala Gly Glu Gln Val Leu Val Arg Gly Leu Gly Met
245 250 255

Gly Phe Phe Asp Ile Met Ala Leu Thr Thr Ile Asp Arg Gly Gly Ile
260 265 270

Phe His Glu Asp Pro Ser Thr Arg Ser Gly Leu Arg Tyr Glu Ala Ser
275 280 285

Gly Glu Glu Pro His Phe Val Ile Ser Ser Gly Arg Gly Tyr Pro Tyr
290 295 300

Leu Pro Lys Ser Asp Tyr Lys Ser Leu Pro Pro Gly Ala Lys Leu Ala
305 310 315 320

Arg Leu Lys Ala Val Ile Ala Ala Ile Asn Ala Gln Asn Arg Gly Val
325 330 335

Ala Ser Ile Asn Tyr Asp Ala Glu Val Trp Pro Ala Val Ala Arg Asp

```
            340                 345                 350

Ala Tyr Glu Ala Tyr Tyr Glu Thr Leu Asp Arg Val Ser Pro Glu Ser
        355                 360                 365

Ile Arg Thr Gly Leu Asp Lys Ile Val Glu Ile Ile Asp Glu Val Asp
    370                 375                 380

Val Asp Lys Leu Pro Lys Ala Leu Ala Ala His Thr Asp Asp Val Phe
385                 390                 395                 400

Asp Leu His Ala Trp Glu Phe Pro Leu Ala Gly Ile Asn Glu Ser Val
                405                 410                 415

Glu Ala Leu Thr Ala Arg Ile Ala Asp Gly Met Ala Arg Asp Ile Arg
            420                 425                 430

His Ala Val Thr Ala Trp Asp Ser Pro Leu Lys Ser Ala Leu Trp Ser
        435                 440                 445

Ile Ser Ala Ala Arg Lys Pro Ser Ser Ile Leu Gly Ala Glu Gly Arg
    450                 455                 460

Leu Thr Phe Glu Ser Arg Arg Asn Arg Phe Ala Ala Val Met Ala Ile
465                 470                 475                 480

Gly Gln Met Val Gly Ser Gly Pro Pro Leu Phe Arg Thr Arg Glu Leu
                485                 490                 495

Leu Ala Leu Val Asp Ala Gly Leu Ala His Phe Ala Gly Ala Arg Pro
            500                 505                 510

Arg Leu Ser Val Ser Asp Gly Gln Trp Gln Ile Ser Ser Pro Thr Thr
        515                 520                 525

Gly Asp Thr Pro Leu Arg Ser Lys Val Leu Val Asp Ala Trp Met His
    530                 535                 540

Asn Pro Asp Val Arg Arg Asn Ala Asp Pro Leu Ala Leu Ser Leu Glu
545                 550                 555                 560

Asp Ala Asp Arg Val Arg Pro Phe Asn Asp Tyr Ser Val Asp Gly Thr
                565                 570                 575

Ala Ala Pro Thr Gly Ser Pro Glu Val Asp Pro Ala Thr Arg Leu Leu
            580                 585                 590

Val His Pro Asn Gly Asn Leu Asp Pro Arg Val His Leu Ile Gly Ile
        595                 600                 605

Pro Thr Tyr Gly Gln Leu Ala Asp Thr Thr Ile Ser Pro Met Pro Gly
    610                 615                 620

Thr Asn Pro Leu Met Leu Gln Glu Thr Asp Lys Thr Ala Val His Val
625                 630                 635                 640

Leu Lys Gln Leu Gly Leu Ile
                645
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<210> 2011

<211> 1356
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1333)
<223> RXA01011

<400> 2011
cccgcaaacc gatttcactc gccgactcat cgacgcgatc ccaggatcgc gctatcgtgg 60

tggcgaactc aatcttggac tataggagca gatcttaaaa atg tca gat ctc atc 115
Met Ser Asp Leu Ile
1 5

gac atg ctg gtt gga gaa gac ctc cca cag ctg cgt gac aac cgt ccc 163
Asp Met Leu Val Gly Glu Asp Leu Pro Gln Leu Arg Asp Asn Arg Pro
10 15 20

caa gct cgc gac aat gca caa aag agc ttc gaa gct ctg ctc gaa ccg 211
Gln Ala Arg Asp Asn Ala Gln Lys Ser Phe Glu Ala Leu Leu Glu Pro
25 30 35

gtc aac cca gga acc ttc agc ttc ggc gag cgt tac gcc gtg gcc acc 259
Val Asn Pro Gly Thr Phe Ser Phe Gly Glu Arg Tyr Ala Val Ala Thr
40 45 50

tat gtt gca ggt ttg cac caa ttc gcg cca gct gta gat ctc tac caa 307
Tyr Val Ala Gly Leu His Gln Phe Ala Pro Ala Val Asp Leu Tyr Gln
55 60 65

gat ttg ctt ctc gac gac gcc cca acc acc ctg gca aac gcc gtc tcc 355
Asp Leu Leu Leu Asp Asp Ala Pro Thr Thr Leu Ala Asn Ala Val Ser
70 75 80 85

gat gcc atc gac gag ggc cta tcc gca ggc cca tac ggc acc tac cgt 403
Asp Ala Ile Asp Glu Gly Leu Ser Ala Gly Pro Tyr Gly Thr Tyr Arg
90 95 100

gaa cct gga ctt gag tcc gaa tca gag cca ggc gga tct gtg cgc aac 451
Glu Pro Gly Leu Glu Ser Glu Ser Glu Pro Gly Gly Ser Val Arg Asn
105 110 115

gat gcc gcc aag ctt ggc gag cga ctt gca gca gca ttt gat tac gca 499
Asp Ala Ala Lys Leu Gly Glu Arg Leu Ala Ala Ala Phe Asp Tyr Ala
120 125 130

cac cta cta gtt ttc cac ccc cgt gat tcc cgc ccc gag gtc ctt ggt 547
His Leu Leu Val Phe His Pro Arg Asp Ser Arg Pro Glu Val Leu Gly
135 140 145

cga ctc tcc ggc gct ggc tgg agc gcg gat gac acc gtg aca ttg gct 595
Arg Leu Ser Gly Ala Gly Trp Ser Ala Asp Asp Thr Val Thr Leu Ala
150 155 160 165

cag ctg gtg tcg ttc ctg gca ttc cag ctg cgt gtt gcc tac ggc ctg 643
Gln Leu Val Ser Phe Leu Ala Phe Gln Leu Arg Val Ala Tyr Gly Leu
170 175 180

cgc acc ctc aaa ggt gaa gac att cag gtg aaa gct cct cgc ctg agt 691

```
Arg Thr Leu Lys Gly Glu Asp Ile Gln Val Lys Ala Pro Arg Leu Ser
            185                 190                 195

att cct gaa gcg aag tgg gaa ctg tcc aac aac ggc ttt gag atc tcc   739
Ile Pro Glu Ala Lys Trp Glu Leu Ser Asn Asn Gly Phe Glu Ile Ser
        200                 205                 210

acc tat gaa gaa ctc aac cgc cct gaa gcg ttt gtg aac cac tct ttg   787
Thr Tyr Glu Glu Leu Asn Arg Pro Glu Ala Phe Val Asn His Ser Leu
    215                 220                 225

ggc tgg aag cca tgg gta cca cca gta gca aag gca gat ctc acc gaa   835
Gly Trp Lys Pro Trp Val Pro Pro Val Ala Lys Ala Asp Leu Thr Glu
230                 235                 240                 245

gaa cag ctg gat tct ttg atc cag cct gag cgc gct gat atg cca tac   883
Glu Gln Leu Asp Ser Leu Ile Gln Pro Glu Arg Ala Asp Met Pro Tyr
                250                 255                 260

ttc cgt ctc ttg gca cgc gat cct gca gca ttg aag gcg cgt acc ctg   931
Phe Arg Leu Leu Ala Arg Asp Pro Ala Ala Leu Lys Ala Arg Thr Leu
            265                 270                 275

acc gat ctg gat atc ttc ttc aac act gac ggc gaa ggc cta gga cgt   979
Thr Asp Leu Asp Ile Phe Phe Asn Thr Asp Gly Glu Gly Leu Gly Arg
        280                 285                 290

gca gag cgt gaa ctc ggc gcc acc gtt act tcc cgc tac aac ggc tgc  1027
Ala Glu Arg Glu Leu Gly Ala Thr Val Thr Ser Arg Tyr Asn Gly Cys
    295                 300                 305

gtg tac tgc gca tcc gtg cac gca gga cgt gct cag gaa gaa tcc ggt  1075
Val Tyr Cys Ala Ser Val His Ala Gly Arg Ala Gln Glu Glu Ser Gly
310                 315                 320                 325

cga gct gat gat gtc aac gca ctg ttg gca agc atc gac tcc gat ctg  1123
Arg Ala Asp Asp Val Asn Ala Leu Leu Ala Ser Ile Asp Ser Asp Leu
                330                 335                 340

ggt tct gac cag tgg aat gtc atc cgt gac gct gct cgc gca ctg agc  1171
Gly Ser Asp Gln Trp Asn Val Ile Arg Asp Ala Ala Arg Ala Leu Ser
            345                 350                 355

tcc acc cct gct gct ttc aac cag gga tgc atc acc aag ctg cgt ggc  1219
Ser Thr Pro Ala Ala Phe Asn Gln Gly Cys Ile Thr Lys Leu Arg Gly
        360                 365                 370

gtt gga ttc agc gac ctg cag atc gtg gac ttg atc aac tct gtg gcg  1267
Val Gly Phe Ser Asp Leu Gln Ile Val Asp Leu Ile Asn Ser Val Ala
    375                 380                 385

ttc ttc aac tgg gcg aac cgc ctg atg ttg tca ctg ggt gaa ccc gaa  1315
Phe Phe Asn Trp Ala Asn Arg Leu Met Leu Ser Leu Gly Glu Pro Glu
390                 395                 400                 405

gtg cca aag cgt ttc ctg taaaacgcat aaccccgaat acc                1356
Val Pro Lys Arg Phe Leu
                410
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<210> 2012

<211> 411
<212> PRT
<213> Corynebacterium glutamicum

<400> 2012

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Met Ser Asp Leu Ile Asp Met Leu Val Gly Glu Asp Leu Pro Gln Leu
  1               5                  10                  15

Arg Asp Asn Arg Pro Gln Ala Arg Asp Asn Ala Gln Lys Ser Phe Glu
             20                  25                  30

Ala Leu Leu Glu Pro Val Asn Pro Gly Thr Phe Ser Phe Gly Glu Arg
         35                  40                  45

Tyr Ala Val Ala Thr Tyr Val Ala Gly Leu His Gln Phe Ala Pro Ala
     50                  55                  60

Val Asp Leu Tyr Gln Asp Leu Leu Leu Asp Asp Ala Pro Thr Thr Leu
 65                  70                  75                  80

Ala Asn Ala Val Ser Asp Ala Ile Asp Glu Gly Leu Ser Ala Gly Pro
                 85                  90                  95

Tyr Gly Thr Tyr Arg Glu Pro Gly Leu Glu Ser Glu Ser Glu Pro Gly
            100                 105                 110

Gly Ser Val Arg Asn Asp Ala Ala Lys Leu Gly Glu Arg Leu Ala Ala
        115                 120                 125

Ala Phe Asp Tyr Ala His Leu Leu Val Phe His Pro Arg Asp Ser Arg
    130                 135                 140

Pro Glu Val Leu Gly Arg Leu Ser Gly Ala Gly Trp Ser Ala Asp Asp
145                 150                 155                 160

Thr Val Thr Leu Ala Gln Leu Val Ser Phe Leu Ala Phe Gln Leu Arg
                165                 170                 175

Val Ala Tyr Gly Leu Arg Thr Leu Lys Gly Glu Asp Ile Gln Val Lys
            180                 185                 190

Ala Pro Arg Leu Ser Ile Pro Glu Ala Lys Trp Glu Leu Ser Asn Asn
        195                 200                 205

Gly Phe Glu Ile Ser Thr Tyr Glu Glu Leu Asn Arg Pro Glu Ala Phe
    210                 215                 220

Val Asn His Ser Leu Gly Trp Lys Pro Trp Val Pro Pro Val Ala Lys
225                 230                 235                 240

Ala Asp Leu Thr Glu Glu Gln Leu Asp Ser Leu Ile Gln Pro Glu Arg
                245                 250                 255

Ala Asp Met Pro Tyr Phe Arg Leu Leu Ala Arg Asp Pro Ala Ala Leu
            260                 265                 270

Lys Ala Arg Thr Leu Thr Asp Leu Asp Ile Phe Phe Asn Thr Asp Gly
        275                 280                 285

Glu Gly Leu Gly Arg Ala Glu Arg Glu Leu Gly Ala Thr Val Thr Ser
    290                 295                 300
```

```
Arg Tyr Asn Gly Cys Val Tyr Cys Ala Ser Val His Ala Gly Arg Ala
305                 310                 315                 320

Gln Glu Glu Ser Gly Arg Ala Asp Asp Val Asn Ala Leu Leu Ala Ser
                325                 330                 335

Ile Asp Ser Asp Leu Gly Ser Asp Gln Trp Asn Val Ile Arg Asp Ala
            340                 345                 350

Ala Arg Ala Leu Ser Ser Thr Pro Ala Ala Phe Asn Gln Gly Cys Ile
        355                 360                 365

Thr Lys Leu Arg Gly Val Gly Phe Ser Asp Leu Gln Ile Val Asp Leu
    370                 375                 380

Ile Asn Ser Val Ala Phe Phe Asn Trp Ala Asn Arg Leu Met Leu Ser
385                 390                 395                 400

Leu Gly Glu Pro Glu Val Pro Lys Arg Phe Leu
                405                 410
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09/25/2003 09:55:55

<210> 2013
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> RXA01017

<400> 2013

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gaaatttgag ggggcgctac ccttagaagg tgcgcaatga caccacgata gttcgcgcct 60

agtgtggatt gctagaaaac tttaagaaag aggaaataat atg gct caa aaa gta   115
                                            Met Ala Gln Lys Val
                                              1               5

acc ttc tgg ttc gat acc acc tgc cca ttc tgc tgg gtc acc tcc cgc   163
Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys Trp Val Thr Ser Arg
                  10                  15                  20

tgg att aag gaa gtc gaa caa gtc cgc gat att gaa atc cag tgg gtt   211
Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile Glu Ile Gln Trp Val
              25                  30                  35

cca atg agc ctc gct gtc cta aac gaa ggc cgt gat ctc cca gag gat   259
Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg Asp Leu Pro Glu Asp
          40                  45                  50

tac aag gag cgc atg aag gct gca tgg gga cca gca cgc gtt ttc gca   307
Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro Ala Arg Val Phe Ala
      55                  60                  65

gct gtc gcc acc gac cat gct gac aag ctc ggc gac ctg tac acc gca   355
Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly Asp Leu Tyr Thr Ala
 70                  75                  80                  85

atg ggt acc cgc atc cac aac gac ggt cgc gga cca atc gaa ggt tcc   403
```

```
Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly Pro Ile Glu Gly Ser
                 90                  95                 100

ttc aat gat gtc atc gca gag gca ctt gaa gag gtc ggc cta gac gct   451
Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu Val Gly Leu Asp Ala
            105                 110                 115

gca ctt ggt gaa gtt gca gac acc acc gaa tgg gac gac gca ctt cgc   499
Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp Asp Asp Ala Leu Arg
        120                 125                 130

gca ttc cac cag acc gca atg gac gag gtc ggc aac gat gtc gga acc   547
Ala Phe His Gln Thr Ala Met Asp Glu Val Gly Asn Asp Val Gly Thr
    135                 140                 145

cca gtg gtc aag ctc ggc gac acc gct ttc ttc ggc cca gtg ctc acc   595
Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe Gly Pro Val Leu Thr
150                 155                 160                 165

cgc atc cca cgc ggc gag gaa gca gga gag atc ttc gac gct tcc ttc   643
Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile Phe Asp Ala Ser Phe
                170                 175                 180

aag ctc gca agc tat ccc cac ttc ttt gaa atc aag cgc agc cgc act   691
Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile Lys Arg Ser Arg Thr
            185                 190                 195

gag aac cca cag ttc gac taattaacgc tgtctctgct tat                732
Glu Asn Pro Gln Phe Asp
        200
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CONFIDENTIAL

<210> 2014
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 2014

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Met Ala Gln Lys Val Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys
  1               5                  10                  15

Trp Val Thr Ser Arg Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile
             20                  25                  30

Glu Ile Gln Trp Val Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg
         35                  40                  45

Asp Leu Pro Glu Asp Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro
     50                  55                  60

Ala Arg Val Phe Ala Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly
 65                  70                  75                  80

Asp Leu Tyr Thr Ala Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly
                 85                  90                  95

Pro Ile Glu Gly Ser Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu
            100                 105                 110

Val Gly Leu Asp Ala Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp
        115                 120                 125
```

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Asp Asp Ala Leu Arg Ala Phe His Gln Thr Ala Met Asp Glu Val Gly
    130                 135                 140

Asn Asp Val Gly Thr Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe
145                 150                 155                 160

Gly Pro Val Leu Thr Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile
                165                 170                 175

Phe Asp Ala Ser Phe Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile
            180                 185                 190

Lys Arg Ser Arg Thr Glu Asn Pro Gln Phe Asp
        195                 200


<210> 2015
<211> 622
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(622)
<223> RXA01021

<400> 2015
cgagaggctt ttttggctct aagcctttta gtcgtgcgaa cgaaatctta agcagcctcg 60

gtgccaccga gatcgattgg tcgctgtaag gtatctgatt atg tcc agt tcc gaa   115
                                        Met Ser Ser Ser Glu
                                          1               5

agc tcg cgt tcc gaa ggc tcg cag cca gca ccg tct gta cag cct gaa   163
Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro Ser Val Gln Pro Glu
                 10                  15                  20

cgc cgt gct gat tca acg ggg gct cct gcg gca gct tcc aag gaa gct   211
Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala
             25                  30                  35

tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct   259
Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala
         40                  45                  50

gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc   307
Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val
     55                  60                  65

ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg   355
Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met
 70                  75                  80                  85

aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc   403
Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val
                 90                  95                 100

gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga   451
Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg
            105                 110                 115
```

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gga aat tct gga gta gtc ctt agt cag gtc ctt cgc gct att gct cag   499
Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln
        120                 125                 130

gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta   547
Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Glu Ala Leu
    135                 140                 145

tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag   595
Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Glu
150                 155                 160                 165

ggc act gtt gtc act gtg ttg cgt tct                              622
Gly Thr Val Val Thr Val Leu Arg Ser
                170
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<210> 2016
<211> 174
<212> PRT
<213> Corynebacterium glutamicum

<400> 2016

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Met Ser Ser Ser Glu Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro
  1               5                  10                  15

Ser Val Gln Pro Glu Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala
             20                  25                  30

Ala Ser Lys Glu Ala Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu
         35                  40                  45

Trp Ala Arg Thr Ala Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile
     50                  55                  60

Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn
 65                  70                  75                  80

Met Thr Tyr Thr Met Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly
                 85                  90                  95

Glu Leu Gly Asp Val Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser
            100                 105                 110

Val Arg Gly Ala Arg Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu
        115                 120                 125

Arg Ala Ile Ala Gln Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr
    130                 135                 140

Ile Gln Glu Ala Leu Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile
145                 150                 155                 160

Thr Asp Pro Val Glu Gly Thr Val Val Thr Val Leu Arg Ser
                165                 170
```

<210> 2017
<211> 612
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(589)
<223> RXA01029

<400> 2017
atgggtggtt gtcttaatta agggtgttgc gtgaaacacg caaccggaga ggagggtgaa 60

gtgtggggtt ccttgcgggc gtatgtccgg ggtgcttgct atg ctt caa acg att 115
Met Leu Gln Thr Ile
1 5

tca ttc aag aaa ctt aat tta tta aca act ctt aaa aga aaa gga gag 163
Ser Phe Lys Lys Leu Asn Leu Leu Thr Thr Leu Lys Arg Lys Gly Glu
10 15 20

ctg gtc atc atg atc act cgt cac gat gtt ccc tac atc atc gct ccg 211
Leu Val Ile Met Ile Thr Arg His Asp Val Pro Tyr Ile Ile Ala Pro
25 30 35

cct gtc tac gcg atc ttt gcg agc ctg atg acc acg cca cca tgg ttt 259
Pro Val Tyr Ala Ile Phe Ala Ser Leu Met Thr Thr Pro Pro Trp Phe
40 45 50

tat cga acc acc tac acc att gac ggt ttc gat ttt aag atc agc tgg 307
Tyr Arg Thr Thr Tyr Thr Ile Asp Gly Phe Asp Phe Lys Ile Ser Trp
55 60 65

gtc tac acc atc acc atc tac atc agc ctc atg atc ctc att atc ggg 355
Val Tyr Thr Ile Thr Ile Tyr Ile Ser Leu Met Ile Leu Ile Ile Gly
70 75 80 85

ttc tac caa gcc aat atg cgc aaa gcg tgc cct tat gag gaa gat cct 403
Phe Tyr Gln Ala Asn Met Arg Lys Ala Cys Pro Tyr Glu Glu Asp Pro
90 95 100

ttg gtc gat att tgg cac aag gtg tgg agc act gca ctc ttt atc cta 451
Leu Val Asp Ile Trp His Lys Val Trp Ser Thr Ala Leu Phe Ile Leu
105 110 115

cct atc gtt tta tcc atc gcg gtg tac tca ctg atc aca cag cgc ggg 499
Pro Ile Val Leu Ser Ile Ala Val Tyr Ser Leu Ile Thr Gln Arg Gly
120 125 130

ttt gac tgg tat gtc atg gtg ttt att ctc cct gta ggc ttg atg atc 547
Phe Asp Trp Tyr Val Met Val Phe Ile Leu Pro Val Gly Leu Met Ile
135 140 145

gct tat gga ttc ttc aag ccc tgt gat tgc gac aaa cac cgt 589
Ala Tyr Gly Phe Phe Lys Pro Cys Asp Cys Asp Lys His Arg
150 155 160

taaggtatac ttgtccaaga ctt 612

<210> 2018
<211> 163
<212> PRT
<213> Corynebacterium glutamicum

<400> 2018
Met Leu Gln Thr Ile Ser Phe Lys Lys Leu Asn Leu Leu Thr Thr Leu
1 5 10 15

Lys Arg Lys Gly Glu Leu Val Ile Met Ile Thr Arg His Asp Val Pro
20 25 30

Tyr Ile Ile Ala Pro Pro Val Tyr Ala Ile Phe Ala Ser Leu Met Thr
35 40 45

Thr Pro Pro Trp Phe Tyr Arg Thr Thr Tyr Thr Ile Asp Gly Phe Asp
50 55 60

Phe Lys Ile Ser Trp Val Tyr Thr Ile Thr Ile Tyr Ile Ser Leu Met
65 70 75 80

Ile Leu Ile Ile Gly Phe Tyr Gln Ala Asn Met Arg Lys Ala Cys Pro
85 90 95

Tyr Glu Glu Asp Pro Leu Val Asp Ile Trp His Lys Val Trp Ser Thr
100 105 110

Ala Leu Phe Ile Leu Pro Ile Val Leu Ser Ile Ala Val Tyr Ser Leu
115 120 125

Ile Thr Gln Arg Gly Phe Asp Trp Tyr Val Met Val Phe Ile Leu Pro
130 135 140

Val Gly Leu Met Ile Ala Tyr Gly Phe Phe Lys Pro Cys Asp Cys Asp
145 150 155 160

Lys His Arg

<210> 2019
<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(766)
<223> RXA01031

<400> 2019
cagctgaact tgatcatttt gatgatctgc cagtacagcg ccaagaagat cttggcacct 60

tagttgttat ctctgctgtt cacgcaagcg actctgcggc atg aaa ctg ctg caa 115
Met Lys Leu Leu Gln
1 5

tac gca ggt ggt gct gtc tat gtc gat cca gaa gat tct gcg cag tcc 163
Tyr Ala Gly Gly Ala Val Tyr Val Asp Pro Glu Asp Ser Ala Gln Ser
10 15 20

caa gac ctg gat gcc agc act gca cgt gat gtt atc gac gct acc aac 211
Gln Asp Leu Asp Ala Ser Thr Ala Arg Asp Val Ile Asp Ala Thr Asn
25 30 35

```
acc gcc atg acc act att acc tct cgc ccc acc atg att gtg cac ctg   259
Thr Ala Met Thr Thr Ile Thr Ser Arg Pro Thr Met Ile Val His Leu
         40                  45                  50

cac aag gtg cga aaa gtc att gag att tta tgc aac cct gca ctc ggc   307
His Lys Val Arg Lys Val Ile Glu Ile Leu Cys Asn Pro Ala Leu Gly
     55                  60                  65

ggt gaa cct gtc aat atc gac cag gac gag acc gga aaa cag gtg tac   355
Gly Glu Pro Val Asn Ile Asp Gln Asp Glu Thr Gly Lys Gln Val Tyr
 70                  75                  80                  85

aca ccc acc cca acg ctt gtc gcc tat cgc ttt atc tct gac aaa gaa   403
Thr Pro Thr Pro Thr Leu Val Ala Tyr Arg Phe Ile Ser Asp Lys Glu
                 90                  95                 100

atc ctg ctt cat tac ctg gcg cag gcg ggt gtg cag ggt gtg gag gtt   451
Ile Leu Leu His Tyr Leu Ala Gln Ala Gly Val Gln Gly Val Glu Val
            105                 110                 115

ttt gac ggg tcg cct gac atg ctg agc cgt tgg aat gcg gga cgc att   499
Phe Asp Gly Ser Pro Asp Met Leu Ser Arg Trp Asn Ala Gly Arg Ile
        120                 125                 130

ccg gtc tta ctt ttg cag cct gcg tct gct ggt cac ggc ttg aat ttc   547
Pro Val Leu Leu Leu Gln Pro Ala Ser Ala Gly His Gly Leu Asn Phe
    135                 140                 145

cag cac ggc ggg cat cgc ttg gtg tgg tac aac ctg ccc gat aat aac   595
Gln His Gly Gly His Arg Leu Val Trp Tyr Asn Leu Pro Asp Asn Asn
150                 155                 160                 165

gag cat tat atg caa gcg aat gct cgt cta cat cgc att ggt caa aag   643
Glu His Tyr Met Gln Ala Asn Ala Arg Leu His Arg Ile Gly Gln Lys
                170                 175                 180

aat ccc gtg acc att cac cgc att att acc gct gat act tat gat gcg   691
Asn Pro Val Thr Ile His Arg Ile Ile Thr Ala Asp Thr Tyr Asp Ala
            185                 190                 195

aat atg ccg gcg att ctg gcc ggt aaa gca aat aga cag caa cgt ctc   739
Asn Met Pro Ala Ile Leu Ala Gly Lys Ala Asn Arg Gln Gln Arg Leu
        200                 205                 210

atc gac gcc gtg cgc cgt gat cca gtc taagaccggc acgatcgcac         786
Ile Asp Ala Val Arg Arg Asp Pro Val
    215                 220

cgt                                                              789
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20050209.0009

<210> 2020
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 2020

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Met Lys Leu Leu Gln Tyr Ala Gly Gly Ala Val Tyr Val Asp Pro Glu
  1               5                  10                  15

Asp Ser Ala Gln Ser Gln Asp Leu Asp Ala Ser Thr Ala Arg Asp Val
```

```
            20                  25                  30

Ile Asp Ala Thr Asn Thr Ala Met Thr Thr Ile Thr Ser Arg Pro Thr
         35                  40                  45

Met Ile Val His Leu His Lys Val Arg Lys Val Ile Glu Ile Leu Cys
     50                  55                  60

Asn Pro Ala Leu Gly Gly Glu Pro Val Asn Ile Asp Gln Asp Glu Thr
 65                  70                  75                  80

Gly Lys Gln Val Tyr Thr Pro Thr Pro Thr Leu Val Ala Tyr Arg Phe
                 85                  90                  95

Ile Ser Asp Lys Glu Ile Leu Leu His Tyr Leu Ala Gln Ala Gly Val
            100                 105                 110

Gln Gly Val Glu Val Phe Asp Gly Ser Pro Asp Met Leu Ser Arg Trp
        115                 120                 125

Asn Ala Gly Arg Ile Pro Val Leu Leu Leu Gln Pro Ala Ser Ala Gly
    130                 135                 140

His Gly Leu Asn Phe Gln His Gly Gly His Arg Leu Val Trp Tyr Asn
145                 150                 155                 160

Leu Pro Asp Asn Asn Glu His Tyr Met Gln Ala Asn Ala Arg Leu His
                165                 170                 175

Arg Ile Gly Gln Lys Asn Pro Val Thr Ile His Arg Ile Ile Thr Ala
            180                 185                 190

Asp Thr Tyr Asp Ala Asn Met Pro Ala Ile Leu Ala Gly Lys Ala Asn
        195                 200                 205

Arg Gln Gln Arg Leu Ile Asp Ala Val Arg Arg Asp Pro Val
    210                 215                 220
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<210> 2021
<211> 498
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(475)
<223> RXA01032

<400> 2021
agctaatcag caccacctac aacaccacaa acacacccca atcagcatga tcgtgccggt 60

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tggggtgtgt cttatcccct aagaaagtga cacctttacc atg tca gac cac gac   115
                                              Met Ser Asp His Asp
                                                1               5

gcc cca caa aca ccg atc ccc aag ggg ttt tgg cag cag atc gac cac   163
Ala Pro Gln Thr Pro Ile Pro Lys Gly Phe Trp Gln Gln Ile Asp His
            10                  15                  20

caa ctc gat cgc ctc ggc acg cag cgc cca gag acc ttc gca gca ctg   211
```

```
Gln Leu Asp Arg Leu Gly Thr Gln Arg Pro Glu Thr Phe Ala Ala Leu
            25                  30                  35

cgt gac att ttg ctt gat cct gcc tac acc gcc att gtt cat gac cgt   259
Arg Asp Ile Leu Leu Asp Pro Ala Tyr Thr Ala Ile Val His Asp Arg
        40                  45                  50

aat cgc tac ggc gtt gtc acc ttt gac acc aac tca gcc ttc ttc tca   307
Asn Arg Tyr Gly Val Val Thr Phe Asp Thr Asn Ser Ala Phe Phe Ser
    55                  60                  65

ggc tct ggc gga gac aac ggc tta gcc gac gta ctc att aac tgt gat   355
Gly Ser Gly Gly Asp Asn Gly Leu Ala Asp Val Leu Ile Asn Cys Asp
70                  75                  80                  85

tgg cgc atg act gac tac cgc gcc gag tac tac tac gtc atg aca cat   403
Trp Arg Met Thr Asp Tyr Arg Ala Glu Tyr Tyr Tyr Val Met Thr His
                90                  95                  100

aaa tac acc aag gaa tcg ttt acc tat atc gag ggc gac gtg aaa cgc   451
Lys Tyr Thr Lys Glu Ser Phe Thr Tyr Ile Glu Gly Asp Val Lys Arg
            105                 110                 115

ggc gac ctc atc ccg cct aat aat taaggacaac cgccatgact cag         498
Gly Asp Leu Ile Pro Pro Asn Asn
        120                 125
```

CONFIDENTIAL

<210> 2022
<211> 125
<212> PRT
<213> Corynebacterium glutamicum

<400> 2022

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Met Ser Asp His Asp Ala Pro Gln Thr Pro Ile Pro Lys Gly Phe Trp
  1               5                  10                  15

Gln Gln Ile Asp His Gln Leu Asp Arg Leu Gly Thr Gln Arg Pro Glu
            20                  25                  30

Thr Phe Ala Ala Leu Arg Asp Ile Leu Leu Asp Pro Ala Tyr Thr Ala
        35                  40                  45

Ile Val His Asp Arg Asn Arg Tyr Gly Val Val Thr Phe Asp Thr Asn
    50                  55                  60

Ser Ala Phe Phe Ser Gly Ser Gly Gly Asp Asn Gly Leu Ala Asp Val
65                  70                  75                  80

Leu Ile Asn Cys Asp Trp Arg Met Thr Asp Tyr Arg Ala Glu Tyr Tyr
                85                  90                  95

Tyr Val Met Thr His Lys Tyr Thr Lys Glu Ser Phe Thr Tyr Ile Glu
            100                 105                 110

Gly Asp Val Lys Arg Gly Asp Leu Ile Pro Pro Asn Asn
        115                 120                 125
```

<210> 2023
<211> 459

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(436)
<223> RXA01033

<400> 2023
acgtcatgac acataaatac accaaggaat cgtttaccta tatcgagggc gacgtgaaac 60

gcggcgacct catcccgcct aataattaag gacaaccgcc atg act cag atc gcc 115
Met Thr Gln Ile Ala
1 5

atg tat ctc gca gga ccc atg aca ggt atc cct gaa tac aac tac ccc 163
Met Tyr Leu Ala Gly Pro Met Thr Gly Ile Pro Glu Tyr Asn Tyr Pro
10 15 20

acc ttc cat gca gcg gct aat aag ttc cgt gca gct ggc tac acc gta 211
Thr Phe His Ala Ala Ala Asn Lys Phe Arg Ala Ala Gly Tyr Thr Val
25 30 35

ctc tcc ccc gct gaa gac gaa tat gaa tcc cag ctc act gca cca ttg 259
Leu Ser Pro Ala Glu Asp Glu Tyr Glu Ser Gln Leu Thr Ala Pro Leu
40 45 50

cct gag aac gct gag cac aaa tac gac cac tac ttg cgt ctc ggt atc 307
Pro Glu Asn Ala Glu His Lys Tyr Asp His Tyr Leu Arg Leu Gly Ile
55 60 65

gaa aag ctg ctc aag gct gat gct gtc cac atg ctt cag gga tgg cag 355
Glu Lys Leu Leu Lys Ala Asp Ala Val His Met Leu Gln Gly Trp Gln
70 75 80 85

agt agc gcc ggt gcc act ctt gag cac gat att gca cag aaa ttg agg 403
Ser Ser Ala Gly Ala Thr Leu Glu His Asp Ile Ala Gln Lys Leu Arg
90 95 100

ctt gcc att acc tat gaa gaa cca cca gca tcc taaggcgcct ccggcatagc 456
Leu Ala Ile Thr Tyr Glu Glu Pro Pro Ala Ser
105 110

gta 459

<210> 2024
<211> 112
<212> PRT
<213> Corynebacterium glutamicum

<400> 2024
Met Thr Gln Ile Ala Met Tyr Leu Ala Gly Pro Met Thr Gly Ile Pro
1 5 10 15

Glu Tyr Asn Tyr Pro Thr Phe His Ala Ala Ala Asn Lys Phe Arg Ala
20 25 30

Ala Gly Tyr Thr Val Leu Ser Pro Ala Glu Asp Glu Tyr Glu Ser Gln
35 40 45

```
Leu Thr Ala Pro Leu Pro Glu Asn Ala Glu His Lys Tyr Asp His Tyr
     50                  55                  60

Leu Arg Leu Gly Ile Glu Lys Leu Leu Lys Ala Asp Ala Val His Met
 65                  70                  75                  80

Leu Gln Gly Trp Gln Ser Ser Ala Gly Ala Thr Leu Glu His Asp Ile
                 85                  90                  95

Ala Gln Lys Leu Arg Leu Ala Ile Thr Tyr Glu Glu Pro Pro Ala Ser
            100                 105                 110
```

<210> 2025
<211> 477
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(454)
<223> RXA01034

<400> 2025
agaaagtatg tcaataactt tgacataacc taaacacaat aaattatgta gtattatgtg 60

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acactaagtt attacattta ttacatgatt ggttaggact atg gac atg gcc att   115
                                           Met Asp Met Ala Ile
                                             1               5

att cag tcg gtc gaa tac aca tct gat gtc tca cat gag cgc atc acc   163
Ile Gln Ser Val Glu Tyr Thr Ser Asp Val Ser His Glu Arg Ile Thr
                 10                  15                  20

aat gtc gtc tct gta ggc gtg gtc tac gag ggt aaa cag tat gta gtg   211
Asn Val Val Ser Val Gly Val Val Tyr Glu Gly Lys Gln Tyr Val Val
             25                  30                  35

gac ctt aat ggt gac gac att gat act gag ctc gat atg atc acg ctc   259
Asp Leu Asn Gly Asp Asp Ile Asp Thr Glu Leu Asp Met Ile Thr Leu
         40                  45                  50

aaa gaa gtc atc aag att ggt cgt gag gaa tct gca cgc cag atc cgt   307
Lys Glu Val Ile Lys Ile Gly Arg Glu Glu Ser Ala Arg Gln Ile Arg
     55                  60                  65

cgt gga tct gta gat gca gag ctg cac cgt aag gcg cgt ttg tgg gct   355
Arg Gly Ser Val Asp Ala Glu Leu His Arg Lys Ala Arg Leu Trp Ala
 70                  75                  80                  85

att gac aat gac atg gcc gtt ggt caa cgt ggt atc gtg cca cag gaa   403
Ile Asp Asn Asp Met Ala Val Gly Gln Arg Gly Ile Val Pro Gln Glu
                 90                  95                 100

atc atc gac gcg tac aaa gag tac tgc gaa aaa gaa ggc att cct ttc   451
Ile Ile Asp Ala Tyr Lys Glu Tyr Cys Glu Lys Glu Gly Ile Pro Phe
            105                 110                 115
```

gaa taagagccct gtggagaatt gtt 477
Glu

<210> 2026
<211> 118
<212> PRT
<213> Corynebacterium glutamicum

<400> 2026
Met Asp Met Ala Ile Ile Gln Ser Val Glu Tyr Thr Ser Asp Val Ser
1 5 10 15

His Glu Arg Ile Thr Asn Val Val Ser Val Gly Val Val Tyr Glu Gly
20 25 30

Lys Gln Tyr Val Val Asp Leu Asn Gly Asp Asp Ile Asp Thr Glu Leu
35 40 45

Asp Met Ile Thr Leu Lys Glu Val Ile Lys Ile Gly Arg Glu Glu Ser
50 55 60

Ala Arg Gln Ile Arg Arg Gly Ser Val Asp Ala Glu Leu His Arg Lys
65 70 75 80

Ala Arg Leu Trp Ala Ile Asp Asn Asp Met Ala Val Gly Gln Arg Gly
85 90 95

Ile Val Pro Gln Glu Ile Ile Asp Ala Tyr Lys Glu Tyr Cys Glu Lys
100 105 110

Glu Gly Ile Pro Phe Glu
115

<210> 2027
<211> 729
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(706)
<223> RXA01035

<400> 2027
ggcagtgatg caccgcactt gagaaaaata aatcatctca agaaacaaac taatacgtta 60

ttattgtaat ttaattagag aaaagaaagt gacttttaaa gtg ctt att cgc atc 115
Val Leu Ile Arg Ile
1 5

gcc gag cat caa ggc cgg ctc cat gtc cat agc ccc tac tca aag gct 163
Ala Glu His Gln Gly Arg Leu His Val His Ser Pro Tyr Ser Lys Ala
10 15 20

ttt gcc gcc cgc gct cga aag ctc aac ggt ctc tgg tca ccc gaa acg 211
Phe Ala Ala Arg Ala Arg Lys Leu Asn Gly Leu Trp Ser Pro Glu Thr
25 30 35

```
aag acc tgg cat ttc agc ccc gat aaa gaa caa ccg gtg aga cgc gca   259
Lys Thr Trp His Phe Ser Pro Asp Lys Glu Gln Pro Val Arg Arg Ala
         40                  45                  50

ctc aag gat gtc tac ggc tgg gat gaa ttc acc aca ccc gag cta tgc   307
Leu Lys Asp Val Tyr Gly Trp Asp Glu Phe Thr Thr Pro Glu Leu Cys
     55                  60                  65

acg gtg cag ctc act gtg acc cca gag gca gtg ctc aac aaa cac aca   355
Thr Val Gln Leu Thr Val Thr Pro Glu Ala Val Leu Asn Lys His Thr
 70                  75                  80                  85

ctc acc atc gct ggt gtt aca ctt ctg agc cgt tta cgc aga aat tac   403
Leu Thr Ile Ala Gly Val Thr Leu Leu Ser Arg Leu Arg Arg Asn Tyr
                 90                  95                 100

tcg gtg tgg ttg ggt gat aat gtc cgc atc atc agt ggc aat ttc cca   451
Ser Val Trp Leu Gly Asp Asn Val Arg Ile Ile Ser Gly Asn Phe Pro
            105                 110                 115

gaa gca gca gga tca ccc cag tac ccc ctc atc atg ggt gtg aag gct   499
Glu Ala Ala Gly Ser Pro Gln Tyr Pro Leu Ile Met Gly Val Lys Ala
        120                 125                 130

caa ccc gtt gtt atc cat gtg cag gaa ttc cct gta gat gct gtt tcg   547
Gln Pro Val Val Ile His Val Gln Glu Phe Pro Val Asp Ala Val Ser
    135                 140                 145

act att ccc ccg cga ttt aat cct att gtt atc act gca ccg ccg agc   595
Thr Ile Pro Pro Arg Phe Asn Pro Ile Val Ile Thr Ala Pro Pro Ser
150                 155                 160                 165

att gat att gct gct ctt cga gct gaa cgc gaa cag ctc acc cga cgc   643
Ile Asp Ile Ala Ala Leu Arg Ala Glu Arg Glu Gln Leu Thr Arg Arg
                170                 175                 180

atc agc gaa att gac aag aaa atc gca cgt gct gtg cat cca acc att   691
Ile Ser Glu Ile Asp Lys Lys Ile Ala Arg Ala Val His Pro Thr Ile
            185                 190                 195

cag act gag gct gcc taataatgat gcagactctc aag                    729
Gln Thr Glu Ala Ala
        200
```

<210> 2028
<211> 202
<212> PRT
<213> Corynebacterium glutamicum

<400> 2028

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Val Leu Ile Arg Ile Ala Glu His Gln Gly Arg Leu His Val His Ser
  1               5                  10                  15

Pro Tyr Ser Lys Ala Phe Ala Ala Arg Ala Arg Lys Leu Asn Gly Leu
             20                  25                  30

Trp Ser Pro Glu Thr Lys Thr Trp His Phe Ser Pro Asp Lys Glu Gln
         35                  40                  45

Pro Val Arg Arg Ala Leu Lys Asp Val Tyr Gly Trp Asp Glu Phe Thr
```

```
     50                  55                  60

Thr Pro Glu Leu Cys Thr Val Gln Leu Thr Val Thr Pro Glu Ala Val
 65                  70                  75                  80

Leu Asn Lys His Thr Leu Thr Ile Ala Gly Val Thr Leu Leu Ser Arg
                 85                  90                  95

Leu Arg Arg Asn Tyr Ser Val Trp Leu Gly Asp Asn Val Arg Ile Ile
            100                 105                 110

Ser Gly Asn Phe Pro Glu Ala Ala Gly Ser Pro Gln Tyr Pro Leu Ile
        115                 120                 125

Met Gly Val Lys Ala Gln Pro Val Val Ile His Val Gln Glu Phe Pro
    130                 135                 140

Val Asp Ala Val Ser Thr Ile Pro Pro Arg Phe Asn Pro Ile Val Ile
145                 150                 155                 160

Thr Ala Pro Pro Ser Ile Asp Ile Ala Ala Leu Arg Ala Glu Arg Glu
                165                 170                 175

Gln Leu Thr Arg Arg Ile Ser Glu Ile Asp Lys Lys Ile Ala Arg Ala
            180                 185                 190

Val His Pro Thr Ile Gln Thr Glu Ala Ala
        195                 200
```

US 20050153417 A1

<210> 2029
<211> 576
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(553)
<223> RXA01036

<400> 2029

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ctgaggctgc ctaataatga tgcagactct caagcggaaa attccgctca tctcatgcaa 60

tgacctcaaa gaagtgcagt tacttttttct taaaggtcag atg cac aca gtc ggc   115
                                            Met His Thr Val Gly
                                              1               5

tac aag cta gat acc gat ctt cgc aag ctc act aat acc gat gtg ctt   163
Tyr Lys Leu Asp Thr Asp Leu Arg Lys Leu Thr Asn Thr Asp Val Leu
                 10                  15                  20

gat ctt att aac gcg ctc ttc ggc acc act gtg acc agc gca gat gac   211
Asp Leu Ile Asn Ala Leu Phe Gly Thr Thr Val Thr Ser Ala Asp Asp
             25                  30                  35

gaa gca gca gat ttc att gac tct gat cct cag ttt gca gtg ctc gtt   259
Glu Ala Ala Asp Phe Ile Asp Ser Asp Pro Gln Phe Ala Val Leu Val
         40                  45                  50

gag ctg gcc tac cac gac tgt gca cgc cgc gct gcc atg ggt cta tcc   307
Glu Leu Ala Tyr His Asp Cys Ala Arg Arg Ala Ala Met Gly Leu Ser
```

```
     55                  60                  65

agg gta cag cag ctc atc tat gac aat gcg gct aaa tca acc tac tac   355
Arg Val Gln Gln Leu Ile Tyr Asp Asn Ala Ala Lys Ser Thr Tyr Tyr
 70                  75                  80                  85

cgc agc gtc gca gct aga cat cgc aaa cac atc cgt gaa ctc cac gag   403
Arg Ser Val Ala Ala Arg His Arg Lys His Ile Arg Glu Leu His Glu
                 90                  95                 100

caa aca cag cga gat ggt att cac ttc gac aac ccg ttg tct cgt gca   451
Gln Thr Gln Arg Asp Gly Ile His Phe Asp Asn Pro Leu Ser Arg Ala
            105                 110                 115

gtc atc aac gat ctc agc atg tcc atg aac cgt gct cga cta aac cgc   499
Val Ile Asn Asp Leu Ser Met Ser Met Asn Arg Ala Arg Leu Asn Arg
        120                 125                 130

atc gct tca tgg aaa tca gcc ggc gta cag cgc tat ctc aac ccc act   547
Ile Ala Ser Trp Lys Ser Ala Gly Val Gln Arg Tyr Leu Asn Pro Thr
    135                 140                 145

atc tct tagaaccaca cacaaccaag aaa                                576
Ile Ser
150
```

<210> 2030
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 2030

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Met His Thr Val Gly Tyr Lys Leu Asp Thr Asp Leu Arg Lys Leu Thr
  1               5                  10                  15

Asn Thr Asp Val Leu Asp Leu Ile Asn Ala Leu Phe Gly Thr Thr Val
             20                  25                  30

Thr Ser Ala Asp Asp Glu Ala Ala Asp Phe Ile Asp Ser Asp Pro Gln
         35                  40                  45

Phe Ala Val Leu Val Glu Leu Ala Tyr His Asp Cys Ala Arg Arg Ala
     50                  55                  60

Ala Met Gly Leu Ser Arg Val Gln Gln Leu Ile Tyr Asp Asn Ala Ala
 65                  70                  75                  80

Lys Ser Thr Tyr Tyr Arg Ser Val Ala Ala Arg His Arg Lys His Ile
                 85                  90                  95

Arg Glu Leu His Glu Gln Thr Gln Arg Asp Gly Ile His Phe Asp Asn
            100                 105                 110

Pro Leu Ser Arg Ala Val Ile Asn Asp Leu Ser Met Ser Met Asn Arg
        115                 120                 125

Ala Arg Leu Asn Arg Ile Ala Ser Trp Lys Ser Ala Gly Val Gln Arg
    130                 135                 140

Tyr Leu Asn Pro Thr Ile Ser
```

145 150

<210> 2031
<211> 651
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(628)
<223> RXA01037

<400> 2031
cgactaaacc gcatcgcttc atggaaatca gccggcgtac agcgctatct caaccccact 60

atctcttaga accacacaca accaagaaag cagtcactac atg acc acc tca tca 115
Met Thr Thr Ser Ser
1 5

ccc ctt aag tcc aaa aat tcc ctt aac ggc gcg cag acc aca ttt gtc 163
Pro Leu Lys Ser Lys Asn Ser Leu Asn Gly Ala Gln Thr Thr Phe Val
10 15 20

cgc aat tgt gtt gca gac ggc cca acc gag gta aaa gcc acc att gat 211
Arg Asn Cys Val Ala Asp Gly Pro Thr Glu Val Lys Ala Thr Ile Asp
25 30 35

gca cgt ggc ggt atc gaa cag ctc cgt gac aat gag att tca cag ctc 259
Ala Arg Gly Gly Ile Glu Gln Leu Arg Asp Asn Glu Ile Ser Gln Leu
40 45 50

ccc gac aag ctg tgg ttc aat agc gca acc tcc gca tcc aat gac gag 307
Pro Asp Lys Leu Trp Phe Asn Ser Ala Thr Ser Ala Ser Asn Asp Glu
55 60 65

ttc acc acc gat aac atc cga ctt ggg ttg ctc tac aac atg gca ctg 355
Phe Thr Thr Asp Asn Ile Arg Leu Gly Leu Leu Tyr Asn Met Ala Leu
70 75 80 85

aat aag gca tcg gct cat cgc tat gag ctt gct gcc cgc tgg tac gcc 403
Asn Lys Ala Ser Ala His Arg Tyr Glu Leu Ala Ala Arg Trp Tyr Ala
90 95 100

att gtt agc cct cag cca tcg caa gaa gct agc cac aag cgc atc gcg 451
Ile Val Ser Pro Gln Pro Ser Gln Glu Ala Ser His Lys Arg Ile Ala
105 110 115

tcc tgg cac ctt acc cag ctg cac gca ctg gtg acc cta tct cgc acc 499
Ser Trp His Leu Thr Gln Leu His Ala Leu Val Thr Leu Ser Arg Thr
120 125 130

cta ggg gtc atc att cct ggt gat gag atc gac gct cta gcg cag tct 547
Leu Gly Val Ile Ile Pro Gly Asp Glu Ile Asp Ala Leu Ala Gln Ser
135 140 145

atg gag aat gct cgt caa gtt ggc acc gag aat tgg tcc act gtc acc 595
Met Glu Asn Ala Arg Gln Val Gly Thr Glu Asn Trp Ser Thr Val Thr
150 155 160 165

atg cgc acc tac gtg acc aac cgc aag gca tcc taatgactcg cgatattttc 648

```
Met Arg Thr Tyr Val Thr Asn Arg Lys Ala Ser
                170                 175

cac                                                                    651
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<210> 2032
<211> 176
<212> PRT
<213> Corynebacterium glutamicum

<400> 2032

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Met Thr Thr Ser Ser Pro Leu Lys Ser Lys Asn Ser Leu Asn Gly Ala
  1               5                  10                  15

Gln Thr Thr Phe Val Arg Asn Cys Val Ala Asp Gly Pro Thr Glu Val
             20                  25                  30

Lys Ala Thr Ile Asp Ala Arg Gly Gly Ile Glu Gln Leu Arg Asp Asn
         35                  40                  45

Glu Ile Ser Gln Leu Pro Asp Lys Leu Trp Phe Asn Ser Ala Thr Ser
     50                  55                  60

Ala Ser Asn Asp Glu Phe Thr Thr Asp Asn Ile Arg Leu Gly Leu Leu
 65                  70                  75                  80

Tyr Asn Met Ala Leu Asn Lys Ala Ser Ala His Arg Tyr Glu Leu Ala
                 85                  90                  95

Ala Arg Trp Tyr Ala Ile Val Ser Pro Gln Pro Ser Gln Glu Ala Ser
            100                 105                 110

His Lys Arg Ile Ala Ser Trp His Leu Thr Gln Leu His Ala Leu Val
        115                 120                 125

Thr Leu Ser Arg Thr Leu Gly Val Ile Ile Pro Gly Asp Glu Ile Asp
    130                 135                 140

Ala Leu Ala Gln Ser Met Glu Asn Ala Arg Gln Val Gly Thr Glu Asn
145                 150                 155                 160

Trp Ser Thr Val Thr Met Arg Thr Tyr Val Thr Asn Arg Lys Ala Ser
                165                 170                 175
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<210> 2033
<211> 870
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(847)
<223> RXA01038

<400> 2033

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acgctctagc gcagtctatg gagaatgctc gtcaagttgg caccgagaat tggtccactg 60
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tcaccatgcg cacctacgtg accaaccgca aggcatccta atg act cgc gat att   115
                                                Met Thr Arg Asp Ile
                                                  1               5

ttc cac gag gct gca aaa ctc atc gca cac ctg ggg tgg agg gac gct   163
Phe His Glu Ala Ala Lys Leu Ile Ala His Leu Gly Trp Arg Asp Ala
                 10                  15                  20

ttt cca gca cta cag cgc act gac cca gcg cca aca cat gct gtg ccg   211
Phe Pro Ala Leu Gln Arg Thr Asp Pro Ala Pro Thr His Ala Val Pro
             25                  30                  35

atc agg gcc ttt gat ctc aag gcg ggc gcc gtc atc acc gat gaa aat   259
Ile Arg Ala Phe Asp Leu Lys Ala Gly Ala Val Ile Thr Asp Glu Asn
         40                  45                  50

cga agc aat gct tat atc tat gac acc ctt gtc atc acg cag cca tat   307
Arg Ser Asn Ala Tyr Ile Tyr Asp Thr Leu Val Ile Thr Gln Pro Tyr
     55                  60                  65

aag cac gag tta cct cat caa aac acc cac cct ttt gag tgg gcc ctg   355
Lys His Glu Leu Pro His Gln Asn Thr His Pro Phe Glu Trp Ala Leu
 70                  75                  80                  85

gaa caa att gcc acg ctt gat ccg gcg ttc tcg atc aag ctc gat cgc   403
Glu Gln Ile Ala Thr Leu Asp Pro Ala Phe Ser Ile Lys Leu Asp Arg
                 90                  95                 100

tca gtg acc gtc cct gaa att gga ctc tac gcc cgc aca ctg cat gac   451
Ser Val Thr Val Pro Glu Ile Gly Leu Tyr Ala Arg Thr Leu His Asp
             105                 110                 115

ctt aat act cgg cat caa gac ttc ttg gca cag cgc aac gcc atg ttg   499
Leu Asn Thr Arg His Gln Asp Phe Leu Ala Gln Arg Asn Ala Met Leu
         120                 125                 130

ctt gtt gtt gcc cgt cgt ggt gtt gat cca aaa aat atc gca gac gta   547
Leu Val Val Ala Arg Arg Gly Val Asp Pro Lys Asn Ile Ala Asp Val
     135                 140                 145

ctt ggt tta acc acc aat cag ata cat cgg att ctc agt gct act ccg   595
Leu Gly Leu Thr Thr Asn Gln Ile His Arg Ile Leu Ser Ala Thr Pro
150                 155                 160                 165

gct gat tcc cct act gat tta ggc gtt aac ccc gcc aca aca atg ggt   643
Ala Asp Ser Pro Thr Asp Leu Gly Val Asn Pro Ala Thr Thr Met Gly
                 170                 175                 180

gat gta gtg agg ttt atc aag aaa cgt cgc acc act atg caa cta cgc   691
Asp Val Val Arg Phe Ile Lys Lys Arg Arg Thr Thr Met Gln Leu Arg
             185                 190                 195

ggc acc gct gtc cgt gca ctg ctc tat cac ggc ctt acg ccg gca gtc   739
Gly Thr Ala Val Arg Ala Leu Leu Tyr His Gly Leu Thr Pro Ala Val
         200                 205                 210

atc tcc cga cta agc ggc atg tcg cgt gcg ggt gtc atc aac gca gcc   787
Ile Ser Arg Leu Ser Gly Met Ser Arg Ala Gly Val Ile Asn Ala Ala
     215                 220                 225
```

```
aag gca ttc ccc acc acc atc aac cac aag gtc aag aaa aga aag cag   835
Lys Ala Phe Pro Thr Thr Ile Asn His Lys Val Lys Lys Arg Lys Gln
230                 235                 240                 245

cac ttc cat gtc taatctcggc acatactatg cag                        870
His Phe His Val
```

<210> 2034
<211> 249
<212> PRT
<213> Corynebacterium glutamicum

<400> 2034

```
Met Thr Arg Asp Ile Phe His Glu Ala Ala Lys Leu Ile Ala His Leu
  1               5                  10                  15

Gly Trp Arg Asp Ala Phe Pro Ala Leu Gln Arg Thr Asp Pro Ala Pro
             20                  25                  30

Thr His Ala Val Pro Ile Arg Ala Phe Asp Leu Lys Ala Gly Ala Val
         35                  40                  45

Ile Thr Asp Glu Asn Arg Ser Asn Ala Tyr Ile Tyr Asp Thr Leu Val
     50                  55                  60

Ile Thr Gln Pro Tyr Lys His Glu Leu Pro His Gln Asn Thr His Pro
 65                  70                  75                  80

Phe Glu Trp Ala Leu Glu Gln Ile Ala Thr Leu Asp Pro Ala Phe Ser
                 85                  90                  95

Ile Lys Leu Asp Arg Ser Val Thr Val Pro Glu Ile Gly Leu Tyr Ala
            100                 105                 110

Arg Thr Leu His Asp Leu Asn Thr Arg His Gln Asp Phe Leu Ala Gln
        115                 120                 125

Arg Asn Ala Met Leu Leu Val Val Ala Arg Arg Gly Val Asp Pro Lys
    130                 135                 140

Asn Ile Ala Asp Val Leu Gly Leu Thr Thr Asn Gln Ile His Arg Ile
145                 150                 155                 160

Leu Ser Ala Thr Pro Ala Asp Ser Pro Thr Asp Leu Gly Val Asn Pro
                165                 170                 175

Ala Thr Thr Met Gly Asp Val Val Arg Phe Ile Lys Lys Arg Arg Thr
            180                 185                 190

Thr Met Gln Leu Arg Gly Thr Ala Val Arg Ala Leu Leu Tyr His Gly
        195                 200                 205

Leu Thr Pro Ala Val Ile Ser Arg Leu Ser Gly Met Ser Arg Ala Gly
    210                 215                 220

Val Ile Asn Ala Ala Lys Ala Phe Pro Thr Thr Ile Asn His Lys Val
225                 230                 235                 240

Lys Lys Arg Lys Gln His Phe His Val
```

245

<210> 2035
<211> 699
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(676)
<223> RXA01039

<400> 2035
aaacctatat gttaatagta acagaaatta ataagatact agagtttaat ttgtagtatc 60

cagggaacat taaacgggta aaggtaaagg acaaacgaac atg gcg att aaa ggc 115
Met Ala Ile Lys Gly
1 5

gca atg ccg aaa aat cga gta cca ggt gtg gca gca ggt gcg ttt att 163
Ala Met Pro Lys Asn Arg Val Pro Gly Val Ala Ala Gly Ala Phe Ile
10 15 20

gct gct gcc gtt att gca ggt gga tca ggc gtg acc ttt ctc gcc caa 211
Ala Ala Ala Val Ile Ala Gly Gly Ser Gly Val Thr Phe Leu Ala Gln
25 30 35

ggc ggt ggt gat gtc aat aca gtg gcc gtc gtc gag cca cag gac gag 259
Gly Gly Gly Asp Val Asn Thr Val Ala Val Val Glu Pro Gln Asp Glu
40 45 50

gta aaa aat cag gtc gtg aca gaa acc gaa att gtc acg aag gtt cac 307
Val Lys Asn Gln Val Val Thr Glu Thr Glu Ile Val Thr Lys Val His
55 60 65

gat cct tct tca tct gac gcc agt gat gct gac agc aac aca ggc acc 355
Asp Pro Ser Ser Ser Asp Ala Ser Asp Ala Asp Ser Asn Thr Gly Thr
70 75 80 85

gcc gaa ggc gca gac tca gat cac aaa gaa ccc cgt gag cac gac agt 403
Ala Glu Gly Ala Asp Ser Asp His Lys Glu Pro Arg Glu His Asp Ser
90 95 100

gct caa gag cca acg gct ccg acc gac ccc acc ttg acc att acc ggc 451
Ala Gln Glu Pro Thr Ala Pro Thr Asp Pro Thr Leu Thr Ile Thr Gly
105 110 115

aac ggt gac aca cca gta tca gca ctt gat gct gtc gca gga cct gcc 499
Asn Gly Asp Thr Pro Val Ser Ala Leu Asp Ala Val Ala Gly Pro Ala
120 125 130

cgt cca ggt acg gtg cac gtc att gag aat ggc gaa acc ttg tcc tct 547
Arg Pro Gly Thr Val His Val Ile Glu Asn Gly Glu Thr Leu Ser Ser
135 140 145

att tct cag gac agt ggt gtg ccg gtt ggg ttg atc att gat cgc aac 595
Ile Ser Gln Asp Ser Gly Val Pro Val Gly Leu Ile Ile Asp Arg Asn
150 155 160 165

aag ctt gtt gat cca gac ctg atc tat gca ggc acg cca ttg gcg att 643

```
Lys Leu Val Asp Pro Asp Leu Ile Tyr Ala Gly Thr Pro Leu Ala Ile
                170                 175                 180

ccg act gag cag gaa ctt gct gct gcg ata cag taatgtagtg gtagagggtt 696
Pro Thr Glu Gln Glu Leu Ala Ala Ala Ile Gln
            185                 190

aaa                                                               699
```

<210> 2036
<211> 192
<212> PRT
<213> Corynebacterium glutamicum

<400> 2036

```
Met Ala Ile Lys Gly Ala Met Pro Lys Asn Arg Val Pro Gly Val Ala
  1               5                  10                  15

Ala Gly Ala Phe Ile Ala Ala Ala Val Ile Ala Gly Gly Ser Gly Val
             20                  25                  30

Thr Phe Leu Ala Gln Gly Gly Gly Asp Val Asn Thr Val Ala Val Val
         35                  40                  45

Glu Pro Gln Asp Glu Val Lys Asn Gln Val Val Thr Glu Thr Glu Ile
     50                  55                  60

Val Thr Lys Val His Asp Pro Ser Ser Ser Asp Ala Ser Asp Ala Asp
 65                  70                  75                  80

Ser Asn Thr Gly Thr Ala Glu Gly Ala Asp Ser Asp His Lys Glu Pro
                85                  90                  95

Arg Glu His Asp Ser Ala Gln Glu Pro Thr Ala Pro Thr Asp Pro Thr
            100                 105                 110

Leu Thr Ile Thr Gly Asn Gly Asp Thr Pro Val Ser Ala Leu Asp Ala
        115                 120                 125

Val Ala Gly Pro Ala Arg Pro Gly Thr Val His Val Ile Glu Asn Gly
    130                 135                 140

Glu Thr Leu Ser Ser Ile Ser Gln Asp Ser Gly Val Pro Val Gly Leu
145                 150                 155                 160

Ile Ile Asp Arg Asn Lys Leu Val Asp Pro Asp Leu Ile Tyr Ala Gly
                165                 170                 175

Thr Pro Leu Ala Ile Pro Thr Glu Gln Glu Leu Ala Ala Ala Ile Gln
            180                 185                 190
```

<210> 2037
<211> 1026
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1003)
<223> RXA01040

<400> 2037
taatttctgt tactattaac atataggttt tttaaagttt cgtctacata aacctgcaac 60

```
agaaatcact acacccagtt ctcgaaaggc tttttctctc atg acc tac cca gtt   115
                                            Met Thr Tyr Pro Val
                                              1               5

acc cct caa cct gtg cag cca gca cca gtc gcc gaa aag atc aag gca   163
Thr Pro Gln Pro Val Gln Pro Ala Pro Val Ala Glu Lys Ile Lys Ala
                 10                  15                  20

tca agc ctc aaa gaa ggc act cag gta ttt atc aaa ggt cgg gtt aat   211
Ser Ser Leu Lys Glu Gly Thr Gln Val Phe Ile Lys Gly Arg Val Asn
             25                  30                  35

tac tcc cgc atc gca agc ttt att act ggt acc gag cgc gaa aac cgt   259
Tyr Ser Arg Ile Ala Ser Phe Ile Thr Gly Thr Glu Arg Glu Asn Arg
         40                  45                  50

aat cgc gac agg ctt cac cca atc gaa ttc gac tac acc tcc ctg act   307
Asn Arg Asp Arg Leu His Pro Ile Glu Phe Asp Tyr Thr Ser Leu Thr
     55                  60                  65

ttg agc cac cct gaa atc atc tac ggc aac ccg caa caa aag acc aat   355
Leu Ser His Pro Glu Ile Ile Tyr Gly Asn Pro Gln Gln Lys Thr Asn
 70                  75                  80                  85

gaa gaa ctc ttc ctt gag cag cga atc ttt gtc ggc aag aag cgt cct   403
Glu Glu Leu Phe Leu Glu Gln Arg Ile Phe Val Gly Lys Lys Arg Pro
                 90                  95                 100

gaa gag ggt cca aaa ttc tcc att gac aac aag agc aac cgt cta cca   451
Glu Glu Gly Pro Lys Phe Ser Ile Asp Asn Lys Ser Asn Arg Leu Pro
            105                 110                 115

cag gtt tgg gtg cca tcc acc aat gct gat ggt act tat gag cag ctt   499
Gln Val Trp Val Pro Ser Thr Asn Ala Asp Gly Thr Tyr Glu Gln Leu
        120                 125                 130

gaa ggt ctc gaa ggt gag ctc gac gca ggg ctc aac gtc att att ctc   547
Glu Gly Leu Glu Gly Glu Leu Asp Ala Gly Leu Asn Val Ile Ile Leu
    135                 140                 145

atc gag ttc tat aag cca cgt aca cag gtt aat cgc ggc tcc cgc ctc   595
Ile Glu Phe Tyr Lys Pro Arg Thr Gln Val Asn Arg Gly Ser Arg Leu
150                 155                 160                 165

aac gcc gtg ttc ctg cag gag ccc att cgt tac tac acc cct ggt tac   643
Asn Ala Val Phe Leu Gln Glu Pro Ile Arg Tyr Tyr Thr Pro Gly Tyr
                170                 175                 180

aat gca gat aag ctc gct gcc ctc gga atc gta ctt aac gca ccg cca   691
Asn Ala Asp Lys Leu Ala Ala Leu Gly Ile Val Leu Asn Ala Pro Pro
            185                 190                 195

aag gac act att cag ctc gtt cct aat gag gtc gct gca gga caa gac   739
```

```
Lys Asp Thr Ile Gln Leu Val Pro Asn Glu Val Ala Ala Gly Gln Asp
        200                 205                 210

cag tcc acc acc gat gca tcc ggt ctc ccg ctt cca ggc cag gga tat   787
Gln Ser Thr Thr Asp Ala Ser Gly Leu Pro Leu Pro Gly Gln Gly Tyr
    215                 220                 225

agc gca cct gat cag cca tat cag gcg cag cct cag tat cag cag gca   835
Ser Ala Pro Asp Gln Pro Tyr Gln Ala Gln Pro Gln Tyr Gln Gln Ala
230                 235                 240                 245

acc cca gcg gct gca cct cag cag tac cag gcc cca cag ccc cag tac   883
Thr Pro Ala Ala Ala Pro Gln Gln Tyr Gln Ala Pro Gln Pro Gln Tyr
                250                 255                 260

cag cag tca gct cca cag gca caa cct gca ccg gca cca gtt gcg cag   931
Gln Gln Ser Ala Pro Gln Ala Gln Pro Ala Pro Ala Pro Val Ala Gln
            265                 270                 275

ttc cag cag gca agc gcc tca ggc acc tgc tca gcc agc aca gca gca   979
Phe Gln Gln Ala Ser Ala Ser Gly Thr Cys Ser Ala Ser Thr Ala Ala
        280                 285                 290

gta tca ggc acc act tcc tgc cgg taatcctctt gcagcaggtc agc        1026
Val Ser Gly Thr Thr Ser Cys Arg
    295                 300


<210> 2038
<211> 301
<212> PRT
<213> Corynebacterium glutamicum

<400> 2038
Met Thr Tyr Pro Val Thr Pro Gln Pro Val Gln Pro Ala Pro Val Ala
  1               5                  10                  15

Glu Lys Ile Lys Ala Ser Ser Leu Lys Glu Gly Thr Gln Val Phe Ile
            20                  25                  30

Lys Gly Arg Val Asn Tyr Ser Arg Ile Ala Ser Phe Ile Thr Gly Thr
        35                  40                  45

Glu Arg Glu Asn Arg Asn Arg Asp Arg Leu His Pro Ile Glu Phe Asp
    50                  55                  60

Tyr Thr Ser Leu Thr Leu Ser His Pro Glu Ile Ile Tyr Gly Asn Pro
65                  70                  75                  80

Gln Gln Lys Thr Asn Glu Glu Leu Phe Leu Glu Gln Arg Ile Phe Val
                85                  90                  95

Gly Lys Lys Arg Pro Glu Glu Gly Pro Lys Phe Ser Ile Asp Asn Lys
            100                 105                 110

Ser Asn Arg Leu Pro Gln Val Trp Val Pro Ser Thr Asn Ala Asp Gly
        115                 120                 125

Thr Tyr Glu Gln Leu Glu Gly Leu Glu Gly Glu Leu Asp Ala Gly Leu
    130                 135                 140
```

```
Asn Val Ile Ile Leu Ile Glu Phe Tyr Lys Pro Arg Thr Gln Val Asn
145                 150                 155                 160

Arg Gly Ser Arg Leu Asn Ala Val Phe Leu Gln Glu Pro Ile Arg Tyr
                165                 170                 175

Tyr Thr Pro Gly Tyr Asn Ala Asp Lys Leu Ala Ala Leu Gly Ile Val
            180                 185                 190

Leu Asn Ala Pro Pro Lys Asp Thr Ile Gln Leu Val Pro Asn Glu Val
        195                 200                 205

Ala Ala Gly Gln Asp Gln Ser Thr Thr Asp Ala Ser Gly Leu Pro Leu
    210                 215                 220

Pro Gly Gln Gly Tyr Ser Ala Pro Asp Gln Pro Tyr Gln Ala Gln Pro
225                 230                 235                 240

Gln Tyr Gln Gln Ala Thr Pro Ala Ala Ala Pro Gln Gln Tyr Gln Ala
                245                 250                 255

Pro Gln Pro Gln Tyr Gln Gln Ser Ala Pro Gln Ala Gln Pro Ala Pro
            260                 265                 270

Ala Pro Val Ala Gln Phe Gln Gln Ala Ser Ala Ser Gly Thr Cys Ser
        275                 280                 285

Ala Ser Thr Ala Ala Val Ser Gly Thr Thr Ser Cys Arg
    290                 295                 300


<210> 2039
<211> 276
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(253)
<223> RXA01041

<400> 2039
acagcaggca atgcctaccc aagccccaca aacaccggca caaccagttc agccaccagc 60

accacaagcc ggttctgcat ttaccgatgc tccgggtgct gtg cca cag gca cca   115
                                        Val Pro Gln Ala Pro
                                          1               5

gca gtt cag gct gct ccc gct gta gct cag gcg cct gtc gcg cca gta   163
Ala Val Gln Ala Ala Pro Ala Val Ala Gln Ala Pro Val Ala Pro Val
                 10                  15                  20

gtt gat atg acc gag cca gca tcc cca tgg gat ctt cca gct gca cct   211
Val Asp Met Thr Glu Pro Ala Ser Pro Trp Asp Leu Pro Ala Ala Pro
             25                  30                  35

agt cag cca gcg cag cca gct cag ggc atc acc tac ccg gca           253
Ser Gln Pro Ala Gln Pro Ala Gln Gly Ile Thr Tyr Pro Ala
         40                  45                  50

taacaaccag cacaaccctt aga                                         276
```

<210> 2040
<211> 51
<212> PRT
<213> Corynebacterium glutamicum

<400> 2040
Val Pro Gln Ala Pro Ala Val Gln Ala Ala Pro Ala Val Ala Gln Ala
1 5 10 15

Pro Val Ala Pro Val Val Asp Met Thr Glu Pro Ala Ser Pro Trp Asp
20 25 30

Leu Pro Ala Ala Pro Ser Gln Pro Ala Gln Pro Ala Gln Gly Ile Thr
35 40 45

Tyr Pro Ala
50

<210> 2041
<211> 1401
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1378)
<223> RXA01042

<400> 2041
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ttttttcacc agggtcgagg cgcggtctgt gtgcccacct cgacccactt ttcgcccacc 60

acttttcgtc aacctaccaa caacaaagcc caggtcactt atg gtc aac cct ttt   115
                                        Met Val Asn Pro Phe
                                          1               5

cac acg ctt gat aac tca ccg ttt gat ccg gtg gca cag ttt cct gcg   163
His Thr Leu Asp Asn Ser Pro Phe Asp Pro Val Ala Gln Phe Pro Ala
            10                  15                  20

ttt tat cac aac ccg ctt atc aat cac ttg ggc cgc cgt cgc gcc tgg   211
Phe Tyr His Asn Pro Leu Ile Asn His Leu Gly Arg Arg Arg Ala Trp
        25                  30                  35

aca atc tca gac atc aac aaa cgc ccc atc aat gtc caa cag atg ctg   259
Thr Ile Ser Asp Ile Asn Lys Arg Pro Ile Asn Val Gln Gln Met Leu
    40                  45                  50

acc acg gcc acc tac ggt agc ccc gtt att cat ggt gcc cgc att gaa   307
Thr Thr Ala Thr Tyr Gly Ser Pro Val Ile His Gly Ala Arg Ile Glu
55                  60                  65

gac gca gca acc tcc cta ctt acc ctg gat gaa ctg cgt aca cag att   355
Asp Ala Ala Thr Ser Leu Leu Thr Leu Asp Glu Leu Arg Thr Gln Ile
70                  75                  80                  85

ccc acc gct gcc aac aat gcg ttt tat ctc gat gct gtc caa gat ggc   403
Pro Thr Ala Ala Asn Asn Ala Phe Tyr Leu Asp Ala Val Gln Asp Gly
            90                  95                  100
```

```
tgt ctt att tta gat att gaa aaa acc tgt ccc ccc gag gtc gca gcc   451
Cys Leu Ile Leu Asp Ile Glu Lys Thr Cys Pro Pro Glu Val Ala Ala
            105                 110                 115

aca cta ctc acg ctc tcc ccc acc gcc ttt tac aca gag gtg tcc atg   499
Thr Leu Leu Thr Leu Ser Pro Thr Ala Phe Tyr Thr Glu Val Ser Met
        120                 125                 130

agt ggt cgt ggc tat cac ctc gtt atg ccg ata cca gag aat ttt gca   547
Ser Gly Arg Gly Tyr His Leu Val Met Pro Ile Pro Glu Asn Phe Ala
    135                 140                 145

gcg ttt cct gcc gta cac aac aaa ccc agt atc aaa cac ccc aag cgc   595
Ala Phe Pro Ala Val His Asn Lys Pro Ser Ile Lys His Pro Lys Arg
150                 155                 160                 165

tgg ttc gaa att ctt acc tca cag tgg atc acc ttc acc cga caa cca   643
Trp Phe Glu Ile Leu Thr Ser Gln Trp Ile Thr Phe Thr Arg Gln Pro
                170                 175                 180

atc cca gag cat gtt ctc cat cac agt gaa tct gct aac aca agt gct   691
Ile Pro Glu His Val Leu His His Ser Glu Ser Ala Asn Thr Ser Ala
            185                 190                 195

gtg cca tgg ttg aat gat caa cca ctt aca tgg gaa aac gtc ttt gca   739
Val Pro Trp Leu Asn Asp Gln Pro Leu Thr Trp Glu Asn Val Phe Ala
        200                 205                 210

gac tta gct aaa act gtt gca ccc aac tta aaa acc ggt gcc gga ctt   787
Asp Leu Ala Lys Thr Val Ala Pro Asn Leu Lys Thr Gly Ala Gly Leu
    215                 220                 225

acc atc aca ccc aat gca ctg atg cca cca gat ctc agc gat gct gag   835
Thr Ile Thr Pro Asn Ala Leu Met Pro Pro Asp Leu Ser Asp Ala Glu
230                 235                 240                 245

cgc att cgc gac gat gaa gtc atc gac tcg acc tgt cga tta ttt gcc   883
Arg Ile Arg Asp Asp Glu Val Ile Asp Ser Thr Cys Arg Leu Phe Ala
                250                 255                 260

gaa cat tac tcg aaa aca ctt gcg gac ttc tat gat gat gca tcc cgg   931
Glu His Tyr Ser Lys Thr Leu Ala Asp Phe Tyr Asp Asp Ala Ser Arg
            265                 270                 275

ttc gag ttc agc caa att ggt gtc att atc aat cta ctg ctc ccc act   979
Phe Glu Phe Ser Gln Ile Gly Val Ile Ile Asn Leu Leu Leu Pro Thr
        280                 285                 290

atg agg atg cat ccc acc acg atc agt ctc gac aaa ccc atc aac tcc   1027
Met Arg Met His Pro Thr Thr Ile Ser Leu Asp Lys Pro Ile Asn Ser
    295                 300                 305

gat cac atc atc aga ctt ctg ttc gct gtc gct act cgc gtg atc act   1075
Asp His Ile Ile Arg Leu Leu Phe Ala Val Ala Thr Arg Val Ile Thr
310                 315                 320                 325

cac cgc agc aaa cat gat gag gag cga tct ggc gtt ccg tat ctg atg   1123
His Arg Ser Lys His Asp Glu Glu Arg Ser Gly Val Pro Tyr Leu Met
                330                 335                 340
```

```
tat cag gtt att tcc tgc ctt gac atg cga gaa cac ccc gac aat ggc   1171
Tyr Gln Val Ile Ser Cys Leu Asp Met Arg Glu His Pro Asp Asn Gly
            345                 350                 355

gac tac cgt gtc gta ccc tcc cgg cat aat aga gac caa cac agc aac   1219
Asp Tyr Arg Val Val Pro Ser Arg His Asn Arg Asp Gln His Ser Asn
        360                 365                 370

aac ccc tca gct cat gtg gtc cac caa caa cca caa ccc cag ccc agc   1267
Asn Pro Ser Ala His Val Val His Gln Gln Pro Gln Pro Gln Pro Ser
    375                 380                 385

gca gca gat tcg cca cat cac tac cgt gca cta ccc caa gaa aac acg   1315
Ala Ala Asp Ser Pro His His Tyr Arg Ala Leu Pro Gln Glu Asn Thr
390                 395                 400                 405

gtg tcc gaa cac agt ttt aaa atc tat aac cca cca gcc aca ccc cct   1363
Val Ser Glu His Ser Phe Lys Ile Tyr Asn Pro Pro Ala Thr Pro Pro
                410                 415                 420

cta gga ggt gaa aat tagatttatt attaaaacac ttg                    1401
Leu Gly Gly Glu Asn
            425
```

CONFIDENTIAL

<210> 2042
<211> 426
<212> PRT
<213> Corynebacterium glutamicum

<400> 2042

```
Met Val Asn Pro Phe His Thr Leu Asp Asn Ser Pro Phe Asp Pro Val
  1               5                  10                  15

Ala Gln Phe Pro Ala Phe Tyr His Asn Pro Leu Ile Asn His Leu Gly
             20                  25                  30

Arg Arg Arg Ala Trp Thr Ile Ser Asp Ile Asn Lys Arg Pro Ile Asn
         35                  40                  45

Val Gln Gln Met Leu Thr Thr Ala Thr Tyr Gly Ser Pro Val Ile His
     50                  55                  60

Gly Ala Arg Ile Glu Asp Ala Ala Thr Ser Leu Leu Thr Leu Asp Glu
 65                  70                  75                  80

Leu Arg Thr Gln Ile Pro Thr Ala Ala Asn Asn Ala Phe Tyr Leu Asp
                 85                  90                  95

Ala Val Gln Asp Gly Cys Leu Ile Leu Asp Ile Glu Lys Thr Cys Pro
            100                 105                 110

Pro Glu Val Ala Ala Thr Leu Leu Thr Leu Ser Pro Thr Ala Phe Tyr
        115                 120                 125

Thr Glu Val Ser Met Ser Gly Arg Gly Tyr His Leu Val Met Pro Ile
    130                 135                 140

Pro Glu Asn Phe Ala Ala Phe Pro Ala Val His Asn Lys Pro Ser Ile
145                 150                 155                 160
```

```
Lys His Pro Lys Arg Trp Phe Glu Ile Leu Thr Ser Gln Trp Ile Thr
                165                 170                 175

Phe Thr Arg Gln Pro Ile Pro Glu His Val Leu His His Ser Glu Ser
            180                 185                 190

Ala Asn Thr Ser Ala Val Pro Trp Leu Asn Asp Gln Pro Leu Thr Trp
        195                 200                 205

Glu Asn Val Phe Ala Asp Leu Ala Lys Thr Val Ala Pro Asn Leu Lys
    210                 215                 220

Thr Gly Ala Gly Leu Thr Ile Thr Pro Asn Ala Leu Met Pro Pro Asp
225                 230                 235                 240

Leu Ser Asp Ala Glu Arg Ile Arg Asp Asp Glu Val Ile Asp Ser Thr
                245                 250                 255

Cys Arg Leu Phe Ala Glu His Tyr Ser Lys Thr Leu Ala Asp Phe Tyr
            260                 265                 270

Asp Asp Ala Ser Arg Phe Glu Phe Ser Gln Ile Gly Val Ile Ile Asn
        275                 280                 285

Leu Leu Leu Pro Thr Met Arg Met His Pro Thr Thr Ile Ser Leu Asp
    290                 295                 300

Lys Pro Ile Asn Ser Asp His Ile Ile Arg Leu Leu Phe Ala Val Ala
305                 310                 315                 320

Thr Arg Val Ile Thr His Arg Ser Lys His Asp Glu Glu Arg Ser Gly
                325                 330                 335

Val Pro Tyr Leu Met Tyr Gln Val Ile Ser Cys Leu Asp Met Arg Glu
            340                 345                 350

His Pro Asp Asn Gly Asp Tyr Arg Val Val Pro Ser Arg His Asn Arg
        355                 360                 365

Asp Gln His Ser Asn Asn Pro Ser Ala His Val Val His Gln Gln Pro
    370                 375                 380

Gln Pro Gln Pro Ser Ala Ala Asp Ser Pro His His Tyr Arg Ala Leu
385                 390                 395                 400

Pro Gln Glu Asn Thr Val Ser Glu His Ser Phe Lys Ile Tyr Asn Pro
                405                 410                 415

Pro Ala Thr Pro Pro Leu Gly Gly Glu Asn
            420                 425
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<210> 2043
<211> 696
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(673)
<223> RXA01043

<400> 2043
tactaggtat agcaacggat taaataatca ctataattaa ttctttccgt actcatttta 60

atcactacct attcaccact tgaacggagc gtttttcgcc atg ttg aaa ttc cgc 115
Met Leu Lys Phe Arg
1 5

atc atc tcc aca gtc act act gga tct cag cca act cca cga aaa agc 163
Ile Ile Ser Thr Val Thr Thr Gly Ser Gln Pro Thr Pro Arg Lys Ser
10 15 20

tgg agc cac ccc gac acc act ctc ctg gtc acc atg gtc act gca cca 211
Trp Ser His Pro Asp Thr Thr Leu Leu Val Thr Met Val Thr Ala Pro
25 30 35

tcg ctg tgc tca gcc atc aac gtg tgg aac gca act gag cgt att ccc 259
Ser Leu Cys Ser Ala Ile Asn Val Trp Asn Ala Thr Glu Arg Ile Pro
40 45 50

gct caa aaa atc ctt aat gtc gaa gaa gta cac gtt ctt ggt gag tgc 307
Ala Gln Lys Ile Leu Asn Val Glu Glu Val His Val Leu Gly Glu Cys
55 60 65

agc gac gcc atc atc tct acg tca cta acc aaa aag gac aat ccg cac 355
Ser Asp Ala Ile Ile Ser Thr Ser Leu Thr Lys Lys Asp Asn Pro His
70 75 80 85

gca ctt gtg ccc gat gat ttc gac caa atc ggc gat gtg ttt ggc tat 403
Ala Leu Val Pro Asp Asp Phe Asp Gln Ile Gly Asp Val Phe Gly Tyr
90 95 100

gcg caa gac aat gta gct gtt ttt gat gtc att gtc gca gca ctg ggc 451
Ala Gln Asp Asn Val Ala Val Phe Asp Val Ile Val Ala Ala Leu Gly
105 110 115

ggt gct ggt tat ggc ctg cta ccc gga ctg gtc atg cac cac att gat 499
Gly Ala Gly Tyr Gly Leu Leu Pro Gly Leu Val Met His His Ile Asp
120 125 130

gag cac acc gtt gca ctt gtc ttt gat act gat tcc cct act ggg acg 547
Glu His Thr Val Ala Leu Val Phe Asp Thr Asp Ser Pro Thr Gly Thr
135 140 145

cat atc ctc ggt gag cgc tgc gtg tac tcc gac atc att cac atg act 595
His Ile Leu Gly Glu Arg Cys Val Tyr Ser Asp Ile Ile His Met Thr
150 155 160 165

gac gat aag tct gcc cgt ggc tgg ggt gca gtc att gcc ata gca cga 643
Asp Asp Lys Ser Ala Arg Gly Trp Gly Ala Val Ile Ala Ile Ala Arg
170 175 180

gcc atc atc ctc aaa gtc gaa cag atc atg tagtacccca ccatgactca 693
Ala Ile Ile Leu Lys Val Glu Gln Ile Met
185 190

ctt 696

<210> 2044
<211> 191

<212> PRT
<213> Corynebacterium glutamicum

<400> 2044

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Met Leu Lys Phe Arg Ile Ile Ser Thr Val Thr Thr Gly Ser Gln Pro
  1               5                  10                  15

Thr Pro Arg Lys Ser Trp Ser His Pro Asp Thr Thr Leu Leu Val Thr
             20                  25                  30

Met Val Thr Ala Pro Ser Leu Cys Ser Ala Ile Asn Val Trp Asn Ala
         35                  40                  45

Thr Glu Arg Ile Pro Ala Gln Lys Ile Leu Asn Val Glu Glu Val His
     50                  55                  60

Val Leu Gly Glu Cys Ser Asp Ala Ile Ile Ser Thr Ser Leu Thr Lys
 65                  70                  75                  80

Lys Asp Asn Pro His Ala Leu Val Pro Asp Asp Phe Asp Gln Ile Gly
                 85                  90                  95

Asp Val Phe Gly Tyr Ala Gln Asp Asn Val Ala Val Phe Asp Val Ile
            100                 105                 110

Val Ala Ala Leu Gly Gly Ala Gly Tyr Gly Leu Leu Pro Gly Leu Val
        115                 120                 125

Met His His Ile Asp Glu His Thr Val Ala Leu Val Phe Asp Thr Asp
    130                 135                 140

Ser Pro Thr Gly Thr His Ile Leu Gly Glu Arg Cys Val Tyr Ser Asp
145                 150                 155                 160

Ile Ile His Met Thr Asp Asp Lys Ser Ala Arg Gly Trp Gly Ala Val
                165                 170                 175

Ile Ala Ile Ala Arg Ala Ile Ile Leu Lys Val Glu Gln Ile Met
            180                 185                 190
```

<210> 2045
<211> 1380
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1357)
<223> RXA01044

<400> 2045

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cagatagcca ctacctacac gcatctgttg tgctgaaaca acagcgcgac actcactctt 60

ctcattactc aacaacttac ttttaaggac tacataactt atg tct ctc tac ctt   115
                                          Met Ser Leu Tyr Leu
                                            1               5

gac gac act ttg tct cgc atc gtt gaa ctt gat ctc aaa gac acc cgc   163
Asp Asp Thr Leu Ser Arg Ile Val Glu Leu Asp Leu Lys Asp Thr Arg
                10                  15                  20
```

```
att gtg ccg ttt ctt gct ggt gaa cca ggt atc ggt aaa acc tca ttc   211
Ile Val Pro Phe Leu Ala Gly Glu Pro Gly Ile Gly Lys Thr Ser Phe
            25                  30                  35

atc tac ggc atc ggc gaa cgt gca ggc tac aaa gtc ttc agt atc tcg   259
Ile Tyr Gly Ile Gly Glu Arg Ala Gly Tyr Lys Val Phe Ser Ile Ser
        40                  45                  50

gtt aac acc ctt gcc gat aag ggt gac ctc acg ggc gct cgc acc ctg   307
Val Asn Thr Leu Ala Asp Lys Gly Asp Leu Thr Gly Ala Arg Thr Leu
    55                  60                  65

cag gac cct gcc gat ggc aag tgg aag cag atg ttt ttc ccg cac gcg   355
Gln Asp Pro Ala Asp Gly Lys Trp Lys Gln Met Phe Phe Pro His Ala
70                  75                  80                  85

acc ttc gtc gaa gca aat gac tat gca cta gca aac cca aac gaa acg   403
Thr Phe Val Glu Ala Asn Asp Tyr Ala Leu Ala Asn Pro Asn Glu Thr
                90                  95                  100

gtc gtc att ctt ctc gat gag att aac cga act gat tcg gat gtc acc   451
Val Val Ile Leu Leu Asp Glu Ile Asn Arg Thr Asp Ser Asp Val Thr
            105                 110                 115

tct gcc tcg atg act atc tct act gag cgt cgc gtt ggt acc acc gat   499
Ser Ala Ser Met Thr Ile Ser Thr Glu Arg Arg Val Gly Thr Thr Asp
        120                 125                 130

cta gca ccc aat gtc cgc ctt gct gtc acc gga aac ctc acc ggt aat   547
Leu Ala Pro Asn Val Arg Leu Ala Val Thr Gly Asn Leu Thr Gly Asn
    135                 140                 145

gtc acc cac ctt gat tca gca tct ctg acc agg ttc tcc ctc tat gag   595
Val Thr His Leu Asp Ser Ala Ser Leu Thr Arg Phe Ser Leu Tyr Glu
150                 155                 160                 165

gtc aag cca tcc gca gag acc ttc atg aac atc atg ggc ggc cgc ctc   643
Val Lys Pro Ser Ala Glu Thr Phe Met Asn Ile Met Gly Gly Arg Leu
                170                 175                 180

aac aag tac atc cgt acc gtg ctg acc aaa tac ccg gaa tac atc ttc   691
Asn Lys Tyr Ile Arg Thr Val Leu Thr Lys Tyr Pro Glu Tyr Ile Phe
            185                 190                 195

atg aag cca act act gct act gct ctt att acc act ggc gat gat gat   739
Met Lys Pro Thr Thr Ala Thr Ala Leu Ile Thr Thr Gly Asp Asp Asp
        200                 205                 210

gac gac cat aca acc aat gcg aag caa atg atg gac ttc aac gct gtg   787
Asp Asp His Thr Thr Asn Ala Lys Gln Met Met Asp Phe Asn Ala Val
    215                 220                 225

ctc ggt tca gac caa gac atg gtt caa ttt acc gca cct aga act atc   835
Leu Gly Ser Asp Gln Asp Met Val Gln Phe Thr Ala Pro Arg Thr Ile
230                 235                 240                 245

gaa ggt ttg tcc gtc tgg ctc aac aac gcc gat gat gac ttt ctt cgt   883
Glu Gly Leu Ser Val Trp Leu Asn Asn Ala Asp Asp Asp Phe Leu Arg
                250                 255                 260
```

```
cta ctt cta caa gaa aag gtg gat ggt ctt gct cga tcc atg agc ttg   931
Leu Leu Leu Gln Glu Lys Val Asp Gly Leu Ala Arg Ser Met Ser Leu
            265                 270                 275

ctg cag gct acg ctc gaa tct cac acc ggc gat acc gct ttt acc gca   979
Leu Gln Ala Thr Leu Glu Ser His Thr Gly Asp Thr Ala Phe Thr Ala
        280                 285                 290

gaa gtc ctc agc gaa atg acc aat gat ctg ctg agc tcc gca tcg caa   1027
Glu Val Leu Ser Glu Met Thr Asn Asp Leu Leu Ser Ser Ala Ser Gln
    295                 300                 305

gct cct agt ggt cca atc aaa cca ttt gtc tac gac cga ctc gct gct   1075
Ala Pro Ser Gly Pro Ile Lys Pro Phe Val Tyr Asp Arg Leu Ala Ala
310                 315                 320                 325

gca cca agc aat act gta ctg gaa caa gag gtt cac aca ctc agt ctc   1123
Ala Pro Ser Asn Thr Val Leu Glu Gln Glu Val His Thr Leu Ser Leu
                330                 335                 340

aat gac cgc gcc gat gtc ttg ttg ttt gcc ctc cat gac act gta aac   1171
Asn Asp Arg Ala Asp Val Leu Leu Phe Ala Leu His Asp Thr Val Asn
            345                 350                 355

aac gct gca cca agc atc atc gct cac ctt gca tct gaa ggc gta ctt   1219
Asn Ala Ala Pro Ser Ile Ile Ala His Leu Ala Ser Glu Gly Val Leu
        360                 365                 370

gat gaa ctg ccc aaa gac aga atc agc aaa att gtt tca ctc ggt cct   1267
Asp Glu Leu Pro Lys Asp Arg Ile Ser Lys Ile Val Ser Leu Gly Pro
    375                 380                 385

gta cca acg gca aac tat cac gcc ttg acc aga cag gat aca acg ttg   1315
Val Pro Thr Ala Asn Tyr His Ala Leu Thr Arg Gln Asp Thr Thr Leu
390                 395                 400                 405

act cga aat ctc ggt ccc gct gtc ttg ggc ttc ttg gaa agt           1357
Thr Arg Asn Leu Gly Pro Ala Val Leu Gly Phe Leu Glu Ser
                410                 415

taaagcaatt tcctaagtac ctt                                        1380
```

<210> 2046
<211> 419
<212> PRT
<213> Corynebacterium glutamicum

<400> 2046

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Met Ser Leu Tyr Leu Asp Asp Thr Leu Ser Arg Ile Val Glu Leu Asp
  1               5                  10                  15

Leu Lys Asp Thr Arg Ile Val Pro Phe Leu Ala Gly Glu Pro Gly Ile
             20                  25                  30

Gly Lys Thr Ser Phe Ile Tyr Gly Ile Gly Glu Arg Ala Gly Tyr Lys
         35                  40                  45

Val Phe Ser Ile Ser Val Asn Thr Leu Ala Asp Lys Gly Asp Leu Thr
     50                  55                  60
```

```
Gly Ala Arg Thr Leu Gln Asp Pro Ala Asp Gly Lys Trp Lys Gln Met
 65                  70                  75                  80

Phe Phe Pro His Ala Thr Phe Val Glu Ala Asn Asp Tyr Ala Leu Ala
                85                  90                  95

Asn Pro Asn Glu Thr Val Val Ile Leu Leu Asp Glu Ile Asn Arg Thr
            100                 105                 110

Asp Ser Asp Val Thr Ser Ala Ser Met Thr Ile Ser Thr Glu Arg Arg
        115                 120                 125

Val Gly Thr Thr Asp Leu Ala Pro Asn Val Arg Leu Ala Val Thr Gly
    130                 135                 140

Asn Leu Thr Gly Asn Val Thr His Leu Asp Ser Ala Ser Leu Thr Arg
145                 150                 155                 160

Phe Ser Leu Tyr Glu Val Lys Pro Ser Ala Glu Thr Phe Met Asn Ile
                165                 170                 175

Met Gly Gly Arg Leu Asn Lys Tyr Ile Arg Thr Val Leu Thr Lys Tyr
            180                 185                 190

Pro Glu Tyr Ile Phe Met Lys Pro Thr Thr Ala Thr Ala Leu Ile Thr
        195                 200                 205

Thr Gly Asp Asp Asp Asp Asp His Thr Thr Asn Ala Lys Gln Met Met
    210                 215                 220

Asp Phe Asn Ala Val Leu Gly Ser Asp Gln Asp Met Val Gln Phe Thr
225                 230                 235                 240

Ala Pro Arg Thr Ile Glu Gly Leu Ser Val Trp Leu Asn Asn Ala Asp
                245                 250                 255

Asp Asp Phe Leu Arg Leu Leu Leu Gln Glu Lys Val Asp Gly Leu Ala
            260                 265                 270

Arg Ser Met Ser Leu Leu Gln Ala Thr Leu Glu Ser His Thr Gly Asp
        275                 280                 285

Thr Ala Phe Thr Ala Glu Val Leu Ser Glu Met Thr Asn Asp Leu Leu
    290                 295                 300

Ser Ser Ala Ser Gln Ala Pro Ser Gly Pro Ile Lys Pro Phe Val Tyr
305                 310                 315                 320

Asp Arg Leu Ala Ala Ala Pro Ser Asn Thr Val Leu Glu Gln Glu Val
                325                 330                 335

His Thr Leu Ser Leu Asn Asp Arg Ala Asp Val Leu Leu Phe Ala Leu
            340                 345                 350

His Asp Thr Val Asn Asn Ala Ala Pro Ser Ile Ile Ala His Leu Ala
        355                 360                 365

Ser Glu Gly Val Leu Asp Glu Leu Pro Lys Asp Arg Ile Ser Lys Ile
    370                 375                 380

Val Ser Leu Gly Pro Val Pro Thr Ala Asn Tyr His Ala Leu Thr Arg
```

385 390 395 400

Gln Asp Thr Thr Leu Thr Arg Asn Leu Gly Pro Ala Val Leu Gly Phe
405 410 415

Leu Glu Ser

<210> 2047
<211> 1947
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1924)
<223> RXA01045

<400> 2047
cagctgaggt agtcatctgt ctacctgcgt ggagtagaca ctaaatcctg tccacgcacc 60

cttacccttc ttgacactag taattgaaag cgatcccctc atg gtt acc ttc agc 115
Met Val Thr Phe Ser
1 5

gtc gca aat cac gcg cct cat act ttt agc cca ttc gat att gaa cca 163
Val Ala Asn His Ala Pro His Thr Phe Ser Pro Phe Asp Ile Glu Pro
10 15 20

cca ctc acc ggt aac gcc acc acc gac gaa cat ggt tac gaa cac acc 211
Pro Leu Thr Gly Asn Ala Thr Thr Asp Glu His Gly Tyr Glu His Thr
25 30 35

tca gtg cta gaa aaa cta gcc tcc aac cac ctg ttc aat cca atc aat 259
Ser Val Leu Glu Lys Leu Ala Ser Asn His Leu Phe Asn Pro Ile Asn
40 45 50

ccg caa cac cca gtc act atc aca gcc acc gaa aac gga tca acc gtt 307
Pro Gln His Pro Val Thr Ile Thr Ala Thr Glu Asn Gly Ser Thr Val
55 60 65

gat ctt gat gca gca gca cta gca caa cat ctt gct cta gcg att acc 355
Asp Leu Asp Ala Ala Ala Leu Ala Gln His Leu Ala Leu Ala Ile Thr
70 75 80 85

cca gac tca atg ctg gca aat cat caa ggc tac aac cgt gac atg atg 403
Pro Asp Ser Met Leu Ala Asn His Gln Gly Tyr Asn Arg Asp Met Met
90 95 100

ggt cta ctt tcg cag ctt act aac cat gtt ggc ttt gat cgc cga ttc 451
Gly Leu Leu Ser Gln Leu Thr Asn His Val Gly Phe Asp Arg Arg Phe
105 110 115

att gtt gac caa ctc ttt atc tcc caa gtg ctc aaa gcg aat cgt cta 499
Ile Val Asp Gln Leu Phe Ile Ser Gln Val Leu Lys Ala Asn Arg Leu
120 125 130

cca gca ccg gca aac aac gtt att tac acc gtg ccc aat gac gtt atc 547
Pro Ala Pro Ala Asn Asn Val Ile Tyr Thr Val Pro Asn Asp Val Ile
135 140 145

```
cca tct gct aaa gac atc ttg tcc acc act gca aaa atg aac aat cca   595
Pro Ser Ala Lys Asp Ile Leu Ser Thr Thr Ala Lys Met Asn Asn Pro
150                 155                 160                 165

ctg aca gtt act gca agt gcc cca att act gtt gac gac att cac aca   643
Leu Thr Val Thr Ala Ser Ala Pro Ile Thr Val Asp Asp Ile His Thr
                170                 175                 180

gcc tat gag gta ttt ttc gct tct ctt gcc tca gtg ttt ttc cct tat   691
Ala Tyr Glu Val Phe Phe Ala Ser Leu Ala Ser Val Phe Phe Pro Tyr
            185                 190                 195

acc tac ggt gcg gta ttc ctt aac aac gca gaa ttc gtt gag ttt gtt   739
Thr Tyr Gly Ala Val Phe Leu Asn Asn Ala Glu Phe Val Glu Phe Val
        200                 205                 210

gat tac ctt att aac gaa gca aca aca ctg cac tcg gca tca ctc atc   787
Asp Tyr Leu Ile Asn Glu Ala Thr Thr Leu His Ser Ala Ser Leu Ile
    215                 220                 225

tcc aac aac acc ttt aat agg ttc caa tca atg cgt aac atc tcc att   835
Ser Asn Asn Thr Phe Asn Arg Phe Gln Ser Met Arg Asn Ile Ser Ile
230                 235                 240                 245

gat aat ctc acc gcc gag ttt ctc tta cgc aaa aat gaa gca gag aca   883
Asp Asn Leu Thr Ala Glu Phe Leu Leu Arg Lys Asn Glu Ala Glu Thr
                250                 255                 260

act gat gat tat tca ttc ccc cgc gta ctt gtt tcc ctg ctg cat tct   931
Thr Asp Asp Tyr Ser Phe Pro Arg Val Leu Val Ser Leu Leu His Ser
            265                 270                 275

tgg gtg aaa ctc aat cac gat gat gct cgt gct aac aat gat gca ccc   979
Trp Val Lys Leu Asn His Asp Asp Ala Arg Ala Asn Asn Asp Ala Pro
        280                 285                 290

acc tgt gca cta gca ccg ttt agt gtg gct caa tgg atc atg ccg gag   1027
Thr Cys Ala Leu Ala Pro Phe Ser Val Ala Gln Trp Ile Met Pro Glu
    295                 300                 305

acc att gtg ttt att aat gct gaa gct cat gct cat gca tcc tcc cag   1075
Thr Ile Val Phe Ile Asn Ala Glu Ala His Ala His Ala Ser Ser Gln
310                 315                 320                 325

gac att gag aag aaa tgg aag gaa att aat gcg gcg tta aca ggg tct   1123
Asp Ile Glu Lys Lys Trp Lys Glu Ile Asn Ala Ala Leu Thr Gly Ser
                330                 335                 340

att cgt att atg tcg cca aat gca att tcc aag ctg caa tct gct cag   1171
Ile Arg Ile Met Ser Pro Asn Ala Ile Ser Lys Leu Gln Ser Ala Gln
            345                 350                 355

cat ctc ggg atg caa gca caa atg cag gcc atg cgt gct cga aaa gat   1219
His Leu Gly Met Gln Ala Gln Met Gln Ala Met Arg Ala Arg Lys Asp
        360                 365                 370

cac cac aac atg cag aag cgt tcc tca caa gaa aac gac ttt tcc aag   1267
His His Asn Met Gln Lys Arg Ser Ser Gln Glu Asn Asp Phe Ser Lys
    375                 380                 385
```

```
gca ctc ccc tca cca cag act atc gtg ctt tct gtc gca gag gtt ctg   1315
Ala Leu Pro Ser Pro Gln Thr Ile Val Leu Ser Val Ala Glu Val Leu
390                 395                 400                 405

cgc aaa ctc act cac gta cgc caa tcg cac aac cct cag aaa tac cag   1363
Arg Lys Leu Thr His Val Arg Gln Ser His Asn Pro Gln Lys Tyr Gln
                410                 415                 420

aag aag tct ctg acc aga gct tct cgc cga cac ccg gat aac cct aat   1411
Lys Lys Ser Leu Thr Arg Ala Ser Arg Arg His Pro Asp Asn Pro Asn
            425                 430                 435

gtc cct ggc acc att aag agc aag ctc ttc tac cct gac ctg cat gtt   1459
Val Pro Gly Thr Ile Lys Ser Lys Leu Phe Tyr Pro Asp Leu His Val
        440                 445                 450

tat gta gat act tct ggt tcg att agt gaa gaa agc tac cgc aac tct   1507
Tyr Val Asp Thr Ser Gly Ser Ile Ser Glu Glu Ser Tyr Arg Asn Ser
    455                 460                 465

gtg gtt ctg ctc atg cag ctt gcc acc aaa ctg gac atc aac ctc tat   1555
Val Val Leu Leu Met Gln Leu Ala Thr Lys Leu Asp Ile Asn Leu Tyr
470                 475                 480                 485

ttc tcc acc ttc tct cac gtg ctc tcc gaa gaa gta cta ttg ccg acc   1603
Phe Ser Thr Phe Ser His Val Leu Ser Glu Glu Val Leu Leu Pro Thr
                490                 495                 500

aag ggt aaa aca cca cag caa ttg gca gct ctt att tcg gcc atc cca   1651
Lys Gly Lys Thr Pro Gln Gln Leu Ala Ala Leu Ile Ser Ala Ile Pro
            505                 510                 515

aag gtc tct ggc ggt act gac tat cac cag att tgg gat tac atc cag   1699
Lys Val Ser Gly Gly Thr Asp Tyr His Gln Ile Trp Asp Tyr Ile Gln
        520                 525                 530

atc aat ccg cag cgc caa gaa cgc atg aat ctt gtg tta act gac ttc   1747
Ile Asn Pro Gln Arg Gln Glu Arg Met Asn Leu Val Leu Thr Asp Phe
    535                 540                 545

gga ttc atg ccg aat cgc ggc tta aac atc gac cac cca agt tct att   1795
Gly Phe Met Pro Asn Arg Gly Leu Asn Ile Asp His Pro Ser Ser Ile
550                 555                 560                 565

ttc tac gtc cca atc ctg cct gac tac ggc agc tgg tca atg gtt cga   1843
Phe Tyr Val Pro Ile Leu Pro Asp Tyr Gly Ser Trp Ser Met Val Arg
                570                 575                 580

aga gat atg tct cat ttc gca aat gaa atg gtt gac ttc gac ccc tat   1891
Arg Asp Met Ser His Phe Ala Asn Glu Met Val Asp Phe Asp Pro Tyr
            585                 590                 595

atc cac agc cga cta ctc ggc gta cac gga aaa tagcagctga tccatctagg 1944
Ile His Ser Arg Leu Leu Gly Val His Gly Lys
        600                 605

gtc                                                               1947
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<210> 2048
<211> 608

<212> PRT
<213> Corynebacterium glutamicum

<400> 2048

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Met Val Thr Phe Ser Val Ala Asn His Ala Pro His Thr Phe Ser Pro
  1               5                  10                  15

Phe Asp Ile Glu Pro Pro Leu Thr Gly Asn Ala Thr Thr Asp Glu His
             20                  25                  30

Gly Tyr Glu His Thr Ser Val Leu Glu Lys Leu Ala Ser Asn His Leu
         35                  40                  45

Phe Asn Pro Ile Asn Pro Gln His Pro Val Thr Ile Thr Ala Thr Glu
     50                  55                  60

Asn Gly Ser Thr Val Asp Leu Asp Ala Ala Ala Leu Ala Gln His Leu
 65                  70                  75                  80

Ala Leu Ala Ile Thr Pro Asp Ser Met Leu Ala Asn His Gln Gly Tyr
                 85                  90                  95

Asn Arg Asp Met Met Gly Leu Leu Ser Gln Leu Thr Asn His Val Gly
            100                 105                 110

Phe Asp Arg Arg Phe Ile Val Asp Gln Leu Phe Ile Ser Gln Val Leu
        115                 120                 125

Lys Ala Asn Arg Leu Pro Ala Pro Ala Asn Asn Val Ile Tyr Thr Val
    130                 135                 140

Pro Asn Asp Val Ile Pro Ser Ala Lys Asp Ile Leu Ser Thr Thr Ala
145                 150                 155                 160

Lys Met Asn Asn Pro Leu Thr Val Thr Ala Ser Ala Pro Ile Thr Val
                165                 170                 175

Asp Asp Ile His Thr Ala Tyr Glu Val Phe Phe Ala Ser Leu Ala Ser
            180                 185                 190

Val Phe Phe Pro Tyr Thr Tyr Gly Ala Val Phe Leu Asn Asn Ala Glu
        195                 200                 205

Phe Val Glu Phe Val Asp Tyr Leu Ile Asn Glu Ala Thr Thr Leu His
    210                 215                 220

Ser Ala Ser Leu Ile Ser Asn Asn Thr Phe Asn Arg Phe Gln Ser Met
225                 230                 235                 240

Arg Asn Ile Ser Ile Asp Asn Leu Thr Ala Glu Phe Leu Leu Arg Lys
                245                 250                 255

Asn Glu Ala Glu Thr Thr Asp Asp Tyr Ser Phe Pro Arg Val Leu Val
            260                 265                 270

Ser Leu Leu His Ser Trp Val Lys Leu Asn His Asp Asp Ala Arg Ala
        275                 280                 285

Asn Asn Asp Ala Pro Thr Cys Ala Leu Ala Pro Phe Ser Val Ala Gln
    290                 295                 300
```

```
Trp Ile Met Pro Glu Thr Ile Val Phe Ile Asn Ala Glu Ala His Ala
305                 310                 315                 320

His Ala Ser Ser Gln Asp Ile Glu Lys Lys Trp Lys Glu Ile Asn Ala
                325                 330                 335

Ala Leu Thr Gly Ser Ile Arg Ile Met Ser Pro Asn Ala Ile Ser Lys
            340                 345                 350

Leu Gln Ser Ala Gln His Leu Gly Met Gln Ala Gln Met Gln Ala Met
        355                 360                 365

Arg Ala Arg Lys Asp His His Asn Met Gln Lys Arg Ser Ser Gln Glu
    370                 375                 380

Asn Asp Phe Ser Lys Ala Leu Pro Ser Pro Gln Thr Ile Val Leu Ser
385                 390                 395                 400

Val Ala Glu Val Leu Arg Lys Leu Thr His Val Arg Gln Ser His Asn
                405                 410                 415

Pro Gln Lys Tyr Gln Lys Lys Ser Leu Thr Arg Ala Ser Arg Arg His
            420                 425                 430

Pro Asp Asn Pro Asn Val Pro Gly Thr Ile Lys Ser Lys Leu Phe Tyr
        435                 440                 445

Pro Asp Leu His Val Tyr Val Asp Thr Ser Gly Ser Ile Ser Glu Glu
    450                 455                 460

Ser Tyr Arg Asn Ser Val Val Leu Leu Met Gln Leu Ala Thr Lys Leu
465                 470                 475                 480

Asp Ile Asn Leu Tyr Phe Ser Thr Phe Ser His Val Leu Ser Glu Glu
                485                 490                 495

Val Leu Leu Pro Thr Lys Gly Lys Thr Pro Gln Gln Leu Ala Ala Leu
            500                 505                 510

Ile Ser Ala Ile Pro Lys Val Ser Gly Gly Thr Asp Tyr His Gln Ile
        515                 520                 525

Trp Asp Tyr Ile Gln Ile Asn Pro Gln Arg Gln Glu Arg Met Asn Leu
    530                 535                 540

Val Leu Thr Asp Phe Gly Phe Met Pro Asn Arg Gly Leu Asn Ile Asp
545                 550                 555                 560

His Pro Ser Ser Ile Phe Tyr Val Pro Ile Leu Pro Asp Tyr Gly Ser
                565                 570                 575

Trp Ser Met Val Arg Arg Asp Met Ser His Phe Ala Asn Glu Met Val
            580                 585                 590

Asp Phe Asp Pro Tyr Ile His Ser Arg Leu Leu Gly Val His Gly Lys
        595                 600                 605
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<210> 2049
<211> 1902
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1879)
<223> RXA01046

<400> 2049
tagcgatcct aggcaaaatg caccagctaa ccccaccgct caaccgccat ctgcccccac 60

ctcacactca tcacagcagg gtctccctcc gggcgccatt atg atc cct ttt cca 115
Met Ile Pro Phe Pro
1 5

ggg caa ccg cag cag caa agc gca ccc aat gac gag acc cgt ttc atc 163
Gly Gln Pro Gln Gln Gln Ser Ala Pro Asn Asp Glu Thr Arg Phe Ile
10 15 20

gac ctt aac gaa cgt cat aaa gat gat gaa cca gcc ctg ttt cgc gat 211
Asp Leu Asn Glu Arg His Lys Asp Asp Glu Pro Ala Leu Phe Arg Asp
25 30 35

gat gtt att gat caa act ctc gct att ttg atc agt aaa aat aag ccc 259
Asp Val Ile Asp Gln Thr Leu Ala Ile Leu Ile Ser Lys Asn Lys Pro
40 45 50

aat gcg cta ctc gtt ggg cct gcc ggt aca ggt aaa tcc cgt atc gca 307
Asn Ala Leu Leu Val Gly Pro Ala Gly Thr Gly Lys Ser Arg Ile Ala
55 60 65

gaa gat att gcg cgc cgc ctt gcc aat gat gac gta tct att ccc gat 355
Glu Asp Ile Ala Arg Arg Leu Ala Asn Asp Asp Val Ser Ile Pro Asp
70 75 80 85

cag ctt gtc ggc cac cgt att ctt gat gtc tcc att gca gag ctt gtt 403
Gln Leu Val Gly His Arg Ile Leu Asp Val Ser Ile Ala Glu Leu Val
90 95 100

gct ggt gct ggc gtt gtt ggt cag ctc aag aaa cgc att ctg gat ctc 451
Ala Gly Ala Gly Val Val Gly Gln Leu Lys Lys Arg Ile Leu Asp Leu
105 110 115

atc aag tat gcg acc gac ccg agt aac aaa gtc att atc ttt att gac 499
Ile Lys Tyr Ala Thr Asp Pro Ser Asn Lys Val Ile Ile Phe Ile Asp
120 125 130

gag att cac caa att gct ggt gat cag tcc agt cac agt gga tcg caa 547
Glu Ile His Gln Ile Ala Gly Asp Gln Ser Ser His Ser Gly Ser Gln
135 140 145

gcc aaa gtt gct cag att ctc aaa ccc tat ctt gcc cgt ggt gac ctt 595
Ala Lys Val Ala Gln Ile Leu Lys Pro Tyr Leu Ala Arg Gly Asp Leu
150 155 160 165

cgt gtt att ggt gcc acc acc acc cag gaa gct cgt gac ttc gat cat 643
Arg Val Ile Gly Ala Thr Thr Thr Gln Glu Ala Arg Asp Phe Asp His
170 175 180

```
gat cca gcc ctc aaa cgc cgt ttt agc aga gta aat gtc gat gaa ttt   691
Asp Pro Ala Leu Lys Arg Arg Phe Ser Arg Val Asn Val Asp Glu Phe
            185                 190                 195

gat cga gat caa acg ctc act att ctt cat gct gca cgt gat ggt tac   739
Asp Arg Asp Gln Thr Leu Thr Ile Leu His Ala Ala Arg Asp Gly Tyr
        200                 205                 210

ctc aaa cat ttc aac aac gct gtc acg gta tct gac gac gta ctg ggc   787
Leu Lys His Phe Asn Asn Ala Val Thr Val Ser Asp Asp Val Leu Gly
    215                 220                 225

tat gtc tac acc tac tcg cag caa ttc aac cca ggc aat aca gca caa   835
Tyr Val Tyr Thr Tyr Ser Gln Gln Phe Asn Pro Gly Asn Thr Ala Gln
230                 235                 240                 245

cct gat gca gca ctg acg ctg ttt gat aag gcg ttg gct tcc cta act   883
Pro Asp Ala Ala Leu Thr Leu Phe Asp Lys Ala Leu Ala Ser Leu Thr
                250                 255                 260

atg gag aaa cag cgt ctg atc aac aac cat gtc att gcg ccg tcg ctc   931
Met Glu Lys Gln Arg Leu Ile Asn Asn His Val Ile Ala Pro Ser Leu
            265                 270                 275

aag ttc cct gtg tca gaa agg cac atc cat aac acc gct cgc aaa ctt   979
Lys Phe Pro Val Ser Glu Arg His Ile His Asn Thr Ala Arg Lys Leu
        280                 285                 290

gcc ttt ggc tct caa gtg cca gcc tcc atc aat act gat gat gct cgt   1027
Ala Phe Gly Ser Gln Val Pro Ala Ser Ile Asn Thr Asp Asp Ala Arg
    295                 300                 305

gac aaa ctc gaa acg ttg ttt ggt caa gat cat att att gag cca gta   1075
Asp Lys Leu Glu Thr Leu Phe Gly Gln Asp His Ile Ile Glu Pro Val
310                 315                 320                 325

ctc acc gct atc aag cgt gaa cag ctt ggt att ttc cct cgc acc aaa   1123
Leu Thr Ala Ile Lys Arg Glu Gln Leu Gly Ile Phe Pro Arg Thr Lys
                330                 335                 340

cca ttg agc tgg gtg ttt gct ggt tca tct ggt gtg ggt aaa aca gaa   1171
Pro Leu Ser Trp Val Phe Ala Gly Ser Ser Gly Val Gly Lys Thr Glu
            345                 350                 355

atg gcg cgt att ctc tct cgc gcc att aat ggc ggc gat ccc atc att   1219
Met Ala Arg Ile Leu Ser Arg Ala Ile Asn Gly Gly Asp Pro Ile Ile
        360                 365                 370

atc aat ggt ccc gaa tac att agt cct gag tcc att act ggc ctt atc   1267
Ile Asn Gly Pro Glu Tyr Ile Ser Pro Glu Ser Ile Thr Gly Leu Ile
    375                 380                 385

gga tca tcc gat ggc tat atc ggc tct aat tct aag cgt gct aaa cca   1315
Gly Ser Ser Asp Gly Tyr Ile Gly Ser Asn Ser Lys Arg Ala Lys Pro
390                 395                 400                 405

ctc gac ccg ctg att tct aat ccg cgt cag gtg att gtg ctc gat gaa   1363
Leu Asp Pro Leu Ile Ser Asn Pro Arg Gln Val Ile Val Leu Asp Glu
                410                 415                 420

ttt gag aag tct cac cct cat ttc cag caa ttg ttc atg gca gct ctt   1411
```

```
Phe Glu Lys Ser His Pro His Phe Gln Gln Leu Phe Met Ala Ala Leu
            425                 430                 435

gat aca ggc act atg gcg atg gct aat ggc acg aca ttg aat ttc tct   1459
Asp Thr Gly Thr Met Ala Met Ala Asn Gly Thr Thr Leu Asn Phe Ser
        440                 445                 450

cag gcc att atc att gcc acc acc aat gca gcc cgc gac aaa atc ggt   1507
Gln Ala Ile Ile Ile Ala Thr Thr Asn Ala Ala Arg Asp Lys Ile Gly
    455                 460                 465

cgt gac agc ttt gga ttc gat tca gat aat tca ggt gtc ctc ggt tct   1555
Arg Asp Ser Phe Gly Phe Asp Ser Asp Asn Ser Gly Val Leu Gly Ser
470                 475                 480                 485

gct caa gca gca act gat ccg cgt gca cag gaa cgc ctc aag tca ctg   1603
Ala Gln Ala Ala Thr Asp Pro Arg Ala Gln Glu Arg Leu Lys Ser Leu
                490                 495                 500

atg tcc aag gat ttc ctg ttg aac tgc tca acc gtt tcc aga ata tct   1651
Met Ser Lys Asp Phe Leu Leu Asn Cys Ser Thr Val Ser Arg Ile Ser
            505                 510                 515

ttg cct tca acc gca ttg atg cag gca cct acc gtg aga ttc tgg aca   1699
Leu Pro Ser Thr Ala Leu Met Gln Ala Pro Thr Val Arg Phe Trp Thr
        520                 525                 530

atc tct acc agc gtc gcc gtg acg ccg tgc tgc tta gcc acc ccg cat   1747
Ile Ser Thr Ser Val Ala Val Thr Pro Cys Cys Leu Ala Thr Pro His
    535                 540                 545

tac gca gca cag atc cct gca gat att gat tca gac act ctt gat cag   1795
Tyr Ala Ala Gln Ile Pro Ala Asp Ile Asp Ser Asp Thr Leu Asp Gln
550                 555                 560                 565

ctg gtg gaa acc acc ttt atc tca gat ttt ggt gca cgt cct gct gca   1843
Leu Val Glu Thr Thr Phe Ile Ser Asp Phe Gly Ala Arg Pro Ala Ala
                570                 575                 580

cgc acc atc gaa gac cac atc gca tcc ttg ctg atg tgaccaacct        1889
Arg Thr Ile Glu Asp His Ile Ala Ser Leu Leu Met
            585                 590

tttaggagta cat                                                   1902


<210> 2050
<211> 593
<212> PRT
<213> Corynebacterium glutamicum

<400> 2050
Met Ile Pro Phe Pro Gly Gln Pro Gln Gln Gln Ser Ala Pro Asn Asp
  1               5                  10                  15

Glu Thr Arg Phe Ile Asp Leu Asn Glu Arg His Lys Asp Asp Glu Pro
            20                  25                  30

Ala Leu Phe Arg Asp Asp Val Ile Asp Gln Thr Leu Ala Ile Leu Ile
        35                  40                  45
```

```
Ser Lys Asn Lys Pro Asn Ala Leu Leu Val Gly Pro Ala Gly Thr Gly
     50                  55                  60

Lys Ser Arg Ile Ala Glu Asp Ile Ala Arg Arg Leu Ala Asn Asp Asp
 65                  70                  75                  80

Val Ser Ile Pro Asp Gln Leu Val Gly His Arg Ile Leu Asp Val Ser
                 85                  90                  95

Ile Ala Glu Leu Val Ala Gly Ala Gly Val Val Gly Gln Leu Lys Lys
            100                 105                 110

Arg Ile Leu Asp Leu Ile Lys Tyr Ala Thr Asp Pro Ser Asn Lys Val
        115                 120                 125

Ile Ile Phe Ile Asp Glu Ile His Gln Ile Ala Gly Asp Gln Ser Ser
    130                 135                 140

His Ser Gly Ser Gln Ala Lys Val Ala Gln Ile Leu Lys Pro Tyr Leu
145                 150                 155                 160

Ala Arg Gly Asp Leu Arg Val Ile Gly Ala Thr Thr Thr Gln Glu Ala
                165                 170                 175

Arg Asp Phe Asp His Asp Pro Ala Leu Lys Arg Arg Phe Ser Arg Val
            180                 185                 190

Asn Val Asp Glu Phe Asp Arg Asp Gln Thr Leu Thr Ile Leu His Ala
        195                 200                 205

Ala Arg Asp Gly Tyr Leu Lys His Phe Asn Asn Ala Val Thr Val Ser
    210                 215                 220

Asp Asp Val Leu Gly Tyr Val Tyr Thr Tyr Ser Gln Gln Phe Asn Pro
225                 230                 235                 240

Gly Asn Thr Ala Gln Pro Asp Ala Ala Leu Thr Leu Phe Asp Lys Ala
                245                 250                 255

Leu Ala Ser Leu Thr Met Glu Lys Gln Arg Leu Ile Asn Asn His Val
            260                 265                 270

Ile Ala Pro Ser Leu Lys Phe Pro Val Ser Glu Arg His Ile His Asn
        275                 280                 285

Thr Ala Arg Lys Leu Ala Phe Gly Ser Gln Val Pro Ala Ser Ile Asn
    290                 295                 300

Thr Asp Asp Ala Arg Asp Lys Leu Glu Thr Leu Phe Gly Gln Asp His
305                 310                 315                 320

Ile Ile Glu Pro Val Leu Thr Ala Ile Lys Arg Glu Gln Leu Gly Ile
                325                 330                 335

Phe Pro Arg Thr Lys Pro Leu Ser Trp Val Phe Ala Gly Ser Ser Gly
            340                 345                 350

Val Gly Lys Thr Glu Met Ala Arg Ile Leu Ser Arg Ala Ile Asn Gly
        355                 360                 365

Gly Asp Pro Ile Ile Ile Asn Gly Pro Glu Tyr Ile Ser Pro Glu Ser
```

```
    370                 375                 380

Ile Thr Gly Leu Ile Gly Ser Ser Asp Gly Tyr Ile Gly Ser Asn Ser
385                 390                 395                 400

Lys Arg Ala Lys Pro Leu Asp Pro Leu Ile Ser Asn Pro Arg Gln Val
                405                 410                 415

Ile Val Leu Asp Glu Phe Glu Lys Ser His Pro His Phe Gln Gln Leu
            420                 425                 430

Phe Met Ala Ala Leu Asp Thr Gly Thr Met Ala Met Ala Asn Gly Thr
        435                 440                 445

Thr Leu Asn Phe Ser Gln Ala Ile Ile Ile Ala Thr Thr Asn Ala Ala
    450                 455                 460

Arg Asp Lys Ile Gly Arg Asp Ser Phe Gly Phe Asp Ser Asp Asn Ser
465                 470                 475                 480

Gly Val Leu Gly Ser Ala Gln Ala Ala Thr Asp Pro Arg Ala Gln Glu
                485                 490                 495

Arg Leu Lys Ser Leu Met Ser Lys Asp Phe Leu Leu Asn Cys Ser Thr
            500                 505                 510

Val Ser Arg Ile Ser Leu Pro Ser Thr Ala Leu Met Gln Ala Pro Thr
        515                 520                 525

Val Arg Phe Trp Thr Ile Ser Thr Ser Val Ala Val Thr Pro Cys Cys
    530                 535                 540

Leu Ala Thr Pro His Tyr Ala Ala Gln Ile Pro Ala Asp Ile Asp Ser
545                 550                 555                 560

Asp Thr Leu Asp Gln Leu Val Glu Thr Thr Phe Ile Ser Asp Phe Gly
                565                 570                 575

Ala Arg Pro Ala Ala Arg Thr Ile Glu Asp His Ile Ala Ser Leu Leu
            580                 585                 590

Met
```

<210> 2051
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> RXA01047

<400> 2051
aaccaccttt atctcagatt ttggtgcacg tcctgctgca cgcaccatcg aagaccacat 60

cgcatccttg ctgatgtgac caacctttta ggagtacatc atg att gat acc act 115
                                                Met Ile Asp Thr Thr
                                                  1   5

```
gct aac agc acc tca ggc acc cta cct aca ctc act gct gac caa gct   163
Ala Asn Ser Thr Ser Gly Thr Leu Pro Thr Leu Thr Ala Asp Gln Ala
                10                  15                  20

gcg ttt atc acc ggt ttt tgc gag gct gct atc ttc aca gcc acc gtc   211
Ala Phe Ile Thr Gly Phe Cys Glu Ala Ala Ile Phe Thr Ala Thr Val
            25                  30                  35

aca ata gat aac gaa cct ata ttt ctt gat gaa gcg ttc ttc tta ggt   259
Thr Ile Asp Asn Glu Pro Ile Phe Leu Asp Glu Ala Phe Phe Leu Gly
        40                  45                  50

caa gaa acc tat acc gac att ctc atg aat caa ctc cgc acc aat gaa   307
Gln Glu Thr Tyr Thr Asp Ile Leu Met Asn Gln Leu Arg Thr Asn Glu
    55                  60                  65

gcc att gtt aaa gac tgt ctc gac ttc ttc ctt gac aac tac acc aca   355
Ala Ile Val Lys Asp Cys Leu Asp Phe Phe Leu Asp Asn Tyr Thr Thr
70                  75                  80                  85

atg aac aag ctc att gtt gat ggt cta tgc cca gat tgg gag cac cac   403
Met Asn Lys Leu Ile Val Asp Gly Leu Cys Pro Asp Trp Glu His His
                90                  95                  100

ggc cat gat ttc cta ctc acc cgt gac cat cat ggt gcc gga ttc tgg   451
Gly His Asp Phe Leu Leu Thr Arg Asp His His Gly Ala Gly Phe Trp
            105                 110                 115

gat cgt ggc tac gac gaa tac ggt gcc caa ctc acc gac aat gcc gaa   499
Asp Arg Gly Tyr Asp Glu Tyr Gly Ala Gln Leu Thr Asp Asn Ala Glu
        120                 125                 130

aaa tat tca gaa aac tgt ctc aat ttc tgg att gag cct gat agt gac   547
Lys Tyr Ser Glu Asn Cys Leu Asn Phe Trp Ile Glu Pro Asp Ser Asp
    135                 140                 145

cct ctc att atc aac ttc gag tac cac taacacccct tgaccttatt         594
Pro Leu Ile Ile Asn Phe Glu Tyr His
150                 155

ttt                                                               597
```

<210> 2052
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 2052

```
Met Ile Asp Thr Thr Ala Asn Ser Thr Ser Gly Thr Leu Pro Thr Leu
  1               5                  10                  15

Thr Ala Asp Gln Ala Ala Phe Ile Thr Gly Phe Cys Glu Ala Ala Ile
            20                  25                  30

Phe Thr Ala Thr Val Thr Ile Asp Asn Glu Pro Ile Phe Leu Asp Glu
        35                  40                  45

Ala Phe Phe Leu Gly Gln Glu Thr Tyr Thr Asp Ile Leu Met Asn Gln
    50                  55                  60
```

```
Leu Arg Thr Asn Glu Ala Ile Val Lys Asp Cys Leu Asp Phe Phe Leu
 65                  70                  75                  80

Asp Asn Tyr Thr Thr Met Asn Lys Leu Ile Val Asp Gly Leu Cys Pro
                 85                  90                  95

Asp Trp Glu His His Gly His Asp Phe Leu Leu Thr Arg Asp His His
            100                 105                 110

Gly Ala Gly Phe Trp Asp Arg Gly Tyr Asp Glu Tyr Gly Ala Gln Leu
        115                 120                 125

Thr Asp Asn Ala Glu Lys Tyr Ser Glu Asn Cys Leu Asn Phe Trp Ile
    130                 135                 140

Glu Pro Asp Ser Asp Pro Leu Ile Ile Asn Phe Glu Tyr His
145                 150                 155


<210> 2053
<211> 444
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(421)
<223> RXA01058

<400> 2053
ctcccgtaat aggggtaatt ttgcaattaa ctgcgcttaa agtaagaaac attgctaatc 60

tttatctggg taattaacaa tcgattttaa ggatattctc atg cgt aaa ctt cgt   115
                                            Met Arg Lys Leu Arg
                                              1               5

act gct tcc gtt gca ctg ctg acc gca ggt gca ctt gca ctg acc gct   163
Thr Ala Ser Val Ala Leu Leu Thr Ala Gly Ala Leu Ala Leu Thr Ala
                  10                  15                  20

act cct gca atg gct cag tcc acc acc ggt tct tct gca tct tct cag   211
Thr Pro Ala Met Ala Gln Ser Thr Thr Gly Ser Ser Ala Ser Ser Gln
             25                  30                  35

gtt ggc gac gca ctc ggt gct agc gac tac gag cgc gac atc tgg ggt   259
Val Gly Asp Ala Leu Gly Ala Ser Asp Tyr Glu Arg Asp Ile Trp Gly
         40                  45                  50

tcc tct aag gac ttc gac gat gta acc cca ttc ggt tcc gct tgg tac   307
Ser Ser Lys Asp Phe Asp Asp Val Thr Pro Phe Gly Ser Ala Trp Tyr
     55                  60                  65

ggc tac acc ctg gcc gca acc gca gtt gct atc tcc ggt ctt gtg tac   355
Gly Tyr Thr Leu Ala Ala Thr Ala Val Ala Ile Ser Gly Leu Val Tyr
 70                  75                  80                  85

gca aac ctt cct gca atc gag cag gct gct gca cag gcc ggc atc aag   403
Ala Asn Leu Pro Ala Ile Glu Gln Ala Ala Ala Gln Ala Gly Ile Lys
                 90                  95                 100
```

```
ctg gag atc cca cgc tac taattgccac tgcaatctta aat                  444
Leu Glu Ile Pro Arg Tyr
            105


<210> 2054
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

<400> 2054
Met Arg Lys Leu Arg Thr Ala Ser Val Ala Leu Leu Thr Ala Gly Ala
  1               5                  10                  15

Leu Ala Leu Thr Ala Thr Pro Ala Met Ala Gln Ser Thr Thr Gly Ser
             20                  25                  30

Ser Ala Ser Ser Gln Val Gly Asp Ala Leu Gly Ala Ser Asp Tyr Glu
         35                  40                  45

Arg Asp Ile Trp Gly Ser Ser Lys Asp Phe Asp Asp Val Thr Pro Phe
     50                  55                  60

Gly Ser Ala Trp Tyr Gly Tyr Thr Leu Ala Ala Thr Ala Val Ala Ile
 65                  70                  75                  80

Ser Gly Leu Val Tyr Ala Asn Leu Pro Ala Ile Glu Gln Ala Ala Ala
                 85                  90                  95

Gln Ala Gly Ile Lys Leu Glu Ile Pro Arg Tyr
            100                 105


<210> 2055
<211> 453
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(430)
<223> RXA01063

<400> 2055
actttcttgt agaggtctgg gtagtggata agttaatcaa ctatgaaata gactaactta 60

atcattaaca ttaatggatt ttcggagaat agggatagac atg gca gac gag aaa   115
                                        Met Ala Asp Glu Lys
                                          1               5

aag gtt cat gta cgt gcc aca ctg cgc ttt gat tca gac acc cac cag   163
Lys Val His Val Arg Ala Thr Leu Arg Phe Asp Ser Asp Thr His Gln
                 10                  15                  20

cgg gca att tat tgg gca gat cga aaa ggt atc tcg ctg agc gcg tat   211
Arg Ala Ile Tyr Trp Ala Asp Arg Lys Gly Ile Ser Leu Ser Ala Tyr
             25                  30                  35

gca gaa gag gcg atc aga gag aag att gat cgt gat aac ggt gtg cac   259
Ala Glu Glu Ala Ile Arg Glu Lys Ile Asp Arg Asp Asn Gly Val His
         40                  45                  50
```

```
gtt att ccg aat tca ctg ttg gat aac cgc atg aac caa atc att gat   307
Val Ile Pro Asn Ser Leu Leu Asp Asn Arg Met Asn Gln Ile Ile Asp
     55                  60                  65

cag ctc agc tcg ttt ggt cgt gag ttg gcg aac aac acg aca gtt gta   355
Gln Leu Ser Ser Phe Gly Arg Glu Leu Ala Asn Asn Thr Thr Val Val
 70                  75                  80                  85

act agt ggt ttc aac acc att atc ggt atg act cgt ggc gac tcg tat   403
Thr Ser Gly Phe Asn Thr Ile Ile Gly Met Thr Arg Gly Asp Ser Tyr
                 90                  95                 100

ctc tct gat gat ctc gat gac ctg ggt taaacccgat gaacgagcag         450
Leu Ser Asp Asp Leu Asp Asp Leu Gly
            105                 110

gaa                                                               453
```

<210> 2056
<211> 110
<212> PRT
<213> Corynebacterium glutamicum

<400> 2056

```
Met Ala Asp Glu Lys Lys Val His Val Arg Ala Thr Leu Arg Phe Asp
  1               5                  10                  15

Ser Asp Thr His Gln Arg Ala Ile Tyr Trp Ala Asp Arg Lys Gly Ile
             20                  25                  30

Ser Leu Ser Ala Tyr Ala Glu Glu Ala Ile Arg Glu Lys Ile Asp Arg
         35                  40                  45

Asp Asn Gly Val His Val Ile Pro Asn Ser Leu Leu Asp Asn Arg Met
     50                  55                  60

Asn Gln Ile Ile Asp Gln Leu Ser Ser Phe Gly Arg Glu Leu Ala Asn
 65                  70                  75                  80

Asn Thr Thr Val Val Thr Ser Gly Phe Asn Thr Ile Ile Gly Met Thr
                 85                  90                  95

Arg Gly Asp Ser Tyr Leu Ser Asp Asp Leu Asp Asp Leu Gly
            100                 105                 110
```

<210> 2057
<211> 849
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(826)
<223> RXA01066

<400> 2057

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aaacgtattc cttgacctgc gcatcaaggt gctgaagaac tggcaatccg atccaaaggc 60
```

```
tttgaaccgc ctgggcttct agctttaagg gggtgagttc atg cgt agg gac agt   115
                                             Met Arg Arg Asp Ser
                                               1               5

ttt cgg gac cgc gcg cta gta gtc aaa act tat gat ttt ggc gaa gcc   163
Phe Arg Asp Arg Ala Leu Val Val Lys Thr Tyr Asp Phe Gly Glu Ala
                 10                  15                  20

gac cgc att att gtg ctg ctc acc cga gac cac ggc atc gtg cgc gga   211
Asp Arg Ile Ile Val Leu Leu Thr Arg Asp His Gly Ile Val Arg Gly
             25                  30                  35

gtt gcc aaa gga gta cgc cga tcc aaa tcc cgg ttt ggg tca agg ctg   259
Val Ala Lys Gly Val Arg Arg Ser Lys Ser Arg Phe Gly Ser Arg Leu
         40                  45                  50

cag ctt ttt gtg gaa ctc gac gtg cag ctc tac cca ggt aga aaa ctg   307
Gln Leu Phe Val Glu Leu Asp Val Gln Leu Tyr Pro Gly Arg Lys Leu
     55                  60                  65

tcc acc atc tct ggc gcg gac acc gtc ggc tac tac gca tca ggc atc   355
Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr Tyr Ala Ser Gly Ile
 70                  75                  80                  85

atc gag gac ttc act cgg tat tcc tgt gcg tcc gcc atc ctg gaa atc   403
Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser Ala Ile Leu Glu Ile
                 90                  95                 100

gcc acc cac atc gca gga ctg gaa aac gat ccg cac ctg ttt gaa gaa   451
Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro His Leu Phe Glu Glu
            105                 110                 115

acc acc cgg gcg ttg aaa aac att cag gac tcc cca gaa ccc atc ctc   499
Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser Pro Glu Pro Ile Leu
        120                 125                 130

aac cta gac gag ttc atg ctc cgc gcc atg aac cac gcc ggc tgg gca   547
Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn His Ala Gly Trp Ala
    135                 140                 145

cca agc ctt ttc gac tgc gca gcc tgc ggc cga cca gga cct cac aac   595
Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg Pro Gly Pro His Asn
150                 155                 160                 165

gca ttc cac cca ggc gtc ggc ggg gca gtg tgc ctg tac tgc cga ccg   643
Ala Phe His Pro Gly Val Gly Gly Ala Val Cys Leu Tyr Cys Arg Pro
                170                 175                 180

ccg gga agc gcc gaa gtc cca cca gaa gca cta cac atg atg tgg ttg   691
Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu His Met Met Trp Leu
            185                 190                 195

gtc gcc aac ggc caa gca gcc cgc att ccc cgg gaa cac cca gag cag   739
Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg Glu His Pro Glu Gln
        200                 205                 210

caa acc acc att cac caa ctg aca acc gcg cat ctg cag tgg cat att   787
Gln Thr Thr Ile His Gln Leu Thr Thr Ala His Leu Gln Trp His Ile
    215                 220                 225

gaa aga aag ctg ccc acg ctg gcg gtg ctg gat cag gcc tagtgcttag    836
```

```
Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp Gln Ala
230                 235                 240

gcttaggcgt ccg                                                    849


<210> 2058
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

<400> 2058
Met Arg Arg Asp Ser Phe Arg Asp Arg Ala Leu Val Val Lys Thr Tyr
  1               5                  10                  15

Asp Phe Gly Glu Ala Asp Arg Ile Ile Val Leu Leu Thr Arg Asp His
             20                  25                  30

Gly Ile Val Arg Gly Val Ala Lys Gly Val Arg Arg Ser Lys Ser Arg
         35                  40                  45

Phe Gly Ser Arg Leu Gln Leu Phe Val Glu Leu Asp Val Gln Leu Tyr
     50                  55                  60

Pro Gly Arg Lys Leu Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr
 65                  70                  75                  80

Tyr Ala Ser Gly Ile Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser
                 85                  90                  95

Ala Ile Leu Glu Ile Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro
            100                 105                 110

His Leu Phe Glu Glu Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser
        115                 120                 125

Pro Glu Pro Ile Leu Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn
    130                 135                 140

His Ala Gly Trp Ala Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg
145                 150                 155                 160

Pro Gly Pro His Asn Ala Phe His Pro Gly Val Gly Gly Ala Val Cys
                165                 170                 175

Leu Tyr Cys Arg Pro Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu
            180                 185                 190

His Met Met Trp Leu Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg
        195                 200                 205

Glu His Pro Glu Gln Gln Thr Thr Ile His Gln Leu Thr Thr Ala His
    210                 215                 220

Leu Gln Trp His Ile Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp
225                 230                 235                 240

Gln Ala
```

<210> 2059
<211> 1194
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1171)
<223> RXA01068

<400> 2059
tggtctacca agacaagctg ttccctgatt tcacgcagca agatctgtac gacgcggtcc 60

tggaatacgc caagcgggat cgcagattcg gaagcgcata atg ccc acc aac cag 115
Met Pro Thr Asn Gln
1 5

ccg acg cca gcc caa atc aaa cgc tgg cgc gga tac ctg gcc aat gag 163
Pro Thr Pro Ala Gln Ile Lys Arg Trp Arg Gly Tyr Leu Ala Asn Glu
10 15 20

caa gca gag gcc gca gcc tac cgc gac ctg gcc aaa cga cgc gaa ggc 211
Gln Ala Glu Ala Ala Ala Tyr Arg Asp Leu Ala Lys Arg Arg Glu Gly
25 30 35

gaa gag cga gac atc ctc cta gcg ctc gcc gac gct gaa cac cga cac 259
Glu Glu Arg Asp Ile Leu Leu Ala Leu Ala Asp Ala Glu His Arg His
40 45 50

gcc gct tac tgg gtg gaa aag ctc ggc cct gat gcc gaa aac cca cca 307
Ala Ala Tyr Trp Val Glu Lys Leu Gly Pro Asp Ala Glu Asn Pro Pro
55 60 65

aaa gcc gac gtc aaa acc cgc ctg ctc ggt ttt cta gca cgc cga ttc 355
Lys Ala Asp Val Lys Thr Arg Leu Leu Gly Phe Leu Ala Arg Arg Phe
70 75 80 85

ggc tcc gtg ttc acc ctg gca ctc atg cag tcc gcc gaa acg cgc agc 403
Gly Ser Val Phe Thr Leu Ala Leu Met Gln Ser Ala Glu Thr Arg Ser
90 95 100

ccc tac gac gac gat gcc gac gcc tcc cgc caa atc agc gcc gac gaa 451
Pro Tyr Asp Asp Asp Ala Asp Ala Ser Arg Gln Ile Ser Ala Asp Glu
105 110 115

cgc atc cac gcc gaa gtc gtt cga ggc cta gcc agc cgc ggc aga gaa 499
Arg Ile His Ala Glu Val Val Arg Gly Leu Ala Ser Arg Gly Arg Glu
120 125 130

cgc atg agc ggc aac ttc cgt gcc gcc gta ttc gga atc aac gac ggc 547
Arg Met Ser Gly Asn Phe Arg Ala Ala Val Phe Gly Ile Asn Asp Gly
135 140 145

ctg gtc tcc aac gtc gcc ctc gtc atg ggt gtc atg gcc acc ggc gtg 595
Leu Val Ser Asn Val Ala Leu Val Met Gly Val Met Ala Thr Gly Val
150 155 160 165

ccc gcc caa att gtt ctc atc acc ggc att tcc ggt ctg ctc tcc ggc 643
Pro Ala Gln Ile Val Leu Ile Thr Gly Ile Ser Gly Leu Leu Ser Gly
170 175 180

```
gcg cta tcc atg gcc gcc ggc gaa tac atc tca gtg cgc tcc caa aca   691
Ala Leu Ser Met Ala Ala Gly Glu Tyr Ile Ser Val Arg Ser Gln Thr
            185                 190                 195

gag ctt ctc gac gcc tcc ctc cca gac ccc aaa gcc cgc gaa gcc ctc   739
Glu Leu Leu Asp Ala Ser Leu Pro Asp Pro Lys Ala Arg Glu Ala Leu
        200                 205                 210

cac gcc ctc gac gtc gaa tcc aac gaa ctg gaa ctc gtc tac cga gcc   787
His Ala Leu Asp Val Glu Ser Asn Glu Leu Glu Leu Val Tyr Arg Ala
    215                 220                 225

cgc gga atg agc gaa gac gaa gcg cgg gca aaa gcg tca caa gtt ttc   835
Arg Gly Met Ser Glu Asp Glu Ala Arg Ala Lys Ala Ser Gln Val Phe
230                 235                 240                 245

caa aga atc agc gac caa aaa cgc atc agc gac aac gtc ctc ggc agc   883
Gln Arg Ile Ser Asp Gln Lys Arg Ile Ser Asp Asn Val Leu Gly Ser
                250                 255                 260

acc gaa atc caa agc gcc ggc tcc gct cgt tcg gcc gcc aca ttc agc   931
Thr Glu Ile Gln Ser Ala Gly Ser Ala Arg Ser Ala Ala Thr Phe Ser
            265                 270                 275

ttc ctg tcc ttt gcc atc ggc gca ttc ctc ccg atc gtc cca tac gtc   979
Phe Leu Ser Phe Ala Ile Gly Ala Phe Leu Pro Ile Val Pro Tyr Val
        280                 285                 290

ttc ggc atg gaa ggc ctc gcc ggg gca gtg gtg tcc cta gtc ctc gtc   1027
Phe Gly Met Glu Gly Leu Ala Gly Ala Val Val Ser Leu Val Leu Val
    295                 300                 305

gga cta tca ctg atg gca acg ggc gcg acc acc ggc ctg cta tcg gga   1075
Gly Leu Ser Leu Met Ala Thr Gly Ala Thr Thr Gly Leu Leu Ser Gly
310                 315                 320                 325

aag cca ccg gga atc cgc gcg gtg cgt cag ctg tcg atc ggc tac ggc   1123
Lys Pro Pro Gly Ile Arg Ala Val Arg Gln Leu Ser Ile Gly Tyr Gly
                330                 335                 340

gcg gcg ctg gtc acc tac gtg ctc ggc ctc ctg ttc ggc atg atc ctt   1171
Ala Ala Leu Val Thr Tyr Val Leu Gly Leu Leu Phe Gly Met Ile Leu
            345                 350                 355

taaaagctct tgcttctcga cgt                                        1194
```

<210> 2060
<211> 357
<212> PRT
<213> Corynebacterium glutamicum

<400> 2060

```
Met Pro Thr Asn Gln Pro Thr Pro Ala Gln Ile Lys Arg Trp Arg Gly
  1               5                  10                  15

Tyr Leu Ala Asn Glu Gln Ala Glu Ala Ala Ala Tyr Arg Asp Leu Ala
             20                  25                  30

Lys Arg Arg Glu Gly Glu Glu Arg Asp Ile Leu Leu Ala Leu Ala Asp
         35                  40                  45
```

```
Ala Glu His Arg His Ala Ala Tyr Trp Val Glu Lys Leu Gly Pro Asp
     50                  55                  60

Ala Glu Asn Pro Pro Lys Ala Asp Val Lys Thr Arg Leu Leu Gly Phe
 65                  70                  75                  80

Leu Ala Arg Arg Phe Gly Ser Val Phe Thr Leu Ala Leu Met Gln Ser
                 85                  90                  95

Ala Glu Thr Arg Ser Pro Tyr Asp Asp Asp Ala Asp Ala Ser Arg Gln
            100                 105                 110

Ile Ser Ala Asp Glu Arg Ile His Ala Glu Val Val Arg Gly Leu Ala
        115                 120                 125

Ser Arg Gly Arg Glu Arg Met Ser Gly Asn Phe Arg Ala Ala Val Phe
    130                 135                 140

Gly Ile Asn Asp Gly Leu Val Ser Asn Val Ala Leu Val Met Gly Val
145                 150                 155                 160

Met Ala Thr Gly Val Pro Ala Gln Ile Val Leu Ile Thr Gly Ile Ser
                165                 170                 175

Gly Leu Leu Ser Gly Ala Leu Ser Met Ala Ala Gly Glu Tyr Ile Ser
            180                 185                 190

Val Arg Ser Gln Thr Glu Leu Leu Asp Ala Ser Leu Pro Asp Pro Lys
        195                 200                 205

Ala Arg Glu Ala Leu His Ala Leu Asp Val Glu Ser Asn Glu Leu Glu
    210                 215                 220

Leu Val Tyr Arg Ala Arg Gly Met Ser Glu Asp Glu Ala Arg Ala Lys
225                 230                 235                 240

Ala Ser Gln Val Phe Gln Arg Ile Ser Asp Gln Lys Arg Ile Ser Asp
                245                 250                 255

Asn Val Leu Gly Ser Thr Glu Ile Gln Ser Ala Gly Ser Ala Arg Ser
            260                 265                 270

Ala Ala Thr Phe Ser Phe Leu Ser Phe Ala Ile Gly Ala Phe Leu Pro
        275                 280                 285

Ile Val Pro Tyr Val Phe Gly Met Glu Gly Leu Ala Gly Ala Val Val
    290                 295                 300

Ser Leu Val Leu Val Gly Leu Ser Leu Met Ala Thr Gly Ala Thr Thr
305                 310                 315                 320

Gly Leu Leu Ser Gly Lys Pro Pro Gly Ile Arg Ala Val Arg Gln Leu
                325                 330                 335

Ser Ile Gly Tyr Gly Ala Ala Leu Val Thr Tyr Val Leu Gly Leu Leu
            340                 345                 350

Phe Gly Met Ile Leu
        355
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<210> 2061
<211> 828
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(805)
<223> RXA01074

<400> 2061
cgaatgaaat cactgggcgg gagttcaccc tcggcgagga gcctgagcgc tactagcttt 60

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gccacatttc actaaacgcc ccgcacaacc ccaagcagcc ttg gcg gaa gcc gca   115
                                             Leu Ala Glu Ala Ala
                                               1               5

ggt cta cgc tgg ctc gcc gaa gca tct tca gct gtg gca cag gtt gtt   163
Gly Leu Arg Trp Leu Ala Glu Ala Ser Ser Ala Val Ala Gln Val Val
                  10                  15                  20

agc gcc gac gca gag cag atc acg act gtt ggc gtc gaa acg caa ttg   211
Ser Ala Asp Ala Glu Gln Ile Thr Thr Val Gly Val Glu Thr Gln Leu
              25                  30                  35

ccc aca ccc gat gcg gcc ttc aag gcc ggc gaa gag ctc gcc cgc atc   259
Pro Thr Pro Asp Ala Ala Phe Lys Ala Gly Glu Glu Leu Ala Arg Ile
          40                  45                  50

cac ctt gcc ggc gcc cca gcg ttc ggc tgt cca cca gcg ggc tgg gcg   307
His Leu Ala Gly Ala Pro Ala Phe Gly Cys Pro Pro Ala Gly Trp Ala
      55                  60                  65

ggg tta aac tac atc ggc acc cag gga caa gca tgc tta tcg acg ccc   355
Gly Leu Asn Tyr Ile Gly Thr Gln Gly Gln Ala Cys Leu Ser Thr Pro
  70                  75                  80                  85

acc tgg ggt gtt ttt tac tcc cag caa cgc gta ctc ccg ttt gcg cgc   403
Thr Trp Gly Val Phe Tyr Ser Gln Gln Arg Val Leu Pro Phe Ala Arg
                  90                  95                 100

cgg gca cgc agg cga aat cac ctc acc gag cac gca ctc tgg gtc gtg   451
Arg Ala Arg Arg Arg Asn His Leu Thr Glu His Ala Leu Trp Val Val
             105                 110                 115

gaa gcc gct tgt gat ttg att agc gaa ctt ccc gat gac gtt ccc ccc   499
Glu Ala Ala Cys Asp Leu Ile Ser Glu Leu Pro Asp Asp Val Pro Pro
         120                 125                 130

gcc aga atc cac ggc gac ttg tgg ttt ggc aac cta ctt ttt ggc aca   547
Ala Arg Ile His Gly Asp Leu Trp Phe Gly Asn Leu Leu Phe Gly Thr
     135                 140                 145

gac ggg cct gtg ttt att gac ccc gca gct cac ggc ggt cat ccc gaa   595
Asp Gly Pro Val Phe Ile Asp Pro Ala Ala His Gly Gly His Pro Glu
150                 155                 160                 165

act gat ctc gcg atg ctt gat gta ttt ggc gca ccc tat ctc gat gaa   643
Thr Asp Leu Ala Met Leu Asp Val Phe Gly Ala Pro Tyr Leu Asp Glu
                170                 175                 180
```

```
atc cgg gaa ggt tat ctg tct atc aac ccg ctg cca gac ggg tgg cgt   691
Ile Arg Glu Gly Tyr Leu Ser Ile Asn Pro Leu Pro Asp Gly Trp Arg
            185                 190                 195

gaa cgc acc ccc atg cac caa ctc cac cct ttg gcc gta cat gcg gcg   739
Glu Arg Thr Pro Met His Gln Leu His Pro Leu Ala Val His Ala Ala
        200                 205                 210

tct cat ggg cca agc tac ggc gtg gaa cta ctc cac gcc gcc aaa gcg   787
Ser His Gly Pro Ser Tyr Gly Val Glu Leu Leu His Ala Ala Lys Ala
    215                 220                 225

aca ctc aaa ctg ttg gat taacgccacc aattttcctg cgg                828
Thr Leu Lys Leu Leu Asp
230                 235
```

<210> 2062
<211> 235
<212> PRT
<213> Corynebacterium glutamicum

<400> 2062

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Leu Ala Glu Ala Ala Gly Leu Arg Trp Leu Ala Glu Ala Ser Ser Ala
  1               5                  10                  15

Val Ala Gln Val Val Ser Ala Asp Ala Glu Gln Ile Thr Thr Val Gly
             20                  25                  30

Val Glu Thr Gln Leu Pro Thr Pro Asp Ala Ala Phe Lys Ala Gly Glu
         35                  40                  45

Glu Leu Ala Arg Ile His Leu Ala Gly Ala Pro Ala Phe Gly Cys Pro
     50                  55                  60

Pro Ala Gly Trp Ala Gly Leu Asn Tyr Ile Gly Thr Gln Gly Gln Ala
 65                  70                  75                  80

Cys Leu Ser Thr Pro Thr Trp Gly Val Phe Tyr Ser Gln Gln Arg Val
                 85                  90                  95

Leu Pro Phe Ala Arg Arg Ala Arg Arg Arg Asn His Leu Thr Glu His
            100                 105                 110

Ala Leu Trp Val Val Glu Ala Ala Cys Asp Leu Ile Ser Glu Leu Pro
        115                 120                 125

Asp Asp Val Pro Pro Ala Arg Ile His Gly Asp Leu Trp Phe Gly Asn
    130                 135                 140

Leu Leu Phe Gly Thr Asp Gly Pro Val Phe Ile Asp Pro Ala Ala His
145                 150                 155                 160

Gly Gly His Pro Glu Thr Asp Leu Ala Met Leu Asp Val Phe Gly Ala
                165                 170                 175

Pro Tyr Leu Asp Glu Ile Arg Glu Gly Tyr Leu Ser Ile Asn Pro Leu
            180                 185                 190

Pro Asp Gly Trp Arg Glu Arg Thr Pro Met His Gln Leu His Pro Leu
```

```
        195                 200                 205

Ala Val His Ala Ala Ser His Gly Pro Ser Tyr Gly Val Glu Leu Leu
    210                 215                 220

His Ala Ala Lys Ala Thr Leu Lys Leu Leu Asp
225                 230                 235


<210> 2063
<211> 1143
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1120)
<223> RXA01076

<400> 2063
tcctcccatt aagcaccttg tcttccggaa gcttccaccc caaattccaa accccaaatt 60

ccatgccccg gatggacatt tttcattaca ctcgggggct atg act cca gct cac   115
                                            Met Thr Pro Ala His
                                              1               5

ata ttt tct gaa ggt cca atc aat agt gtt gtt ctc agc cag gat gag   163
Ile Phe Ser Glu Gly Pro Ile Asn Ser Val Val Leu Ser Gln Asp Glu
                  10                  15                  20

gat gga aat ttc acc acc tcc tac cag gac acg ttc tct gat cca tca   211
Asp Gly Asn Phe Thr Thr Ser Tyr Gln Asp Thr Phe Ser Asp Pro Ser
              25                  30                  35

ttt ttg ggg gaa ggt gac gtt cta att gag gtt ggt tgg tcc agc ttg   259
Phe Leu Gly Glu Gly Asp Val Leu Ile Glu Val Gly Trp Ser Ser Leu
          40                  45                  50

aat tac aag gac gca atg gct ctg aag ggt gat aag gga gtg gtg cgt   307
Asn Tyr Lys Asp Ala Met Ala Leu Lys Gly Asp Lys Gly Val Val Arg
      55                  60                  65

act gtg cca ctg att cca ggt atc gat gtg gtg ggc act gtg atc gag   355
Thr Val Pro Leu Ile Pro Gly Ile Asp Val Val Gly Thr Val Ile Glu
  70                  75                  80                  85

agc gct gat cct cgc ttt ggt cgt ggt gat gaa gtg gtg ctg aat ggc   403
Ser Ala Asp Pro Arg Phe Gly Arg Gly Asp Glu Val Val Leu Asn Gly
                  90                  95                 100

gct ggt ttg ggg gag aac cgg cat gga ggt ttc acg cag cgg ctg aaa   451
Ala Gly Leu Gly Glu Asn Arg His Gly Gly Phe Thr Gln Arg Leu Lys
              105                 110                 115

gtg ccg tct gaa ccg ttg ctg cat att cca ttt aac ttc tcc gcg cag   499
Val Pro Ser Glu Pro Leu Leu His Ile Pro Phe Asn Phe Ser Ala Gln
          120                 125                 130

cag gtg ggt gcg ttg ggt act gca ggt ttc acg gct gcg cta tcg gtg   547
Gln Val Gly Ala Leu Gly Thr Ala Gly Phe Thr Ala Ala Leu Ser Val
      135                 140                 145
```

```
aat gct ctg gtc gat caa ggt atc aaa ccg gag gat ggg gag att ctg   595
Asn Ala Leu Val Asp Gln Gly Ile Lys Pro Glu Asp Gly Glu Ile Leu
150                 155                 160                 165

gta act ggt tcg act ggt ggt gtg ggt tcg att gca ctt cac ctg ctg   643
Val Thr Gly Ser Thr Gly Gly Val Gly Ser Ile Ala Leu His Leu Leu
                170                 175                 180

aat aag ttg gga tat acg acg gtc gcg gtg acg ggg cgt cga gaa gcg   691
Asn Lys Leu Gly Tyr Thr Thr Val Ala Val Thr Gly Arg Arg Glu Ala
            185                 190                 195

cat gcc gaa tac ctg acc agc ctg ggc gca agc gac atc att gat cgc   739
His Ala Glu Tyr Leu Thr Ser Leu Gly Ala Ser Asp Ile Ile Asp Arg
        200                 205                 210

gcg gag ctt tct gaa aag ggc cgg ccg ctg cag aag ggg cgt tgg gcg   787
Ala Glu Leu Ser Glu Lys Gly Arg Pro Leu Gln Lys Gly Arg Trp Ala
    215                 220                 225

ggt gta gtg gat tca gtg gga tcc cac aca ctt gtc aat gcg att gct   835
Gly Val Val Asp Ser Val Gly Ser His Thr Leu Val Asn Ala Ile Ala
230                 235                 240                 245

cag aca aaa tgg ggc gga att gtc acg gcg tgt ggc atg gct cag ggg   883
Gln Thr Lys Trp Gly Gly Ile Val Thr Ala Cys Gly Met Ala Gln Gly
                250                 255                 260

ccg gat ctg ccg gga acg gtg ttg ccg ttt att ctt cgt ggc gtg cat   931
Pro Asp Leu Pro Gly Thr Val Leu Pro Phe Ile Leu Arg Gly Val His
            265                 270                 275

ttg gtt ggc att aac tct gtc gat gca ccc cgt gag ctg cgt cga cgt   979
Leu Val Gly Ile Asn Ser Val Asp Ala Pro Arg Glu Leu Arg Arg Arg
        280                 285                 290

gcg tgg gcg ttg ctg tcc gag cat ctt gat acc gcg gtg cta gat gat   1027
Ala Trp Ala Leu Leu Ser Glu His Leu Asp Thr Ala Val Leu Asp Asp
    295                 300                 305

atg acc act gtg att gat gtc aag gat gtt gct caa gct ggc gaa gat   1075
Met Thr Thr Val Ile Asp Val Lys Asp Val Ala Gln Ala Gly Glu Asp
310                 315                 320                 325

ttg atg gct ggc aag ctt cac gga cgt acc gcg gtg cgt gtt cat       1120
Leu Met Ala Gly Lys Leu His Gly Arg Thr Ala Val Arg Val His
                330                 335                 340

tagcaggtca agcgcgtaat tga                                        1143
```

<210> 2064
<211> 340
<212> PRT
<213> Corynebacterium glutamicum

<400> 2064

```
Met Thr Pro Ala His Ile Phe Ser Glu Gly Pro Ile Asn Ser Val Val
  1               5                  10                  15
```

```
Leu Ser Gln Asp Glu Asp Gly Asn Phe Thr Thr Ser Tyr Gln Asp Thr
            20                  25                  30

Phe Ser Asp Pro Ser Phe Leu Gly Glu Gly Asp Val Leu Ile Glu Val
        35                  40                  45

Gly Trp Ser Ser Leu Asn Tyr Lys Asp Ala Met Ala Leu Lys Gly Asp
    50                  55                  60

Lys Gly Val Val Arg Thr Val Pro Leu Ile Pro Gly Ile Asp Val Val
65                  70                  75                  80

Gly Thr Val Ile Glu Ser Ala Asp Pro Arg Phe Gly Arg Gly Asp Glu
                85                  90                  95

Val Val Leu Asn Gly Ala Gly Leu Gly Glu Asn Arg His Gly Gly Phe
            100                 105                 110

Thr Gln Arg Leu Lys Val Pro Ser Glu Pro Leu Leu His Ile Pro Phe
        115                 120                 125

Asn Phe Ser Ala Gln Gln Val Gly Ala Leu Gly Thr Ala Gly Phe Thr
    130                 135                 140

Ala Ala Leu Ser Val Asn Ala Leu Val Asp Gln Gly Ile Lys Pro Glu
145                 150                 155                 160

Asp Gly Glu Ile Leu Val Thr Gly Ser Thr Gly Gly Val Gly Ser Ile
                165                 170                 175

Ala Leu His Leu Leu Asn Lys Leu Gly Tyr Thr Thr Val Ala Val Thr
            180                 185                 190

Gly Arg Arg Glu Ala His Ala Glu Tyr Leu Thr Ser Leu Gly Ala Ser
        195                 200                 205

Asp Ile Ile Asp Arg Ala Glu Leu Ser Glu Lys Gly Arg Pro Leu Gln
    210                 215                 220

Lys Gly Arg Trp Ala Gly Val Val Asp Ser Val Gly Ser His Thr Leu
225                 230                 235                 240

Val Asn Ala Ile Ala Gln Thr Lys Trp Gly Gly Ile Val Thr Ala Cys
                245                 250                 255

Gly Met Ala Gln Gly Pro Asp Leu Pro Gly Thr Val Leu Pro Phe Ile
            260                 265                 270

Leu Arg Gly Val His Leu Val Gly Ile Asn Ser Val Asp Ala Pro Arg
        275                 280                 285

Glu Leu Arg Arg Arg Ala Trp Ala Leu Leu Ser Glu His Leu Asp Thr
    290                 295                 300

Ala Val Leu Asp Asp Met Thr Thr Val Ile Asp Val Lys Asp Val Ala
305                 310                 315                 320

Gln Ala Gly Glu Asp Leu Met Ala Gly Lys Leu His Gly Arg Thr Ala
                325                 330                 335

Val Arg Val His
```

340

<210> 2065
<211> 957
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(934)
<223> RXA01078

<400> 2065
atcattcacg agctcgatag ccgacaggtt tctgaactca cagaagccct ggccaaagtc 60

tccaccaccc gcagctaaaa ctttttgaaa ggagctcatc atg agc aac gca gta 115
Met Ser Asn Ala Val
1 5

ccc cac aac gtt tcc ttc aac ttt gtt ccc cgc gct tac cgt cca gaa 163
Pro His Asn Val Ser Phe Asn Phe Val Pro Arg Ala Tyr Arg Pro Glu
10 15 20

aag ccc cgc aca ttc ggc atg aca gaa att cgt gca ccg tac tac tcc 211
Lys Pro Arg Thr Phe Gly Met Thr Glu Ile Arg Ala Pro Tyr Tyr Ser
25 30 35

act ttc ggc acc cga cac ctc cag gat gtc ttc gat gtt gca ggc cag 259
Thr Phe Gly Thr Arg His Leu Gln Asp Val Phe Asp Val Ala Gly Gln
40 45 50

tgg gtg gac ggc atc aaa tgg gca ggc ggt tcc ttc tcc ctg gtg ccg 307
Trp Val Asp Gly Ile Lys Trp Ala Gly Gly Ser Phe Ser Leu Val Pro
55 60 65

acc gaa cag gtg cgt gct ttt agc gac atc gcc cat gaa aac aat gcc 355
Thr Glu Gln Val Arg Ala Phe Ser Asp Ile Ala His Glu Asn Asn Ala
70 75 80 85

tat gtg tct tcc ggt ggc tgg att gaa act gtg ctt cgc tac ggc gac 403
Tyr Val Ser Ser Gly Gly Trp Ile Glu Thr Val Leu Arg Tyr Gly Asp
90 95 100

gac gca gtt gat cat tac tta aag gaa gcc aag gaa gtc ggc ttc gat 451
Asp Ala Val Asp His Tyr Leu Lys Glu Ala Lys Glu Val Gly Phe Asp
105 110 115

gtt att gag att tcc acc gga ttc atc atg ctc aac act tca ggt ctt 499
Val Ile Glu Ile Ser Thr Gly Phe Ile Met Leu Asn Thr Ser Gly Leu
120 125 130

cag cgc ctg gta gaa aaa gtg gtc aag gca ggc ctc aaa gca aaa cct 547
Gln Arg Leu Val Glu Lys Val Val Lys Ala Gly Leu Lys Ala Lys Pro
135 140 145

gaa cta gga cta cag att ggt tcc gga ggc gac tct ggt gag gct gaa 595
Glu Leu Gly Leu Gln Ile Gly Ser Gly Gly Asp Ser Gly Glu Ala Glu
150 155 160 165

ctt gca gcc gaa gga aag aaa gac att ggc gat ctg gtt gac cgc ggt 643

```
Leu Ala Ala Glu Gly Lys Lys Asp Ile Gly Asp Leu Val Asp Arg Gly
                170                 175                 180

aaa aaa gct ctc gac gcc ggc gca tcc atc atc atg atc gaa tcc gaa   691
Lys Lys Ala Leu Asp Ala Gly Ala Ser Ile Ile Met Ile Glu Ser Glu
            185                 190                 195

ggc atc acc gaa aac gtc acc gaa tgg gat aca ggc gct gcc gcg tcc   739
Gly Ile Thr Glu Asn Val Thr Glu Trp Asp Thr Gly Ala Ala Ala Ser
        200                 205                 210

atc atc aat gga ctg gga tta gaa aac gtc atg ttc gaa gcc gcc gac   787
Ile Ile Asn Gly Leu Gly Leu Glu Asn Val Met Phe Glu Ala Ala Asp
    215                 220                 225

ggc ccc gtc ttt gag tgg tat gtc aaa aac tac ggc aac gaa tgc aac   835
Gly Pro Val Phe Glu Trp Tyr Val Lys Asn Tyr Gly Asn Glu Cys Asn
230                 235                 240                 245

ctg ttc gtc gac cac agt caa att ctg caa ctt gaa ggg ctg cgc caa   883
Leu Phe Val Asp His Ser Gln Ile Leu Gln Leu Glu Gly Leu Arg Gln
                250                 255                 260

aac atc tgg ggc aac aag agc acc tgg gga cga gta atc aac cct gcg   931
Asn Ile Trp Gly Asn Lys Ser Thr Trp Gly Arg Val Ile Asn Pro Ala
            265                 270                 275

cct taaataccag gtcagggagg gca                                    957
Pro
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US20050100900A1

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<210> 2066
<211> 278
<212> PRT
<213> Corynebacterium glutamicum

<400> 2066
Met Ser Asn Ala Val Pro His Asn Val Ser Phe Asn Phe Val Pro Arg
  1               5                  10                  15

Ala Tyr Arg Pro Glu Lys Pro Arg Thr Phe Gly Met Thr Glu Ile Arg
             20                  25                  30

Ala Pro Tyr Tyr Ser Thr Phe Gly Thr Arg His Leu Gln Asp Val Phe
         35                  40                  45

Asp Val Ala Gly Gln Trp Val Asp Gly Ile Lys Trp Ala Gly Gly Ser
     50                  55                  60

Phe Ser Leu Val Pro Thr Glu Gln Val Arg Ala Phe Ser Asp Ile Ala
 65                  70                  75                  80

His Glu Asn Asn Ala Tyr Val Ser Ser Gly Gly Trp Ile Glu Thr Val
                 85                  90                  95

Leu Arg Tyr Gly Asp Asp Ala Val Asp His Tyr Leu Lys Glu Ala Lys
            100                 105                 110

Glu Val Gly Phe Asp Val Ile Glu Ile Ser Thr Gly Phe Ile Met Leu
        115                 120                 125
```

```
Asn Thr Ser Gly Leu Gln Arg Leu Val Glu Lys Val Val Lys Ala Gly
    130                 135                 140

Leu Lys Ala Lys Pro Glu Leu Gly Leu Gln Ile Gly Ser Gly Gly Asp
145                 150                 155                 160

Ser Gly Glu Ala Glu Leu Ala Ala Glu Gly Lys Lys Asp Ile Gly Asp
                165                 170                 175

Leu Val Asp Arg Gly Lys Lys Ala Leu Asp Ala Gly Ala Ser Ile Ile
            180                 185                 190

Met Ile Glu Ser Glu Gly Ile Thr Glu Asn Val Thr Glu Trp Asp Thr
        195                 200                 205

Gly Ala Ala Ala Ser Ile Ile Asn Gly Leu Gly Leu Glu Asn Val Met
    210                 215                 220

Phe Glu Ala Ala Asp Gly Pro Val Phe Glu Trp Tyr Val Lys Asn Tyr
225                 230                 235                 240

Gly Asn Glu Cys Asn Leu Phe Val Asp His Ser Gln Ile Leu Gln Leu
                245                 250                 255

Glu Gly Leu Arg Gln Asn Ile Trp Gly Asn Lys Ser Thr Trp Gly Arg
            260                 265                 270

Val Ile Asn Pro Ala Pro
        275


<210> 2067
<211> 399
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(376)
<223> RXA01083

<400> 2067
gtcgacatac tggcacgcaa gatctgtgta cccggcccac gtgcctaaaa ctaggtgagc 60

gagaccttcg agcagttcct cgaaggagag tgatccacct atg ttt ccg cga att   115
                                               Met Phe Pro Arg Ile
                                                 1               5

ccg ctg gca atg tgt gct gtc gca gca atc cct gct gtt gtg ctc agg   163
Pro Leu Ala Met Cys Ala Val Ala Ala Ile Pro Ala Val Val Leu Arg
                 10                  15                  20

ttt tct gag ctg tcg gcg tca cct gtg gcg acc atg ctg att ttt ggt   211
Phe Ser Glu Leu Ser Ala Ser Pro Val Ala Thr Met Leu Ile Phe Gly
             25                  30                  35

acc gca gtg gtt gct gcc tct ttt gtg ttg gcg tgg gca gct gaa gct   259
Thr Ala Val Val Ala Ala Ser Phe Val Leu Ala Trp Ala Ala Glu Ala
         40                  45                  50
```

```
gtg cgc aaa gat att tct ggt gcg ttg gca gtg gcc ttg ctt gcg tta   307
Val Arg Lys Asp Ile Ser Gly Ala Leu Ala Val Ala Leu Leu Ala Leu
     55                  60                  65

gtt gca gtg ctt cct gaa tat gct tct gaa acg gtt gtc gag cac act   355
Val Ala Val Leu Pro Glu Tyr Ala Ser Glu Thr Val Val Glu His Thr
 70                  75                  80                  85

tat caa aca tcg gcg gcg aat taagaaggtg aacagttgac gca             399
Tyr Gln Thr Ser Ala Ala Asn
                 90
```

<210> 2068
<211> 92
<212> PRT
<213> Corynebacterium glutamicum

<400> 2068

```
Met Phe Pro Arg Ile Pro Leu Ala Met Cys Ala Val Ala Ala Ile Pro
  1               5                  10                  15

Ala Val Val Leu Arg Phe Ser Glu Leu Ser Ala Ser Pro Val Ala Thr
             20                  25                  30

Met Leu Ile Phe Gly Thr Ala Val Val Ala Ala Ser Phe Val Leu Ala
         35                  40                  45

Trp Ala Ala Glu Ala Val Arg Lys Asp Ile Ser Gly Ala Leu Ala Val
     50                  55                  60

Ala Leu Leu Ala Leu Val Ala Val Leu Pro Glu Tyr Ala Ser Glu Thr
 65                  70                  75                  80

Val Val Glu His Thr Tyr Gln Thr Ser Ala Ala Asn
                 85                  90
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<210> 2069
<211> 1305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1282)
<223> RXA01088

<400> 2069

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tgccttgagt ctaattctcc cgcccgtgcg atgggtttaa gctggactga taaacctttt 60

gtgaaccgaa ttttttaact gatttgaaga agcgagaata atg gga ctg tgg atc   115
                                          Met Gly Leu Trp Ile
                                            1               5

gat gca acc gct ggc gtt gca ggg gat atg ttg ctg gga gca ctc att   163
Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu Leu Gly Ala Leu Ile
                 10                  15                  20

gat gca ggt gca gaa cta gaa aaa atc caa cag gtt gtg gaa gca gtc   211
Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln Val Val Glu Ala Val
```

```
                25                  30                  35

atc ccc ggt gac gtg ctc ttg cgc acc gaa gag gta gtg cgc caa ggc   259
Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu Val Val Arg Gln Gly
         40                  45                  50

caa cga ggc atc aag ctg cat gtg gac gca caa cat gaa cac cat cat   307
Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln His Glu His His His
     55                  60                  65

cac cgc cac tta agc acc att aaa gaa ctg ctt gtc aat gct gac atc   355
His Arg His Leu Ser Thr Ile Lys Glu Leu Leu Val Asn Ala Asp Ile
 70                  75                  80                  85

cct gaa caa acc aag cag gat gcc tta ggc gtt ttt gaa ctc atc gct   403
Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val Phe Glu Leu Ile Ala
                 90                  95                 100

atc gct gaa gga aaa gtc cac ggc atc gag ccg gag aaa atc cac ttc   451
Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro Glu Lys Ile His Phe
            105                 110                 115

cat gag gta gga gct tgg gat tcc atc gca gac att gtg ggt gtg tgc   499
His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp Ile Val Gly Val Cys
        120                 125                 130

gaa gcg atc agg cag ctt aac cca ggt ttg att gct gca tct ccg att   547
Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile Ala Ala Ser Pro Ile
    135                 140                 145

gct tta gga ttc gga cgc atc aag gca gct cac gga gat att cca gtg   595
Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His Gly Asp Ile Pro Val
150                 155                 160                 165

cca gtt cca gcc gtg gca gag ctg gtg aaa ggc tgg ccc acc caa acc   643
Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly Trp Pro Thr Gln Thr
                170                 175                 180

gga gct ctt atg gag agc acc gaa cct gtt ggt gaa tta gcc acc cca   691
Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly Glu Leu Ala Thr Pro
            185                 190                 195

act ggt gtt gcg ttg atc cgt cac ttt gcc acc caa gat ggc cct ttc   739
Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr Gln Asp Gly Pro Phe
        200                 205                 210

cca ggt ggc atc atc aat gaa gtt ggc att ggt gca gga aca aaa gat   787
Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly Ala Gly Thr Lys Asp
    215                 220                 225

aca gaa ggc cgt cca aat ata gtg cgc gca att ttg ttc aac acc tct   835
Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile Leu Phe Asn Thr Ser
230                 235                 240                 245

agg agt aac cca gat acc cgc aca ctg gtg caa tta gaa gcc aat gtt   883
Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln Leu Glu Ala Asn Val
                250                 255                 260

gat gat caa gac cca cgg ctg tgg cca gga gta ata gag atc ctc ttt   931
Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val Ile Glu Ile Leu Phe
            265                 270                 275
```

```
gcc gct ggc gca gta gat gca tgg ctg act cca att ttg atg aag aag   979
Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro Ile Leu Met Lys Lys
        280                 285                 290

ggc cgt cct gca cat agg gtg tca gca ttg gtg gat agc tcc gag gtg   1027
Gly Arg Pro Ala His Arg Val Ser Ala Leu Val Asp Ser Ser Glu Val
    295                 300                 305

gaa gca gtg aaa acc gca tta ttt gca gcc acc acg act ttt ggg atc   1075
Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr Thr Thr Phe Gly Ile
310                 315                 320                 325

aga tca tgg gaa gtc gaa cga gaa ggc ttg gac cgt cgt ttc gaa caa   1123
Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp Arg Arg Phe Glu Gln
                330                 335                 340

gtc gag gtg gac gga cac acc atc aac atc aaa atc ggt tcc cgt gat   1171
Val Glu Val Asp Gly His Thr Ile Asn Ile Lys Ile Gly Ser Arg Asp
            345                 350                 355

gat caa gta atc agt gca cag tcc gag ttt gaa gat att cgg tct gca   1219
Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu Asp Ile Arg Ser Ala
        360                 365                 370

gcg gtg gcc ttg gga att tca gag cgg gaa gtt gtg gca aga att ccg   1267
Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val Val Ala Arg Ile Pro
    375                 380                 385

caa ggc acc acc gag taacaaccaa aaggtcgact gct                    1305
Gln Gly Thr Thr Glu
390
```

<210> 2070
<211> 394
<212> PRT
<213> Corynebacterium glutamicum

<400> 2070

```
Met Gly Leu Trp Ile Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu
  1               5                  10                  15

Leu Gly Ala Leu Ile Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln
             20                  25                  30

Val Val Glu Ala Val Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu
         35                  40                  45

Val Val Arg Gln Gly Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln
     50                  55                  60

His Glu His His His His Arg His Leu Ser Thr Ile Lys Glu Leu Leu
 65                  70                  75                  80

Val Asn Ala Asp Ile Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val
                 85                  90                  95

Phe Glu Leu Ile Ala Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro
            100                 105                 110
```

```
Glu Lys Ile His Phe His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp
        115                 120                 125

Ile Val Gly Val Cys Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile
    130                 135                 140

Ala Ala Ser Pro Ile Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His
145                 150                 155                 160

Gly Asp Ile Pro Val Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly
                165                 170                 175

Trp Pro Thr Gln Thr Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly
            180                 185                 190

Glu Leu Ala Thr Pro Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr
        195                 200                 205

Gln Asp Gly Pro Phe Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly
    210                 215                 220

Ala Gly Thr Lys Asp Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile
225                 230                 235                 240

Leu Phe Asn Thr Ser Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln
                245                 250                 255

Leu Glu Ala Asn Val Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val
            260                 265                 270

Ile Glu Ile Leu Phe Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro
        275                 280                 285

Ile Leu Met Lys Lys Gly Arg Pro Ala His Arg Val Ser Ala Leu Val
    290                 295                 300

Asp Ser Ser Glu Val Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr
305                 310                 315                 320

Thr Thr Phe Gly Ile Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp
                325                 330                 335

Arg Arg Phe Glu Gln Val Glu Val Asp Gly His Thr Ile Asn Ile Lys
            340                 345                 350

Ile Gly Ser Arg Asp Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu
        355                 360                 365

Asp Ile Arg Ser Ala Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val
    370                 375                 380

Val Ala Arg Ile Pro Gln Gly Thr Thr Glu
385                 390
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<210> 2071
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(571)
<223> RXA01091

<400> 2071
tcgtcggaaa aactggcgat actattgata acgggcatgg gttcaccttc gataaagcac 60

ggtctatgct ggactatcgc cttttgacac gagtatcgca atg gtc ccg aac aca 115
Met Val Pro Asn Thr
1 5

gtc ctt atc cat gac gaa acc gcc gat ctg gcg acg cag atc cag cgg 163
Val Leu Ile His Asp Glu Thr Ala Asp Leu Ala Thr Gln Ile Gln Arg
10 15 20

ctg gaa cat atc atg gcg tgc ctg cgc gat ccg gtc agc gga tgc ccg 211
Leu Glu His Ile Met Ala Cys Leu Arg Asp Pro Val Ser Gly Cys Pro
25 30 35

tgg gat att gaa cag acc ttt gcc agc atc gcg ccc cac acg att gag 259
Trp Asp Ile Glu Gln Thr Phe Ala Ser Ile Ala Pro His Thr Ile Glu
40 45 50

gaa ggc tac gag gtt gcc gac gcc atc gcg cag gaa gac tgg ccc gag 307
Glu Gly Tyr Glu Val Ala Asp Ala Ile Ala Gln Glu Asp Trp Pro Glu
55 60 65

cta cgc ggc gag ttg ggc gat ttg ctg ttt cag acc gtg ttt cac gcc 355
Leu Arg Gly Glu Leu Gly Asp Leu Leu Phe Gln Thr Val Phe His Ala
70 75 80 85

caa atg gcg cgc gag gca ggc cat ttc gct ttg gtt gac gtg gtg aag 403
Gln Met Ala Arg Glu Ala Gly His Phe Ala Leu Val Asp Val Val Lys
90 95 100

gca att tcg gac aag atg gtt ttg cgc cat ccg cac gtg ttc ggc gcg 451
Ala Ile Ser Asp Lys Met Val Leu Arg His Pro His Val Phe Gly Ala
105 110 115

cag tcg aac gcg aaa tcc gcc gac cag cag gtg aag att ggg aag tca 499
Gln Ser Asn Ala Lys Ser Ala Asp Gln Gln Val Lys Ile Gly Lys Ser
120 125 130

tca agg cgc ccg agc gcg cgg gca aag cgc aaa agg gcg ttt tgg atg 547
Ser Arg Arg Pro Ser Ala Arg Ala Lys Arg Lys Arg Ala Phe Trp Met
135 140 145

gcg tcg cgc tgg gac tgc ctg ccc tgatgcgcgc gacgaagctg caa 594
Ala Ser Arg Trp Asp Cys Leu Pro
150 155

<210> 2072
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 2072
Met Val Pro Asn Thr Val Leu Ile His Asp Glu Thr Ala Asp Leu Ala
1 5 10 15

```
Thr Gln Ile Gln Arg Leu Glu His Ile Met Ala Cys Leu Arg Asp Pro
            20                  25                  30

Val Ser Gly Cys Pro Trp Asp Ile Glu Gln Thr Phe Ala Ser Ile Ala
        35                  40                  45

Pro His Thr Ile Glu Glu Gly Tyr Glu Val Ala Asp Ala Ile Ala Gln
    50                  55                  60

Glu Asp Trp Pro Glu Leu Arg Gly Glu Leu Gly Asp Leu Leu Phe Gln
65                  70                  75                  80

Thr Val Phe His Ala Gln Met Ala Arg Glu Ala Gly His Phe Ala Leu
                85                  90                  95

Val Asp Val Val Lys Ala Ile Ser Asp Lys Met Val Leu Arg His Pro
            100                 105                 110

His Val Phe Gly Ala Gln Ser Asn Ala Lys Ser Ala Asp Gln Gln Val
        115                 120                 125

Lys Ile Gly Lys Ser Ser Arg Arg Pro Ser Ala Arg Ala Lys Arg Lys
    130                 135                 140

Arg Ala Phe Trp Met Ala Ser Arg Trp Asp Cys Leu Pro
145                 150                 155


<210> 2073
<211> 280
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(280)
<223> RXA01092

<400> 2073
tgaacccatg cccgttatca atagtatcgc cagtttttcc gacgagatga cccgctggcg 60

gcgtcacctg catcaaaacc ccgaaatcag ctttgattgt gtg gaa act gcg gcc   115
                                            Val Glu Thr Ala Ala
                                              1               5

ttc gtg gcc gag cag ctg cgc agc ttc ggg gtg gat gaa att cac acc   163
Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp Glu Ile His Thr
                10                  15                  20

ggc atc gcg aaa acc ggt atc atc gcc ctg att cac ggg cgc gag gct   211
Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala
            25                  30                  35

ggc ccc gtc gtc ggc ctg cgc gcc gat atg gac gcg ctg ccg ctg acc   259
Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Thr
        40                  45                  50

gag att acc ggc gtc tac tat                                      280
Glu Ile Thr Gly Val Tyr Tyr
    55                  60
```

<210> 2074
<211> 60
<212> PRT
<213> Corynebacterium glutamicum

<400> 2074
Val Glu Thr Ala Ala Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val
1 5 10 15

Asp Glu Ile His Thr Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile
20 25 30

His Gly Arg Glu Ala Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp
35 40 45

Ala Leu Pro Leu Thr Glu Ile Thr Gly Val Tyr Tyr
50 55 60

<210> 2075
<211> 280
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(280)
<223> RXA01092

<400> 2075
tgaacccatg cccgttatca atagtatcgc cagtttttcc gacgagatga cccgctggcg 60

gcgtcacctg catcaaaacc ccgaaatcag ctttgattgt gtg gaa act gcg gcc 115
Val Glu Thr Ala Ala
1 5

ttc gtg gcc gag cag ctg cgc agc ttc ggg gtg gat gaa att cac acc 163
Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp Glu Ile His Thr
10 15 20

ggc atc gcg aaa acc ggt atc atc gcc ctg att cac ggg cgc gag gct 211
Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala
25 30 35

ggc ccc gtc gtc ggc ctg cgc gcc gat atg gac gcg ctg ccg ctg acc 259
Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Thr
40 45 50

gag att acc ggc gtc tac tat 280
Glu Ile Thr Gly Val Tyr Tyr
55 60

<210> 2076
<211> 60
<212> PRT
<213> Corynebacterium glutamicum

<400> 2076
Val Glu Thr Ala Ala Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val

```
  1               5                  10                  15

Asp Glu Ile His Thr Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile
            20                  25                  30

His Gly Arg Glu Ala Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp
        35                  40                  45

Ala Leu Pro Leu Thr Glu Ile Thr Gly Val Tyr Tyr
    50                  55                  60


<210> 2077
<211> 822
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(799)
<223> RXA01096

<400> 2077
accgtgaaac aaaccggcgg tgcgtgccac actggtgccc acacatgttt cgacaatgac 60

gttttgctgt aaaagcaaca acgattaagg aagaaatctt atg aag cca cgc gtg   115
                                            Met Lys Pro Arg Val
                                              1               5

ctg tca gca tta ggc att gga gct ggc gcc ctg gtt gtc tgg atc agc   163
Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu Val Val Trp Ile Ser
                10                  15                  20

tca cgc atg aac tgg gta acc atc gag gct ttc gac gat aaa tca ggt   211
Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe Asp Asp Lys Ser Gly
            25                  30                  35

agt gtc acc caa tct att gtg ggt gca acc tgg tct aca gaa atc atg   259
Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp Ser Thr Glu Ile Met
        40                  45                  50

gcg ctt gca ctt gct ttg ctc gct gcc ttc gcc gcc gcg ttg gtg ctc   307
Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala Ala Ala Leu Val Leu
    55                  60                  65

aag cgc atg ggt cgg cgc atc att ggt ggt att tcg gcg ctg atc gcg   355
Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile Ser Ala Leu Ile Ala
70                  75                  80                  85

gtg ggt gcc agc ctg tct cca ctc gcg ctt ctc acc caa gac cca gac   403
Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu Thr Gln Asp Pro Asp
                90                  95                  100

gca gaa cgg gcc cga acc ctg ctg acc tcc ggt gtg gcc tca cag aag   451
Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly Val Ala Ser Gln Lys
            105                 110                 115

gct aat tcc gga acc ctg ctg tct gat tgg gcg gag atc atc aat acc   499
Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala Glu Ile Ile Asn Thr
        120                 125                 130
```

```
acc acc cat cca ctg gcg gca gtg gta gcc atg att ggc tgc gcg cta   547
Thr Thr His Pro Leu Ala Ala Val Val Ala Met Ile Gly Cys Ala Leu
    135                 140                 145

gcc cta gtc ggc ggc gtt gtc ctt gcc atg cgc cct gcc gag gac acc   595
Ala Leu Val Gly Gly Val Val Leu Ala Met Arg Pro Ala Glu Asp Thr
150                 155                 160                 165

gcg aaa agc aat cag tat gag cgt aaa cag gct cgc gct gag aaa atc   643
Ala Lys Ser Asn Gln Tyr Glu Arg Lys Gln Ala Arg Ala Glu Lys Ile
                170                 175                 180

cac acc gat ttg gcc caa gat cca gac tcc ggt cgt gtg atg tgg acg   691
His Thr Asp Leu Ala Gln Asp Pro Asp Ser Gly Arg Val Met Trp Thr
            185                 190                 195

cac tcg atg aag aca ttg act tca ccg aga aga ctc aga aat cca aag   739
His Ser Met Lys Thr Leu Thr Ser Pro Arg Arg Leu Arg Asn Pro Lys
        200                 205                 210

aaa ccc cag gtc aaa gct agg gtg tgg cac cct gat ttc ttt cgc cat   787
Lys Pro Gln Val Lys Ala Arg Val Trp His Pro Asp Phe Phe Arg His
    215                 220                 225

gtg tgt tcg gga taaccttaaa cacagcattg gtt                        822
Val Cys Ser Gly
230
```

EFS Web 2.2.0.D

<210> 2078
<211> 233
<212> PRT
<213> Corynebacterium glutamicum

<400> 2078

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Met Lys Pro Arg Val Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu
  1               5                  10                  15

Val Val Trp Ile Ser Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe
             20                  25                  30

Asp Asp Lys Ser Gly Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp
         35                  40                  45

Ser Thr Glu Ile Met Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala
     50                  55                  60

Ala Ala Leu Val Leu Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile
 65                  70                  75                  80

Ser Ala Leu Ile Ala Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu
                 85                  90                  95

Thr Gln Asp Pro Asp Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly
            100                 105                 110

Val Ala Ser Gln Lys Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala
        115                 120                 125

Glu Ile Ile Asn Thr Thr Thr His Pro Leu Ala Ala Val Val Ala Met
    130                 135                 140
```

```
Ile Gly Cys Ala Leu Ala Leu Val Gly Gly Val Val Leu Ala Met Arg
145                 150                 155                 160

Pro Ala Glu Asp Thr Ala Lys Ser Asn Gln Tyr Glu Arg Lys Gln Ala
                165                 170                 175

Arg Ala Glu Lys Ile His Thr Asp Leu Ala Gln Asp Pro Asp Ser Gly
            180                 185                 190

Arg Val Met Trp Thr His Ser Met Lys Thr Leu Thr Ser Pro Arg Arg
        195                 200                 205

Leu Arg Asn Pro Lys Lys Pro Gln Val Lys Ala Arg Val Trp His Pro
    210                 215                 220

Asp Phe Phe Arg His Val Cys Ser Gly
225                 230
```

<210> 2079
<211> 1368
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1345)
<223> RXA01102

<400> 2079

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attctatggt tgttgggaga gatgacttaa tttggaatca cgggctttaa cacgcgctga 60

cattgagcaa cttcccagca tgtggaaaag cccaggtttc gtg gct gtc ctc gtg   115
                                            Val Ala Val Leu Val
                                              1               5

gcg gtt gca gca gcg ttc ggc agt tgg tca ctc ctt ctt ccc gtc gta   163
Ala Val Ala Ala Ala Phe Gly Ser Trp Ser Leu Leu Leu Pro Val Val
                  10                  15                  20

ccg cta gcg gtc ctc aac aac ggc gga tca agc gct gtc gcc ggt gcc   211
Pro Leu Ala Val Leu Asn Asn Gly Gly Ser Ser Ala Val Ala Gly Ala
              25                  30                  35

acc act ggc atc ttc atg gca gct aca gtg atc act cag att ttc act   259
Thr Thr Gly Ile Phe Met Ala Ala Thr Val Ile Thr Gln Ile Phe Thr
          40                  45                  50

ccc gct gcg ctg cgg aaa att ggc tac acc cca gtg atg gct ttc gcc   307
Pro Ala Ala Leu Arg Lys Ile Gly Tyr Thr Pro Val Met Ala Phe Ala
      55                  60                  65

gca ttc atg ctg ggt gtg cca gcc atc ggg tac atc ttc agc gtc gag   355
Ala Phe Met Leu Gly Val Pro Ala Ile Gly Tyr Ile Phe Ser Val Glu
  70                  75                  80                  85

cca att cca gtg ctg gta gtg tcc gca ctt cga gga att ggg ttc ggt   403
Pro Ile Pro Val Leu Val Val Ser Ala Leu Arg Gly Ile Gly Phe Gly
                  90                  95                 100
```

```
gcg ctc acc gtc gca gaa tct gcg ttg gtg gct gaa ctc gtt ccc gta   451
Ala Leu Thr Val Ala Glu Ser Ala Leu Val Ala Glu Leu Val Pro Val
            105                 110                 115

cgc ttc ttg ggc aaa gct tct gga atg ttg ggc gta ttt att ggc ctt   499
Arg Phe Leu Gly Lys Ala Ser Gly Met Leu Gly Val Phe Ile Gly Leu
        120                 125                 130

tcc caa atg ctt ttc ctg cct gcc ggg ttg gcg tta ggt gac caa ttt   547
Ser Gln Met Leu Phe Leu Pro Ala Gly Leu Ala Leu Gly Asp Gln Phe
    135                 140                 145

ggc tac aac gtg gtc tat gtt tta ggt gcc gtt atc gca cta gtt gca   595
Gly Tyr Asn Val Val Tyr Val Leu Gly Ala Val Ile Ala Leu Val Ala
150                 155                 160                 165

gcg gtg atg tgt ctg cgt att ccg cag gtt aag gca gcg gca aag cag   643
Ala Val Met Cys Leu Arg Ile Pro Gln Val Lys Ala Ala Ala Lys Gln
                170                 175                 180

caa cca cag gtg agc gaa cag gag cgt tct gtt tcc acc tgg aag ttg   691
Gln Pro Gln Val Ser Glu Gln Glu Arg Ser Val Ser Thr Trp Lys Leu
            185                 190                 195

gtg ctg gtt ccc tcc ttg gct gtt acc agt ttg tca atg act ttt ggc   739
Val Leu Val Pro Ser Leu Ala Val Thr Ser Leu Ser Met Thr Phe Gly
        200                 205                 210

gca gtg tct tca ttc ctt cca gct gca gtc att gag tta gat cca gga   787
Ala Val Ser Ser Phe Leu Pro Ala Ala Val Ile Glu Leu Asp Pro Gly
    215                 220                 225

tta ggt gct gca tta gcg ggt att att tta tcc att acc ggt ggt tct   835
Leu Gly Ala Ala Leu Ala Gly Ile Ile Leu Ser Ile Thr Gly Gly Ser
230                 235                 240                 245

tca atg gtg ttc cgc tac ctg tcc ggc gtt atc gct gac cgc cgc ggt   883
Ser Met Val Phe Arg Tyr Leu Ser Gly Val Ile Ala Asp Arg Arg Gly
                250                 255                 260

gtg cct ggt acc acg atg att cct gct cag atc att ggg ttc tta ggt   931
Val Pro Gly Thr Thr Met Ile Pro Ala Gln Ile Ile Gly Phe Leu Gly
            265                 270                 275

gtc gtt tta atc acc gtc aca atc ttc caa ggc tgg tcc gtg tgg ctt   979
Val Val Leu Ile Thr Val Thr Ile Phe Gln Gly Trp Ser Val Trp Leu
        280                 285                 290

ttg att ata ggt gca gtg atg ttt ggt ggt gct ttt ggc atg gtg caa   1027
Leu Ile Ile Gly Ala Val Met Phe Gly Gly Ala Phe Gly Met Val Gln
    295                 300                 305

aac gaa gcg ttg ctt tca atg ttt ttc cgg ctt cct cgc act aga gtc   1075
Asn Glu Ala Leu Leu Ser Met Phe Phe Arg Leu Pro Arg Thr Arg Val
310                 315                 320                 325

tcc gaa gcc tcc gcc atc tgg aat atc gcc ttt gat tcg gga aca gga   1123
Ser Glu Ala Ser Ala Ile Trp Asn Ile Ala Phe Asp Ser Gly Thr Gly
                330                 335                 340

atc gga agc ttc ctc ctt ggc ata gtt gcc gca tcg ctt gct tac agt   1171
```

```
Ile Gly Ser Phe Leu Leu Gly Ile Val Ala Ala Ser Leu Ala Tyr Ser
            345                 350                 355

ggt gct ttt ggt tcc gga gcc gtg gtg att ttg ttt gga atc gtt ttg   1219
Gly Ala Phe Gly Ser Gly Ala Val Val Ile Leu Phe Gly Ile Val Leu
        360                 365                 370

acc acc gcc gat cga atc att ggg cgg cac cgc att act gaa tac aac   1267
Thr Thr Ala Asp Arg Ile Ile Gly Arg His Arg Ile Thr Glu Tyr Asn
    375                 380                 385

aac acc cgc gcg cgt ttg cgc cag gtg cca gtc gct cgg cgt gca gtg   1315
Asn Thr Arg Ala Arg Leu Arg Gln Val Pro Val Ala Arg Arg Ala Val
390                 395                 400                 405

caa ggg ctg cgc aac agg cgc aaa gat cgc taaaacgctt ttcgacgcca     1365
Gln Gly Leu Arg Asn Arg Arg Lys Asp Arg
                410                 415

ccc                                                               1368
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<210> 2080
<211> 415
<212> PRT
<213> Corynebacterium glutamicum

<400> 2080

```
Val Ala Val Leu Val Ala Val Ala Ala Ala Phe Gly Ser Trp Ser Leu
  1               5                  10                  15

Leu Leu Pro Val Val Pro Leu Ala Val Leu Asn Asn Gly Gly Ser Ser
             20                  25                  30

Ala Val Ala Gly Ala Thr Thr Gly Ile Phe Met Ala Ala Thr Val Ile
         35                  40                  45

Thr Gln Ile Phe Thr Pro Ala Ala Leu Arg Lys Ile Gly Tyr Thr Pro
     50                  55                  60

Val Met Ala Phe Ala Ala Phe Met Leu Gly Val Pro Ala Ile Gly Tyr
 65                  70                  75                  80

Ile Phe Ser Val Glu Pro Ile Pro Val Leu Val Val Ser Ala Leu Arg
                 85                  90                  95

Gly Ile Gly Phe Gly Ala Leu Thr Val Ala Glu Ser Ala Leu Val Ala
            100                 105                 110

Glu Leu Val Pro Val Arg Phe Leu Gly Lys Ala Ser Gly Met Leu Gly
        115                 120                 125

Val Phe Ile Gly Leu Ser Gln Met Leu Phe Leu Pro Ala Gly Leu Ala
    130                 135                 140

Leu Gly Asp Gln Phe Gly Tyr Asn Val Val Tyr Val Leu Gly Ala Val
145                 150                 155                 160

Ile Ala Leu Val Ala Ala Val Met Cys Leu Arg Ile Pro Gln Val Lys
                165                 170                 175
```

```
Ala Ala Ala Lys Gln Gln Pro Gln Val Ser Glu Gln Glu Arg Ser Val
            180                 185                 190

Ser Thr Trp Lys Leu Val Leu Val Pro Ser Leu Ala Val Thr Ser Leu
        195                 200                 205

Ser Met Thr Phe Gly Ala Val Ser Ser Phe Leu Pro Ala Ala Val Ile
    210                 215                 220

Glu Leu Asp Pro Gly Leu Gly Ala Ala Leu Ala Gly Ile Ile Leu Ser
225                 230                 235                 240

Ile Thr Gly Gly Ser Ser Met Val Phe Arg Tyr Leu Ser Gly Val Ile
                245                 250                 255

Ala Asp Arg Arg Gly Val Pro Gly Thr Thr Met Ile Pro Ala Gln Ile
            260                 265                 270

Ile Gly Phe Leu Gly Val Val Leu Ile Thr Val Thr Ile Phe Gln Gly
        275                 280                 285

Trp Ser Val Trp Leu Leu Ile Ile Gly Ala Val Met Phe Gly Gly Ala
    290                 295                 300

Phe Gly Met Val Gln Asn Glu Ala Leu Leu Ser Met Phe Phe Arg Leu
305                 310                 315                 320

Pro Arg Thr Arg Val Ser Glu Ala Ser Ala Ile Trp Asn Ile Ala Phe
                325                 330                 335

Asp Ser Gly Thr Gly Ile Gly Ser Phe Leu Leu Gly Ile Val Ala Ala
            340                 345                 350

Ser Leu Ala Tyr Ser Gly Ala Phe Gly Ser Gly Ala Val Val Ile Leu
        355                 360                 365

Phe Gly Ile Val Leu Thr Thr Ala Asp Arg Ile Ile Gly Arg His Arg
    370                 375                 380

Ile Thr Glu Tyr Asn Asn Thr Arg Ala Arg Leu Arg Gln Val Pro Val
385                 390                 395                 400

Ala Arg Arg Ala Val Gln Gly Leu Arg Asn Arg Arg Lys Asp Arg
                405                 410                 415
```

09600 09601 09602 09603 09604 09605 09606 09607 09608 09609 09610 09611 09612 09613 09614 09615 09616 09617 09618 09619 09620 09621 09622 09623 09624 09625 09626 09627 09628 09629 09630 09631 09632 09633 09634 09635 09636 09637 09638 09639 09640 09641 09642 09643 09644 09645 09646 09647 09648 09649 09650 09651 09652 09653 09654 09655 09656 09657 09658 09659 09660 09661 09662 09663 09664 09665 09666 09667 09668 09669 09670 09671 09672 09673 09674 09675 09676 09677 09678 09679 09680 09681 09682 09683 09684 09685 09686 09687 09688 09689 09690 09691 09692 09693 09694 09695 09696 09697 09698 09699 09700 09701 09702 09703 09704 09705 09706 09707 09708 09709 09710 09711 09712 09713 09714 09715 09716 09717 09718 09719 09720 09721 09722 09723 09724 09725 09726 09727 09728 09729 09730 09731 09732 09733 09734 09735 09736 09737 09738 09739 09740 09741 09742 09743 09744 09745 09746 09747 09748 09749 09750 09751 09752 09753 09754 09755 09756 09757 09758 09759 09760 09761 09762 09763 09764 09765 09766 09767 09768 09769 09770 09771 09772 09773 09774 09775 09776 09777 09778 09779 09780 09781 09782 09783 09784 09785 09786 09787 09788 09789 09790 09791 09792 09793 09794 09795 09796 09797 09798 09799 09800 09801 09802 09803 09804 09805 09806 09807 09808 09809 09810 09811 09812 09813 09814 09815 09816 09817 09818 09819 09820 09821 09822 09823 09824 09825 09826 09827 09828 09829 09830 09831 09832 09833 09834 09835 09836 09837 09838 09839 09840 09841 09842 09843 09844 09845 09846 09847 09848 09849 09850 09851 09852 09853 09854 09855 09856 09857 09858 09859 09860 09861 09862 09863 09864 09865 09866 09867 09868 09869 09870 09871 09872 09873 09874 09875 09876 09877 09878 09879 09880 09881 09882 09883 09884 09885 09886 09887 09888 09889 09890 09891 09892 09893 09894 09895 09896 09897 09898 09899 09900 09901 09902 09903 09904 09905 09906 09907 09908 09909 09910 09911 09912 09913 09914 09915 09916 09917 09918 09919 09920 09921 09922 09923 09924 09925 09926 09927 09928 09929 09930 09931 09932 09933 09934 09935 09936 09937 09938 09939 09940 09941 09942 09943 09944 09945 09946 09947 09948 09949 09950 09951 09952 09953 09954 09955 09956 09957 09958 09959 09960 09961 09962 09963 09964 09965 09966 09967 09968 09969 09970 09971 09972 09973 09974 09975 09976 09977 09978 09979 09980 09981 09982 09983 09984 09985 09986 09987 09988 09989 09990 09991 09992 09993 09994 09995 09996 09997 09998 09999

<210> 2081
<211> 348
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(325)
<223> RXA01103

<400> 2081
ccgaagcaga gtacaaggct gttgcccgtg cgctgcgcgg tgccgtagag atggatcctc 60

gtcaaacagg aatcccatcc actaagggag cgctctagac atg aac tct tct ccc 115
                                                Met Asn Ser Ser Pro

```
                                                    1               5

atc tct gat atg gtc act gcg gct gtg cag aac gaa cca gat gcg ggc   163
Ile Ser Asp Met Val Thr Ala Ala Val Gln Asn Glu Pro Asp Ala Gly
                 10                  15                  20

gac cga tgg ttt att tat ggt ttg ttc ctc atc gcc ggg ctt ttc ttt   211
Asp Arg Trp Phe Ile Tyr Gly Leu Phe Leu Ile Ala Gly Leu Phe Phe
             25                  30                  35

ggc ggt gcc tgg tct gca tat aaa tca gaa aac aaa atc ctc atg gtt   259
Gly Gly Ala Trp Ser Ala Tyr Lys Ser Glu Asn Lys Ile Leu Met Val
         40                  45                  50

gca gcc ggc ctc atc gca gtg ctg gca gtg gct gga gga att cta tgg   307
Ala Ala Gly Leu Ile Ala Val Leu Ala Val Ala Gly Gly Ile Leu Trp
     55                  60                  65

ttg ttg gga gag atg act taatttggaa tcacgggctt taa                348
Leu Leu Gly Glu Met Thr
 70                  75
```

0305305

<210> 2082
<211> 75
<212> PRT
<213> Corynebacterium glutamicum

<400> 2082
Met Asn Ser Ser Pro Ile Ser Asp Met Val Thr Ala Ala Val Gln Asn
  1   5   10   15

Glu Pro Asp Ala Gly Asp Arg Trp Phe Ile Tyr Gly Leu Phe Leu Ile
             20   25   30

Ala Gly Leu Phe Phe Gly Gly Ala Trp Ser Ala Tyr Lys Ser Glu Asn
         35   40   45

Lys Ile Leu Met Val Ala Ala Gly Leu Ile Ala Val Leu Ala Val Ala
     50   55   60

Gly Gly Ile Leu Trp Leu Leu Gly Glu Met Thr
 65   70   75

<210> 2083
<211> 1323
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1300)
<223> RXA01107

<400> 2083
gggtacatca gagttcattt gaattagact taaaacttaa aatgaccacc ccagatttac 60

```
ctgaattaaa cccgctttca cctttgagat actggaagga atg gat ttc acc tct   115
                                              Met Asp Phe Thr Ser
                                                1               5
```

```
gtg aat gat cga aac gtc cct gca ccc aac acc tcc att cct ttc cca   163
Val Asn Asp Arg Asn Val Pro Ala Pro Asn Thr Ser Ile Pro Phe Pro
                10                  15                  20

gtt gac ctg aat cga gtg acg gag gct gtt gat tcc ttg ggc tac cac   211
Val Asp Leu Asn Arg Val Thr Glu Ala Val Asp Ser Leu Gly Tyr His
            25                  30                  35

tat ttg agc tca gaa gat cgc atc atc gtg ccg tgg caa gat cac cgc   259
Tyr Leu Ser Ser Glu Asp Arg Ile Ile Val Pro Trp Gln Asp His Arg
        40                  45                  50

att tcg atg tac ttc agc cac gaa tca ggg caa atg ctc acc atc ctt   307
Ile Ser Met Tyr Phe Ser His Glu Ser Gly Gln Met Leu Thr Ile Leu
    55                  60                  65

ggt cgc acg cgc ctt aat ttg gac atg ttt gcc atc aac gat gcg gcg   355
Gly Arg Thr Arg Leu Asn Leu Asp Met Phe Ala Ile Asn Asp Ala Ala
70                  75                  80                  85

cga gct gtc acc gaa tgg aat gcc gaa cgc atc ggg cca aca gcc ctc   403
Arg Ala Val Thr Glu Trp Asn Ala Glu Arg Ile Gly Pro Thr Ala Leu
                90                  95                  100

gtc cat ctg ggc aac gac ggc gaa gtg gaa ttg aaa ttc cgc acg acc   451
Val His Leu Gly Asn Asp Gly Glu Val Glu Leu Lys Phe Arg Thr Thr
            105                 110                 115

atc tgc atc gat gaa ggg tta agc acc caa cag cta cgc caa ttc atc   499
Ile Cys Ile Asp Glu Gly Leu Ser Thr Gln Gln Leu Arg Gln Phe Ile
        120                 125                 130

aac ctg tcc ttg gac acc acc gcc atg gct gtg acc tat att ctg gag   547
Asn Leu Ser Leu Asp Thr Thr Ala Met Ala Val Thr Tyr Ile Leu Glu
    135                 140                 145

cgt ttt tca gaa ctt aac ttc agc gac acc gga agc cct gac gac acg   595
Arg Phe Ser Glu Leu Asn Phe Ser Asp Thr Gly Ser Pro Asp Asp Thr
150                 155                 160                 165

aac aat gcc gat gaa ctc agc gac gaa caa gac caa gca gat ctc gta   643
Asn Asn Ala Asp Glu Leu Ser Asp Glu Gln Asp Gln Ala Asp Leu Val
                170                 175                 180

gag aaa atc cgg ggg ctg tac gtt ccc act cca gtt gaa gag ctc atc   691
Glu Lys Ile Arg Gly Leu Tyr Val Pro Thr Pro Val Glu Glu Leu Ile
            185                 190                 195

gaa tcc cta gaa gac gca gag tgg gaa gaa tca gac atg gca gac gag   739
Glu Ser Leu Glu Asp Ala Glu Trp Glu Glu Ser Asp Met Ala Asp Glu
        200                 205                 210

gat gca gaa gac gac tac cta gac gat gac tca gaa atc gaa tgg gaa   787
Asp Ala Glu Asp Asp Tyr Leu Asp Asp Asp Ser Glu Ile Glu Trp Glu
    215                 220                 225

aca gac gat gac tac ttc gaa cct gaa gaa gtc gac atg gac gaa ctc   835
Thr Asp Asp Asp Tyr Phe Glu Pro Glu Glu Val Asp Met Asp Glu Leu
230                 235                 240                 245
```

```
ctc aac ggt ttc ctc gaa gat tct gac atc ccc cag gaa gtc acc ttg   883
Leu Asn Gly Phe Leu Glu Asp Ser Asp Ile Pro Gln Glu Val Thr Leu
                250                 255                 260

gaa cgc att cgg gca caa ctg cat gcc atc ggc gtg gta aaa acc agc   931
Glu Arg Ile Arg Ala Gln Leu His Ala Ile Gly Val Val Lys Thr Ser
            265                 270                 275

ggc gaa gac gat ttc atc atc gcg tgg atc aac gaa gtg ttt tta ggc   979
Gly Glu Asp Asp Phe Ile Ile Ala Trp Ile Asn Glu Val Phe Leu Gly
        280                 285                 290

ttc ttc gtt gat aat ggc ccc act ttc ctg gtg aaa ggt cac tgg gat   1027
Phe Phe Val Asp Asn Gly Pro Thr Phe Leu Val Lys Gly His Trp Asp
    295                 300                 305

ccc agc atg gac ccc aca cgc gac ttc atg aaa ctg ttc atg atg tgc   1075
Pro Ser Met Asp Pro Thr Arg Asp Phe Met Lys Leu Phe Met Met Cys
310                 315                 320                 325

aat cag tgg aac gaa aac tct ctg act acc aaa gct ttt tgc cat act   1123
Asn Gln Trp Asn Glu Asn Ser Leu Thr Thr Lys Ala Phe Cys His Thr
                330                 335                 340

gat gac aag ggt ctc cag gtc cgg gta gag ttc gcg gtc tct gtc gct   1171
Asp Asp Lys Gly Leu Gln Val Arg Val Glu Phe Ala Val Ser Val Ala
            345                 350                 355

gaa ggc ctc aac gac gat caa cta cag cac aac atc gca ctg tca att   1219
Glu Gly Leu Asn Asp Asp Gln Leu Gln His Asn Ile Ala Leu Ser Ile
        360                 365                 370

cat cat att ttg caa gcg att gat tcc atc agc aca gaa gcc act gga   1267
His His Ile Leu Gln Ala Ile Asp Ser Ile Ser Thr Glu Ala Thr Gly
    375                 380                 385

tca tca acg gtg gaa tgg ccg gag aaa aac cgc tgatcattaa ggtcttccaa 1320
Ser Ser Thr Val Glu Trp Pro Glu Lys Asn Arg
390                 395                 400

gaa                                                               1323
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<210> 2084
<211> 400
<212> PRT
<213> Corynebacterium glutamicum

<400> 2084

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Met Asp Phe Thr Ser Val Asn Asp Arg Asn Val Pro Ala Pro Asn Thr
  1               5                  10                  15

Ser Ile Pro Phe Pro Val Asp Leu Asn Arg Val Thr Glu Ala Val Asp
             20                  25                  30

Ser Leu Gly Tyr His Tyr Leu Ser Ser Glu Asp Arg Ile Ile Val Pro
         35                  40                  45

Trp Gln Asp His Arg Ile Ser Met Tyr Phe Ser His Glu Ser Gly Gln
     50                  55                  60
```

```
Met Leu Thr Ile Leu Gly Arg Thr Arg Leu Asn Leu Asp Met Phe Ala
 65                  70                  75                  80

Ile Asn Asp Ala Ala Arg Ala Val Thr Glu Trp Asn Ala Glu Arg Ile
                 85                  90                  95

Gly Pro Thr Ala Leu Val His Leu Gly Asn Asp Gly Glu Val Glu Leu
            100                 105                 110

Lys Phe Arg Thr Thr Ile Cys Ile Asp Glu Gly Leu Ser Thr Gln Gln
        115                 120                 125

Leu Arg Gln Phe Ile Asn Leu Ser Leu Asp Thr Thr Ala Met Ala Val
    130                 135                 140

Thr Tyr Ile Leu Glu Arg Phe Ser Glu Leu Asn Phe Ser Asp Thr Gly
145                 150                 155                 160

Ser Pro Asp Asp Thr Asn Asn Ala Asp Glu Leu Ser Asp Glu Gln Asp
                165                 170                 175

Gln Ala Asp Leu Val Glu Lys Ile Arg Gly Leu Tyr Val Pro Thr Pro
            180                 185                 190

Val Glu Glu Leu Ile Glu Ser Leu Glu Asp Ala Glu Trp Glu Glu Ser
        195                 200                 205

Asp Met Ala Asp Glu Asp Ala Glu Asp Asp Tyr Leu Asp Asp Asp Ser
    210                 215                 220

Glu Ile Glu Trp Glu Thr Asp Asp Asp Tyr Phe Glu Pro Glu Glu Val
225                 230                 235                 240

Asp Met Asp Glu Leu Leu Asn Gly Phe Leu Glu Asp Ser Asp Ile Pro
                245                 250                 255

Gln Glu Val Thr Leu Glu Arg Ile Arg Ala Gln Leu His Ala Ile Gly
            260                 265                 270

Val Val Lys Thr Ser Gly Glu Asp Asp Phe Ile Ile Ala Trp Ile Asn
        275                 280                 285

Glu Val Phe Leu Gly Phe Phe Val Asp Asn Gly Pro Thr Phe Leu Val
    290                 295                 300

Lys Gly His Trp Asp Pro Ser Met Asp Pro Thr Arg Asp Phe Met Lys
305                 310                 315                 320

Leu Phe Met Met Cys Asn Gln Trp Asn Glu Asn Ser Leu Thr Thr Lys
                325                 330                 335

Ala Phe Cys His Thr Asp Asp Lys Gly Leu Gln Val Arg Val Glu Phe
            340                 345                 350

Ala Val Ser Val Ala Glu Gly Leu Asn Asp Asp Gln Leu Gln His Asn
        355                 360                 365

Ile Ala Leu Ser Ile His His Ile Leu Gln Ala Ile Asp Ser Ile Ser
    370                 375                 380

Thr Glu Ala Thr Gly Ser Ser Thr Val Glu Trp Pro Glu Lys Asn Arg
```

385 390 395 400

<210> 2085
<211> 774
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> RXA01108

<400> 2085
gtggccagtg gaagttctgc gactaatcca cagagcttaa aactccggtt gtcagttcag 60

gttgcaaagt taacagtcaa cggctgtatt ctttagagcc atg aca tac ccc ggc 115
Met Thr Tyr Pro Gly
1 5

atc acc tct gac cac aat cct tat gat gga tac aca ggc gat gac ggg 163
Ile Thr Ser Asp His Asn Pro Tyr Asp Gly Tyr Thr Gly Asp Asp Gly
10 15 20

gcc gga aac aag cgc aac ctc cca aac cga aag aaa ata aac aaa tcg 211
Ala Gly Asn Lys Arg Asn Leu Pro Asn Arg Lys Lys Ile Asn Lys Ser
25 30 35

gtg gga gtt tac gct ggt gtg ttt gcc cta aca ttg gct tta tac gcc 259
Val Gly Val Tyr Ala Gly Val Phe Ala Leu Thr Leu Ala Leu Tyr Ala
40 45 50

att ggg gga gcc gca tgg gga ctg ctc cga ccc act tat acc gct tat 307
Ile Gly Gly Ala Ala Trp Gly Leu Leu Arg Pro Thr Tyr Thr Ala Tyr
55 60 65

gtt gaa gac gct gaa aca gcc tcc ata gcg gtg gaa acc aac act tct 355
Val Glu Asp Ala Glu Thr Ala Ser Ile Ala Val Glu Thr Asn Thr Ser
70 75 80 85

ttt gcc ggc tat gcc tgg ttt gcg atc gcc acc ggt gtg ctt gca gca 403
Phe Ala Gly Tyr Ala Trp Phe Ala Ile Ala Thr Gly Val Leu Ala Ala
90 95 100

gca atc gca tta ttc gtt ttc ctg cgc acc cct caa cat cga ggc cca 451
Ala Ile Ala Leu Phe Val Phe Leu Arg Thr Pro Gln His Arg Gly Pro
105 110 115

gtt atg ctc cta tgg ctg gga att gta tct atc gca ggt tcc gtg gca 499
Val Met Leu Leu Trp Leu Gly Ile Val Ser Ile Ala Gly Ser Val Ala
120 125 130

ttc ctg gtg ttt gga aac gtg gcc tcg acg atg ctt cat ggt tca cca 547
Phe Leu Val Phe Gly Asn Val Ala Ser Thr Met Leu His Gly Ser Pro
135 140 145

tct gat tac gcc tca gcg atc ggt gcg tct ttc cag gta gca ccc act 595
Ser Asp Tyr Ala Ser Ala Ile Gly Ala Ser Phe Gln Val Ala Pro Thr

```
150                 155                 160                 165

att acc cct ggt gtt gcg ttt ggg gtc gct cca ttt ttg agt gtg tgc   643
Ile Thr Pro Gly Val Ala Phe Gly Val Ala Pro Phe Leu Ser Val Cys
                170                 175                 180

atg tat tgg tgc gcg gca ttt gtg aca cct gaa gaa gag ata gac cag   691
Met Tyr Trp Cys Ala Ala Phe Val Thr Pro Glu Glu Glu Ile Asp Gln
            185                 190                 195

gac gac gca ggc cag ggg act tcg aaa gca tcg ggg tct gag atg act   739
Asp Asp Ala Gly Gln Gly Thr Ser Lys Ala Ser Gly Ser Glu Met Thr
        200                 205                 210

ggg gct agt ggc taggggctag atgtgcgcaa aca                        774
Gly Ala Ser Gly
    215
```

<210> 2086
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 2086

```
Met Thr Tyr Pro Gly Ile Thr Ser Asp His Asn Pro Tyr Asp Gly Tyr
  1               5                  10                  15

Thr Gly Asp Asp Gly Ala Gly Asn Lys Arg Asn Leu Pro Asn Arg Lys
            20                  25                  30

Lys Ile Asn Lys Ser Val Gly Val Tyr Ala Gly Val Phe Ala Leu Thr
        35                  40                  45

Leu Ala Leu Tyr Ala Ile Gly Gly Ala Ala Trp Gly Leu Leu Arg Pro
    50                  55                  60

Thr Tyr Thr Ala Tyr Val Glu Asp Ala Glu Thr Ala Ser Ile Ala Val
65                  70                  75                  80

Glu Thr Asn Thr Ser Phe Ala Gly Tyr Ala Trp Phe Ala Ile Ala Thr
                85                  90                  95

Gly Val Leu Ala Ala Ala Ile Ala Leu Phe Val Phe Leu Arg Thr Pro
            100                 105                 110

Gln His Arg Gly Pro Val Met Leu Leu Trp Leu Gly Ile Val Ser Ile
        115                 120                 125

Ala Gly Ser Val Ala Phe Leu Val Phe Gly Asn Val Ala Ser Thr Met
    130                 135                 140

Leu His Gly Ser Pro Ser Asp Tyr Ala Ser Ala Ile Gly Ala Ser Phe
145                 150                 155                 160

Gln Val Ala Pro Thr Ile Thr Pro Gly Val Ala Phe Gly Val Ala Pro
                165                 170                 175

Phe Leu Ser Val Cys Met Tyr Trp Cys Ala Ala Phe Val Thr Pro Glu
            180                 185                 190
```

```
Glu Glu Ile Asp Gln Asp Asp Ala Gly Gln Gly Thr Ser Lys Ala Ser
        195                 200                 205

Gly Ser Glu Met Thr Gly Ala Ser Gly
    210                 215
```

<210> 2087
<211> 765
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(742)
<223> RXA01109

<400> 2087

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gggtcgtcag ctagattgct ttgctagggt aatctgcgtg aaccgtccgg gaatttttaa 60

gttttccgga gcatgtcgat gatttatcag gagcagaact ttg tct att agc ctt   115
                                              Leu Ser Ile Ser Leu
                                                1               5

tcc tca aag aag gtt gct ttc gca gca ctc atg gtc acc cca ctt ctc   163
Ser Ser Lys Lys Val Ala Phe Ala Ala Leu Met Val Thr Pro Leu Leu
                  10                  15                  20

ttg acc gca tgt ggc agt gat tca tct gat act gaa gca gcc tca tcc   211
Leu Thr Ala Cys Gly Ser Asp Ser Ser Asp Thr Glu Ala Ala Ser Ser
              25                  30                  35

agc gca gcg acg acg aca aat tct tcc tca tcc agc gca gcg acc tcg   259
Ser Ala Ala Thr Thr Thr Asn Ser Ser Ser Ser Ser Ala Ala Thr Ser
          40                  45                  50

gcg gaa gca gca gaa acc acc tcg tcc gaa tct gaa tct tcc gaa gca   307
Ala Glu Ala Ala Glu Thr Thr Ser Ser Glu Ser Glu Ser Ser Glu Ala
      55                  60                  65

aca acc att aac gaa gag cag caa gca cag ctt gat gta ctg tct caa   355
Thr Thr Ile Asn Glu Glu Gln Gln Ala Gln Leu Asp Val Leu Ser Gln
  70                  75                  80                  85

gag ctg tct gag aac cca att acc ttc gct gaa gct gcg cca gtt gaa   403
Glu Leu Ser Glu Asn Pro Ile Thr Phe Ala Glu Ala Ala Pro Val Glu
                  90                  95                 100

aac ggc gag acc gct tcc cca gaa gac aca gct gcc atc gag gct ctg   451
Asn Gly Glu Thr Ala Ser Pro Glu Asp Thr Ala Ala Ile Glu Ala Leu
             105                 110                 115

gtt cgc gga tac act gac acc aac acc ttg cgt agc tcc ctt gcg tac   499
Val Arg Gly Tyr Thr Asp Thr Asn Thr Leu Arg Ser Ser Leu Ala Tyr
         120                 125                 130

acc atc aac aac acc tgc acc cgc gtt ctt gaa gcc agc ggc gct gac   547
Thr Ile Asn Asn Thr Cys Thr Arg Val Leu Glu Ala Ser Gly Ala Asp
    135                 140                 145

gct acc cag ctt gat ctc aac acc atc cct gat atc cca ctg ggt ggc   595
```

```
Ala Thr Gln Leu Asp Leu Asn Thr Ile Pro Asp Ile Pro Leu Gly Gly
150                 155                 160                 165

gaa ggc acc gga act gtt gat tcc atc acc gat gtt gtg gtc aac ggc   643
Glu Gly Thr Gly Thr Val Asp Ser Ile Thr Asp Val Val Val Asn Gly
                170                 175                 180

cag gaa gca tcc gca tgg gtc gta gca acc gcc ggt gga acc acc gac   691
Gln Glu Ala Ser Ala Trp Val Val Ala Thr Ala Gly Gly Thr Thr Asp
            185                 190                 195

tct gca acc cag cgc ttc ttc aac gaa ggt ggc cag tgg aag ttc tgc   739
Ser Ala Thr Gln Arg Phe Phe Asn Glu Gly Gly Gln Trp Lys Phe Cys
        200                 205                 210

gac taatccacag agcttaaaac tcc                                    765
Asp
```

<210> 2088
<211> 214
<212> PRT
<213> Corynebacterium glutamicum

<400> 2088

```
Leu Ser Ile Ser Leu Ser Ser Lys Lys Val Ala Phe Ala Ala Leu Met
  1               5                  10                  15

Val Thr Pro Leu Leu Leu Thr Ala Cys Gly Ser Asp Ser Ser Asp Thr
             20                  25                  30

Glu Ala Ala Ser Ser Ser Ala Ala Thr Thr Thr Asn Ser Ser Ser Ser
         35                  40                  45

Ser Ala Ala Thr Ser Ala Glu Ala Ala Glu Thr Thr Ser Ser Glu Ser
     50                  55                  60

Glu Ser Ser Glu Ala Thr Thr Ile Asn Glu Glu Gln Gln Ala Gln Leu
 65                  70                  75                  80

Asp Val Leu Ser Gln Glu Leu Ser Glu Asn Pro Ile Thr Phe Ala Glu
                 85                  90                  95

Ala Ala Pro Val Glu Asn Gly Glu Thr Ala Ser Pro Glu Asp Thr Ala
            100                 105                 110

Ala Ile Glu Ala Leu Val Arg Gly Tyr Thr Asp Thr Asn Thr Leu Arg
        115                 120                 125

Ser Ser Leu Ala Tyr Thr Ile Asn Asn Thr Cys Thr Arg Val Leu Glu
    130                 135                 140

Ala Ser Gly Ala Asp Ala Thr Gln Leu Asp Leu Asn Thr Ile Pro Asp
145                 150                 155                 160

Ile Pro Leu Gly Gly Glu Gly Thr Gly Thr Val Asp Ser Ile Thr Asp
                165                 170                 175

Val Val Val Asn Gly Gln Glu Ala Ser Ala Trp Val Val Ala Thr Ala
            180                 185                 190
```

```
Gly Gly Thr Thr Asp Ser Ala Thr Gln Arg Phe Phe Asn Glu Gly Gly
        195                 200                 205

Gln Trp Lys Phe Cys Asp
    210
```

<210> 2089
<211> 1053
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1030)
<223> RXA01119

<400> 2089

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ccgtaaagac gttggcgaag tcatcatcaa cggtgccgtt gcccgtggcg aagccgaacc 60

agagatgttg gaagctgtcg cagaagaaaa gaccgcgtag ttg gca gga gtt atc   115
                                          Leu Ala Gly Val Ile
                                            1               5

acc ggc ttt gcc atc atc ctg tcg gtt atc ggc gtt gga ttt ctt ctg   163
Thr Gly Phe Ala Ile Ile Leu Ser Val Ile Gly Val Gly Phe Leu Leu
                  10                  15                  20

gca aag ctg ggg gtc atc aat gat gac aaa cag cgc ttg gtg tta aac   211
Ala Lys Leu Gly Val Ile Asn Asp Asp Lys Gln Arg Leu Val Leu Asn
              25                  30                  35

cgc att gct ttt tat gcg gca act cca gcg ctg ctt ttc aat gtc gtt   259
Arg Ile Ala Phe Tyr Ala Ala Thr Pro Ala Leu Leu Phe Asn Val Val
          40                  45                  50

gcc cga tca gat ccc agc gcg ttg atc tca ccg gtc att gtg gtg aca   307
Ala Arg Ser Asp Pro Ser Ala Leu Ile Ser Pro Val Ile Val Val Thr
      55                  60                  65

ttt gtg gcc acg atc gtc aca gca gct gtg tac tgc gtg att tcg gcg   355
Phe Val Ala Thr Ile Val Thr Ala Ala Val Tyr Cys Val Ile Ser Ala
  70                  75                  80                  85

att ttc ttt aag aag gat atc gcc act acg gcg aca gga gct gcg gct   403
Ile Phe Phe Lys Lys Asp Ile Ala Thr Thr Ala Thr Gly Ala Ala Ala
                  90                  95                 100

tct gcc tac gtg aac tcc aac aac att ggc ctg ccg gtg tct att tat   451
Ser Ala Tyr Val Asn Ser Asn Asn Ile Gly Leu Pro Val Ser Ile Tyr
              105                 110                 115

gtg ctg gga aca ggc gca tat gtg gca ccg att ctg gtc atg cag atg   499
Val Leu Gly Thr Gly Ala Tyr Val Ala Pro Ile Leu Val Met Gln Met
          120                 125                 130

gtg att ttc gcg ccc atg atc ctg gcc gcg ctg acc tct ggt gat gtg   547
Val Ile Phe Ala Pro Met Ile Leu Ala Ala Leu Thr Ser Gly Asp Val
      135                 140                 145
```

```
aaa ggc tcg cgc ggg caa aaa ata tgg gct gcg gtg aaa ggt tca ctg   595
Lys Gly Ser Arg Gly Gln Lys Ile Trp Ala Ala Val Lys Gly Ser Leu
150                 155                 160                 165

ctc agc cca att gtg ttg gcc tct atc gcg ggc ctg atc gtg tgt ctg   643
Leu Ser Pro Ile Val Leu Ala Ser Ile Ala Gly Leu Ile Val Cys Leu
                170                 175                 180

tta gaa att cag ctg cca gcc gca gtc atg gaa ccc acc atc att ttg   691
Leu Glu Ile Gln Leu Pro Ala Ala Val Met Glu Pro Thr Ile Ile Leu
            185                 190                 195

ggc ggc gca tcc att ccg ttg att ctg atg agc ttc ggc gca tca ttg   739
Gly Gly Ala Ser Ile Pro Leu Ile Leu Met Ser Phe Gly Ala Ser Leu
        200                 205                 210

ccc tca acc aac gtg ctg gct tcc aag gcg gat cgc ccc agc gtt ctt   787
Pro Ser Thr Asn Val Leu Ala Ser Lys Ala Asp Arg Pro Ser Val Leu
    215                 220                 225

act gct act gcg ata aaa att gtg ggt atg ccc gcc atc act tgg ctg   835
Thr Ala Thr Ala Ile Lys Ile Val Gly Met Pro Ala Ile Thr Trp Leu
230                 235                 240                 245

atc gcc aag gcg ttt ggt ctg gag ggc gat tac ctc tac gcc gct gtt   883
Ile Ala Lys Ala Phe Gly Leu Glu Gly Asp Tyr Leu Tyr Ala Ala Val
                250                 255                 260

att ttg gcg gcg ctg ccc gcc gcg cag aat gtg tac aac tac gcg gcg   931
Ile Leu Ala Ala Leu Pro Ala Ala Gln Asn Val Tyr Asn Tyr Ala Ala
            265                 270                 275

acg tac cgc aag ggc gag atc gtc gcc cgc gat acg gtc ttc ctc acc   979
Thr Tyr Arg Lys Gly Glu Ile Val Ala Arg Asp Thr Val Phe Leu Thr
        280                 285                 290

acg ttc cta gcg ctg ctg ggc atg cta gga atc gcg gcc cta ttt ggt   1027
Thr Phe Leu Ala Leu Leu Gly Met Leu Gly Ile Ala Ala Leu Phe Gly
    295                 300                 305

cgc tagggcttca ggctgctttt cga                                    1053
Arg
310
```

US 2006/0160179 A1 Jul. 20, 2006

<2210> 2090
<211> 310
<212> PRT
<213> Corynebacterium glutamicum

<400> 2090

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Leu Ala Gly Val Ile Thr Gly Phe Ala Ile Ile Leu Ser Val Ile Gly
  1               5                  10                  15

Val Gly Phe Leu Leu Ala Lys Leu Gly Val Ile Asn Asp Asp Lys Gln
             20                  25                  30

Arg Leu Val Leu Asn Arg Ile Ala Phe Tyr Ala Ala Thr Pro Ala Leu
         35                  40                  45

Leu Phe Asn Val Val Ala Arg Ser Asp Pro Ser Ala Leu Ile Ser Pro
```

```
     50                  55                  60

Val Ile Val Val Thr Phe Val Ala Thr Ile Val Thr Ala Ala Val Tyr
 65                  70                  75                  80

Cys Val Ile Ser Ala Ile Phe Phe Lys Lys Asp Ile Ala Thr Thr Ala
                 85                  90                  95

Thr Gly Ala Ala Ala Ser Ala Tyr Val Asn Ser Asn Asn Ile Gly Leu
            100                 105                 110

Pro Val Ser Ile Tyr Val Leu Gly Thr Gly Ala Tyr Val Ala Pro Ile
        115                 120                 125

Leu Val Met Gln Met Val Ile Phe Ala Pro Met Ile Leu Ala Ala Leu
    130                 135                 140

Thr Ser Gly Asp Val Lys Gly Ser Arg Gly Gln Lys Ile Trp Ala Ala
145                 150                 155                 160

Val Lys Gly Ser Leu Leu Ser Pro Ile Val Leu Ala Ser Ile Ala Gly
                165                 170                 175

Leu Ile Val Cys Leu Leu Glu Ile Gln Leu Pro Ala Ala Val Met Glu
            180                 185                 190

Pro Thr Ile Ile Leu Gly Gly Ala Ser Ile Pro Leu Ile Leu Met Ser
        195                 200                 205

Phe Gly Ala Ser Leu Pro Ser Thr Asn Val Leu Ala Ser Lys Ala Asp
    210                 215                 220

Arg Pro Ser Val Leu Thr Ala Thr Ala Ile Lys Ile Val Gly Met Pro
225                 230                 235                 240

Ala Ile Thr Trp Leu Ile Ala Lys Ala Phe Gly Leu Glu Gly Asp Tyr
                245                 250                 255

Leu Tyr Ala Ala Val Ile Leu Ala Ala Leu Pro Ala Ala Gln Asn Val
            260                 265                 270

Tyr Asn Tyr Ala Ala Thr Tyr Arg Lys Gly Glu Ile Val Ala Arg Asp
        275                 280                 285

Thr Val Phe Leu Thr Thr Phe Leu Ala Leu Leu Gly Met Leu Gly Ile
    290                 295                 300

Ala Ala Leu Phe Gly Arg
305                 310


<210> 2091
<211> 645
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(622)
<223> RXA01122
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<400> 2091
tattcgacca aggctgagca aaaaggcgct aagctgtggg gagatcgcaa gcccctatcc 60

ggcctctact aagccccgaa gttgaaggga aactccccca atg ccg ttt cca gca 115
Met Pro Phe Pro Ala
1 5

ctg ttg ttg ccg ctg att ttc tgg aca gga att gca gct ttg tcc tct 163
Leu Leu Leu Pro Leu Ile Phe Trp Thr Gly Ile Ala Ala Leu Ser Ser
10 15 20

tgg gcg gtc agc cgt gca ctt ccg ctg cgc gcc gat aat tcc att gag 211
Trp Ala Val Ser Arg Ala Leu Pro Leu Arg Ala Asp Asn Ser Ile Glu
25 30 35

att gat gcg ccg gtg gaa aag gtc tgg gat ttc atc gag gag acc aac 259
Ile Asp Ala Pro Val Glu Lys Val Trp Asp Phe Ile Glu Glu Thr Asn
40 45 50

cgc gtg ccg gag tgg aat gag cac att ctg tac gtg cag gcg cct ggt 307
Arg Val Pro Glu Trp Asn Glu His Ile Leu Tyr Val Gln Ala Pro Gly
55 60 65

gag atc gag cag ggc atg aag ctc aag atg aaa aca agg cac cca gag 355
Glu Ile Glu Gln Gly Met Lys Leu Lys Met Lys Thr Arg His Pro Glu
70 75 80 85

acc aat cgc ctc act ttg aag ttt cgc ccc acc atc gac gtg ctg cgt 403
Thr Asn Arg Leu Thr Leu Lys Phe Arg Pro Thr Ile Asp Val Leu Arg
90 95 100

cca cac cgt gaa ttg acg tgg tcc acc aaa att gtt gcg cgt tgg ctg 451
Pro His Arg Glu Leu Thr Trp Ser Thr Lys Ile Val Ala Arg Trp Leu
105 110 115

ctc acc gtc acc gac acg atc gag ctg aag cct ttg gaa gat ggt cgc 499
Leu Thr Val Thr Asp Thr Ile Glu Leu Lys Pro Leu Glu Asp Gly Arg
120 125 130

act gag gtg gat caa tca atg tcc ttt agt ggc gta cta tcc ccc gga 547
Thr Glu Val Asp Gln Ser Met Ser Phe Ser Gly Val Leu Ser Pro Gly
135 140 145

gtg ccc ttt ttg gcc agc atc agc agg atc aaa gag aac tca aac cgc 595
Val Pro Phe Leu Ala Ser Ile Ser Arg Ile Lys Glu Asn Ser Asn Arg
150 155 160 165

cag ttg aaa gca ctg atc gaa gcc gag taaacctcca acccctacat 642
Gln Leu Lys Ala Leu Ile Glu Ala Glu
170

aac 645

<210> 2092
<211> 174
<212> PRT
<213> Corynebacterium glutamicum

<400> 2092
Met Pro Phe Pro Ala Leu Leu Leu Pro Leu Ile Phe Trp Thr Gly Ile

```
  1               5                  10                  15

Ala Ala Leu Ser Ser Trp Ala Val Ser Arg Ala Leu Pro Leu Arg Ala
            20                  25                  30

Asp Asn Ser Ile Glu Ile Asp Ala Pro Val Glu Lys Val Trp Asp Phe
        35                  40                  45

Ile Glu Glu Thr Asn Arg Val Pro Glu Trp Asn Glu His Ile Leu Tyr
    50                  55                  60

Val Gln Ala Pro Gly Glu Ile Glu Gln Gly Met Lys Leu Lys Met Lys
65                  70                  75                  80

Thr Arg His Pro Glu Thr Asn Arg Leu Thr Leu Lys Phe Arg Pro Thr
                85                  90                  95

Ile Asp Val Leu Arg Pro His Arg Glu Leu Thr Trp Ser Thr Lys Ile
            100                 105                 110

Val Ala Arg Trp Leu Leu Thr Val Thr Asp Thr Ile Glu Leu Lys Pro
        115                 120                 125

Leu Glu Asp Gly Arg Thr Glu Val Asp Gln Ser Met Ser Phe Ser Gly
    130                 135                 140

Val Leu Ser Pro Gly Val Pro Phe Leu Ala Ser Ile Ser Arg Ile Lys
145                 150                 155                 160

Glu Asn Ser Asn Arg Gln Leu Lys Ala Leu Ile Glu Ala Glu
                165                 170
```

CS2005050009A1

<210> 2093
<211> 570
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(547)
<223> RXA01123

<400> 2093

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aaagagcagt gatttttccc gatccccccc tggccgccta gcggaaatta ttgataccgc 60

gtggcggttg gtggaaacac gtggctgggc gaatgtgagc atg cga acc ctg gcc   115
                                        Met Arg Thr Leu Ala
                                          1               5

gcg gag cta aat atc aag gcg ccg tcg ctg tac aag cat gta aaa acg   163
Ala Glu Leu Asn Ile Lys Ala Pro Ser Leu Tyr Lys His Val Lys Thr
                  10                  15                  20

cgc gag gat atc gcc gca cac atc gcc acg aag gca ttt att cag ctg   211
Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys Ala Phe Ile Gln Leu
              25                  30                  35

ggg caa agc ctg cat gaa cat tgt gaa agt gtg gag gat ttg ctt gcg   259
Gly Gln Ser Leu His Glu His Cys Glu Ser Val Glu Asp Leu Leu Ala
          40                  45                  50
```

```
gaa tac cgc tcc atg gct cgg gaa aat cca aat att tac cgg ctt ctc   307
Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn Ile Tyr Arg Leu Leu
     55                  60                  65

acc agt tca gag ttc ccc cgc gag cta ctt cca gaa ggc cta gaa act   355
Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro Glu Gly Leu Glu Thr
 70                  75                  80                  85

tgg gca gga acg cca ttc tac ctg gtc acc ggc cac gat ccg atc aag   403
Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly His Asp Pro Ile Lys
                 90                  95                 100

ggt caa gca ctg tgg gca ttc gcg cac ggc atg gcc atc ctg gaa atc   451
Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met Ala Ile Leu Glu Ile
            105                 110                 115

gac gcc cga ttc gcc ggc ccc aac aat gga tcc ccc gcg gat ggc gtg   499
Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser Pro Ala Asp Gly Val
        120                 125                 130

tgg gag atc ggc gcg cgg gca ttt gac aca caa gta ttc gac caa ggc   547
Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln Val Phe Asp Gln Gly
    135                 140                 145

tgagcaaaaa ggcgctaagc tgt                                        570


<210> 2094
<211> 149
<212> PRT
<213> Corynebacterium glutamicum

<400> 2094
Met Arg Thr Leu Ala Ala Glu Leu Asn Ile Lys Ala Pro Ser Leu Tyr
  1               5                  10                  15

Lys His Val Lys Thr Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys
             20                  25                  30

Ala Phe Ile Gln Leu Gly Gln Ser Leu His Glu His Cys Glu Ser Val
         35                  40                  45

Glu Asp Leu Leu Ala Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn
     50                  55                  60

Ile Tyr Arg Leu Leu Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro
 65                  70                  75                  80

Glu Gly Leu Glu Thr Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly
                 85                  90                  95

His Asp Pro Ile Lys Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met
            100                 105                 110

Ala Ile Leu Glu Ile Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser
        115                 120                 125

Pro Ala Asp Gly Val Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln
    130                 135                 140
```

Val Phe Asp Gln Gly
145

<210> 2095
<211> 302
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(279)
<223> RXA01127

<400> 2095

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gga att ggc ctc gca gca tcc ggc aac atc gat gcc acg ggc acc aac   48
Gly Ile Gly Leu Ala Ala Ser Gly Asn Ile Asp Ala Thr Gly Thr Asn
  1               5                  10                  15

cct tcc atg ttc gag cca gtc cac ggc tct gca cca gat atc gca ggc   96
Pro Ser Met Phe Glu Pro Val His Gly Ser Ala Pro Asp Ile Ala Gly
             20                  25                  30

cag gga atc gca gac cca acg gca gca atc cta tcc gct gcg atg ctg   144
Gln Gly Ile Ala Asp Pro Thr Ala Ala Ile Leu Ser Ala Ala Met Leu
         35                  40                  45

ctg cgt cac tta ggt gat gaa gac aac gca gta cgt att gaa aca gcc   192
Leu Arg His Leu Gly Asp Glu Asp Asn Ala Val Arg Ile Glu Thr Ala
     50                  55                  60

atc gca gct gat gtg gct ggc cga gat aac tct cag ccg att tct acc   240
Ile Ala Ala Asp Val Ala Gly Arg Asp Asn Ser Gln Pro Ile Ser Thr
 65                  70                  75                  80

act gag gtg gga gac cgc atc gtc aag gcg ctg caa agc taaatttcaa    289
Thr Glu Val Gly Asp Arg Ile Val Lys Ala Leu Gln Ser
                 85                  90

cgccgacccc ctt                                                   302
```

<210> 2096
<211> 93
<212> PRT
<213> Corynebacterium glutamicum

<400> 2096

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Gly Ile Gly Leu Ala Ala Ser Gly Asn Ile Asp Ala Thr Gly Thr Asn
  1               5                  10                  15

Pro Ser Met Phe Glu Pro Val His Gly Ser Ala Pro Asp Ile Ala Gly
             20                  25                  30

Gln Gly Ile Ala Asp Pro Thr Ala Ala Ile Leu Ser Ala Ala Met Leu
         35                  40                  45

Leu Arg His Leu Gly Asp Glu Asp Asn Ala Val Arg Ile Glu Thr Ala
     50                  55                  60

Ile Ala Ala Asp Val Ala Gly Arg Asp Asn Ser Gln Pro Ile Ser Thr
```

```
 65                  70                  75                  80

Thr Glu Val Gly Asp Arg Ile Val Lys Ala Leu Gln Ser
                 85                  90


<210> 2097
<211> 1989
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1966)
<223> RXA01129

<400> 2097
caatataacg cactttaaca tatttccccc catctttttg ttctcaaatt tatttgtact 60

cgaatgcagg atttcgagac aatgaggcag tttttctttt atg gtt aat ctc atg   115
                                            Met Val Asn Leu Met
                                              1               5

tcg gtc gaa ctc gaa gaa atc cgc gat ttc tta gca gga ttt gaa cct   163
Ser Val Glu Leu Glu Glu Ile Arg Asp Phe Leu Ala Gly Phe Glu Pro
                 10                  15                  20

ttc gcg cag cta cca gcc gag gaa cta gat cag tta cct gga aaa atg   211
Phe Ala Gln Leu Pro Ala Glu Glu Leu Asp Gln Leu Pro Gly Lys Met
             25                  30                  35

agc ttg cgc tat ttt cgg cgt ggg gaa gag atc atc cca att ggt gtg   259
Ser Leu Arg Tyr Phe Arg Arg Gly Glu Glu Ile Ile Pro Ile Gly Val
         40                  45                  50

ccc aat cat tac atg ggg gta atc aga tcg ggt gcc att gat gtt ctt   307
Pro Asn His Tyr Met Gly Val Ile Arg Ser Gly Ala Ile Asp Val Leu
     55                  60                  65

gat cag gag ggc gta ctg ctg gat cgc cgt gac gcg ggg cgc tcg ttt   355
Asp Gln Glu Gly Val Leu Leu Asp Arg Arg Asp Ala Gly Arg Ser Phe
 70                  75                  80                  85

ggc tat tcc acg atg ggg cca gaa cga aat tct cgg tac cgt atg gtt   403
Gly Tyr Ser Thr Met Gly Pro Glu Arg Asn Ser Arg Tyr Arg Met Val
                 90                  95                 100

gcc gtg gaa gat tcc ttg gtg ttg cgt ctg ggg cgt gat gat ttt gat   451
Ala Val Glu Asp Ser Leu Val Leu Arg Leu Gly Arg Asp Asp Phe Asp
             105                 110                 115

gag tta gcc aag cgc aac cct gat ctg aac cgt tac tac tcc agc tgg   499
Glu Leu Ala Lys Arg Asn Pro Asp Leu Asn Arg Tyr Tyr Ser Ser Trp
         120                 125                 130

tcg aag cgt atc cgc gcc gct gct gat caa ttg cgc caa gaa tct agt   547
Ser Lys Arg Ile Arg Ala Ala Ala Asp Gln Leu Arg Gln Glu Ser Ser
     135                 140                 145

tcg aag gtg ctg cgc acg aag ttg ggg gag ttc aag atc gcc aac ccg   595
Ser Lys Val Leu Arg Thr Lys Leu Gly Glu Phe Lys Ile Ala Asn Pro
```

```
150                 155                 160                 165

att tcc tgc agc ccg gac acc acg atc atg gat gct gcc atc aag atg   643
Ile Ser Cys Ser Pro Asp Thr Thr Ile Met Asp Ala Ala Ile Lys Met
                170                 175                 180

cat gag ttc ggg gtg tct tcg ttg ctg gtg cag atc gat ggg gaa ctc   691
His Glu Phe Gly Val Ser Ser Leu Leu Val Gln Ile Asp Gly Glu Leu
            185                 190                 195

aaa ggc atc atc acc gat cac tat atg cgc agc agg gtg gtg gcg aag   739
Lys Gly Ile Ile Thr Asp His Tyr Met Arg Ser Arg Val Val Ala Lys
        200                 205                 210

cat ttg gat att cag ctg ccg gtc tct gag gtc atg acg gtg gat ccg   787
His Leu Asp Ile Gln Leu Pro Val Ser Glu Val Met Thr Val Asp Pro
    215                 220                 225

cgt tgc gcg acc tcg cag ggg ttg gct ttt gag gcc atg ttg ttg atg   835
Arg Cys Ala Thr Ser Gln Gly Leu Ala Phe Glu Ala Met Leu Leu Met
230                 235                 240                 245

tcg gag ctg cgc att cac cac ttg ccg att gtg gat gat ggc caa atc   883
Ser Glu Leu Arg Ile His His Leu Pro Ile Val Asp Asp Gly Gln Ile
                250                 255                 260

tcc ggc atc gtc act gca gct gac atc atg cgc ttg ctg cgc cac gat   931
Ser Gly Ile Val Thr Ala Ala Asp Ile Met Arg Leu Leu Arg His Asp
            265                 270                 275

ccg att tac ctc act gcg gat ctg tcg cga aaa aat acc gtg gag gaa   979
Pro Ile Tyr Leu Thr Ala Asp Leu Ser Arg Lys Asn Thr Val Glu Glu
        280                 285                 290

ttg gcc aac acc ttc cag tcg gca gcg gag gtg gct tcg aga ttt att   1027
Leu Ala Asn Thr Phe Gln Ser Ala Ala Glu Val Ala Ser Arg Phe Ile
    295                 300                 305

gat cgg gga gct tct gcg gaa gaa gtc agt agc ttg ctc acc gtg gct   1075
Asp Arg Gly Ala Ser Ala Glu Glu Val Ser Ser Leu Leu Thr Val Ala
310                 315                 320                 325

gcg gat tct ttg gca aga agg ctc ctt gtg ctg gcg gag cgg aaa ttt   1123
Ala Asp Ser Leu Ala Arg Arg Leu Leu Val Leu Ala Glu Arg Lys Phe
                330                 335                 340

ggt gca ccg cca gtt ccg tat tgc ttt gtg gtg gtg ggc tcg cag ggc   1171
Gly Ala Pro Pro Val Pro Tyr Cys Phe Val Val Val Gly Ser Gln Gly
            345                 350                 355

agg aaa gaa atg gga ctg gcc tct gat caa gac aat gcc ctt gtt ctg   1219
Arg Lys Glu Met Gly Leu Ala Ser Asp Gln Asp Asn Ala Leu Val Leu
        360                 365                 370

gac aat tcc tac aat gac cgc gag cat gga cag tat ttt gca gcg ctg   1267
Asp Asn Ser Tyr Asn Asp Arg Glu His Gly Gln Tyr Phe Ala Ala Leu
    375                 380                 385

agt gaa ttc gtg tgc cag ggc ctc gac cgc gca gga cag gtg ctg tgt   1315
Ser Glu Phe Val Cys Gln Gly Leu Asp Arg Ala Gly Gln Val Leu Cys
390                 395                 400                 405
```

```
ccg ggt gac atg atg gca tcc aat ccg gag tgg cgg aaa act gct gac   1363
Pro Gly Asp Met Met Ala Ser Asn Pro Glu Trp Arg Lys Thr Ala Asp
                410                 415                 420

cag tgg atc tcc acc ttc cat tcc tgg att act gcg ccg gag ccg gat   1411
Gln Trp Ile Ser Thr Phe His Ser Trp Ile Thr Ala Pro Glu Pro Asp
            425                 430                 435

gcg ttg ctg cat gcc cag aca ttc ttt gat ttc agg gga att tac ggc   1459
Ala Leu Leu His Ala Gln Thr Phe Phe Asp Phe Arg Gly Ile Tyr Gly
        440                 445                 450

gac acc gag atg gct aag gat gtc cac caa aat gcg gtg aat atg gcc   1507
Asp Thr Glu Met Ala Lys Asp Val His Gln Asn Ala Val Asn Met Ala
    455                 460                 465

agg ggt gcg cgt cgc atg cat gca cac ttg gct agt ctt gcg gcc cgg   1555
Arg Gly Ala Arg Arg Met His Ala His Leu Ala Ser Leu Ala Ala Arg
470                 475                 480                 485

cgc gat cct ccg ctg ggg ttt ttc cgt ggt ctt gtg gtg gag cgt tct   1603
Arg Asp Pro Pro Leu Gly Phe Phe Arg Gly Leu Val Val Glu Arg Ser
                490                 495                 500

ggt gaa tac ggc gcg acg atg gat att aag aag ggt ggc acc gcg ggc   1651
Gly Glu Tyr Gly Ala Thr Met Asp Ile Lys Lys Gly Gly Thr Ala Gly
            505                 510                 515

atc gtg cag atg gcg agg ctg tat gcg ctg gcc acg ggt agt gat gcg   1699
Ile Val Gln Met Ala Arg Leu Tyr Ala Leu Ala Thr Gly Ser Asp Ala
        520                 525                 530

att ggg act cgg gag cgg ttg att gct gcg tcg ggc cat ggt cag gtg   1747
Ile Gly Thr Arg Glu Arg Leu Ile Ala Ala Ser Gly His Gly Gln Val
    535                 540                 545

tcg cgt aag ggt gcg cag gat ttg ttg gat gcc ttt gat ttc tta gcg   1795
Ser Arg Lys Gly Ala Gln Asp Leu Leu Asp Ala Phe Asp Phe Leu Ala
550                 555                 560                 565

gcg atg gcg ttc cag cac cag gcg cgg ttg atc aag gtg ggg gag aag   1843
Ala Met Ala Phe Gln His Gln Ala Arg Leu Ile Lys Val Gly Glu Lys
                570                 575                 580

ccg aac tat cac att gat ccc aag acg ttg ggc aag atg gat cgg gag   1891
Pro Asn Tyr His Ile Asp Pro Lys Thr Leu Gly Lys Met Asp Arg Glu
            585                 590                 595

cat ttg cgc gat gca ttt tcc att att aaa gat atg cag tcg gcg tta   1939
His Leu Arg Asp Ala Phe Ser Ile Ile Lys Asp Met Gln Ser Ala Leu
        600                 605                 610

gct act aaa tat ccg gtg agg aac atc tagtgttggg gcgtcgaaaa         1986
Ala Thr Lys Tyr Pro Val Arg Asn Ile
    615                 620

gcg                                                              1989
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<210> 2098

<211> 622
<212> PRT
<213> Corynebacterium glutamicum

<400> 2098

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Met Val Asn Leu Met Ser Val Glu Leu Glu Glu Ile Arg Asp Phe Leu
  1               5                  10                  15

Ala Gly Phe Glu Pro Phe Ala Gln Leu Pro Ala Glu Glu Leu Asp Gln
             20                  25                  30

Leu Pro Gly Lys Met Ser Leu Arg Tyr Phe Arg Arg Gly Glu Glu Ile
         35                  40                  45

Ile Pro Ile Gly Val Pro Asn His Tyr Met Gly Val Ile Arg Ser Gly
     50                  55                  60

Ala Ile Asp Val Leu Asp Gln Glu Gly Val Leu Leu Asp Arg Arg Asp
 65                  70                  75                  80

Ala Gly Arg Ser Phe Gly Tyr Ser Thr Met Gly Pro Glu Arg Asn Ser
                 85                  90                  95

Arg Tyr Arg Met Val Ala Val Glu Asp Ser Leu Val Leu Arg Leu Gly
            100                 105                 110

Arg Asp Asp Phe Asp Glu Leu Ala Lys Arg Asn Pro Asp Leu Asn Arg
        115                 120                 125

Tyr Tyr Ser Ser Trp Ser Lys Arg Ile Arg Ala Ala Ala Asp Gln Leu
    130                 135                 140

Arg Gln Glu Ser Ser Ser Lys Val Leu Arg Thr Lys Leu Gly Glu Phe
145                 150                 155                 160

Lys Ile Ala Asn Pro Ile Ser Cys Ser Pro Asp Thr Thr Ile Met Asp
                165                 170                 175

Ala Ala Ile Lys Met His Glu Phe Gly Val Ser Ser Leu Leu Val Gln
            180                 185                 190

Ile Asp Gly Glu Leu Lys Gly Ile Ile Thr Asp His Tyr Met Arg Ser
        195                 200                 205

Arg Val Val Ala Lys His Leu Asp Ile Gln Leu Pro Val Ser Glu Val
    210                 215                 220

Met Thr Val Asp Pro Arg Cys Ala Thr Ser Gln Gly Leu Ala Phe Glu
225                 230                 235                 240

Ala Met Leu Leu Met Ser Glu Leu Arg Ile His His Leu Pro Ile Val
                245                 250                 255

Asp Asp Gly Gln Ile Ser Gly Ile Val Thr Ala Ala Asp Ile Met Arg
            260                 265                 270

Leu Leu Arg His Asp Pro Ile Tyr Leu Thr Ala Asp Leu Ser Arg Lys
        275                 280                 285

Asn Thr Val Glu Glu Leu Ala Asn Thr Phe Gln Ser Ala Ala Glu Val
    290                 295                 300
```

```
Ala Ser Arg Phe Ile Asp Arg Gly Ala Ser Ala Glu Glu Val Ser Ser
305                 310                 315                 320

Leu Leu Thr Val Ala Ala Asp Ser Leu Ala Arg Arg Leu Leu Val Leu
                325                 330                 335

Ala Glu Arg Lys Phe Gly Ala Pro Pro Val Pro Tyr Cys Phe Val Val
            340                 345                 350

Val Gly Ser Gln Gly Arg Lys Glu Met Gly Leu Ala Ser Asp Gln Asp
        355                 360                 365

Asn Ala Leu Val Leu Asp Asn Ser Tyr Asn Asp Arg Glu His Gly Gln
    370                 375                 380

Tyr Phe Ala Ala Leu Ser Glu Phe Val Cys Gln Gly Leu Asp Arg Ala
385                 390                 395                 400

Gly Gln Val Leu Cys Pro Gly Asp Met Met Ala Ser Asn Pro Glu Trp
                405                 410                 415

Arg Lys Thr Ala Asp Gln Trp Ile Ser Thr Phe His Ser Trp Ile Thr
            420                 425                 430

Ala Pro Glu Pro Asp Ala Leu Leu His Ala Gln Thr Phe Phe Asp Phe
        435                 440                 445

Arg Gly Ile Tyr Gly Asp Thr Glu Met Ala Lys Asp Val His Gln Asn
    450                 455                 460

Ala Val Asn Met Ala Arg Gly Ala Arg Arg Met His Ala His Leu Ala
465                 470                 475                 480

Ser Leu Ala Ala Arg Arg Asp Pro Pro Leu Gly Phe Phe Arg Gly Leu
                485                 490                 495

Val Val Glu Arg Ser Gly Glu Tyr Gly Ala Thr Met Asp Ile Lys Lys
            500                 505                 510

Gly Gly Thr Ala Gly Ile Val Gln Met Ala Arg Leu Tyr Ala Leu Ala
        515                 520                 525

Thr Gly Ser Asp Ala Ile Gly Thr Arg Glu Arg Leu Ile Ala Ala Ser
    530                 535                 540

Gly His Gly Gln Val Ser Arg Lys Gly Ala Gln Asp Leu Leu Asp Ala
545                 550                 555                 560

Phe Asp Phe Leu Ala Ala Met Ala Phe Gln His Gln Ala Arg Leu Ile
                565                 570                 575

Lys Val Gly Glu Lys Pro Asn Tyr His Ile Asp Pro Lys Thr Leu Gly
            580                 585                 590

Lys Met Asp Arg Glu His Leu Arg Asp Ala Phe Ser Ile Ile Lys Asp
        595                 600                 605

Met Gln Ser Ala Leu Ala Thr Lys Tyr Pro Val Arg Asn Ile
    610                 615                 620
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<210> 2099
<211> 990
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(967)
<223> RXA01131

<400> 2099
gaattcattc aaggtggtaa ggcggttttc gctcttttaa tacagtttta aggtagatt 60

tgggagagaa gatttccctt aagaaaggtt cttaacaacc atg ccg cct gcg acg 115
Met Pro Pro Ala Thr
1 5

ctg ttc aat gtt ttg act tca gct gga ctt gac cct cac cag tca ggt 163
Leu Phe Asn Val Leu Thr Ser Ala Gly Leu Asp Pro His Gln Ser Gly
10 15 20

gat gcc att gtt gtc gag tct gcc cat ttc aca ttg acg ttc acg tgg 211
Asp Ala Ile Val Val Glu Ser Ala His Phe Thr Leu Thr Phe Thr Trp
25 30 35

gat gag tgg ctg cga gct caa gcg acg tgg gtg ggg gag ttg agt gcg 259
Asp Glu Trp Leu Arg Ala Gln Ala Thr Trp Val Gly Glu Leu Ser Ala
40 45 50

tcg gat tat gtg cgt tct att gtg gcg att aac tct gcc cat gat gca 307
Ser Asp Tyr Val Arg Ser Ile Val Ala Ile Asn Ser Ala His Asp Ala
55 60 65

cgg gca acg ccg aag atg atg ttg gat gcc ccg act ggt ctg aca acg 355
Arg Ala Thr Pro Lys Met Met Leu Asp Ala Pro Thr Gly Leu Thr Thr
70 75 80 85

gtg ctt aag gcg gat aag ggt cag ttg cag gcg ttt gcc gtg gag gcg 403
Val Leu Lys Ala Asp Lys Gly Gln Leu Gln Ala Phe Ala Val Glu Ala
90 95 100

ctg ccg att ggc gat ggc ctc agc gag gct cag ttg gcg ggg ttt gtg 451
Leu Pro Ile Gly Asp Gly Leu Ser Glu Ala Gln Leu Ala Gly Phe Val
105 110 115

gct gcc gcg ttt gat ggc gcc atc gac ctc act cgt gag ttt cat gca 499
Ala Ala Ala Phe Asp Gly Ala Ile Asp Leu Thr Arg Glu Phe His Ala
120 125 130

ctt tac ccg gag cgc tcg ccg cag gag cgc ggc gca atg ctc aac att 547
Leu Tyr Pro Glu Arg Ser Pro Gln Glu Arg Gly Ala Met Leu Asn Ile
135 140 145

aag ctt gtc gac gcc tcc ccc tct caa aca gtt acg ccc gtg cga gta 595
Lys Leu Val Asp Ala Ser Pro Ser Gln Thr Val Thr Pro Val Arg Val
150 155 160 165

gct aac tgg ttc atg gat cag ggg gtg gag gaa gtt cct tat gat gca 643
Ala Asn Trp Phe Met Asp Gln Gly Val Glu Glu Val Pro Tyr Asp Ala
170 175 180

```
gct tct ggg cgc atc agc ttt gag ctg ggt gac acc cca gtg gat gtg   691
Ala Ser Gly Arg Ile Ser Phe Glu Leu Gly Asp Thr Pro Val Asp Val
            185                 190                 195

att ttg gat gat ccc gag ttg ttg aag atc caa gcc gtg gtg gtt gct   739
Ile Leu Asp Asp Pro Glu Leu Leu Lys Ile Gln Ala Val Val Val Ala
        200                 205                 210

gac cgc gat gtg gaa gcc act gaa gtt tta cat ttg tgt aat cga gcg   787
Asp Arg Asp Val Glu Ala Thr Glu Val Leu His Leu Cys Asn Arg Ala
    215                 220                 225

aac ctg gat tct gat cac tcc acc att ttt atg cgt tcg gat ggg gat   835
Asn Leu Asp Ser Asp His Ser Thr Ile Phe Met Arg Ser Asp Gly Asp
230                 235                 240                 245

gat gtg gat ttc gtc gcc acg gtt gcg gtg ccg att cgt gct ggt ctg   883
Asp Val Asp Phe Val Ala Thr Val Ala Val Pro Ile Arg Ala Gly Leu
                250                 255                 260

aac gat ttc cag ttg agt caa gcc ctg cat gat ggg gta gtg ggg gtt   931
Asn Asp Phe Gln Leu Ser Gln Ala Leu His Asp Gly Val Val Gly Val
            265                 270                 275

gtt ggg cag gta cga gct gtg atc aat cag cta cac tagtgaagtc        977
Val Gly Gln Val Arg Ala Val Ile Asn Gln Leu His
        280                 285

catatagtga gaa                                                   990


<210> 2100
<211> 289
<212> PRT
<213> Corynebacterium glutamicum

<400> 2100
Met Pro Pro Ala Thr Leu Phe Asn Val Leu Thr Ser Ala Gly Leu Asp
  1               5                  10                  15

Pro His Gln Ser Gly Asp Ala Ile Val Val Glu Ser Ala His Phe Thr
            20                  25                  30

Leu Thr Phe Thr Trp Asp Glu Trp Leu Arg Ala Gln Ala Thr Trp Val
        35                  40                  45

Gly Glu Leu Ser Ala Ser Asp Tyr Val Arg Ser Ile Val Ala Ile Asn
    50                  55                  60

Ser Ala His Asp Ala Arg Ala Thr Pro Lys Met Met Leu Asp Ala Pro
65                  70                  75                  80

Thr Gly Leu Thr Thr Val Leu Lys Ala Asp Lys Gly Gln Leu Gln Ala
                85                  90                  95

Phe Ala Val Glu Ala Leu Pro Ile Gly Asp Gly Leu Ser Glu Ala Gln
            100                 105                 110

Leu Ala Gly Phe Val Ala Ala Ala Phe Asp Gly Ala Ile Asp Leu Thr
        115                 120                 125
```

```
Arg Glu Phe His Ala Leu Tyr Pro Glu Arg Ser Pro Gln Glu Arg Gly
    130                 135                 140

Ala Met Leu Asn Ile Lys Leu Val Asp Ala Ser Pro Ser Gln Thr Val
145                 150                 155                 160

Thr Pro Val Arg Val Ala Asn Trp Phe Met Asp Gln Gly Val Glu Glu
                165                 170                 175

Val Pro Tyr Asp Ala Ala Ser Gly Arg Ile Ser Phe Glu Leu Gly Asp
            180                 185                 190

Thr Pro Val Asp Val Ile Leu Asp Asp Pro Glu Leu Leu Lys Ile Gln
        195                 200                 205

Ala Val Val Val Ala Asp Arg Asp Val Glu Ala Thr Glu Val Leu His
    210                 215                 220

Leu Cys Asn Arg Ala Asn Leu Asp Ser Asp His Ser Thr Ile Phe Met
225                 230                 235                 240

Arg Ser Asp Gly Asp Asp Val Asp Phe Val Ala Thr Val Ala Val Pro
                245                 250                 255

Ile Arg Ala Gly Leu Asn Asp Phe Gln Leu Ser Gln Ala Leu His Asp
            260                 265                 270

Gly Val Val Gly Val Val Gly Gln Val Arg Ala Val Ile Asn Gln Leu
        275                 280                 285

His
```

US20050202538A1

<210> 2101
<211> 483
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(460)
<223> RXA01137

<400> 2101
tcggtttgaa cgcaactgct tgcgcttggg tgagctttga ggatgtcttc attcctgggg 60

ctcagattct aagccacgat ttccttacct tgtggcatcg gtg cgc cca acc ttc 115
                                              Val Arg Pro Thr Phe
                                                1   5

gtg atc cta cgg atc tcc gaa tac ttc ggt gtc gct gaa gct gcg att 163
Val Ile Leu Arg Ile Ser Glu Tyr Phe Gly Val Ala Glu Ala Ala Ile
                10   15   20

aat gca gcc act gga cgt ctg acc agc ctc agc gaa gtg ttt atc gac 211
Asn Ala Ala Thr Gly Arg Leu Thr Ser Leu Ser Glu Val Phe Ile Asp
            25   30   35

aac gct gcc gag atc caa gac aac ctt tct tcg ctg gtc gcg ctt cag 259
```
```

```
Asn Ala Ala Glu Ile Gln Asp Asn Leu Ser Ser Leu Val Ala Leu Gln
         40                  45                  50

aaa gat ttg gca gag cga gtc aac gtt gaa gga gtc aat cct gtt act   307
Lys Asp Leu Ala Glu Arg Val Asn Val Glu Gly Val Asn Pro Val Thr
     55                  60                  65

cca gtt gat cta ctg gaa ctt cgc ctc ggt tcc gcg cag ctg gcc gtt   355
Pro Val Asp Leu Leu Glu Leu Arg Leu Gly Ser Ala Gln Leu Ala Val
 70                  75                  80                  85

gct gca act gcc att gag gtt cgt gtt gct gga gga gca ggt tat gta   403
Ala Ala Thr Ala Ile Glu Val Arg Val Ala Gly Gly Ala Gly Tyr Val
                 90                  95                 100

aag tct tca tca acg tct cgt cgt ttc cgt gtt gaa atg gga gct tgc   451
Lys Ser Ser Ser Thr Ser Arg Arg Phe Arg Val Glu Met Gly Ala Cys
            105                 110                 115

acg ggt ccg tgatctacag gccacgcaaa act                            483
Thr Gly Pro
        120
```

5,648,240 5,656,465 5,773,571 5,786,177 5,804,414 5,849,696

<210> 2102
<211> 120
<212> PRT
<213> Corynebacterium glutamicum

<400> 2102

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Val Arg Pro Thr Phe Val Ile Leu Arg Ile Ser Glu Tyr Phe Gly Val
  1               5                  10                  15

Ala Glu Ala Ala Ile Asn Ala Ala Thr Gly Arg Leu Thr Ser Leu Ser
             20                  25                  30

Glu Val Phe Ile Asp Asn Ala Ala Glu Ile Gln Asp Asn Leu Ser Ser
         35                  40                  45

Leu Val Ala Leu Gln Lys Asp Leu Ala Glu Arg Val Asn Val Glu Gly
     50                  55                  60

Val Asn Pro Val Thr Pro Val Asp Leu Leu Glu Leu Arg Leu Gly Ser
 65                  70                  75                  80

Ala Gln Leu Ala Val Ala Ala Thr Ala Ile Glu Val Arg Val Ala Gly
                 85                  90                  95

Gly Ala Gly Tyr Val Lys Ser Ser Ser Thr Ser Arg Arg Phe Arg Val
            100                 105                 110

Glu Met Gly Ala Cys Thr Gly Pro
        115                 120
```

<210> 2103
<211> 257
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (34)..(234)
<223> RXA01156

<400> 2103
aagaactaag aaataccgat ttacggcagg agagtg agt gta gtg aac gca aag 54
Val Ser Val Val Asn Ala Lys
1 5

caa acc caa att atg ggt ggc ggc gga cgt gac gag gac aac gcc gag 102
Gln Thr Gln Ile Met Gly Gly Gly Gly Arg Asp Glu Asp Asn Ala Glu
10 15 20

gat tcc gca cag gca tct gga cag gtt cag atc aac acc gaa ggt gtg 150
Asp Ser Ala Gln Ala Ser Gly Gln Val Gln Ile Asn Thr Glu Gly Val
25 30 35

gac agc ttg ctg gat gaa atc gac gga ctg ttg gaa aac aac gcc gag 198
Asp Ser Leu Leu Asp Glu Ile Asp Gly Leu Leu Glu Asn Asn Ala Glu
40 45 50 55

gaa ttc gtt cgt tcc tat gta caa aag ggt ggc gaa tagtcactgt 244
Glu Phe Val Arg Ser Tyr Val Gln Lys Gly Gly Glu
60 65

gagtaccgtg gaa 257

<210> 2104
<211> 67
<212> PRT
<213> Corynebacterium glutamicum

<400> 2104
Val Ser Val Val Asn Ala Lys Gln Thr Gln Ile Met Gly Gly Gly Gly
1 5 10 15

Arg Asp Glu Asp Asn Ala Glu Asp Ser Ala Gln Ala Ser Gly Gln Val
20 25 30

Gln Ile Asn Thr Glu Gly Val Asp Ser Leu Leu Asp Glu Ile Asp Gly
35 40 45

Leu Leu Glu Asn Asn Ala Glu Glu Phe Val Arg Ser Tyr Val Gln Lys
50 55 60

Gly Gly Glu
65

<210> 2105
<211> 1065
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1042)
<223> RXA01158

<400> 2105

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taggacgttc aaggaattgg ctgaatcaac aagcgccaag gtggttaagc gccctcggcg 60

agttatctca aaaaagaaga agaagtctcc tacgggagag atg tcc att gtt gag   115
                                            Met Ser Ile Val Glu
                                              1               5

cac atc aaa gag ttt cga cgc cga ctt ctt atc gct ctg gcg ggc atc   163
His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile Ala Leu Ala Gly Ile
                 10                  15                  20

ctc gtg ggc acc att atc ggc ttt att tgg tac gat ttc tca ttt tgg   211
Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr Asp Phe Ser Phe Trp
             25                  30                  35

cag atc ccc act ttg ggc gag ctg ctg agg gat ccg tac tgt tct ctg   259
Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp Pro Tyr Cys Ser Leu
         40                  45                  50

cct gct gaa tcc cgc tgg gcc atg agc gac tca gag gaa tgt cga ctg   307
Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser Glu Glu Cys Arg Leu
     55                  60                  65

ctc gca acc ggc ccg ttt gat cca ttc atg ctt cgc ctt aaa gta gcg   355
Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu Arg Leu Lys Val Ala
 70                  75                  80                  85

gcg ttg gtg ggt atg gtt ctt ggc tca ccc gtg tgg ctg agc cag ctg   403
Ala Leu Val Gly Met Val Leu Gly Ser Pro Val Trp Leu Ser Gln Leu
                 90                  95                 100

tgg ggc ttt atc acc cca ggt ttg atg aag aat gag cgc cgt tac acc   451
Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn Glu Arg Arg Tyr Thr
             105                 110                 115

gca atc ttc gtc acg att gct gtt gtg ctg ttt gtc ggc ggt gct gtt   499
Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe Val Gly Gly Ala Val
         120                 125                 130

ctt gcg tac ttc gtc gtt gca tat ggt ttg gag ttc ctc ctt acc att   547
Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu Phe Leu Leu Thr Ile
    135                 140                 145

ggt gga gac acc cag gca gcg gcc ctg act ggt gat aag tac ttc gga   595
Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly Asp Lys Tyr Phe Gly
150                 155                 160                 165

ttc ttg ctc gcg ttg ttg gcg att ttc ggc gtg agc ttc gaa gtt cca   643
Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val Ser Phe Glu Val Pro
                170                 175                 180

ctg gtg atc ggc atg ctc aac att gtg ggt atc ttg cct tac gat gcc   691
Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile Leu Pro Tyr Asp Ala
            185                 190                 195

att aaa gat aag cga cgc atg atc atc atg att ttg ttc gtg ttc gct   739
Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile Leu Phe Val Phe Ala
        200                 205                 210

gct ttc atg aca ccc ggc cag gat cct ttc acc atg ttg gtg ttg gcg   787
Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr Met Leu Val Leu Ala
    215                 220                 225
```

```
ctt tca ctc acc gtt ctg gta gag ctt gcc ctg cag ttc tgt cgc ttc   835
Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu Gln Phe Cys Arg Phe
230                 235                 240                 245

aac gac aaa cgc cgg gac aag aag cgc cca gaa tgg ctt gat ggc gat   883
Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu Trp Leu Asp Gly Asp
                250                 255                 260

gac ctc tct gca tca cca ctg gat act tct gct ggt gga gaa gat gct   931
Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala Gly Gly Glu Asp Ala
            265                 270                 275

cca agc cca gtc gaa acc cca gag gcg gtg gag cct tcg cgg atg ctg   979
Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu Pro Ser Arg Met Leu
        280                 285                 290

aac cca agt ggg gag gcg tcg ata agc tat aaa ccc ggg cgc gcc gac   1027
Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys Pro Gly Arg Ala Asp
    295                 300                 305

ttc ggt gac gtg ctc tagggcctag ccaggtaccc tta                    1065
Phe Gly Asp Val Leu
310
```

Sequence Listing

<210> 2106
<211> 314
<212> PRT
<213> Corynebacterium glutamicum

<400> 2106

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Met Ser Ile Val Glu His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile
  1               5                  10                  15

Ala Leu Ala Gly Ile Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr
             20                  25                  30

Asp Phe Ser Phe Trp Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp
         35                  40                  45

Pro Tyr Cys Ser Leu Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser
     50                  55                  60

Glu Glu Cys Arg Leu Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu
 65                  70                  75                  80

Arg Leu Lys Val Ala Ala Leu Val Gly Met Val Leu Gly Ser Pro Val
                 85                  90                  95

Trp Leu Ser Gln Leu Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn
            100                 105                 110

Glu Arg Arg Tyr Thr Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe
        115                 120                 125

Val Gly Gly Ala Val Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu
    130                 135                 140

Phe Leu Leu Thr Ile Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly
145                 150                 155                 160
```

```
Asp Lys Tyr Phe Gly Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val
                165                 170                 175

Ser Phe Glu Val Pro Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile
            180                 185                 190

Leu Pro Tyr Asp Ala Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile
        195                 200                 205

Leu Phe Val Phe Ala Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr
    210                 215                 220

Met Leu Val Leu Ala Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu
225                 230                 235                 240

Gln Phe Cys Arg Phe Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu
                245                 250                 255

Trp Leu Asp Gly Asp Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala
            260                 265                 270

Gly Gly Glu Asp Ala Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu
        275                 280                 285

Pro Ser Arg Met Leu Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys
    290                 295                 300

Pro Gly Arg Ala Asp Phe Gly Asp Val Leu
305                 310


<210> 2107
<211> 438
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(415)
<223> RXA01159

<400> 2107
catcaatcaa tgtgcaaggg tttcatttct ggaaatcgtg gtcaccccac attcaccagt 60

catgaacaag cttgtttaat gtgaatttgg agtagaccac atg tcc ctc gga cca   115
                                            Met Ser Leu Gly Pro
                                              1               5

tgg gaa att gga atc att gtc ctg ctg atc atc gtg ctg ttc ggc gcg   163
Trp Glu Ile Gly Ile Ile Val Leu Leu Ile Ile Val Leu Phe Gly Ala
                  10                  15                  20

aag aag ctg cct gat gca gct cgt tcc atc ggc cgt tcc atg cgc atc   211
Lys Lys Leu Pro Asp Ala Ala Arg Ser Ile Gly Arg Ser Met Arg Ile
              25                  30                  35

ttc aag tct gaa gtc aaa gaa atg aac aag gac ggc gat acc cca gaa   259
Phe Lys Ser Glu Val Lys Glu Met Asn Lys Asp Gly Asp Thr Pro Glu
          40                  45                  50
```

```
caa cag cag cag cct cag cag cag att gcg ccc aac cag atc gag gct   307
Gln Gln Gln Gln Pro Gln Gln Gln Ile Ala Pro Asn Gln Ile Glu Ala
     55                  60                  65

cct cag cca aac ttt gag cag cac tac cag gga cag cag gtt cag cag   355
Pro Gln Pro Asn Phe Glu Gln His Tyr Gln Gly Gln Gln Val Gln Gln
 70                  75                  80                  85

cct cag aac cct cag acc cct gac tac cgt cag aac tac gag gat cca   403
Pro Gln Asn Pro Gln Thr Pro Asp Tyr Arg Gln Asn Tyr Glu Asp Pro
                 90                  95                 100

aac cgc acc tct taaagttggg cagtttgcat cta                         438
Asn Arg Thr Ser
            105
```

<210> 2108
<211> 105
<212> PRT
<213> Corynebacterium glutamicum

<400> 2108

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Met Ser Leu Gly Pro Trp Glu Ile Gly Ile Ile Val Leu Leu Ile Ile
  1               5                  10                  15

Val Leu Phe Gly Ala Lys Lys Leu Pro Asp Ala Ala Arg Ser Ile Gly
             20                  25                  30

Arg Ser Met Arg Ile Phe Lys Ser Glu Val Lys Glu Met Asn Lys Asp
         35                  40                  45

Gly Asp Thr Pro Glu Gln Gln Gln Gln Pro Gln Gln Gln Ile Ala Pro
     50                  55                  60

Asn Gln Ile Glu Ala Pro Gln Pro Asn Phe Glu Gln His Tyr Gln Gly
 65                  70                  75                  80

Gln Gln Val Gln Gln Pro Gln Asn Pro Gln Thr Pro Asp Tyr Arg Gln
                 85                  90                  95

Asn Tyr Glu Asp Pro Asn Arg Thr Ser
            100                 105
```

<210> 2109
<211> 998
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(975)
<223> RXA01160

<400> 2109

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aaa tca tcc aac aaa atc agc gac ctt gcc cgc cag ctt aat ctg ttg   48
Lys Ser Ser Asn Lys Ile Ser Asp Leu Ala Arg Gln Leu Asn Leu Leu
  1               5                  10                  15

ccg tat ttc acc agg tat aaa ggc cgt acc gtc atg gaa gca gcg cgc   96
```

```
Pro Tyr Phe Thr Arg Tyr Lys Gly Arg Thr Val Met Glu Ala Ala Arg
            20                  25                  30

gat ctt ggc caa ccc tcc tcc caa atc atg gaa gac ctc aac aga tta   144
Asp Leu Gly Gln Pro Ser Ser Gln Ile Met Glu Asp Leu Asn Arg Leu
         35                  40                  45

tgg atg tgt ggt ctg cca gga ctt ctt cca ggt gac ttg gtg gag ctt   192
Trp Met Cys Gly Leu Pro Gly Leu Leu Pro Gly Asp Leu Val Glu Leu
     50                  55                  60

gat cat tcc ttt aag gaa gta aaa atc cac aat gct caa ggc atg gat   240
Asp His Ser Phe Lys Glu Val Lys Ile His Asn Ala Gln Gly Met Asp
 65                  70                  75                  80

aaa ccc ttg cgc ctc aca cca act gaa gcc ggt gtt ttg ctg ctg aca   288
Lys Pro Leu Arg Leu Thr Pro Thr Glu Ala Gly Val Leu Leu Leu Thr
                 85                  90                  95

ctt gaa tcc ctg gaa tcc ctc ccc ggt att gcg aaa cag gaa gcg gtc   336
Leu Glu Ser Leu Glu Ser Leu Pro Gly Ile Ala Lys Gln Glu Ala Val
            100                 105                 110

gta tct gct gcg aac aag cta cgc gcc atc atg ggg gag tat tcc tcg   384
Val Ser Ala Ala Asn Lys Leu Arg Ala Ile Met Gly Glu Tyr Ser Ser
        115                 120                 125

act gtt ttc gac tcc act gga gaa gac ctc gat gct gaa gtt cta gag   432
Thr Val Phe Asp Ser Thr Gly Glu Asp Leu Asp Ala Glu Val Leu Glu
    130                 135                 140

atc atc cgc gac gcc atg gat tta cac cag cag gtc agt ttt gaa tac   480
Ile Ile Arg Asp Ala Met Asp Leu His Gln Gln Val Ser Phe Glu Tyr
145                 150                 155                 160

cac tcg cac aga tca gac aac acc agc ctg agg caa gtc agc cct gct   528
His Ser His Arg Ser Asp Asn Thr Ser Leu Arg Gln Val Ser Pro Ala
                165                 170                 175

cat atc ttc acc cat gaa ggc gaa acc tac atc aaa gcc tgg gaa gaa   576
His Ile Phe Thr His Glu Gly Glu Thr Tyr Ile Lys Ala Trp Glu Glu
            180                 185                 190

gct gtg aac caa tgg cgg acg ttt agg ctt gat cgc atc cga agc att   624
Ala Val Asn Gln Trp Arg Thr Phe Arg Leu Asp Arg Ile Arg Ser Ile
        195                 200                 205

gtg ctt ctt gac agc aaa gca gtg cac ccg gcg cga ggg gtt tca gta   672
Val Leu Leu Asp Ser Lys Ala Val His Pro Ala Arg Gly Val Ser Val
    210                 215                 220

tcc acg gac gat cct ttt gag ttc gca aaa tct tcc gat att gcc acg   720
Ser Thr Asp Asp Pro Phe Glu Phe Ala Lys Ser Ser Asp Ile Ala Thr
225                 230                 235                 240

tta ttg ctg cgt gag gac gca atg tgg tta ggc aat tac atg gcc atg   768
Leu Leu Leu Arg Glu Asp Ala Met Trp Leu Gly Asn Tyr Met Ala Met
                245                 250                 255

gag gtg gat gaa acg gtg gaa ccg att cgc gat agc gac gga ttc agc   816
Glu Val Asp Glu Thr Val Glu Pro Ile Arg Asp Ser Asp Gly Phe Ser
```

```
            260                 265                 270

tgg cac aca gtc cac ttt ccg ctg ctt tct agg gat tgg ttc gtc cga   864
Trp His Thr Val His Phe Pro Leu Leu Ser Arg Asp Trp Phe Val Arg
        275                 280                 285

ttc gcg att ggc cat gct gag cat ttg aaa gta act agt ccc gaa gat   912
Phe Ala Ile Gly His Ala Glu His Leu Lys Val Thr Ser Pro Glu Asp
    290                 295                 300

ctt cgg aaa tgc ata aag caa aag gct ttt agt ggt ttg tca gcg tat   960
Leu Arg Lys Cys Ile Lys Gln Lys Ala Phe Ser Gly Leu Ser Ala Tyr
305                 310                 315                 320

gat cat cac gta gag taacacccaa gagtaagacg caa                     998
Asp His His Val Glu
                325
```

<210> 2110
<211> 325
<212> PRT
<213> Corynebacterium glutamicum

<400> 2110

```
Lys Ser Ser Asn Lys Ile Ser Asp Leu Ala Arg Gln Leu Asn Leu Leu
  1               5                  10                  15

Pro Tyr Phe Thr Arg Tyr Lys Gly Arg Thr Val Met Glu Ala Ala Arg
            20                  25                  30

Asp Leu Gly Gln Pro Ser Ser Gln Ile Met Glu Asp Leu Asn Arg Leu
        35                  40                  45

Trp Met Cys Gly Leu Pro Gly Leu Leu Pro Gly Asp Leu Val Glu Leu
    50                  55                  60

Asp His Ser Phe Lys Glu Val Lys Ile His Asn Ala Gln Gly Met Asp
65                  70                  75                  80

Lys Pro Leu Arg Leu Thr Pro Thr Glu Ala Gly Val Leu Leu Leu Thr
                85                  90                  95

Leu Glu Ser Leu Glu Ser Leu Pro Gly Ile Ala Lys Gln Glu Ala Val
            100                 105                 110

Val Ser Ala Ala Asn Lys Leu Arg Ala Ile Met Gly Glu Tyr Ser Ser
        115                 120                 125

Thr Val Phe Asp Ser Thr Gly Glu Asp Leu Asp Ala Glu Val Leu Glu
    130                 135                 140

Ile Ile Arg Asp Ala Met Asp Leu His Gln Gln Val Ser Phe Glu Tyr
145                 150                 155                 160

His Ser His Arg Ser Asp Asn Thr Ser Leu Arg Gln Val Ser Pro Ala
                165                 170                 175

His Ile Phe Thr His Glu Gly Glu Thr Tyr Ile Lys Ala Trp Glu Glu
            180                 185                 190
```

```
Ala Val Asn Gln Trp Arg Thr Phe Arg Leu Asp Arg Ile Arg Ser Ile
        195                 200                 205

Val Leu Leu Asp Ser Lys Ala Val His Pro Ala Arg Gly Val Ser Val
    210                 215                 220

Ser Thr Asp Asp Pro Phe Glu Phe Ala Lys Ser Ser Asp Ile Ala Thr
225                 230                 235                 240

Leu Leu Leu Arg Glu Asp Ala Met Trp Leu Gly Asn Tyr Met Ala Met
                245                 250                 255

Glu Val Asp Glu Thr Val Glu Pro Ile Arg Asp Ser Asp Gly Phe Ser
            260                 265                 270

Trp His Thr Val His Phe Pro Leu Leu Ser Arg Asp Trp Phe Val Arg
        275                 280                 285

Phe Ala Ile Gly His Ala Glu His Leu Lys Val Thr Ser Pro Glu Asp
    290                 295                 300

Leu Arg Lys Cys Ile Lys Gln Lys Ala Phe Ser Gly Leu Ser Ala Tyr
305                 310                 315                 320

Asp His His Val Glu
                325
```

US 7,666,644 B2

<210> 2111
<211> 805
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(805)
<223> RXA01163

<400> 2111
accgtaccca cagacacacc agaattaaca gaaacagact gaaaaacaac atcgctcgac 60

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atgcgcgtaa tcctaacccg cgcacactaa tgtggccgat atg ggc tac acc aac   115
                                            Met Gly Tyr Thr Asn
                                              1               5

ctc aac gac aca cgg gtc ttg cgc gcc ggg tca tgt gat gcc tgg tgg   163
Leu Asn Asp Thr Arg Val Leu Arg Ala Gly Ser Cys Asp Ala Trp Trp
                  10                  15                  20

cgc acg atg tct ccg cta gtg cag cag gga agt gag gca gtc ttt cgg   211
Arg Thr Met Ser Pro Leu Val Gln Gln Gly Ser Glu Ala Val Phe Arg
              25                  30                  35

cgc atc atg ggt ctc tcg cgg cgt cct gat cgg aaa cct ggc ttt gac   259
Arg Ile Met Gly Leu Ser Arg Arg Pro Asp Arg Lys Pro Gly Phe Asp
          40                  45                  50

gat gtc cca cat ttc ggc gca gct gtt cga gtt ccc ggt cta aaa cac   307
Asp Val Pro His Phe Gly Ala Ala Val Arg Val Pro Gly Leu Lys His
      55                  60                  65
```

```
ggc acg ttg gtc aat gct gca ccc ttg aaa gtt ttg ggc gca cgg ggc   355
Gly Thr Leu Val Asn Ala Ala Pro Leu Lys Val Leu Gly Ala Arg Gly
 70                  75                  80                  85

gag ccc aac ccc gcg agt tcg tac cgt ttt gaa tac atc acc ggt gat   403
Glu Pro Asn Pro Ala Ser Ser Tyr Arg Phe Glu Tyr Ile Thr Gly Asp
                90                  95                 100

tcc gca ggt cga gcc atc act gcg acc ggc gct gtc ctc ttt tcc aca   451
Ser Ala Gly Arg Ala Ile Thr Ala Thr Gly Ala Val Leu Phe Ser Thr
            105                 110                 115

cgc ccc tgg aca acc ggc ccg cgt ccc gcg atc gcc atg gct cca tcc   499
Arg Pro Trp Thr Thr Gly Pro Arg Pro Ala Ile Ala Met Ala Pro Ser
        120                 125                 130

acc caa ggc gtc gca cag cac tgc gat ccc tcc cac acc tgc gcc atc   547
Thr Gln Gly Val Ala Gln His Cys Asp Pro Ser His Thr Cys Ala Ile
    135                 140                 145

gga ctc aac gca ttc tat gac aaa ccc ttc gac gca atc att gct tac   595
Gly Leu Asn Ala Phe Tyr Asp Lys Pro Phe Asp Ala Ile Ile Ala Tyr
150                 155                 160                 165

gaa ctc ccc gtc atc ctc tgg ttt cta gct cac gga ctt gac gtt gtg   643
Glu Leu Pro Val Ile Leu Trp Phe Leu Ala His Gly Leu Asp Val Val
                170                 175                 180

ttc atc gat tac ccc cgc gac ccc gca acc ggc gtc caa tac tat tgc   691
Phe Ile Asp Tyr Pro Arg Asp Pro Ala Thr Gly Val Gln Tyr Tyr Cys
            185                 190                 195

gat tcc atc gct gca gct aaa tcg ctt ctc gac gcc gtc ctc gcc tcc   739
Asp Ser Ile Ala Ala Ala Lys Ser Leu Leu Asp Ala Val Leu Ala Ser
        200                 205                 210

aga caa ctc ggc ctt tca ccg gaa gca ccg ctt ggc ctg tgg gga ttc   787
Arg Gln Leu Gly Leu Ser Pro Glu Ala Pro Leu Gly Leu Trp Gly Phe
    215                 220                 225

tcc caa gga ggc ggc gcc                                          805
Ser Gln Gly Gly Gly Ala
230                 235
```

US 20050170464 A1 20050804

<210> 2112
<211> 235
<212> PRT
<213> Corynebacterium glutamicum

<400> 2112

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Met Gly Tyr Thr Asn Leu Asn Asp Thr Arg Val Leu Arg Ala Gly Ser
  1               5                  10                  15

Cys Asp Ala Trp Trp Arg Thr Met Ser Pro Leu Val Gln Gln Gly Ser
             20                  25                  30

Glu Ala Val Phe Arg Arg Ile Met Gly Leu Ser Arg Arg Pro Asp Arg
         35                  40                  45

Lys Pro Gly Phe Asp Asp Val Pro His Phe Gly Ala Ala Val Arg Val
```

```
     50                  55                  60

Pro Gly Leu Lys His Gly Thr Leu Val Asn Ala Ala Pro Leu Lys Val
 65                  70                  75                  80

Leu Gly Ala Arg Gly Glu Pro Asn Pro Ala Ser Ser Tyr Arg Phe Glu
                 85                  90                  95

Tyr Ile Thr Gly Asp Ser Ala Gly Arg Ala Ile Thr Ala Thr Gly Ala
            100                 105                 110

Val Leu Phe Ser Thr Arg Pro Trp Thr Thr Gly Pro Arg Pro Ala Ile
        115                 120                 125

Ala Met Ala Pro Ser Thr Gln Gly Val Ala Gln His Cys Asp Pro Ser
    130                 135                 140

His Thr Cys Ala Ile Gly Leu Asn Ala Phe Tyr Asp Lys Pro Phe Asp
145                 150                 155                 160

Ala Ile Ile Ala Tyr Glu Leu Pro Val Ile Leu Trp Phe Leu Ala His
                165                 170                 175

Gly Leu Asp Val Val Phe Ile Asp Tyr Pro Arg Asp Pro Ala Thr Gly
            180                 185                 190

Val Gln Tyr Tyr Cys Asp Ser Ile Ala Ala Ala Lys Ser Leu Leu Asp
        195                 200                 205

Ala Val Leu Ala Ser Arg Gln Leu Gly Leu Ser Pro Glu Ala Pro Leu
    210                 215                 220

Gly Leu Trp Gly Phe Ser Gln Gly Gly Gly Ala
225                 230                 235


<210> 2113
<211> 696
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(673)
<223> RXA01165

<400> 2113
agaccactca cattgcacat ctgcagctgc caggaagtct ccacccaaca gttttctagg 60

tcacagggat ccattagcca tttggtcctt gtcgaaaggt atg gtg ggg cat gtg   115
                                              Met Val Gly His Val
                                                1               5

cct gca gca ata gca atc cca tat ttc att att gag atc ctc gcc ttc   163
Pro Ala Ala Ile Ala Ile Pro Tyr Phe Ile Ile Glu Ile Leu Ala Phe
                10                  15                  20

att ggt gtc gtc atg tgg ctc ggt ttc ggc tgg gct ttg ggt ctc ctc   211
Ile Gly Val Val Met Trp Leu Gly Phe Gly Trp Ala Leu Gly Leu Leu
            25                  30                  35
```

```
gta ttg ttc ttc gtc ggt gga ctt ctt cta gcc ggc gtg gag ctt cgt   259
Val Leu Phe Phe Val Gly Gly Leu Leu Leu Ala Gly Val Glu Leu Arg
         40                  45                  50

cgc att agt aag agt gcc gcc att cat cag gct tcg ggc cag gga agt   307
Arg Ile Ser Lys Ser Ala Ala Ile His Gln Ala Ser Gly Gln Gly Ser
     55                  60                  65

gcg gga gcg atc gcc gga aac att ggg ctg acc gca gct ggt gcc att   355
Ala Gly Ala Ile Ala Gly Asn Ile Gly Leu Thr Ala Ala Gly Ala Ile
 70                  75                  80                  85

ttg gtg gcc atg ccg ggg ttt gtg tct tcg att atc ggt ttg ttg ttc   403
Leu Val Ala Met Pro Gly Phe Val Ser Ser Ile Ile Gly Leu Leu Phe
                 90                  95                 100

att ttt gca cca acc agg gcg ctg ttc cgc aag gtt ttg gcc aag cgc   451
Ile Phe Ala Pro Thr Arg Ala Leu Phe Arg Lys Val Leu Ala Lys Arg
            105                 110                 115

atg cgc agt gcc atc gag aac cta ggt gtg cgt ggt ttt gaa gcc gtt   499
Met Arg Ser Ala Ile Glu Asn Leu Gly Val Arg Gly Phe Glu Ala Val
        120                 125                 130

aat ggt tac cgc acc cag gca tcc tac gga aac ttc gga gcg gca ttc   547
Asn Gly Tyr Arg Thr Gln Ala Ser Tyr Gly Asn Phe Gly Ala Ala Phe
    135                 140                 145

aat ggt ggt gcg caa caa cca tca aat gag ccg atc gtg att gat gaa   595
Asn Gly Gly Ala Gln Gln Pro Ser Asn Glu Pro Ile Val Ile Asp Glu
150                 155                 160                 165

gac gag atc caa gcc tgg act tct gat ctc aaa cct gaa gat ttc acc   643
Asp Glu Ile Gln Ala Trp Thr Ser Asp Leu Lys Pro Glu Asp Phe Thr
                170                 175                 180

aaa ggt aaa gat gaa tcc gac ggt gag aaa taagtgacac tgtttgttcg     693
Lys Gly Lys Asp Glu Ser Asp Gly Glu Lys
            185                 190

gct                                                               696


<210> 2114
<211> 191
<212> PRT
<213> Corynebacterium glutamicum

<400> 2114
Met Val Gly His Val Pro Ala Ala Ile Ala Ile Pro Tyr Phe Ile Ile
  1               5                  10                  15

Glu Ile Leu Ala Phe Ile Gly Val Val Met Trp Leu Gly Phe Gly Trp
             20                  25                  30

Ala Leu Gly Leu Leu Val Leu Phe Phe Val Gly Gly Leu Leu Leu Ala
         35                  40                  45

Gly Val Glu Leu Arg Arg Ile Ser Lys Ser Ala Ala Ile His Gln Ala
     50                  55                  60
```

```
Ser Gly Gln Gly Ser Ala Gly Ala Ile Ala Gly Asn Ile Gly Leu Thr
 65                  70                  75                  80

Ala Ala Gly Ala Ile Leu Val Ala Met Pro Gly Phe Val Ser Ser Ile
                 85                  90                  95

Ile Gly Leu Leu Phe Ile Phe Ala Pro Thr Arg Ala Leu Phe Arg Lys
            100                 105                 110

Val Leu Ala Lys Arg Met Arg Ser Ala Ile Glu Asn Leu Gly Val Arg
        115                 120                 125

Gly Phe Glu Ala Val Asn Gly Tyr Arg Thr Gln Ala Ser Tyr Gly Asn
    130                 135                 140

Phe Gly Ala Ala Phe Asn Gly Gly Ala Gln Gln Pro Ser Asn Glu Pro
145                 150                 155                 160

Ile Val Ile Asp Glu Asp Glu Ile Gln Ala Trp Thr Ser Asp Leu Lys
                165                 170                 175

Pro Glu Asp Phe Thr Lys Gly Lys Asp Glu Ser Asp Gly Glu Lys
            180                 185                 190
```

<210> 2115
<211> 506
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(483)
<223> RXA01166

<400> 2115

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ctc acc gga gtg att gcc tac gcc atc gcg gga ctt gca gtg aac tct   48
Leu Thr Gly Val Ile Ala Tyr Ala Ile Ala Gly Leu Ala Val Asn Ser
  1               5                  10                  15

tca gag atg ttt gag gaa atc atg tcg gtg tta aat gaa cgc gga gtc   96
Ser Glu Met Phe Glu Glu Ile Met Ser Val Leu Asn Glu Arg Gly Val
             20                  25                  30

agt gat gtg ctg aaa aat atc acc agc tgc gcg gga ggt tcc ttg ttg   144
Ser Asp Val Leu Lys Asn Ile Thr Ser Cys Ala Gly Gly Ser Leu Leu
         35                  40                  45

gcc agt ggc tac tcg tct tcc cgc ggg tgg aca cat cag ggc acg ccg   192
Ala Ser Gly Tyr Ser Ser Ser Arg Gly Trp Thr His Gln Gly Thr Pro
     50                  55                  60

ctg gca gac att ctg gac gat ctg cca ctt gtt gtc gct gag ttt ggg   240
Leu Ala Asp Ile Leu Asp Asp Leu Pro Leu Val Val Ala Glu Phe Gly
 65                  70                  75                  80

aag caa aag ctg ggt cgt gtg gcg cca gaa atc cca gtg ctg ttg tgg   288
Lys Gln Lys Leu Gly Arg Val Ala Pro Glu Ile Pro Val Leu Leu Trp
                 85                  90                  95

ggc tct aaa aat gat gat gtc att ccc att gat ccc att agg gaa ttg   336
```

```
Gly Ser Lys Asn Asp Asp Val Ile Pro Ile Asp Pro Ile Arg Glu Leu
            100                 105                 110

cgt gat agc tgg gcg gac aag ggt acg cca ttg acc tgg cat gaa tcc   384
Arg Asp Ser Trp Ala Asp Lys Gly Thr Pro Leu Thr Trp His Glu Ser
        115                 120                 125

caa gcg ccg cgt gtg cca gga cgc aca ggt ctc aac cat ttc ggg ccc   432
Gln Ala Pro Arg Val Pro Gly Arg Thr Gly Leu Asn His Phe Gly Pro
    130                 135                 140

tat ttt aga aac ctg gaa aag tac tcg gga tgg ctc ata gat cat ctt   480
Tyr Phe Arg Asn Leu Glu Lys Tyr Ser Gly Trp Leu Ile Asp His Leu
145                 150                 155                 160

gtc tgagtgccgt tttaaaggct cgg                                    506
Val
```

<210> 2116
<211> 161
<212> PRT
<213> Corynebacterium glutamicum

<400> 2116

```
Leu Thr Gly Val Ile Ala Tyr Ala Ile Ala Gly Leu Ala Val Asn Ser
  1               5                  10                  15

Ser Glu Met Phe Glu Glu Ile Met Ser Val Leu Asn Glu Arg Gly Val
             20                  25                  30

Ser Asp Val Leu Lys Asn Ile Thr Ser Cys Ala Gly Gly Ser Leu Leu
         35                  40                  45

Ala Ser Gly Tyr Ser Ser Ser Arg Gly Trp Thr His Gln Gly Thr Pro
     50                  55                  60

Leu Ala Asp Ile Leu Asp Asp Leu Pro Leu Val Val Ala Glu Phe Gly
 65                  70                  75                  80

Lys Gln Lys Leu Gly Arg Val Ala Pro Glu Ile Pro Val Leu Leu Trp
                 85                  90                  95

Gly Ser Lys Asn Asp Asp Val Ile Pro Ile Asp Pro Ile Arg Glu Leu
            100                 105                 110

Arg Asp Ser Trp Ala Asp Lys Gly Thr Pro Leu Thr Trp His Glu Ser
        115                 120                 125

Gln Ala Pro Arg Val Pro Gly Arg Thr Gly Leu Asn His Phe Gly Pro
    130                 135                 140

Tyr Phe Arg Asn Leu Glu Lys Tyr Ser Gly Trp Leu Ile Asp His Leu
145                 150                 155                 160

Val
```

<210> 2117

<211> 606
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(583)
<223> RXA01170

<400> 2117
tacaggaaac tttcaggcat aggggagtca tgaaacagaa cggcaagcta aggtgacata 60

gtcacttaaa ctaaacaaga agggtggagg acccaagcac gtg agt ctt tca aac 115
Val Ser Leu Ser Asn
1 5

aaa gct aaa gga atc gtt gca gta atc atc gtc gcc tgg atc gtc gcg 163
Lys Ala Lys Gly Ile Val Ala Val Ile Ile Val Ala Trp Ile Val Ala
10 15 20

atg gct ggc atg gtc gca tac gcg tca agc aat aat gct gat aag aca 211
Met Ala Gly Met Val Ala Tyr Ala Ser Ser Asn Asn Ala Asp Lys Thr
25 30 35

ttt cca act gca ggt gcg cta gaa caa acc gtc gca gca ttt gat agg 259
Phe Pro Thr Ala Gly Ala Leu Glu Gln Thr Val Ala Ala Phe Asp Arg
40 45 50

caa ggc ctt cag gtc tct gca gtc gca ctg gca gac atc tac ggc gat 307
Gln Gly Leu Gln Val Ser Ala Val Ala Leu Ala Asp Ile Tyr Gly Asp
55 60 65

gaa tac gtc tcc gcg gcg att ctg tgc gaa gga act cca acc gca aca 355
Glu Tyr Val Ser Ala Ala Ile Leu Cys Glu Gly Thr Pro Thr Ala Thr
70 75 80 85

ctc gag cag tca ctg ggc gta gac ctg tct gag ctg aac ctg gac gag 403
Leu Glu Gln Ser Leu Gly Val Asp Leu Ser Glu Leu Asn Leu Asp Glu
90 95 100

tct ggt gtt cct tcg ggc gtg tcc tac ttg gct ctg tcc aat cag gat 451
Ser Gly Val Pro Ser Gly Val Ser Tyr Leu Ala Leu Ser Asn Gln Asp
105 110 115

ggg gaa gtt gtc tac gac aag att gat cgt gcc aac gtt gat ctc tgc 499
Gly Glu Val Val Tyr Asp Lys Ile Asp Arg Ala Asn Val Asp Leu Cys
120 125 130

gca acg cca ctc aat ggt gct ttc agc gct tat tca ttg atg cca gtt 547
Ala Thr Pro Leu Asn Gly Ala Phe Ser Ala Tyr Ser Leu Met Pro Val
135 140 145

gcc aag gtt ggc gag aac tcc tgg gcg atc gcc gct tagggtttta 593
Ala Lys Val Gly Glu Asn Ser Trp Ala Ile Ala Ala
150 155 160

agggtcaatc cgc 606

<210> 2118
<211> 161

<212> PRT
<213> Corynebacterium glutamicum

<400> 2118
Val Ser Leu Ser Asn Lys Ala Lys Gly Ile Val Ala Val Ile Ile Val
1 5 10 15

Ala Trp Ile Val Ala Met Ala Gly Met Val Ala Tyr Ala Ser Ser Asn
20 25 30

Asn Ala Asp Lys Thr Phe Pro Thr Ala Gly Ala Leu Glu Gln Thr Val
35 40 45

Ala Ala Phe Asp Arg Gln Gly Leu Gln Val Ser Ala Val Ala Leu Ala
50 55 60

Asp Ile Tyr Gly Asp Glu Tyr Val Ser Ala Ala Ile Leu Cys Glu Gly
65 70 75 80

Thr Pro Thr Ala Thr Leu Glu Gln Ser Leu Gly Val Asp Leu Ser Glu
85 90 95

Leu Asn Leu Asp Glu Ser Gly Val Pro Ser Gly Val Ser Tyr Leu Ala
100 105 110

Leu Ser Asn Gln Asp Gly Glu Val Val Tyr Asp Lys Ile Asp Arg Ala
115 120 125

Asn Val Asp Leu Cys Ala Thr Pro Leu Asn Gly Ala Phe Ser Ala Tyr
130 135 140

Ser Leu Met Pro Val Ala Lys Val Gly Glu Asn Ser Trp Ala Ile Ala
145 150 155 160

Ala

<210> 2119
<211> 816
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> RXA01171

<400> 2119
gtagaaattt tccatgcaga ggaaagccga taatggggca gaacccccttc ccgccaaaat 60

gacataatgt acattatcgg acaattatcc atatctggcc atg tcg cag gcc gct 115
Met Ser Gln Ala Ala
1 5

ggt aag ttt aag ccc atg act tca acg ctc gcc gaa tca aca ctt aca 163
Gly Lys Phe Lys Pro Met Thr Ser Thr Leu Ala Glu Ser Thr Leu Thr
10 15 20

tcc ctt aaa gaa ctt gag gat cca aag atc ctt tcc gtc aat gaa cgc 211
Ser Leu Lys Glu Leu Glu Asp Pro Lys Ile Leu Ser Val Asn Glu Arg

```
                25                  30                  35

cac ggc gat gat cac gca gtg aac ctc acc aag ctt cgc gcc gtt gcc   259
His Gly Asp Asp His Ala Val Asn Leu Thr Lys Leu Arg Ala Val Ala
         40                  45                  50

aaa gag ctg aaa aag aac cag ccg ctg gct cgt gag ctt tgg gca acc   307
Lys Glu Leu Lys Lys Asn Gln Pro Leu Ala Arg Glu Leu Trp Ala Thr
     55                  60                  65

gac gat aca gcc gca cgt ttg gtg gcg ttg ctt att tgc cga ccc aag   355
Asp Asp Thr Ala Ala Arg Leu Val Ala Leu Leu Ile Cys Arg Pro Lys
 70                  75                  80                  85

gaa ttt gat cag tct gaa ctc gac tcg atg atc cat gag gct cgc acg   403
Glu Phe Asp Gln Ser Glu Leu Asp Ser Met Ile His Glu Ala Arg Thr
                 90                  95                 100

ccg aag gtt ctt gat tgg ttg atc aat tat gtg gtc aag aag aat cct   451
Pro Lys Val Leu Asp Trp Leu Ile Asn Tyr Val Val Lys Lys Asn Pro
            105                 110                 115

cat tgg aac gat ctc cgt gtg ctc tgg ctt gaa gat ccc gcc gag aat   499
His Trp Asn Asp Leu Arg Val Leu Trp Leu Glu Asp Pro Ala Glu Asn
        120                 125                 130

gtt gcg gcc gcc ggc tgg gct ctc aac act cat gcc gtt atc aca aag   547
Val Ala Ala Ala Gly Trp Ala Leu Asn Thr His Ala Val Ile Thr Lys
    135                 140                 145

ccg gac gca ttg gac gat tcc gaa atc ctt gac acc att gaa gct cag   595
Pro Asp Ala Leu Asp Asp Ser Glu Ile Leu Asp Thr Ile Glu Ala Gln
150                 155                 160                 165

atg aaa act gcc gag cct cgc gta cag tgg tca atg aat gaa tgt ttg   643
Met Lys Thr Ala Glu Pro Arg Val Gln Trp Ser Met Asn Glu Cys Leu
                170                 175                 180

gcg caa atc ggc atc cat cgt cca gag ctt cgt gat cgt gcc att gcc   691
Ala Gln Ile Gly Ile His Arg Pro Glu Leu Arg Asp Arg Ala Ile Ala
            185                 190                 195

att ggt gag cgc ctg gaa gtt ctc aaa gat tat ccg acc cct cca aat   739
Ile Gly Glu Arg Leu Glu Val Leu Lys Asp Tyr Pro Thr Pro Pro Asn
        200                 205                 210

tgc acc tcg cct ttt gct ccg att tgg atc gaa gag atg gtt cgc agg   787
Cys Thr Ser Pro Phe Ala Pro Ile Trp Ile Glu Glu Met Val Arg Arg
    215                 220                 225

aaa aaa taaccgacct gttccctatc ttt                                816
Lys Lys
230
```

<210> 2120
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 2120

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Met Ser Gln Ala Ala Gly Lys Phe Lys Pro Met Thr Ser Thr Leu Ala
  1               5                  10                  15

Glu Ser Thr Leu Thr Ser Leu Lys Glu Leu Glu Asp Pro Lys Ile Leu
            20                  25                  30

Ser Val Asn Glu Arg His Gly Asp Asp His Ala Val Asn Leu Thr Lys
         35                  40                  45

Leu Arg Ala Val Ala Lys Glu Leu Lys Lys Asn Gln Pro Leu Ala Arg
     50                  55                  60

Glu Leu Trp Ala Thr Asp Asp Thr Ala Ala Arg Leu Val Ala Leu Leu
 65                  70                  75                  80

Ile Cys Arg Pro Lys Glu Phe Asp Gln Ser Glu Leu Asp Ser Met Ile
                 85                  90                  95

His Glu Ala Arg Thr Pro Lys Val Leu Asp Trp Leu Ile Asn Tyr Val
            100                 105                 110

Val Lys Lys Asn Pro His Trp Asn Asp Leu Arg Val Leu Trp Leu Glu
        115                 120                 125

Asp Pro Ala Glu Asn Val Ala Ala Ala Gly Trp Ala Leu Asn Thr His
    130                 135                 140

Ala Val Ile Thr Lys Pro Asp Ala Leu Asp Asp Ser Glu Ile Leu Asp
145                 150                 155                 160

Thr Ile Glu Ala Gln Met Lys Thr Ala Glu Pro Arg Val Gln Trp Ser
                165                 170                 175

Met Asn Glu Cys Leu Ala Gln Ile Gly Ile His Arg Pro Glu Leu Arg
            180                 185                 190

Asp Arg Ala Ile Ala Ile Gly Glu Arg Leu Glu Val Leu Lys Asp Tyr
        195                 200                 205

Pro Thr Pro Pro Asn Cys Thr Ser Pro Phe Ala Pro Ile Trp Ile Glu
    210                 215                 220

Glu Met Val Arg Arg Lys Lys
225                 230
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CONFIDENTIAL

<210> 2121
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> RXA01176

<400> 2121
gagctgtgca ccttgtgacc ttttgtgaca ctgctcaatg ctttacggct acgatgaaca 60

acaaaccgac gttttcgacg ctgtgaagga ctaattgcta gtg cgt tat ttt tac 115
Val Arg Tyr Phe Tyr

```
                                                    1               5

gat act gag ttc att gaa gat ggg cgc acg atc gaa ttg gtc tct att   163
Asp Thr Glu Phe Ile Glu Asp Gly Arg Thr Ile Glu Leu Val Ser Ile
                10                  15                  20

gga atc gtc gca gaa gac ggt cgc gag tat tac gca gtt agc aca cag   211
Gly Ile Val Ala Glu Asp Gly Arg Glu Tyr Tyr Ala Val Ser Thr Gln
            25                  30                  35

ttt gat tcc tcc aag gcg aac gct tgg gtg cgc gcc aac gtg ttg gac   259
Phe Asp Ser Ser Lys Ala Asn Ala Trp Val Arg Ala Asn Val Leu Asp
        40                  45                  50

aaa ttg cct aat cct tcc tcc aaa gtg tgg aaa tct gca gac act ata   307
Lys Leu Pro Asn Pro Ser Ser Lys Val Trp Lys Ser Ala Asp Thr Ile
    55                  60                  65

aag cgc gaa gtt tat gag ttt ctc acc tcc acc gga cca acc cct gaa   355
Lys Arg Glu Val Tyr Glu Phe Leu Thr Ser Thr Gly Pro Thr Pro Glu
70                  75                  80                  85

ctg tgg gcc tgg gtg ggc gca tat gac cac gtg ttg ttg gca caa atg   403
Leu Trp Ala Trp Val Gly Ala Tyr Asp His Val Leu Leu Ala Gln Met
                90                  95                  100

tgg ggc gat atg gcg ggg ctt cct cgg gag atc cct cgt ttt acc cgc   451
Trp Gly Asp Met Ala Gly Leu Pro Arg Glu Ile Pro Arg Phe Thr Arg
            105                 110                 115

gag ctt cgc cag tat tgg gac atg gct ggc cgc cca acg ctg cca gag   499
Glu Leu Arg Gln Tyr Trp Asp Met Ala Gly Arg Pro Thr Leu Pro Glu
        120                 125                 130

ctg ccg aac ggc aac cac gat gcg ttg att gat gcg cgt cat aat tta   547
Leu Pro Asn Gly Asn His Asp Ala Leu Ile Asp Ala Arg His Asn Leu
    135                 140                 145

gcc aag ttc aaa gtg tgc atg gca gcg ctg cct ttg ggt aaa agg gat   595
Ala Lys Phe Lys Val Cys Met Ala Ala Leu Pro Leu Gly Lys Arg Asp
150                 155                 160                 165

cgc gtc tct tagtcgatct gctcccattc cat                            627
Arg Val Ser
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CONFIDENTIAL

<210> 2122
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 2122

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Val Arg Tyr Phe Tyr Asp Thr Glu Phe Ile Glu Asp Gly Arg Thr Ile
  1               5                  10                  15

Glu Leu Val Ser Ile Gly Ile Val Ala Glu Asp Gly Arg Glu Tyr Tyr
            20                  25                  30

Ala Val Ser Thr Gln Phe Asp Ser Ser Lys Ala Asn Ala Trp Val Arg
        35                  40                  45
```

```
Ala Asn Val Leu Asp Lys Leu Pro Asn Pro Ser Ser Lys Val Trp Lys
     50                  55                  60

Ser Ala Asp Thr Ile Lys Arg Glu Val Tyr Glu Phe Leu Thr Ser Thr
 65                  70                  75                  80

Gly Pro Thr Pro Glu Leu Trp Ala Trp Val Gly Ala Tyr Asp His Val
                 85                  90                  95

Leu Leu Ala Gln Met Trp Gly Asp Met Ala Gly Leu Pro Arg Glu Ile
            100                 105                 110

Pro Arg Phe Thr Arg Glu Leu Arg Gln Tyr Trp Asp Met Ala Gly Arg
        115                 120                 125

Pro Thr Leu Pro Glu Leu Pro Asn Gly Asn His Asp Ala Leu Ile Asp
    130                 135                 140

Ala Arg His Asn Leu Ala Lys Phe Lys Val Cys Met Ala Ala Leu Pro
145                 150                 155                 160

Leu Gly Lys Arg Asp Arg Val Ser
                165
```

US 20050059124 A1

<210> 2123
<211> 2109
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2086)
<223> RXA01177

<400> 2123

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tgttcatcgt agccgtaaag cattgagcag tgtcacaaaa ggtcacaagg tgcacagctc 60

agttccttaa aaaccgctgg atacggatac actatttttc atg cac ggt gaa aaa   115
                                            Met His Gly Glu Lys
                                              1               5

ctt gtg gat ggc act gag gga aat ctc agt caa ttc caa tgg cgc gat   163
Leu Val Asp Gly Thr Glu Gly Asn Leu Ser Gln Phe Gln Trp Arg Asp
                  10                  15                  20

atg gct aca aat cag acg ctg aga aaa gca ctg tta gtg ctt tct acc   211
Met Ala Thr Asn Gln Thr Leu Arg Lys Ala Leu Leu Val Leu Ser Thr
              25                  30                  35

atc gct cta ctc ttg act tta tgg cct tca att ttc aat gtt cgg gcc   259
Ile Ala Leu Leu Leu Thr Leu Trp Pro Ser Ile Phe Asn Val Arg Ala
          40                  45                  50

atc gag tct ttt gtt ttc ttc ttc cat att gat act gac gtg tac cgc   307
Ile Glu Ser Phe Val Phe Phe Phe His Ile Asp Thr Asp Val Tyr Arg
     55                  60                  65

gcc ggt gct aat gca ttc ttg cat ggc gag aat ctg tat acc cag gac   355
Ala Gly Ala Asn Ala Phe Leu His Gly Glu Asn Leu Tyr Thr Gln Asp
```

```
 70                  75                  80                  85

tac caa gtt ggt agc att caa ctt ccc ttc acg tac cca ccg att tct   403
Tyr Gln Val Gly Ser Ile Gln Leu Pro Phe Thr Tyr Pro Pro Ile Ser
                 90                  95                 100

gct gcg ctg ttt gtt cca ctt gca atc ctt gca agc agt gta gcc gga   451
Ala Ala Leu Phe Val Pro Leu Ala Ile Leu Ala Ser Ser Val Ala Gly
            105                 110                 115

ata gca tta acg ctt att tcc acg gtg ttg ctg tgg tgg agc gta gct   499
Ile Ala Leu Thr Leu Ile Ser Thr Val Leu Leu Trp Trp Ser Val Ala
        120                 125                 130

atc gtc ttg cgc cga gtg ctc aag ggt ctc acg gat gct gat tcc agg   547
Ile Val Leu Arg Arg Val Leu Lys Gly Leu Thr Asp Ala Asp Ser Arg
    135                 140                 145

ttt gtg tcc tat ttg att ctg cct atg gca ttg tcc acg gaa cct gta   595
Phe Val Ser Tyr Leu Ile Leu Pro Met Ala Leu Ser Thr Glu Pro Val
150                 155                 160                 165

ttc cag acc ctg cag ttt ggc cag gtc aac atc att ttg atg gcg ctg   643
Phe Gln Thr Leu Gln Phe Gly Gln Val Asn Ile Ile Leu Met Ala Leu
                170                 175                 180

gtt ctc atg gat acc ttc acc aaa aag ccc tgg ttg cca cgt ggt ttt   691
Val Leu Met Asp Thr Phe Thr Lys Lys Pro Trp Leu Pro Arg Gly Phe
            185                 190                 195

tgg att ggt ttg gcg gca tcc atc aag ctg acc ccc gca gtc ttt ggc   739
Trp Ile Gly Leu Ala Ala Ser Ile Lys Leu Thr Pro Ala Val Phe Gly
        200                 205                 210

ctt tac ttc cta gtg aag aag gac tgg aag ggc gct gga gta gca att   787
Leu Tyr Phe Leu Val Lys Lys Asp Trp Lys Gly Ala Gly Val Ala Ile
    215                 220                 225

gct tct ggc gta ggt ttt tcc gcc ttg gcg ttt atc ctc tca cct tca   835
Ala Ser Gly Val Gly Phe Ser Ala Leu Ala Phe Ile Leu Ser Pro Ser
230                 235                 240                 245

agt tcc aag att tac tgg act gaa aca ctc aac gac cct tct cgc atc   883
Ser Ser Lys Ile Tyr Trp Thr Glu Thr Leu Asn Asp Pro Ser Arg Ile
                250                 255                 260

ggc aac cta tct tat att gct aac caa tct gtg cgt gga acg ctc agc   931
Gly Asn Leu Ser Tyr Ile Ala Asn Gln Ser Val Arg Gly Thr Leu Ser
            265                 270                 275

cga atg atg cat gaa cag cag gat ctc gtc gaa aag ctt tgg ctt gtg   979
Arg Met Met His Glu Gln Gln Asp Leu Val Glu Lys Leu Trp Leu Val
        280                 285                 290

gca gtt gtc ttg tgc ctt gcc gct gtc gcc gtc gcc atg tgg cgc gtg   1027
Ala Val Val Leu Cys Leu Ala Ala Val Ala Val Ala Met Trp Arg Val
    295                 300                 305

gta cgc gcc ggc aac ccg tac ggc gcc gtc atg ctc aac tcg ttg att   1075
Val Arg Ala Gly Asn Pro Tyr Gly Ala Val Met Leu Asn Ser Leu Ile
310                 315                 320                 325
```

```
gct ctg ctg tgc tcc cct gtt tca tgg tct cac cac tgg gta tgg ctg   1123
Ala Leu Leu Cys Ser Pro Val Ser Trp Ser His His Trp Val Trp Leu
                330                 335                 340

att cca atc gct att ggt ttg ggg gca agt gcg tgg aac cag cgg cgg   1171
Ile Pro Ile Ala Ile Gly Leu Gly Ala Ser Ala Trp Asn Gln Arg Arg
            345                 350                 355

act gct cca gga att gcc gcg acg gct gga gtc ttg gcg ctt ctg acc   1219
Thr Ala Pro Gly Ile Ala Ala Thr Ala Gly Val Leu Ala Leu Leu Thr
        360                 365                 370

acg att ccg atg ttc atc aca aca ttt tgg aac atg cca tac gat tca   1267
Thr Ile Pro Met Phe Ile Thr Thr Phe Trp Asn Met Pro Tyr Asp Ser
    375                 380                 385

gag tct tac cca ttt tgg cca ttg att ctg cag ccg tcg ggc aac gcg   1315
Glu Ser Tyr Pro Phe Trp Pro Leu Ile Leu Gln Pro Ser Gly Asn Ala
390                 395                 400                 405

tat gta gta gtg gtc atc gct att ttg atc gtc gcg att gtg aat cca   1363
Tyr Val Val Val Val Ile Ala Ile Leu Ile Val Ala Ile Val Asn Pro
                410                 415                 420

aca gtt ttg ggc agt ggc aat aaa gct gtt tca ggc cag gca gag aag   1411
Thr Val Leu Gly Ser Gly Asn Lys Ala Val Ser Gly Gln Ala Glu Lys
            425                 430                 435

aag tcc tcc cct gcg ttg ctt gtt gtt tta gcg att gcc att ttc tac   1459
Lys Ser Ser Pro Ala Leu Leu Val Val Leu Ala Ile Ala Ile Phe Tyr
        440                 445                 450

ctc ttt gcc aat att tgg ttt aag gga aac aat caa aac aaa gcg ctc   1507
Leu Phe Ala Asn Ile Trp Phe Lys Gly Asn Asn Gln Asn Lys Ala Leu
    455                 460                 465

att cag tac cca ctg cag act atg gaa ggt cgc ggt ctc act gac ttc   1555
Ile Gln Tyr Pro Leu Gln Thr Met Glu Gly Arg Gly Leu Thr Asp Phe
470                 475                 480                 485

ggc gag ctt att ttt gaa ttc gcg gct tcc tcc aac cag ctt gtt tcc   1603
Gly Glu Leu Ile Phe Glu Phe Ala Ala Ser Ser Asn Gln Leu Val Ser
                490                 495                 500

ctc tgg ata atc ggc gcc ctc aac gcc atc gca ttg gct att acc ctg   1651
Leu Trp Ile Ile Gly Ala Leu Asn Ala Ile Ala Leu Ala Ile Thr Leu
            505                 510                 515

tgg ttc ctc ctt cag cgt ttt gct ggg aag aag agc tcc tgg ctg att   1699
Trp Phe Leu Leu Gln Arg Phe Ala Gly Lys Lys Ser Ser Trp Leu Ile
        520                 525                 530

tat ctc agc acc gtg gct gtt gcg ctg atg atg ttc tca gtg cag gat   1747
Tyr Leu Ser Thr Val Ala Val Ala Leu Met Met Phe Ser Val Gln Asp
    535                 540                 545

gcc ttg cag ttt ggt tcg ctg act ctc gtt gca ctc gca ttg atc act   1795
Ala Leu Gln Phe Gly Ser Leu Thr Leu Val Ala Leu Ala Leu Ile Thr
550                 555                 560                 565
```

```
gtt gat gtg ttg agt gtc aga gag att ggc cgc cgc ggg ctg ctc aca   1843
Val Asp Val Leu Ser Val Arg Glu Ile Gly Arg Arg Gly Leu Leu Thr
                570                 575                 580

gga ctt gca gca gcc ctg ttt gga tgg cca att ctg att gtt atc gga   1891
Gly Leu Ala Ala Ala Leu Phe Gly Trp Pro Ile Leu Ile Val Ile Gly
            585                 590                 595

ttc ctc att cac cga cgt tat gca gca aca atc aca acc act gtc acc   1939
Phe Leu Ile His Arg Arg Tyr Ala Ala Thr Ile Thr Thr Thr Val Thr
        600                 605                 610

gca gct gtg ctg tgg atc tta gga att ctg ctc aat cca gac gcc ttc   1987
Ala Ala Val Leu Trp Ile Leu Gly Ile Leu Leu Asn Pro Asp Ala Phe
    615                 620                 625

aac ctc aac ctg ctg cgt caa tgg ttc aac ggg cgc gat ggt cgg gac   2035
Asn Leu Asn Leu Leu Arg Gln Trp Phe Asn Gly Arg Asp Gly Arg Asp
630                 635                 640                 645

aat ttg tcc ttc tat gct ttc ctt gcc agg tgg gtc agc gaa tcc cca   2083
Asn Leu Ser Phe Tyr Ala Phe Leu Ala Arg Trp Val Ser Glu Ser Pro
                650                 655                 660

gca tgatgttcgt atggttcatc gtc                                    2109
Ala
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Sequence Listing

<210> 2124
<211> 662
<212> PRT
<213> Corynebacterium glutamicum

<400> 2124

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Met His Gly Glu Lys Leu Val Asp Gly Thr Glu Gly Asn Leu Ser Gln
  1               5                  10                  15

Phe Gln Trp Arg Asp Met Ala Thr Asn Gln Thr Leu Arg Lys Ala Leu
             20                  25                  30

Leu Val Leu Ser Thr Ile Ala Leu Leu Leu Thr Leu Trp Pro Ser Ile
         35                  40                  45

Phe Asn Val Arg Ala Ile Glu Ser Phe Val Phe Phe Phe His Ile Asp
     50                  55                  60

Thr Asp Val Tyr Arg Ala Gly Ala Asn Ala Phe Leu His Gly Glu Asn
 65                  70                  75                  80

Leu Tyr Thr Gln Asp Tyr Gln Val Gly Ser Ile Gln Leu Pro Phe Thr
                 85                  90                  95

Tyr Pro Pro Ile Ser Ala Ala Leu Phe Val Pro Leu Ala Ile Leu Ala
            100                 105                 110

Ser Ser Val Ala Gly Ile Ala Leu Thr Leu Ile Ser Thr Val Leu Leu
        115                 120                 125

Trp Trp Ser Val Ala Ile Val Leu Arg Arg Val Leu Lys Gly Leu Thr
    130                 135                 140
```

```
Asp Ala Asp Ser Arg Phe Val Ser Tyr Leu Ile Leu Pro Met Ala Leu
145                 150                 155                 160

Ser Thr Glu Pro Val Phe Gln Thr Leu Gln Phe Gly Gln Val Asn Ile
                165                 170                 175

Ile Leu Met Ala Leu Val Leu Met Asp Thr Phe Thr Lys Lys Pro Trp
            180                 185                 190

Leu Pro Arg Gly Phe Trp Ile Gly Leu Ala Ala Ser Ile Lys Leu Thr
        195                 200                 205

Pro Ala Val Phe Gly Leu Tyr Phe Leu Val Lys Lys Asp Trp Lys Gly
    210                 215                 220

Ala Gly Val Ala Ile Ala Ser Gly Val Gly Phe Ser Ala Leu Ala Phe
225                 230                 235                 240

Ile Leu Ser Pro Ser Ser Ser Lys Ile Tyr Trp Thr Glu Thr Leu Asn
                245                 250                 255

Asp Pro Ser Arg Ile Gly Asn Leu Ser Tyr Ile Ala Asn Gln Ser Val
            260                 265                 270

Arg Gly Thr Leu Ser Arg Met Met His Glu Gln Gln Asp Leu Val Glu
        275                 280                 285

Lys Leu Trp Leu Val Ala Val Val Leu Cys Leu Ala Ala Val Ala Val
    290                 295                 300

Ala Met Trp Arg Val Val Arg Ala Gly Asn Pro Tyr Gly Ala Val Met
305                 310                 315                 320

Leu Asn Ser Leu Ile Ala Leu Leu Cys Ser Pro Val Ser Trp Ser His
                325                 330                 335

His Trp Val Trp Leu Ile Pro Ile Ala Ile Gly Leu Gly Ala Ser Ala
            340                 345                 350

Trp Asn Gln Arg Arg Thr Ala Pro Gly Ile Ala Ala Thr Ala Gly Val
        355                 360                 365

Leu Ala Leu Leu Thr Thr Ile Pro Met Phe Ile Thr Thr Phe Trp Asn
    370                 375                 380

Met Pro Tyr Asp Ser Glu Ser Tyr Pro Phe Trp Pro Leu Ile Leu Gln
385                 390                 395                 400

Pro Ser Gly Asn Ala Tyr Val Val Val Val Ile Ala Ile Leu Ile Val
                405                 410                 415

Ala Ile Val Asn Pro Thr Val Leu Gly Ser Gly Asn Lys Ala Val Ser
            420                 425                 430

Gly Gln Ala Glu Lys Lys Ser Ser Pro Ala Leu Leu Val Val Leu Ala
        435                 440                 445

Ile Ala Ile Phe Tyr Leu Phe Ala Asn Ile Trp Phe Lys Gly Asn Asn
    450                 455                 460
```

```
Gln Asn Lys Ala Leu Ile Gln Tyr Pro Leu Gln Thr Met Glu Gly Arg
465                 470                 475                 480

Gly Leu Thr Asp Phe Gly Glu Leu Ile Phe Glu Phe Ala Ala Ser Ser
                485                 490                 495

Asn Gln Leu Val Ser Leu Trp Ile Ile Gly Ala Leu Asn Ala Ile Ala
            500                 505                 510

Leu Ala Ile Thr Leu Trp Phe Leu Leu Gln Arg Phe Ala Gly Lys Lys
        515                 520                 525

Ser Ser Trp Leu Ile Tyr Leu Ser Thr Val Ala Val Ala Leu Met Met
    530                 535                 540

Phe Ser Val Gln Asp Ala Leu Gln Phe Gly Ser Leu Thr Leu Val Ala
545                 550                 555                 560

Leu Ala Leu Ile Thr Val Asp Val Leu Ser Val Arg Glu Ile Gly Arg
                565                 570                 575

Arg Gly Leu Leu Thr Gly Leu Ala Ala Ala Leu Phe Gly Trp Pro Ile
            580                 585                 590

Leu Ile Val Ile Gly Phe Leu Ile His Arg Arg Tyr Ala Ala Thr Ile
        595                 600                 605

Thr Thr Thr Val Thr Ala Ala Val Leu Trp Ile Leu Gly Ile Leu Leu
    610                 615                 620

Asn Pro Asp Ala Phe Asn Leu Asn Leu Leu Arg Gln Trp Phe Asn Gly
625                 630                 635                 640

Arg Asp Gly Arg Asp Asn Leu Ser Phe Tyr Ala Phe Leu Ala Arg Trp
                645                 650                 655

Val Ser Glu Ser Pro Ala
            660
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<210> 2125
<211> 573
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(550)
<223> RXA01178

<400> 2125

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tcaacctcaa cctgctgcgt caatggttca acgggcgcga tggtcgggac aatttgtcct 60

tctatgcttt ccttgccagg tgggtcagcg aatccccagc atg atg ttc gta tgg   115
                                            Met Met Phe Val Trp
                                              1               5

ttc atc gtc gcc cta gga ctt ggt gcc tgg gca atc cac cgc acc tgg   163
Phe Ile Val Ala Leu Gly Leu Gly Ala Trp Ala Ile His Arg Thr Trp
                 10                  15                  20
```

```
tca cat gga ttc aag gac ctc tcc gtt gca ctg agc atc gca cta cca   211
Ser His Gly Phe Lys Asp Leu Ser Val Ala Leu Ser Ile Ala Leu Pro
            25                  30                  35

acc ttg gtg ctc ccc ata gtg gaa ctc cac cac ctc gtg cta ctt ctt   259
Thr Leu Val Leu Pro Ile Val Glu Leu His His Leu Val Leu Leu Leu
        40                  45                  50

cca ctg atc gca gtg ttg ctt cgt caa gga cgc gtg gca att tcc tac   307
Pro Leu Ile Ala Val Leu Leu Arg Gln Gly Arg Val Ala Ile Ser Tyr
    55                  60                  65

ctc atc gga ttt atc tac cta gtc tca tgg act ccg caa cac ctg tcc   355
Leu Ile Gly Phe Ile Tyr Leu Val Ser Trp Thr Pro Gln His Leu Ser
70                  75                  80                  85

tac tcc acg gta ttc cca ctt aat gat cca gca cca gaa ggg tac gtc   403
Tyr Ser Thr Val Phe Pro Leu Asn Asp Pro Ala Pro Glu Gly Tyr Val
                90                  95                  100

gcc cac ttt gga tgg tat tta ctc gtt gaa cca atg gcg gta gca ccg   451
Ala His Phe Gly Trp Tyr Leu Leu Val Glu Pro Met Ala Val Ala Pro
            105                 110                 115

gca gct ata atc ctc gga gca ttt att gcc tgt gct gca acc aca cct   499
Ala Ala Ile Ile Leu Gly Ala Phe Ile Ala Cys Ala Ala Thr Thr Pro
        120                 125                 130

aaa aca agt cag ctc gtg cag gtc gac aag tca agc gcg gaa aac acc   547
Lys Thr Ser Gln Leu Val Gln Val Asp Lys Ser Ser Ala Glu Asn Thr
    135                 140                 145

aag taagccttac agtccgacag cct                                    573
Lys
150
```

<210> 2126
<211> 150
<212> PRT
<213> Corynebacterium glutamicum

<400> 2126

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Met Met Phe Val Trp Phe Ile Val Ala Leu Gly Leu Gly Ala Trp Ala
  1               5                  10                  15

Ile His Arg Thr Trp Ser His Gly Phe Lys Asp Leu Ser Val Ala Leu
            20                  25                  30

Ser Ile Ala Leu Pro Thr Leu Val Leu Pro Ile Val Glu Leu His His
        35                  40                  45

Leu Val Leu Leu Leu Pro Leu Ile Ala Val Leu Leu Arg Gln Gly Arg
    50                  55                  60

Val Ala Ile Ser Tyr Leu Ile Gly Phe Ile Tyr Leu Val Ser Trp Thr
65                  70                  75                  80

Pro Gln His Leu Ser Tyr Ser Thr Val Phe Pro Leu Asn Asp Pro Ala
                85                  90                  95
```

```
Pro Glu Gly Tyr Val Ala His Phe Gly Trp Tyr Leu Leu Val Glu Pro
            100                 105                 110

Met Ala Val Ala Pro Ala Ala Ile Ile Leu Gly Ala Phe Ile Ala Cys
        115                 120                 125

Ala Ala Thr Thr Pro Lys Thr Ser Gln Leu Val Gln Val Asp Lys Ser
    130                 135                 140

Ser Ala Glu Asn Thr Lys
145                 150


<210> 2127
<211> 1589
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1573)
<223> RXA01184

<400> 2127
taaaacactt ctgaaactac agctgacgtt gtggggaaga actattaaag gaaataaagc 60

ggcaatagtg atgatgtcgc tgatatcttt ttacgccttg atg ggt ttg ttt ggt   115
                                            Met Gly Leu Phe Gly
                                              1               5

ttc ggc atc ttt ttg gct ctt ggg ctt ggg caa gac cac atg ggc atc   163
Phe Gly Ile Phe Leu Ala Leu Gly Leu Gly Gln Asp His Met Gly Ile
                  10                  15                  20

ctt gct ggt gtt gtc tcg gtc ggc atg gtg gct tat tgc att gct gcg   211
Leu Ala Gly Val Val Ser Val Gly Met Val Ala Tyr Cys Ile Ala Ala
              25                  30                  35

ttt atg tgg ccg tca ggt gag ggg cag ctg gat ccg act gca ttt tcc   259
Phe Met Trp Pro Ser Gly Glu Gly Gln Leu Asp Pro Thr Ala Phe Ser
          40                  45                  50

acc atg ccg cta tcg gcg aag caa tta ttg cct gga ttc gct atc ggt   307
Thr Met Pro Leu Ser Ala Lys Gln Leu Leu Pro Gly Phe Ala Ile Gly
      55                  60                  65

acg ctc ctg cag tca cgg ggg att att gcg gtg att tgt acg gtg gcg   355
Thr Leu Leu Gln Ser Arg Gly Ile Ile Ala Val Ile Cys Thr Val Ala
  70                  75                  80                  85

aca tcc att att gct gcg gtg ttt tta cct gtt ggt tcg tgg ccg atg   403
Thr Ser Ile Ile Ala Ala Val Phe Leu Pro Val Gly Ser Trp Pro Met
                  90                  95                 100

atc gtg ttc atg atg gcg gta tcg ctg gtt act acg ttg ctt ttg ggt   451
Ile Val Phe Met Met Ala Val Ser Leu Val Thr Thr Leu Leu Leu Gly
            105                 110                 115

gag ttg ctt ggg gcg ttg acc tcg ggt tct tct tct agg gtg agt aat   499
Glu Leu Leu Gly Ala Leu Thr Ser Gly Ser Ser Ser Arg Val Ser Asn
        120                 125                 130
```

```
gat cgc cgt aca gtt ctt act tcc gtt gtc ttc atg gtg ttt gtt gtt   547
Asp Arg Arg Thr Val Leu Thr Ser Val Val Phe Met Val Phe Val Val
    135                 140                 145

ggc tat aac atg ctg att ggc gcg gat gga atg agt cga atc gat gcc   595
Gly Tyr Asn Met Leu Ile Gly Ala Asp Gly Met Ser Arg Ile Asp Ala
150                 155                 160                 165

att ggg gct tat aca aag tgg aca cca ttt ggg gcg ggt gca ggt gct   643
Ile Gly Ala Tyr Thr Lys Trp Thr Pro Phe Gly Ala Gly Ala Gly Ala
                170                 175                 180

att gag gct ttt gct gtt ggt ttg tgg ggt gag gca ggc ctg tta aca   691
Ile Glu Ala Phe Ala Val Gly Leu Trp Gly Glu Ala Gly Leu Leu Thr
            185                 190                 195

ttg ctg gct ttt gtt tat gtt gct gct ggt ttc tgg tta tgg tca cag   739
Leu Leu Ala Phe Val Tyr Val Ala Ala Gly Phe Trp Leu Trp Ser Gln
        200                 205                 210

ctg att aat cgc gcg ctc act gcg ccg ctg gac caa ggt ggg caa ggg   787
Leu Ile Asn Arg Ala Leu Thr Ala Pro Leu Asp Gln Gly Gly Gln Gly
    215                 220                 225

caa agc gct aaa gac agc gcc ggt gaa ggc aag aag gtt ctc ttt ctg   835
Gln Ser Ala Lys Asp Ser Ala Gly Glu Gly Lys Lys Val Leu Phe Leu
230                 235                 240                 245

cca ggt att cct tgg tca gtt gga ggt gcc att ttc tcg agg tcg ctg   883
Pro Gly Ile Pro Trp Ser Val Gly Gly Ala Ile Phe Ser Arg Ser Leu
                250                 255                 260

cgt tat atg ttc agg gac tcc agg ttg ttg gga tca atg att gtg ttc   931
Arg Tyr Met Phe Arg Asp Ser Arg Leu Leu Gly Ser Met Ile Val Phe
            265                 270                 275

ccg ctt ctt ggc gtg ctg ttt att ttc cag agc ttc acc gtt gag ttt   979
Pro Leu Leu Gly Val Leu Phe Ile Phe Gln Ser Phe Thr Val Glu Phe
        280                 285                 290

ttc atg atc tat gtt ggg ttg atc atg atg gca gtg ttc gca gga tcc   1027
Phe Met Ile Tyr Val Gly Leu Ile Met Met Ala Val Phe Ala Gly Ser
    295                 300                 305

gtt gct acc aat gat ttt ggc tat gac ggc cct tcg ttg tgg cta aat   1075
Val Ala Thr Asn Asp Phe Gly Tyr Asp Gly Pro Ser Leu Trp Leu Asn
310                 315                 320                 325

atc gtt gct ggt gtc aaa gcc cga acg ttg ttg atg ccc agg cac tgg   1123
Ile Val Ala Gly Val Lys Ala Arg Thr Leu Leu Met Pro Arg His Trp
                330                 335                 340

gca tca atg ctg ccg gga agt gtg tca att gtg gtg ttt atg atc atc   1171
Ala Ser Met Leu Pro Gly Ser Val Ser Ile Val Val Phe Met Ile Ile
            345                 350                 355

acc att gtg ctc gcg gag aat aag acc acc gct gtg ctg atc tgt ttt   1219
Thr Ile Val Leu Ala Glu Asn Lys Thr Thr Ala Val Leu Ile Cys Phe
        360                 365                 370
```

```
att ggc ctg ggg atc ttt atc tcc agt gcg gct gta gcg ttg ttg gtc   1267
Ile Gly Leu Gly Ile Phe Ile Ser Ser Ala Ala Val Ala Leu Leu Val
    375                 380                 385

acc aca ttt aat ccg tat ccg act tct aag cca ggc acg agt cct tgg   1315
Thr Thr Phe Asn Pro Tyr Pro Thr Ser Lys Pro Gly Thr Ser Pro Trp
390                 395                 400                 405

ggc gat cga agt ggc tat tcc ggt gct gcg ttc gtg gga gca ttt gcc   1363
Gly Asp Arg Ser Gly Tyr Ser Gly Ala Ala Phe Val Gly Ala Phe Ala
                410                 415                 420

gca ctg tta ctg gga tgg atc ccg acg att cct act atc gca ttg ggt   1411
Ala Leu Leu Leu Gly Trp Ile Pro Thr Ile Pro Thr Ile Ala Leu Gly
            425                 430                 435

atc ttt ggt ctg gtt acc gat cag atg tgg atg atc atc ctc gcg gag   1459
Ile Phe Gly Leu Val Thr Asp Gln Met Trp Met Ile Ile Leu Ala Glu
        440                 445                 450

gtg ctg gcc att att ctc cca gta gct gtg tac atc ggc gtt gct aag   1507
Val Leu Ala Ile Ile Leu Pro Val Ala Val Tyr Ile Gly Val Ala Lys
    455                 460                 465

gtg tgt att cgc aag gtg gag aag gat ctt ccg gag atc ttc gac aag   1555
Val Cys Ile Arg Lys Val Glu Lys Asp Leu Pro Glu Ile Phe Asp Lys
470                 475                 480                 485

gtg aaa act cac gtg aaa tagaaaaatg cggggt                        1589
Val Lys Thr His Val Lys
                490
```

US-09-964-553-2128

<210> 2128
<211> 491
<212> PRT
<213> Corynebacterium glutamicum

<400> 2128

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Met Gly Leu Phe Gly Phe Gly Ile Phe Leu Ala Leu Gly Leu Gly Gln
  1               5                  10                  15

Asp His Met Gly Ile Leu Ala Gly Val Val Ser Val Gly Met Val Ala
             20                  25                  30

Tyr Cys Ile Ala Ala Phe Met Trp Pro Ser Gly Glu Gly Gln Leu Asp
         35                  40                  45

Pro Thr Ala Phe Ser Thr Met Pro Leu Ser Ala Lys Gln Leu Leu Pro
     50                  55                  60

Gly Phe Ala Ile Gly Thr Leu Leu Gln Ser Arg Gly Ile Ile Ala Val
 65                  70                  75                  80

Ile Cys Thr Val Ala Thr Ser Ile Ile Ala Ala Val Phe Leu Pro Val
                 85                  90                  95

Gly Ser Trp Pro Met Ile Val Phe Met Met Ala Val Ser Leu Val Thr
            100                 105                 110

Thr Leu Leu Leu Gly Glu Leu Leu Gly Ala Leu Thr Ser Gly Ser Ser
```

```
        115                 120                 125

Ser Arg Val Ser Asn Asp Arg Arg Thr Val Leu Thr Ser Val Val Phe
    130                 135                 140

Met Val Phe Val Val Gly Tyr Asn Met Leu Ile Gly Ala Asp Gly Met
145                 150                 155                 160

Ser Arg Ile Asp Ala Ile Gly Ala Tyr Thr Lys Trp Thr Pro Phe Gly
                165                 170                 175

Ala Gly Ala Gly Ala Ile Glu Ala Phe Ala Val Gly Leu Trp Gly Glu
            180                 185                 190

Ala Gly Leu Leu Thr Leu Leu Ala Phe Val Tyr Val Ala Ala Gly Phe
        195                 200                 205

Trp Leu Trp Ser Gln Leu Ile Asn Arg Ala Leu Thr Ala Pro Leu Asp
    210                 215                 220

Gln Gly Gly Gln Gly Gln Ser Ala Lys Asp Ser Ala Gly Glu Gly Lys
225                 230                 235                 240

Lys Val Leu Phe Leu Pro Gly Ile Pro Trp Ser Val Gly Gly Ala Ile
                245                 250                 255

Phe Ser Arg Ser Leu Arg Tyr Met Phe Arg Asp Ser Arg Leu Leu Gly
            260                 265                 270

Ser Met Ile Val Phe Pro Leu Leu Gly Val Leu Phe Ile Phe Gln Ser
        275                 280                 285

Phe Thr Val Glu Phe Phe Met Ile Tyr Val Gly Leu Ile Met Met Ala
    290                 295                 300

Val Phe Ala Gly Ser Val Ala Thr Asn Asp Phe Gly Tyr Asp Gly Pro
305                 310                 315                 320

Ser Leu Trp Leu Asn Ile Val Ala Gly Val Lys Ala Arg Thr Leu Leu
                325                 330                 335

Met Pro Arg His Trp Ala Ser Met Leu Pro Gly Ser Val Ser Ile Val
            340                 345                 350

Val Phe Met Ile Ile Thr Ile Val Leu Ala Glu Asn Lys Thr Thr Ala
        355                 360                 365

Val Leu Ile Cys Phe Ile Gly Leu Gly Ile Phe Ile Ser Ser Ala Ala
    370                 375                 380

Val Ala Leu Leu Val Thr Thr Phe Asn Pro Tyr Pro Thr Ser Lys Pro
385                 390                 395                 400

Gly Thr Ser Pro Trp Gly Asp Arg Ser Gly Tyr Ser Gly Ala Ala Phe
                405                 410                 415

Val Gly Ala Phe Ala Ala Leu Leu Leu Gly Trp Ile Pro Thr Ile Pro
            420                 425                 430

Thr Ile Ala Leu Gly Ile Phe Gly Leu Val Thr Asp Gln Met Trp Met
        435                 440                 445
```

```
Ile Ile Leu Ala Glu Val Leu Ala Ile Ile Leu Pro Val Ala Val Tyr
    450                 455                 460

Ile Gly Val Ala Lys Val Cys Ile Arg Lys Val Glu Lys Asp Leu Pro
465                 470                 475                 480

Glu Ile Phe Asp Lys Val Lys Thr His Val Lys
                485                 490


<210> 2129
<211> 1221
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1198)
<223> RXA01186

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agttcaacaa ttacataaca tctgaaagaa tagggacatt atg gct aca cct gta   115
                                        Met Ala Thr Pro Val
                                          1               5

cca ctg gtt ttt aac gca cct aag cgt ggc atg ccc cca acc cac ttt   163
Pro Leu Val Phe Asn Ala Pro Lys Arg Gly Met Pro Pro Thr His Phe
                  10                  15                  20

gcg gat ctt aat gat gag gct cgc att gag gct ctt aaa gag ctc ggc   211
Ala Asp Leu Asn Asp Glu Ala Arg Ile Glu Ala Leu Lys Glu Leu Gly
              25                  30                  35

ttg ccc aaa ttc cga ctc aat cag atc gct cga cac tac tat ggt cgc   259
Leu Pro Lys Phe Arg Leu Asn Gln Ile Ala Arg His Tyr Tyr Gly Arg
          40                  45                  50

ctc gag gct gac cca ctc act atg acg gac ctg cct gaa ggt gct cgt   307
Leu Glu Ala Asp Pro Leu Thr Met Thr Asp Leu Pro Glu Gly Ala Arg
      55                  60                  65

caa gaa gtc aag gat gct ctt ttt cca acg ttg atg tct cct ctg cgc   355
Gln Glu Val Lys Asp Ala Leu Phe Pro Thr Leu Met Ser Pro Leu Arg
  70                  75                  80                  85

gtc gtc gaa acc gat gac gat aca act cag aag acg tta tgg aag ctc   403
Val Val Glu Thr Asp Asp Asp Thr Thr Gln Lys Thr Leu Trp Lys Leu
                  90                  95                 100

cat gat ggc act ttg ctt gag tct gtt ctc atg cgc tat tca gat cgc   451
His Asp Gly Thr Leu Leu Glu Ser Val Leu Met Arg Tyr Ser Asp Arg
              105                 110                 115

tcc acg ctg tgt att tct tcg cag gct ggt tgc ggc atg gcg tgc cca   499
Ser Thr Leu Cys Ile Ser Ser Gln Ala Gly Cys Gly Met Ala Cys Pro
          120                 125                 130

ttc tgt gca act ggt cag ggc ggt ttg gac cgt aac ctt tca atc ggt   547
```

```
Phe Cys Ala Thr Gly Gln Gly Gly Leu Asp Arg Asn Leu Ser Ile Gly
    135                 140                 145

gag atc gtg gat cag gtt cgt aat gct gct gca acg atg cag tca gag   595
Glu Ile Val Asp Gln Val Arg Asn Ala Ala Ala Thr Met Gln Ser Glu
150                 155                 160                 165

ggc ggt cgt ctg tcc aac att gtg ttc atg gga atg ggc gag cct ctc   643
Gly Gly Arg Leu Ser Asn Ile Val Phe Met Gly Met Gly Glu Pro Leu
                170                 175                 180

gct aac tac aag cgc gtg gtg tcg gct gtt cgt cag atc acg cag cca   691
Ala Asn Tyr Lys Arg Val Val Ser Ala Val Arg Gln Ile Thr Gln Pro
            185                 190                 195

agc cct gcg ggc ttc ggc att tcc cag cgc agt gtg act gtc tcc acc   739
Ser Pro Ala Gly Phe Gly Ile Ser Gln Arg Ser Val Thr Val Ser Thr
        200                 205                 210

gtg ggc ctc gct cca gct atc agg aag ctt gcc gac gaa gag atg tcc   787
Val Gly Leu Ala Pro Ala Ile Arg Lys Leu Ala Asp Glu Glu Met Ser
    215                 220                 225

gta act ttg gca gtt tcc ttg cac act cca gac gat gag ttg cgt gac   835
Val Thr Leu Ala Val Ser Leu His Thr Pro Asp Asp Glu Leu Arg Asp
230                 235                 240                 245

act ctc gtg cca gtc aac aat cgt tgg cct gtc gct gag gta ctg gac   883
Thr Leu Val Pro Val Asn Asn Arg Trp Pro Val Ala Glu Val Leu Asp
                250                 255                 260

gct gct cgt tac tac gca gat aag tct ggc cgt cgc gtc tcc atc gag   931
Ala Ala Arg Tyr Tyr Ala Asp Lys Ser Gly Arg Arg Val Ser Ile Glu
            265                 270                 275

tat gcg ctc att cgc gat gtg aat gac cag gat tgg cgc gca gat atg   979
Tyr Ala Leu Ile Arg Asp Val Asn Asp Gln Asp Trp Arg Ala Asp Met
        280                 285                 290

ctg ggc gag aag ctg cat aag gct ttg ggc tcc cgt gtg cac gtc aac   1027
Leu Gly Glu Lys Leu His Lys Ala Leu Gly Ser Arg Val His Val Asn
    295                 300                 305

ttg att cca ttg aac cca act cct ggt tct aag tgg gat gct gca cca   1075
Leu Ile Pro Leu Asn Pro Thr Pro Gly Ser Lys Trp Asp Ala Ala Pro
310                 315                 320                 325

aag gct cgt cag gat gag ttt gtg cgt cgt gtg atc gcc aag ggt gtt   1123
Lys Ala Arg Gln Asp Glu Phe Val Arg Arg Val Ile Ala Lys Gly Val
                330                 335                 340

cca tgc act gtg cgt gat acc aag gga caa gaa atc gct gcg gct tgt   1171
Pro Cys Thr Val Arg Asp Thr Lys Gly Gln Glu Ile Ala Ala Ala Cys
            345                 350                 355

gga cag ctt gct gcg gag gaa tct gct taagccctca aagctcaaaa         1218
Gly Gln Leu Ala Ala Glu Glu Ser Ala
        360                 365

gcc                                                              1221
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<210> 2130
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

<400> 2130

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Met Ala Thr Pro Val Pro Leu Val Phe Asn Ala Pro Lys Arg Gly Met
  1               5                  10                  15

Pro Pro Thr His Phe Ala Asp Leu Asn Asp Glu Ala Arg Ile Glu Ala
             20                  25                  30

Leu Lys Glu Leu Gly Leu Pro Lys Phe Arg Leu Asn Gln Ile Ala Arg
         35                  40                  45

His Tyr Tyr Gly Arg Leu Glu Ala Asp Pro Leu Thr Met Thr Asp Leu
     50                  55                  60

Pro Glu Gly Ala Arg Gln Glu Val Lys Asp Ala Leu Phe Pro Thr Leu
 65                  70                  75                  80

Met Ser Pro Leu Arg Val Val Glu Thr Asp Asp Asp Thr Thr Gln Lys
                 85                  90                  95

Thr Leu Trp Lys Leu His Asp Gly Thr Leu Leu Glu Ser Val Leu Met
            100                 105                 110

Arg Tyr Ser Asp Arg Ser Thr Leu Cys Ile Ser Ser Gln Ala Gly Cys
        115                 120                 125

Gly Met Ala Cys Pro Phe Cys Ala Thr Gly Gln Gly Gly Leu Asp Arg
    130                 135                 140

Asn Leu Ser Ile Gly Glu Ile Val Asp Gln Val Arg Asn Ala Ala Ala
145                 150                 155                 160

Thr Met Gln Ser Glu Gly Gly Arg Leu Ser Asn Ile Val Phe Met Gly
                165                 170                 175

Met Gly Glu Pro Leu Ala Asn Tyr Lys Arg Val Val Ser Ala Val Arg
            180                 185                 190

Gln Ile Thr Gln Pro Ser Pro Ala Gly Phe Gly Ile Ser Gln Arg Ser
        195                 200                 205

Val Thr Val Ser Thr Val Gly Leu Ala Pro Ala Ile Arg Lys Leu Ala
    210                 215                 220

Asp Glu Glu Met Ser Val Thr Leu Ala Val Ser Leu His Thr Pro Asp
225                 230                 235                 240

Asp Glu Leu Arg Asp Thr Leu Val Pro Val Asn Asn Arg Trp Pro Val
                245                 250                 255

Ala Glu Val Leu Asp Ala Ala Arg Tyr Tyr Ala Asp Lys Ser Gly Arg
            260                 265                 270

Arg Val Ser Ile Glu Tyr Ala Leu Ile Arg Asp Val Asn Asp Gln Asp
        275                 280                 285
```

```
Trp Arg Ala Asp Met Leu Gly Glu Lys Leu His Lys Ala Leu Gly Ser
    290                 295                 300

Arg Val His Val Asn Leu Ile Pro Leu Asn Pro Thr Pro Gly Ser Lys
305                 310                 315                 320

Trp Asp Ala Ala Pro Lys Ala Arg Gln Asp Glu Phe Val Arg Arg Val
                325                 330                 335

Ile Ala Lys Gly Val Pro Cys Thr Val Arg Asp Thr Lys Gly Gln Glu
            340                 345                 350

Ile Ala Ala Ala Cys Gly Gln Leu Ala Ala Glu Glu Ser Ala
        355                 360                 365


<210> 2131
<211> 1221
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1198)
<223> RXA01186

<400> 2131
ttgctcatac agccattgaa ctcgtagaat caccgttccg ccacccaaat cagcccaata 60

agttcaacaa ttacataaca tctgaaagaa tagggacatt atg gct aca cct gta   115
                                        Met Ala Thr Pro Val
                                          1               5

cca ctg gtt ttt aac gca cct aag cgt ggc atg ccc cca acc cac ttt   163
Pro Leu Val Phe Asn Ala Pro Lys Arg Gly Met Pro Pro Thr His Phe
                  10                  15                  20

gcg gat ctt aat gat gag gct cgc att gag gct ctt aaa gag ctc ggc   211
Ala Asp Leu Asn Asp Glu Ala Arg Ile Glu Ala Leu Lys Glu Leu Gly
              25                  30                  35

ttg ccc aaa ttc cga ctc aat cag atc gct cga cac tac tat ggt cgc   259
Leu Pro Lys Phe Arg Leu Asn Gln Ile Ala Arg His Tyr Tyr Gly Arg
          40                  45                  50

ctc gag gct gac cca ctc act atg acg gac ctg cct gaa ggt gct cgt   307
Leu Glu Ala Asp Pro Leu Thr Met Thr Asp Leu Pro Glu Gly Ala Arg
      55                  60                  65

caa gaa gtc aag gat gct ctt ttt cca acg ttg atg tct cct ctg cgc   355
Gln Glu Val Lys Asp Ala Leu Phe Pro Thr Leu Met Ser Pro Leu Arg
  70                  75                  80                  85

gtc gtc gaa acc gat gac gat aca act cag aag acg tta tgg aag ctc   403
Val Val Glu Thr Asp Asp Asp Thr Thr Gln Lys Thr Leu Trp Lys Leu
                  90                  95                 100

cat gat ggc act ttg ctt gag tct gtt ctc atg cgc tat tca gat cgc   451
His Asp Gly Thr Leu Leu Glu Ser Val Leu Met Arg Tyr Ser Asp Arg
            105                 110                 115
```

```
tcc acg ctg tgt att tct tcg cag gct ggt tgc ggc atg gcg tgc cca   499
Ser Thr Leu Cys Ile Ser Ser Gln Ala Gly Cys Gly Met Ala Cys Pro
        120                 125                 130

ttc tgt gca act ggt cag ggc ggt ttg gac cgt aac ctt tca atc ggt   547
Phe Cys Ala Thr Gly Gln Gly Gly Leu Asp Arg Asn Leu Ser Ile Gly
    135                 140                 145

gag atc gtg gat cag gtt cgt aat gct gct gca acg atg cag tca gag   595
Glu Ile Val Asp Gln Val Arg Asn Ala Ala Ala Thr Met Gln Ser Glu
150                 155                 160                 165

ggc ggt cgt ctg tcc aac att gtg ttc atg gga atg ggc gag cct ctc   643
Gly Gly Arg Leu Ser Asn Ile Val Phe Met Gly Met Gly Glu Pro Leu
                170                 175                 180

gct aac tac aag cgc gtg gtg tcg gct gtt cgt cag atc acg cag cca   691
Ala Asn Tyr Lys Arg Val Val Ser Ala Val Arg Gln Ile Thr Gln Pro
            185                 190                 195

agc cct gcg ggc ttc ggc att tcc cag cgc agt gtg act gtc tcc acc   739
Ser Pro Ala Gly Phe Gly Ile Ser Gln Arg Ser Val Thr Val Ser Thr
        200                 205                 210

gtg ggc ctc gct cca gct atc agg aag ctt gcc gac gaa gag atg tcc   787
Val Gly Leu Ala Pro Ala Ile Arg Lys Leu Ala Asp Glu Glu Met Ser
    215                 220                 225

gta act ttg gca gtt tcc ttg cac act cca gac gat gag ttg cgt gac   835
Val Thr Leu Ala Val Ser Leu His Thr Pro Asp Asp Glu Leu Arg Asp
230                 235                 240                 245

act ctc gtg cca gtc aac aat cgt tgg cct gtc gct gag gta ctg gac   883
Thr Leu Val Pro Val Asn Asn Arg Trp Pro Val Ala Glu Val Leu Asp
                250                 255                 260

gct gct cgt tac tac gca gat aag tct ggc cgt cgc gtc tcc atc gag   931
Ala Ala Arg Tyr Tyr Ala Asp Lys Ser Gly Arg Arg Val Ser Ile Glu
            265                 270                 275

tat gcg ctc att cgc gat gtg aat gac cag gat tgg cgc gca gat atg   979
Tyr Ala Leu Ile Arg Asp Val Asn Asp Gln Asp Trp Arg Ala Asp Met
        280                 285                 290

ctg ggc gag aag ctg cat aag gct ttg ggc tcc cgt gtg cac gtc aac   1027
Leu Gly Glu Lys Leu His Lys Ala Leu Gly Ser Arg Val His Val Asn
    295                 300                 305

ttg att cca ttg aac cca act cct ggt tct aag tgg gat gct gca cca   1075
Leu Ile Pro Leu Asn Pro Thr Pro Gly Ser Lys Trp Asp Ala Ala Pro
310                 315                 320                 325

aag gct cgt cag gat gag ttt gtg cgt cgt gtg atc gcc aag ggt gtt   1123
Lys Ala Arg Gln Asp Glu Phe Val Arg Arg Val Ile Ala Lys Gly Val
                330                 335                 340

cca tgc act gtg cgt gat acc aag gga caa gaa atc gct gcg gct tgt   1171
Pro Cys Thr Val Arg Asp Thr Lys Gly Gln Glu Ile Ala Ala Ala Cys
            345                 350                 355

gga cag ctt gct gcg gag gaa tct gct taagccctca aagctcaaaa         1218
```

```
Gly Gln Leu Ala Ala Glu Glu Ser Ala
        360                 365

gcc                                                                    1221


<210> 2132
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

<400> 2132
Met Ala Thr Pro Val Pro Leu Val Phe Asn Ala Pro Lys Arg Gly Met
  1               5                  10                  15

Pro Pro Thr His Phe Ala Asp Leu Asn Asp Glu Ala Arg Ile Glu Ala
             20                  25                  30

Leu Lys Glu Leu Gly Leu Pro Lys Phe Arg Leu Asn Gln Ile Ala Arg
         35                  40                  45

His Tyr Tyr Gly Arg Leu Glu Ala Asp Pro Leu Thr Met Thr Asp Leu
     50                  55                  60

Pro Glu Gly Ala Arg Gln Glu Val Lys Asp Ala Leu Phe Pro Thr Leu
 65                  70                  75                  80

Met Ser Pro Leu Arg Val Val Glu Thr Asp Asp Asp Thr Thr Gln Lys
                 85                  90                  95

Thr Leu Trp Lys Leu His Asp Gly Thr Leu Leu Glu Ser Val Leu Met
            100                 105                 110

Arg Tyr Ser Asp Arg Ser Thr Leu Cys Ile Ser Ser Gln Ala Gly Cys
        115                 120                 125

Gly Met Ala Cys Pro Phe Cys Ala Thr Gly Gln Gly Gly Leu Asp Arg
    130                 135                 140

Asn Leu Ser Ile Gly Glu Ile Val Asp Gln Val Arg Asn Ala Ala Ala
145                 150                 155                 160

Thr Met Gln Ser Glu Gly Gly Arg Leu Ser Asn Ile Val Phe Met Gly
                165                 170                 175

Met Gly Glu Pro Leu Ala Asn Tyr Lys Arg Val Val Ser Ala Val Arg
            180                 185                 190

Gln Ile Thr Gln Pro Ser Pro Ala Gly Phe Gly Ile Ser Gln Arg Ser
        195                 200                 205

Val Thr Val Ser Thr Val Gly Leu Ala Pro Ala Ile Arg Lys Leu Ala
    210                 215                 220

Asp Glu Glu Met Ser Val Thr Leu Ala Val Ser Leu His Thr Pro Asp
225                 230                 235                 240

Asp Glu Leu Arg Asp Thr Leu Val Pro Val Asn Asn Arg Trp Pro Val
                245                 250                 255

Ala Glu Val Leu Asp Ala Ala Arg Tyr Tyr Ala Asp Lys Ser Gly Arg
```

```
            260                 265                 270

Arg Val Ser Ile Glu Tyr Ala Leu Ile Arg Asp Val Asn Asp Gln Asp
        275                 280                 285

Trp Arg Ala Asp Met Leu Gly Glu Lys Leu His Lys Ala Leu Gly Ser
    290                 295                 300

Arg Val His Val Asn Leu Ile Pro Leu Asn Pro Thr Pro Gly Ser Lys
305                 310                 315                 320

Trp Asp Ala Ala Pro Lys Ala Arg Gln Asp Glu Phe Val Arg Arg Val
                325                 330                 335

Ile Ala Lys Gly Val Pro Cys Thr Val Arg Asp Thr Lys Gly Gln Glu
            340                 345                 350

Ile Ala Ala Ala Cys Gly Gln Leu Ala Ala Glu Glu Ser Ala
        355                 360                 365
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20050059107

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<210> 2133
<211> 573
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(559)
<223> RXA01187

<400> 2133
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gtgattctac gagttcaatg gctgtatgag caacagacct gtg gat cca ttt gag   115
                                           Val Asp Pro Phe Glu
                                             1               5

acc aac cca aac gac ctt ccc acc ggt tta gac cca gca tac gaa ggt   163
Thr Asn Pro Asn Asp Leu Pro Thr Gly Leu Asp Pro Ala Tyr Glu Gly
                 10                  15                  20

aac agt gag tta aac ccg ctt gga gga aaa aat att ccc gac gag cct   211
Asn Ser Glu Leu Asn Pro Leu Gly Gly Lys Asn Ile Pro Asp Glu Pro
             25                  30                  35

gag gtg act gca aac aca cct gca gtt caa gaa gaa cct gct tac tcg   259
Glu Val Thr Ala Asn Thr Pro Ala Val Gln Glu Glu Pro Ala Tyr Ser
         40                  45                  50

gag cca gaa act gcc gtt gag tcg aag cgt cag gcg aag cag aac aca   307
Glu Pro Glu Thr Ala Val Glu Ser Lys Arg Gln Ala Lys Gln Asn Thr
     55                  60                  65

aag aag tcc gaa cct gtt gtg gct cca aaa caa aca ctt gcc ggt ggc   355
Lys Lys Ser Glu Pro Val Val Ala Pro Lys Gln Thr Leu Ala Gly Gly
 70                  75                  80                  85

acg tgg gta gct ctc atc gta ggc gca ctt ttg cta atc cta ctg ttg   403
Thr Trp Val Ala Leu Ile Val Gly Ala Leu Leu Leu Ile Leu Leu Leu
                 90                  95                 100
```

```
gtc ttc atc atg cag aac caa acc acc gta gag ctt aac ctt ttt gcg   451
Val Phe Ile Met Gln Asn Gln Thr Thr Val Glu Leu Asn Leu Phe Ala
            105                 110                 115

tgg acc ttc caa ttc cca gcc gga atc ggt ttc cta cta gca gcc att   499
Trp Thr Phe Gln Phe Pro Ala Gly Ile Gly Phe Leu Leu Ala Ala Ile
        120                 125                 130

acc ggt gca ttg att atg gcg ctt ggt ggt ggc gtg cgc atg ttt gag   547
Thr Gly Ala Leu Ile Met Ala Leu Gly Gly Gly Val Arg Met Phe Glu
    135                 140                 145

tac cgt cgc agt taagaaaaat ccgt                                   573
Tyr Arg Arg Ser
150
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<210> 2134
<211> 153
<212> PRT
<213> Corynebacterium glutamicum

<400> 2134

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Val Asp Pro Phe Glu Thr Asn Pro Asn Asp Leu Pro Thr Gly Leu Asp
  1               5                  10                  15

Pro Ala Tyr Glu Gly Asn Ser Glu Leu Asn Pro Leu Gly Gly Lys Asn
             20                  25                  30

Ile Pro Asp Glu Pro Glu Val Thr Ala Asn Thr Pro Ala Val Gln Glu
         35                  40                  45

Glu Pro Ala Tyr Ser Glu Pro Glu Thr Ala Val Glu Ser Lys Arg Gln
     50                  55                  60

Ala Lys Gln Asn Thr Lys Lys Ser Glu Pro Val Val Ala Pro Lys Gln
 65                  70                  75                  80

Thr Leu Ala Gly Gly Thr Trp Val Ala Leu Ile Val Gly Ala Leu Leu
                 85                  90                  95

Leu Ile Leu Leu Leu Val Phe Ile Met Gln Asn Gln Thr Thr Val Glu
            100                 105                 110

Leu Asn Leu Phe Ala Trp Thr Phe Gln Phe Pro Ala Gly Ile Gly Phe
        115                 120                 125

Leu Leu Ala Ala Ile Thr Gly Ala Leu Ile Met Ala Leu Gly Gly Gly
    130                 135                 140

Val Arg Met Phe Glu Tyr Arg Arg Ser
145                 150
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<210> 2135
<211> 570
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(547)
<223> RXA01195

<400> 2135
ggtttcgcgc caggcgacat tgtgagtagg atcgtctaaa atcgttttct tatcgcagga 60

aggactcaaa aaggccgtgg aatatttgac ctggggtttg gtg att gtt gca gtg 115
Val Ile Val Ala Val
1 5

tcg gca gtt ctt ctt gct gcc tgg cgg ttt ttc acc tta cgt tct cgg 163
Ser Ala Val Leu Leu Ala Ala Trp Arg Phe Phe Thr Leu Arg Ser Arg
10 15 20

gga acc act gtg att ctg cgt gag ttg cca caa agc ggt gtg cat ggc 211
Gly Thr Thr Val Ile Leu Arg Glu Leu Pro Gln Ser Gly Val His Gly
25 30 35

tgg cgc cat gga tca ttt cgc tac aac ggc aac gac ttg gag tac ttc 259
Trp Arg His Gly Ser Phe Arg Tyr Asn Gly Asn Asp Leu Glu Tyr Phe
40 45 50

aag ctg cgc tct ttg tct ccc atg gct gac ctt att ttg aac cgc ctt 307
Lys Leu Arg Ser Leu Ser Pro Met Ala Asp Leu Ile Leu Asn Arg Leu
55 60 65

tca gta act ttg ctt gat cgt aga gat cca gct gct gat gag gcg gtt 355
Ser Val Thr Leu Leu Asp Arg Arg Asp Pro Ala Ala Asp Glu Ala Val
70 75 80 85

ttt atg tct caa ggc tta aaa att ctg cac att aaa tcc aaa aat gat 403
Phe Met Ser Gln Gly Leu Lys Ile Leu His Ile Lys Ser Lys Asn Asp
90 95 100

cag att gaa tta gct ttg gac gcc cac ggg gag atg gcg ttt act gcc 451
Gln Ile Glu Leu Ala Leu Asp Ala His Gly Glu Met Ala Phe Thr Ala
105 110 115

tgg ttg gaa gca gca cca gat gcg cgg gcg gag cat tca ttg aat cca 499
Trp Leu Glu Ala Ala Pro Asp Ala Arg Ala Glu His Ser Leu Asn Pro
120 125 130

cgt gat ttc aac cgc ttt cga gcc agc aaa gac acc cgc aaa aac cgc 547
Arg Asp Phe Asn Arg Phe Arg Ala Ser Lys Asp Thr Arg Lys Asn Arg
135 140 145

taagtagacg tcattgttat ggt 570

<210> 2136
<211> 149
<212> PRT
<213> Corynebacterium glutamicum

<400> 2136
Val Ile Val Ala Val Ser Ala Val Leu Leu Ala Ala Trp Arg Phe Phe
1 5 10 15

Thr Leu Arg Ser Arg Gly Thr Thr Val Ile Leu Arg Glu Leu Pro Gln
20 25 30

```
Ser Gly Val His Gly Trp Arg His Gly Ser Phe Arg Tyr Asn Gly Asn
         35                  40                  45

Asp Leu Glu Tyr Phe Lys Leu Arg Ser Leu Ser Pro Met Ala Asp Leu
     50                  55                  60

Ile Leu Asn Arg Leu Ser Val Thr Leu Leu Asp Arg Arg Asp Pro Ala
 65                  70                  75                  80

Ala Asp Glu Ala Val Phe Met Ser Gln Gly Leu Lys Ile Leu His Ile
                 85                  90                  95

Lys Ser Lys Asn Asp Gln Ile Glu Leu Ala Leu Asp Ala His Gly Glu
            100                 105                 110

Met Ala Phe Thr Ala Trp Leu Glu Ala Ala Pro Asp Ala Arg Ala Glu
        115                 120                 125

His Ser Leu Asn Pro Arg Asp Phe Asn Arg Phe Arg Ala Ser Lys Asp
    130                 135                 140

Thr Arg Lys Asn Arg
145


<210> 2137
<211> 813
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(790)
<223> RXA01196

<400> 2137
gggcggagca ttcattgaat ccacgtgatt tcaaccgctt tcgagccagc aaagacaccc 60

gcaaaaaccg ctaagtagac gtcattgtta tggtgggtgc atg cgt tta gtc atc   115
                                            Met Arg Leu Val Ile
                                              1               5

gcc cgt tgc tca gtt gat tat gtt ggc cgt ttg gaa gct cat ctt ccg   163
Ala Arg Cys Ser Val Asp Tyr Val Gly Arg Leu Glu Ala His Leu Pro
                 10                  15                  20

tcc gcc gat cgc ctt ttg atg gtt aag gcg gat ggt tct gta tcc atc   211
Ser Ala Asp Arg Leu Leu Met Val Lys Ala Asp Gly Ser Val Ser Ile
             25                  30                  35

cat gcc gat gac cgt gcc tat aag cca ctg aac tgg atg aca cct cca   259
His Ala Asp Asp Arg Ala Tyr Lys Pro Leu Asn Trp Met Thr Pro Pro
         40                  45                  50

tgt tct tta gtt gaa act ccc atc act gat gaa gat ggt gaa gca aca   307
Cys Ser Leu Val Glu Thr Pro Ile Thr Asp Glu Asp Gly Glu Ala Thr
     55                  60                  65

ggg gaa agc ctg tgg gtg gtg gaa aac aaa aag ggc gag cag ctt cga   355
Gly Glu Ser Leu Trp Val Val Glu Asn Lys Lys Gly Glu Gln Leu Arg
```

```
 70                  75                  80                  85

att act gtg gaa gaa att cat tcg gaa caa aac ttc gat cta ggc caa   403
Ile Thr Val Glu Glu Ile His Ser Glu Gln Asn Phe Asp Leu Gly Gln
                 90                  95                 100

gac cca ggt ttg gtg aaa gac gga gtg gaa gat cat ctc caa gag ctt   451
Asp Pro Gly Leu Val Lys Asp Gly Val Glu Asp His Leu Gln Glu Leu
            105                 110                 115

ctt gca gag cac atc act acg ttg ggt gat ggg tac aca ttg att cgt   499
Leu Ala Glu His Ile Thr Thr Leu Gly Asp Gly Tyr Thr Leu Ile Arg
        120                 125                 130

cgg gag tat cca aca gct att ggg cct gtc gat att ttg tgt cgc aac   547
Arg Glu Tyr Pro Thr Ala Ile Gly Pro Val Asp Ile Leu Cys Arg Asn
    135                 140                 145

tct gac ggc gag act gtc gct gtg gag atc aag cgt cgt ggt ggc atc   595
Ser Asp Gly Glu Thr Val Ala Val Glu Ile Lys Arg Arg Gly Gly Ile
150                 155                 160                 165

gac ggc gtt gag cag ttg acc agg tat ttg gaa ttg ctc aac cgt gat   643
Asp Gly Val Glu Gln Leu Thr Arg Tyr Leu Glu Leu Leu Asn Arg Asp
                170                 175                 180

gaa ttg ctc aag cct gtt cat gga gtg ttt gca gcc cag gag att aag   691
Glu Leu Leu Lys Pro Val His Gly Val Phe Ala Ala Gln Glu Ile Lys
            185                 190                 195

cct cag gca aag act ctc gcg gag gat cgt ggc atc aag tgc gtg acg   739
Pro Gln Ala Lys Thr Leu Ala Glu Asp Arg Gly Ile Lys Cys Val Thr
        200                 205                 210

ttg gat tat caa gcg ctt cgt ggc att gag tcc aat gag ctg aca ttg   787
Leu Asp Tyr Gln Ala Leu Arg Gly Ile Glu Ser Asn Glu Leu Thr Leu
    215                 220                 225

ttc taagaacatg ggccgaaaaa ata                                    813
Phe
230
```

<210> 2138
<211> 230
<212> PRT
<213> Corynebacterium glutamicum

<400> 2138

```
Met Arg Leu Val Ile Ala Arg Cys Ser Val Asp Tyr Val Gly Arg Leu
  1               5                  10                  15

Glu Ala His Leu Pro Ser Ala Asp Arg Leu Leu Met Val Lys Ala Asp
             20                  25                  30

Gly Ser Val Ser Ile His Ala Asp Asp Arg Ala Tyr Lys Pro Leu Asn
         35                  40                  45

Trp Met Thr Pro Pro Cys Ser Leu Val Glu Thr Pro Ile Thr Asp Glu
     50                  55                  60
```

```
Asp Gly Glu Ala Thr Gly Glu Ser Leu Trp Val Val Glu Asn Lys Lys
 65                  70                  75                  80

Gly Glu Gln Leu Arg Ile Thr Val Glu Glu Ile His Ser Glu Gln Asn
                 85                  90                  95

Phe Asp Leu Gly Gln Asp Pro Gly Leu Val Lys Asp Gly Val Glu Asp
            100                 105                 110

His Leu Gln Glu Leu Leu Ala Glu His Ile Thr Thr Leu Gly Asp Gly
        115                 120                 125

Tyr Thr Leu Ile Arg Arg Glu Tyr Pro Thr Ala Ile Gly Pro Val Asp
    130                 135                 140

Ile Leu Cys Arg Asn Ser Asp Gly Glu Thr Val Ala Val Glu Ile Lys
145                 150                 155                 160

Arg Arg Gly Gly Ile Asp Gly Val Glu Gln Leu Thr Arg Tyr Leu Glu
                165                 170                 175

Leu Leu Asn Arg Asp Glu Leu Leu Lys Pro Val His Gly Val Phe Ala
            180                 185                 190

Ala Gln Glu Ile Lys Pro Gln Ala Lys Thr Leu Ala Glu Asp Arg Gly
        195                 200                 205

Ile Lys Cys Val Thr Leu Asp Tyr Gln Ala Leu Arg Gly Ile Glu Ser
    210                 215                 220

Asn Glu Leu Thr Leu Phe
225                 230


<210> 2139
<211> 576
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(553)
<223> RXA01197

<400> 2139
agcaacaatc atatctgcca ccctaccttg gggttggcat gtgatgacta gcttgcccaa 60

tcctcaatat tcccccacct gctatgccta aaattaagcc atg tct acc gaa cag   115
                                              Met Ser Thr Glu Gln
                                                1               5

tct ttg aat atc ccc cac gaa tac gtc atc tgc ctc gat cat gtt ggc   163
Ser Leu Asn Ile Pro His Glu Tyr Val Ile Cys Leu Asp His Val Gly
                10                  15                  20

atc gcc gtc cct gac ctc gag gaa gcc atc gaa ttt tac cgt tcc gca   211
Ile Ala Val Pro Asp Leu Glu Glu Ala Ile Glu Phe Tyr Arg Ser Ala
            25                  30                  35

ttc ggc tgg gta aac cac cac caa gaa atc aat gag gaa caa ggc att   259
Phe Gly Trp Val Asn His His Gln Glu Ile Asn Glu Glu Gln Gly Ile
```

```
         40                  45                  50

tca gag gcc atg atc ggc ccc aaa gac att aaa agc aca gaa ggc atg   307
Ser Glu Ala Met Ile Gly Pro Lys Asp Ile Lys Ser Thr Glu Gly Met
     55                  60                  65

att cag ctc atc gcg ccg ctc aac gag gac tcc aca atc gcc aaa ttc   355
Ile Gln Leu Ile Ala Pro Leu Asn Glu Asp Ser Thr Ile Ala Lys Phe
 70                  75                  80                  85

ctc gaa aag aaa ggt ccc ggc atc cag caa atg tgc ctg cgc acc aac   403
Leu Glu Lys Lys Gly Pro Gly Ile Gln Gln Met Cys Leu Arg Thr Asn
                 90                  95                 100

aac atc gat gcg ctc tcc gag cac ctg cgc cgc caa ggc gtg cgc ctg   451
Asn Ile Asp Ala Leu Ser Glu His Leu Arg Arg Gln Gly Val Arg Leu
            105                 110                 115

ctc tac ccc gaa ccc aaa aac ggc acc ggc ggt gcc cgc atc aac ttc   499
Leu Tyr Pro Glu Pro Lys Asn Gly Thr Gly Gly Ala Arg Ile Asn Phe
        120                 125                 130

ctg cac ccc aaa gac gcg ggc ggc gtg ctg ctc gag atc acg cag cct   547
Leu His Pro Lys Asp Ala Gly Gly Val Leu Leu Glu Ile Thr Gln Pro
    135                 140                 145

caa agc taattgctta tcgacgctcc cag                                576
Gln Ser
150
```

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<210> 2140
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 2140

```
Met Ser Thr Glu Gln Ser Leu Asn Ile Pro His Glu Tyr Val Ile Cys
  1               5                  10                  15

Leu Asp His Val Gly Ile Ala Val Pro Asp Leu Glu Glu Ala Ile Glu
            20                  25                  30

Phe Tyr Arg Ser Ala Phe Gly Trp Val Asn His His Gln Glu Ile Asn
        35                  40                  45

Glu Glu Gln Gly Ile Ser Glu Ala Met Ile Gly Pro Lys Asp Ile Lys
    50                  55                  60

Ser Thr Glu Gly Met Ile Gln Leu Ile Ala Pro Leu Asn Glu Asp Ser
65                  70                  75                  80

Thr Ile Ala Lys Phe Leu Glu Lys Lys Gly Pro Gly Ile Gln Gln Met
                85                  90                  95

Cys Leu Arg Thr Asn Asn Ile Asp Ala Leu Ser Glu His Leu Arg Arg
            100                 105                 110

Gln Gly Val Arg Leu Leu Tyr Pro Glu Pro Lys Asn Gly Thr Gly Gly
        115                 120                 125
```

```
Ala Arg Ile Asn Phe Leu His Pro Lys Asp Ala Gly Gly Val Leu Leu
    130                 135                 140

Glu Ile Thr Gln Pro Gln Ser
145                 150


<210> 2141
<211> 426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(403)
<223> RXA01198

<400> 2141
ttcggtagac atggcttaat tttaggcata gcaggtgggg gaatattgag gattgggcaa 60

gctagtcatc acatgccaac cccaaggtag ggtggcagat atg att gtt gct ttt   115
                                              Met Ile Val Ala Phe
                                                1               5

tct gta gcc ccg act gtt act gat aat cca gat gct gag atg gcc gat   163
Ser Val Ala Pro Thr Val Thr Asp Asn Pro Asp Ala Glu Met Ala Asp
                  10                  15                  20

gcg gtc acg gag gcg att cga atc gtc cgc gca tcg ggt ctg cct aat   211
Ala Val Thr Glu Ala Ile Arg Ile Val Arg Ala Ser Gly Leu Pro Asn
              25                  30                  35

gaa act aac gcg atg ttc acg ctc att gag ggg gag tgg gat gag gtg   259
Glu Thr Asn Ala Met Phe Thr Leu Ile Glu Gly Glu Trp Asp Glu Val
          40                  45                  50

atg gcg gtg att aag gag gcc act gag gcg atc tct agg gta tct ccg   307
Met Ala Val Ile Lys Glu Ala Thr Glu Ala Ile Ser Arg Val Ser Pro
      55                  60                  65

cgt aca tcg ttg gta att aag gct gat att cgt ccg gga cac act ggc   355
Arg Thr Ser Leu Val Ile Lys Ala Asp Ile Arg Pro Gly His Thr Gly
  70                  75                  80                  85

caa ttg acg agg aag gtg gag gcg gtg gag gaa cgc cta gct agg gat   403
Gln Leu Thr Arg Lys Val Glu Ala Val Glu Glu Arg Leu Ala Arg Asp
                  90                  95                 100

tagctttgta cttaaacttg ttg                                        426


<210> 2142
<211> 101
<212> PRT
<213> Corynebacterium glutamicum

<400> 2142
Met Ile Val Ala Phe Ser Val Ala Pro Thr Val Thr Asp Asn Pro Asp
  1               5                  10                  15

Ala Glu Met Ala Asp Ala Val Thr Glu Ala Ile Arg Ile Val Arg Ala
```

```
            20                  25                  30

Ser Gly Leu Pro Asn Glu Thr Asn Ala Met Phe Thr Leu Ile Glu Gly
         35                  40                  45

Glu Trp Asp Glu Val Met Ala Val Ile Lys Glu Ala Thr Glu Ala Ile
     50                  55                  60

Ser Arg Val Ser Pro Arg Thr Ser Leu Val Ile Lys Ala Asp Ile Arg
 65                  70                  75                  80

Pro Gly His Thr Gly Gln Leu Thr Arg Lys Val Glu Ala Val Glu Glu
                 85                  90                  95

Arg Leu Ala Arg Asp
            100
```

<210> 2143
<211> 771
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> RXA01207

<400> 2143

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cttcatgatc tcaccggcag agcgcgtttt gttacagcgc gtaaactgtg actttgaaaa 60

atttttgaac aatccgtaca ccaacttcag gagaaaaaca gtg agc aga atc tat  115
                                          Val Ser Arg Ile Tyr
                                            1               5

gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc  163
Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
                 10                  15                  20

gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt  211
Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
             25                  30                  35

tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt  259
Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
         40                  45                  50

ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc  307
Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
     55                  60                  65

ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag  355
Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
 70                  75                  80                  85

gca aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc  403
Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
                 90                  95                 100

gtt ccg cag gca cca agc ctt ccg tgg aac ctt ggc gat acc cgt ggc  451
Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
```

```
            105                 110                 115

acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg   499
Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
        120                 125                 130

cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat   547
Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
    135                 140                 145

act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat   595
Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn
150                 155                 160                 165

gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca   643
Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
                170                 175                 180

acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt   691
Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
            185                 190                 195

gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa   739
Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu
        200                 205                 210

agc ctg cgc taaatgggag tcggtttcgc ggg                            771
Ser Leu Arg
    215
```

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<210> 2144
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 2144

```
Val Ser Arg Ile Tyr Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly
  1               5                  10                  15

Leu Lys Ala Ala Val Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu
             20                  25                  30

Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu
         35                  40                  45

Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro
     50                  55                  60

Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His
 65                  70                  75                  80

Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly
                 85                  90                  95

Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu
            100                 105                 110

Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val
        115                 120                 125
```

```
Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala
    130                 135                 140

Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln
145                 150                 155                 160

Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala
                165                 170                 175

Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys
            180                 185                 190

Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu
        195                 200                 205

Gly Val Ser Ala Glu Ser Leu Arg
    210                 215


<210> 2145
<211> 1350
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1327)
<223> RXA01213

<400> 2145
aactctggca acaacatgcg ccttcactcc ctcaaacaaa ttttcataaa caccccacat 60

catatcaacc aaacggtgta gttcttctaa gctttcaccc atg aca aat ccc aca   115
                                            Met Thr Asn Pro Thr
                                              1               5

gag gag cgc aac gca cgc cgc ctc att tgg gcc aac ggc ctg caa aac   163
Glu Glu Arg Asn Ala Arg Arg Leu Ile Trp Ala Asn Gly Leu Gln Asn
                  10                  15                  20

atc ggc gat caa atc gtt gcc gcc aaa aca gtc ctg ccc tgg ttg ctg   211
Ile Gly Asp Gln Ile Val Ala Ala Lys Thr Val Leu Pro Trp Leu Leu
              25                  30                  35

caa gcc gct ggc gcg ccg ggc ttt ttg ctg gcg ctt ctg gtt cca atc   259
Gln Ala Ala Gly Ala Pro Gly Phe Leu Leu Ala Leu Leu Val Pro Ile
          40                  45                  50

cgc gaa gcc gga tcg atg ctg ccg caa gct gcc att act ggc tgg gtg   307
Arg Glu Ala Gly Ser Met Leu Pro Gln Ala Ala Ile Thr Gly Trp Val
      55                  60                  65

ctg agg cag acg tcg aga agc aaa gtc tgg gtg att ggc tcg aac ggc   355
Leu Arg Gln Thr Ser Arg Ser Lys Val Trp Val Ile Gly Ser Asn Gly
  70                  75                  80                  85

cag ttc gtc tcg gcg ctg ggt atc ggc gtg gct gcg ctg ttt ttg cgt   403
Gln Phe Val Ser Ala Leu Gly Ile Gly Val Ala Ala Leu Phe Leu Arg
                  90                  95                 100

ggg tgg gcg ctg ggc atc acg gtg atc gtg ctg ctt gcg gcg ctg tcg   451
```

```
Gly Trp Ala Leu Gly Ile Thr Val Ile Val Leu Leu Ala Ala Leu Ser
            105                 110                 115

ctg ttt cga tcg atg tgt tcg att gca tcg aag gat gtt cag ggc aag   499
Leu Phe Arg Ser Met Cys Ser Ile Ala Ser Lys Asp Val Gln Gly Lys
        120                 125                 130

gtg att tcc aag ggc aag cgt ggg ctg gta acg ggc cgc gcg acg gtg   547
Val Ile Ser Lys Gly Lys Arg Gly Leu Val Thr Gly Arg Ala Thr Val
    135                 140                 145

att ggc ggt gtg atg ggc ctg gtt gca ggc ctg gcg atc gct att ttc   595
Ile Gly Gly Val Met Gly Leu Val Ala Gly Leu Ala Ile Ala Ile Phe
150                 155                 160                 165

ttg ggc tcg cat tcc ccg acg agg gtg ctg gcc gca gtg gtg atc gcg   643
Leu Gly Ser His Ser Pro Thr Arg Val Leu Ala Ala Val Val Ile Ala
                170                 175                 180

agc tcg ttt agc tgg ctg ttt gcc tcc att gtt ttc gcg cgc atc gaa   691
Ser Ser Phe Ser Trp Leu Phe Ala Ser Ile Val Phe Ala Arg Ile Glu
            185                 190                 195

tac gcg aag cca gcg act cca aaa aac gcg cct tcc gca aac ccg tgg   739
Tyr Ala Lys Pro Ala Thr Pro Lys Asn Ala Pro Ser Ala Asn Pro Trp
        200                 205                 210

gtg cgt cgc tgc atc gcc gca tta aaa gat gat aaa gct ttt cga cgt   787
Val Arg Arg Cys Ile Ala Ala Leu Lys Asp Asp Lys Ala Phe Arg Arg
    215                 220                 225

ttc gtt ctg gtt cgc tca atg atg ctg gtg aca gca ctc tcc acg gct   835
Phe Val Leu Val Arg Ser Met Met Leu Val Thr Ala Leu Ser Thr Ala
230                 235                 240                 245

ttc atc gtc gca ctc gcc gct gaa tcc gga aac agc atc gac tcc ttg   883
Phe Ile Val Ala Leu Ala Ala Glu Ser Gly Asn Ser Ile Asp Ser Leu
                250                 255                 260

gga ttc ttc ctc atc gcc tcc ggc ttg gcg tcc atg gtt ggt ggc cga   931
Gly Phe Phe Leu Ile Ala Ser Gly Leu Ala Ser Met Val Gly Gly Arg
            265                 270                 275

atc tct gga atc tgg tcg gat cat tcc tcc aaa aac gtc atg gcg ggc   979
Ile Ser Gly Ile Trp Ser Asp His Ser Ser Lys Asn Val Met Ala Gly
        280                 285                 290

ggt gcc cta ttc ggt tcc atc gtg tta atc ctc gtg gtg ctc agc tcc   1027
Gly Ala Leu Phe Gly Ser Ile Val Leu Ile Leu Val Val Leu Ser Ser
    295                 300                 305

gcg ttt gca ccc gcg cag atc aac acg ctg gtg ttc ccg ttg agt ttc   1075
Ala Phe Ala Pro Ala Gln Ile Asn Thr Leu Val Phe Pro Leu Ser Phe
310                 315                 320                 325

ttc ctc atc acc ttg gcc cac acc gcc atc cgc gtg gcc cgc aaa act   1123
Phe Leu Ile Thr Leu Ala His Thr Ala Ile Arg Val Ala Arg Lys Thr
                330                 335                 340

tat gta atg gac atg gct gaa ggt gat cag cgc acc cgc tat gtt gcc   1171
Tyr Val Met Asp Met Ala Glu Gly Asp Gln Arg Thr Arg Tyr Val Ala
```

```
            345                 350                 355

gac gcc aac aca cta atg ggt gta gtt ttg ctc att gtt ggc gca tta   1219
Asp Ala Asn Thr Leu Met Gly Val Val Leu Leu Ile Val Gly Ala Leu
        360                 365                 370

tct ggc ttc att gca att ttc gga aac gaa gcc gca ctg ctc ttc ttg   1267
Ser Gly Phe Ile Ala Ile Phe Gly Asn Glu Ala Ala Leu Leu Phe Leu
    375                 380                 385

gcg gca att ggc ctg ctt gga acc att agc gcc cgt ggc ctc aag gaa   1315
Ala Ala Ile Gly Leu Leu Gly Thr Ile Ser Ala Arg Gly Leu Lys Glu
390                 395                 400                 405

gta tcc gcc gga tagttttaca acttttccac cca                         1350
Val Ser Ala Gly
```

<210> 2146
<211> 409
<212> PRT
<213> Corynebacterium glutamicum

<400> 2146

```
Met Thr Asn Pro Thr Glu Glu Arg Asn Ala Arg Arg Leu Ile Trp Ala
  1               5                  10                  15

Asn Gly Leu Gln Asn Ile Gly Asp Gln Ile Val Ala Ala Lys Thr Val
             20                  25                  30

Leu Pro Trp Leu Leu Gln Ala Ala Gly Ala Pro Gly Phe Leu Leu Ala
         35                  40                  45

Leu Leu Val Pro Ile Arg Glu Ala Gly Ser Met Leu Pro Gln Ala Ala
     50                  55                  60

Ile Thr Gly Trp Val Leu Arg Gln Thr Ser Arg Ser Lys Val Trp Val
 65                  70                  75                  80

Ile Gly Ser Asn Gly Gln Phe Val Ser Ala Leu Gly Ile Gly Val Ala
                 85                  90                  95

Ala Leu Phe Leu Arg Gly Trp Ala Leu Gly Ile Thr Val Ile Val Leu
            100                 105                 110

Leu Ala Ala Leu Ser Leu Phe Arg Ser Met Cys Ser Ile Ala Ser Lys
        115                 120                 125

Asp Val Gln Gly Lys Val Ile Ser Lys Gly Lys Arg Gly Leu Val Thr
    130                 135                 140

Gly Arg Ala Thr Val Ile Gly Gly Val Met Gly Leu Val Ala Gly Leu
145                 150                 155                 160

Ala Ile Ala Ile Phe Leu Gly Ser His Ser Pro Thr Arg Val Leu Ala
                165                 170                 175

Ala Val Val Ile Ala Ser Ser Phe Ser Trp Leu Phe Ala Ser Ile Val
            180                 185                 190
```

```
Phe Ala Arg Ile Glu Tyr Ala Lys Pro Ala Thr Pro Lys Asn Ala Pro
        195                 200                 205

Ser Ala Asn Pro Trp Val Arg Arg Cys Ile Ala Ala Leu Lys Asp Asp
    210                 215                 220

Lys Ala Phe Arg Arg Phe Val Leu Val Arg Ser Met Met Leu Val Thr
225                 230                 235                 240

Ala Leu Ser Thr Ala Phe Ile Val Ala Leu Ala Ala Glu Ser Gly Asn
                245                 250                 255

Ser Ile Asp Ser Leu Gly Phe Phe Leu Ile Ala Ser Gly Leu Ala Ser
            260                 265                 270

Met Val Gly Gly Arg Ile Ser Gly Ile Trp Ser Asp His Ser Ser Lys
        275                 280                 285

Asn Val Met Ala Gly Gly Ala Leu Phe Gly Ser Ile Val Leu Ile Leu
    290                 295                 300

Val Val Leu Ser Ser Ala Phe Ala Pro Ala Gln Ile Asn Thr Leu Val
305                 310                 315                 320

Phe Pro Leu Ser Phe Phe Leu Ile Thr Leu Ala His Thr Ala Ile Arg
                325                 330                 335

Val Ala Arg Lys Thr Tyr Val Met Asp Met Ala Glu Gly Asp Gln Arg
            340                 345                 350

Thr Arg Tyr Val Ala Asp Ala Asn Thr Leu Met Gly Val Val Leu Leu
        355                 360                 365

Ile Val Gly Ala Leu Ser Gly Phe Ile Ala Ile Phe Gly Asn Glu Ala
    370                 375                 380

Ala Leu Leu Phe Leu Ala Ala Ile Gly Leu Leu Gly Thr Ile Ser Ala
385                 390                 395                 400

Arg Gly Leu Lys Glu Val Ser Ala Gly
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<210> 2147
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<213> Corynebacterium glutamicum

<220>
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<222> (101)..(529)
<223> RXA01218

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tcacattagc caaaaggcac tttgaggaag tggaactcct atg gca cga ctt cag 115
                                                Met Ala Arg Leu Gln
                                                  1   5

cac gac atg att ttc atc aac cta cca gta tct gac ctt gca gca tct 163

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His Asp Met Ile Phe Ile Asn Leu Pro Val Ser Asp Leu Ala Ala Ser
                 10                  15                  20

aag cgt ttt tat gca ggt ctt ggc ttc aaa gaa aac acc gtc ttc agt   211
Lys Arg Phe Tyr Ala Gly Leu Gly Phe Lys Glu Asn Thr Val Phe Ser
             25                  30                  35

gat gag cac act gca tct ttt gag gtc agt gac gcc atc gtg gtg atg   259
Asp Glu His Thr Ala Ser Phe Glu Val Ser Asp Ala Ile Val Val Met
         40                  45                  50

ctt ctg gaa acc gcg cgc ttc agt gat ttc act aag cgc ccc atc gtg   307
Leu Leu Glu Thr Ala Arg Phe Ser Asp Phe Thr Lys Arg Pro Ile Val
     55                  60                  65

gag aag aac ggc tcc cgc gaa gtg ctc aac tgc ctg tct gta tgt tcc   355
Glu Lys Asn Gly Ser Arg Glu Val Leu Asn Cys Leu Ser Val Cys Ser
 70                  75                  80                  85

acc gag gat gcg gat gag ttc gtg cgt cgc gcc cag gaa ttc gga ggc   403
Thr Glu Asp Ala Asp Glu Phe Val Arg Arg Ala Gln Glu Phe Gly Gly
                 90                  95                 100

acg atc acc cgt gag ctt gca gcg gaa ggc ccc atg tac ggc gga gct   451
Thr Ile Thr Arg Glu Leu Ala Ala Glu Gly Pro Met Tyr Gly Gly Ala
             105                 110                 115

ttt gat gat cca gat gga cac ggt tgg gag ctg atg tac ttc gat cca   499
Phe Asp Asp Pro Asp Gly His Gly Trp Glu Leu Met Tyr Phe Asp Pro
         120                 125                 130

gag gca ctc gct cag atg atg cct gag ggc taaatattct tcagggcttc     549
Glu Ala Leu Ala Gln Met Met Pro Glu Gly
    135                 140

tcg                                                               552


<210> 2148
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 2148
Met Ala Arg Leu Gln His Asp Met Ile Phe Ile Asn Leu Pro Val Ser
  1               5                  10                  15

Asp Leu Ala Ala Ser Lys Arg Phe Tyr Ala Gly Leu Gly Phe Lys Glu
             20                  25                  30

Asn Thr Val Phe Ser Asp Glu His Thr Ala Ser Phe Glu Val Ser Asp
         35                  40                  45

Ala Ile Val Val Met Leu Leu Glu Thr Ala Arg Phe Ser Asp Phe Thr
     50                  55                  60

Lys Arg Pro Ile Val Glu Lys Asn Gly Ser Arg Glu Val Leu Asn Cys
 65                  70                  75                  80

Leu Ser Val Cys Ser Thr Glu Asp Ala Asp Glu Phe Val Arg Arg Ala
                 85                  90                  95
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Gln Glu Phe Gly Gly Thr Ile Thr Arg Glu Leu Ala Ala Glu Gly Pro
            100                 105                 110

Met Tyr Gly Gly Ala Phe Asp Asp Pro Asp Gly His Gly Trp Glu Leu
        115                 120                 125

Met Tyr Phe Asp Pro Glu Ala Leu Ala Gln Met Met Pro Glu Gly
    130                 135                 140


<210> 2149
<211> 507
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(484)
<223> RXA01234

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tgcatttatt cgggtcactt caacgttgaa aagcatagga atg tgg aag ttc atg   115
                                          Met Trp Lys Phe Met
                                            1               5

aag act caa tac gta tgt acc act tat ttc atc gct gca ccc gag gat   163
Lys Thr Gln Tyr Val Cys Thr Thr Tyr Phe Ile Ala Ala Pro Glu Asp
                  10                  15                  20

gaa gac gag gcg tac caa act tat cgc agc cga atg aac tct ttg gca   211
Glu Asp Glu Ala Tyr Gln Thr Tyr Arg Ser Arg Met Asn Ser Leu Ala
              25                  30                  35

gca ttg aac ggc gct gac gta gtt tca gtg gca gat ggc cta cgg atg   259
Ala Leu Asn Gly Ala Asp Val Val Ser Val Ala Asp Gly Leu Arg Met
          40                  45                  50

gaa gta gac cag gat att tgg gga agc ctt gct gag cag tat cag att   307
Glu Val Asp Gln Asp Ile Trp Gly Ser Leu Ala Glu Gln Tyr Gln Ile
      55                  60                  65

gag caa gaa ggc ctg tat ccc act ggt cac aac ttg tac ttt gtt gtc   355
Glu Gln Glu Gly Leu Tyr Pro Thr Gly His Asn Leu Tyr Phe Val Val
  70                  75                  80                  85

acc gtg gtg aac cta gat gat tca gat gag gtt tat gac cga aca atg   403
Thr Val Val Asn Leu Asp Asp Ser Asp Glu Val Tyr Asp Arg Thr Met
                  90                  95                 100

gag cat ctg att atg gat gac cct tat gtg cga gtg gat cgt ttc cca   451
Glu His Leu Ile Met Asp Asp Pro Tyr Val Arg Val Asp Arg Phe Pro
            105                 110                 115

agc act gtc cat gcc agc acc cag atc atg ttg tagaaaaaga aaaagcacca 504
Ser Thr Val His Ala Ser Thr Gln Ile Met Leu
        120                 125

ccc                                                               507
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<210> 2150
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<213> Corynebacterium glutamicum

<400> 2150
Met Trp Lys Phe Met Lys Thr Gln Tyr Val Cys Thr Thr Tyr Phe Ile
1 5 10 15

Ala Ala Pro Glu Asp Glu Asp Glu Ala Tyr Gln Thr Tyr Arg Ser Arg
20 25 30

Met Asn Ser Leu Ala Ala Leu Asn Gly Ala Asp Val Val Ser Val Ala
35 40 45

Asp Gly Leu Arg Met Glu Val Asp Gln Asp Ile Trp Gly Ser Leu Ala
50 55 60

Glu Gln Tyr Gln Ile Glu Gln Glu Gly Leu Tyr Pro Thr Gly His Asn
65 70 75 80

Leu Tyr Phe Val Val Thr Val Val Asn Leu Asp Asp Ser Asp Glu Val
85 90 95

Tyr Asp Arg Thr Met Glu His Leu Ile Met Asp Asp Pro Tyr Val Arg
100 105 110

Val Asp Arg Phe Pro Ser Thr Val His Ala Ser Thr Gln Ile Met Leu
115 120 125

<210> 2151
<211> 564
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(541)
<223> RXA01237

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aaaccaaaaa tcacgacgca ttaagtaaca gagacttaaa ttaagaactc cgaacaacaa 60

cttcggattg tttcattttt gaggatgaaa gagcttttca atg aac gta cag ttt 115
Met Asn Val Gln Phe
1 5

gaa tca gac atg gcc gtc caa cca gga aac acc atg gaa gct acc gtc 163
Glu Ser Asp Met Ala Val Gln Pro Gly Asn Thr Met Glu Ala Thr Val
10 15 20

acc gac att cgt gat gcc aag cgt aaa aca acc cag ctt gat tca gta 211
Thr Asp Ile Arg Asp Ala Lys Arg Lys Thr Thr Gln Leu Asp Ser Val
25 30 35

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acg ccg ttt aag aag aat tgc ccg agc cgc acc ttg ctc gac acc atc   259
Thr Pro Phe Lys Lys Asn Cys Pro Ser Arg Thr Leu Leu Asp Thr Ile
         40                  45                  50

agt gac aag tgg gcg gtg ctg atc ctg ctc agc atg gaa aat ggt cca   307
Ser Asp Lys Trp Ala Val Leu Ile Leu Leu Ser Met Glu Asn Gly Pro
     55                  60                  65

cag cgc aat ggt gaa atc aaa gat cag gtc caa gga att acc cca aag   355
Gln Arg Asn Gly Glu Ile Lys Asp Gln Val Gln Gly Ile Thr Pro Lys
 70                  75                  80                  85

atg ctc acc cag cgt ctt gga gtg ttg gtg gaa gac gga ctg gtc act   403
Met Leu Thr Gln Arg Leu Gly Val Leu Val Glu Asp Gly Leu Val Thr
                 90                  95                 100

cgc acc tcc cac gca gtt gtg ccg cct cgt gtg gat tat cag ctc acc   451
Arg Thr Ser His Ala Val Val Pro Pro Arg Val Asp Tyr Gln Leu Thr
            105                 110                 115

gat ctg ggt gct tct gtc att gag cct tgc cgt gcg atg tat tcc tgg   499
Asp Leu Gly Ala Ser Val Ile Glu Pro Cys Arg Ala Met Tyr Ser Trp
        120                 125                 130

gca gtg gag aac att aag caa gtg gag gcc tac cgc tca gca           541
Ala Val Glu Asn Ile Lys Gln Val Glu Ala Tyr Arg Ser Ala
    135                 140                 145

taagaacact tggcaaacct cac                                        564


<210> 2152
<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 2152
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  1               5                  10                  15

Met Glu Ala Thr Val Thr Asp Ile Arg Asp Ala Lys Arg Lys Thr Thr
             20                  25                  30

Gln Leu Asp Ser Val Thr Pro Phe Lys Lys Asn Cys Pro Ser Arg Thr
         35                  40                  45

Leu Leu Asp Thr Ile Ser Asp Lys Trp Ala Val Leu Ile Leu Leu Ser
     50                  55                  60

Met Glu Asn Gly Pro Gln Arg Asn Gly Glu Ile Lys Asp Gln Val Gln
 65                  70                  75                  80

Gly Ile Thr Pro Lys Met Leu Thr Gln Arg Leu Gly Val Leu Val Glu
                 85                  90                  95

Asp Gly Leu Val Thr Arg Thr Ser His Ala Val Val Pro Pro Arg Val
            100                 105                 110

Asp Tyr Gln Leu Thr Asp Leu Gly Ala Ser Val Ile Glu Pro Cys Arg
        115                 120                 125
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Ala Met Tyr Ser Trp Ala Val Glu Asn Ile Lys Gln Val Glu Ala Tyr
    130                 135                 140

Arg Ser Ala
145
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<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1414)
<223> RXA01267

<400> 2153

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gatttttcga attgaagatg tttctgaaag gtatttagat atg tat gca gaa att   115
                                            Met Tyr Ala Glu Ile
                                              1               5

aat ggc ggt ttt att cca gag ggc acc gtg cgg gta agc ggc gca aaa   163
Asn Gly Gly Phe Ile Pro Glu Gly Thr Val Arg Val Ser Gly Ala Lys
                  10                  15                  20

aac tct gct act aga ctt ctc gcg gcg gca ctg cta acc gat gag gtg   211
Asn Ser Ala Thr Arg Leu Leu Ala Ala Ala Leu Leu Thr Asp Glu Val
              25                  30                  35

gtg cat ctt ggt aat ttc cca acc aag ctt gtg gat gtt gaa cat aaa   259
Val His Leu Gly Asn Phe Pro Thr Lys Leu Val Asp Val Glu His Lys
          40                  45                  50

att cgc ttt att gaa gag ctt ggc gga aaa gtg cat gtc gac cat gat   307
Ile Arg Phe Ile Glu Glu Leu Gly Gly Lys Val His Val Asp His Asp
      55                  60                  65

gag caa att tta gta gtt gat gct aag gat ctt gca gcg cga gaa atg   355
Glu Gln Ile Leu Val Val Asp Ala Lys Asp Leu Ala Ala Arg Glu Met
  70                  75                  80                  85

act act gat gaa ctg aat att ccg att cga act act tat ctc cta gca   403
Thr Thr Asp Glu Leu Asn Ile Pro Ile Arg Thr Thr Tyr Leu Leu Ala
                  90                  95                 100

gca gcg cag att ggg cgt ggg gaa att gct cga gtt cct ttt cct ggg   451
Ala Ala Gln Ile Gly Arg Gly Glu Ile Ala Arg Val Pro Phe Pro Gly
              105                 110                 115

ggg tgt gct att gga gga ggt cct gct ggc gga cga gga tat gat ctt   499
Gly Cys Ala Ile Gly Gly Gly Pro Ala Gly Gly Arg Gly Tyr Asp Leu
          120                 125                 130

cat ctt atg gtc tgg gaa cag cta ggt tgt aaa att ctt gaa aaa gat   547
His Leu Met Val Trp Glu Gln Leu Gly Cys Lys Ile Leu Glu Lys Asp
      135                 140                 145

gat cac att gaa gta act gca ccc cag ggc ttt atc ggg gga gtt att   595
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Asp His Ile Glu Val Thr Ala Pro Gln Gly Phe Ile Gly Gly Val Ile
150                 155                 160                 165

gac ttt cct att tct act gtg gga ggc act gaa aac gcg tta cta tgc   643
Asp Phe Pro Ile Ser Thr Val Gly Gly Thr Glu Asn Ala Leu Leu Cys
                170                 175                 180

gca agt att gct tca ggg gat act aaa att gcc aat gct tat att acc   691
Ala Ser Ile Ala Ser Gly Asp Thr Lys Ile Ala Asn Ala Tyr Ile Thr
            185                 190                 195

cct gag ata act gat ctt att gaa ctt ctg cga cgt atg ggt gcg gag   739
Pro Glu Ile Thr Asp Leu Ile Glu Leu Leu Arg Arg Met Gly Ala Glu
        200                 205                 210

atc act gtc tac ggt acc agc cgt att cat gta aag ggt cga gca ggt   787
Ile Thr Val Tyr Gly Thr Ser Arg Ile His Val Lys Gly Arg Ala Gly
    215                 220                 225

ctt ttg cag ggc gca tat atg gac gta atg ccg gat cgt att gag gca   835
Leu Leu Gln Gly Ala Tyr Met Asp Val Met Pro Asp Arg Ile Glu Ala
230                 235                 240                 245

ttg acg tgg atc gtg tat gga att att tca ggc gga agg att acc gtc   883
Leu Thr Trp Ile Val Tyr Gly Ile Ile Ser Gly Gly Arg Ile Thr Val
                250                 255                 260

gaa ggt gtt cca ttt agc tcg atg gaa gtt cct ttt atc cac ctt gag   931
Glu Gly Val Pro Phe Ser Ser Met Glu Val Pro Phe Ile His Leu Glu
            265                 270                 275

aag gct gga gtg gat ctt ttc cgt aat tca agt tcc gta tat att aca   979
Lys Ala Gly Val Asp Leu Phe Arg Asn Ser Ser Ser Val Tyr Ile Thr
        280                 285                 290

cca gaa tgc ttg cct tca ggc tca gtt cag cca ttt gag cta gcg tgt   1027
Pro Glu Cys Leu Pro Ser Gly Ser Val Gln Pro Phe Glu Leu Ala Cys
    295                 300                 305

gga act cac ccc gga gta att tcg gac atg cag gca ctt ttt gtt ctt   1075
Gly Thr His Pro Gly Val Ile Ser Asp Met Gln Ala Leu Phe Val Leu
310                 315                 320                 325

tta gga tta aaa ggt gca gga act tca cgc gtc tat gac tat cga tac   1123
Leu Gly Leu Lys Gly Ala Gly Thr Ser Arg Val Tyr Asp Tyr Arg Tyr
                330                 335                 340

cca gaa aga att gca ttt gtt gag gaa ttg aca aat cta gtt tcg ggc   1171
Pro Glu Arg Ile Ala Phe Val Glu Glu Leu Thr Asn Leu Val Ser Gly
            345                 350                 355

gac aaa tta agt gca gag gct ggc aag atc act atc cag gga gat gct   1219
Asp Lys Leu Ser Ala Glu Ala Gly Lys Ile Thr Ile Gln Gly Asp Ala
        360                 365                 370

act ttc cgg cca gga tat gcg aac tca act gat cta cgt ggt tct atg   1267
Thr Phe Arg Pro Gly Tyr Ala Asn Ser Thr Asp Leu Arg Gly Ser Met
    375                 380                 385

gct gtt gtt tta gcg gcg ctt tgc gct gat gga aag tcc acg att aat   1315
Ala Val Val Leu Ala Ala Leu Cys Ala Asp Gly Lys Ser Thr Ile Asn
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390                 395                 400                 405

aac gtc cat atg gcg tta cgt ggg tac aac gag ttg gat aaa aaa ctt   1363
Asn Val His Met Ala Leu Arg Gly Tyr Asn Glu Leu Asp Lys Lys Leu
                410                 415                 420

cgt tta ctt ggt gcg gat tta act atc aga gaa ggc gaa gtt cct tca   1411
Arg Leu Leu Gly Ala Asp Leu Thr Ile Arg Glu Gly Glu Val Pro Ser
            425                 430                 435

cct taagaacgaa agttttacat tga                                    1437
Pro
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<210> 2154
<211> 438
<212> PRT
<213> Corynebacterium glutamicum

<400> 2154

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Met Tyr Ala Glu Ile Asn Gly Gly Phe Ile Pro Glu Gly Thr Val Arg
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Val Ser Gly Ala Lys Asn Ser Ala Thr Arg Leu Leu Ala Ala Ala Leu
             20                  25                  30

Leu Thr Asp Glu Val Val His Leu Gly Asn Phe Pro Thr Lys Leu Val
         35                  40                  45

Asp Val Glu His Lys Ile Arg Phe Ile Glu Glu Leu Gly Gly Lys Val
     50                  55                  60

His Val Asp His Asp Glu Gln Ile Leu Val Val Asp Ala Lys Asp Leu
 65                  70                  75                  80

Ala Ala Arg Glu Met Thr Thr Asp Glu Leu Asn Ile Pro Ile Arg Thr
                 85                  90                  95

Thr Tyr Leu Leu Ala Ala Ala Gln Ile Gly Arg Gly Glu Ile Ala Arg
            100                 105                 110

Val Pro Phe Pro Gly Gly Cys Ala Ile Gly Gly Gly Pro Ala Gly Gly
        115                 120                 125

Arg Gly Tyr Asp Leu His Leu Met Val Trp Glu Gln Leu Gly Cys Lys
    130                 135                 140

Ile Leu Glu Lys Asp Asp His Ile Glu Val Thr Ala Pro Gln Gly Phe
145                 150                 155                 160

Ile Gly Gly Val Ile Asp Phe Pro Ile Ser Thr Val Gly Gly Thr Glu
                165                 170                 175

Asn Ala Leu Leu Cys Ala Ser Ile Ala Ser Gly Asp Thr Lys Ile Ala
            180                 185                 190

Asn Ala Tyr Ile Thr Pro Glu Ile Thr Asp Leu Ile Glu Leu Leu Arg
        195                 200                 205

Arg Met Gly Ala Glu Ile Thr Val Tyr Gly Thr Ser Arg Ile His Val
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    210                 215                 220

Lys Gly Arg Ala Gly Leu Leu Gln Gly Ala Tyr Met Asp Val Met Pro
225                 230                 235                 240

Asp Arg Ile Glu Ala Leu Thr Trp Ile Val Tyr Gly Ile Ile Ser Gly
                245                 250                 255

Gly Arg Ile Thr Val Glu Gly Val Pro Phe Ser Ser Met Glu Val Pro
            260                 265                 270

Phe Ile His Leu Glu Lys Ala Gly Val Asp Leu Phe Arg Asn Ser Ser
        275                 280                 285

Ser Val Tyr Ile Thr Pro Glu Cys Leu Pro Ser Gly Ser Val Gln Pro
    290                 295                 300

Phe Glu Leu Ala Cys Gly Thr His Pro Gly Val Ile Ser Asp Met Gln
305                 310                 315                 320

Ala Leu Phe Val Leu Leu Gly Leu Lys Gly Ala Gly Thr Ser Arg Val
                325                 330                 335

Tyr Asp Tyr Arg Tyr Pro Glu Arg Ile Ala Phe Val Glu Glu Leu Thr
            340                 345                 350

Asn Leu Val Ser Gly Asp Lys Leu Ser Ala Glu Ala Gly Lys Ile Thr
        355                 360                 365

Ile Gln Gly Asp Ala Thr Phe Arg Pro Gly Tyr Ala Asn Ser Thr Asp
    370                 375                 380

Leu Arg Gly Ser Met Ala Val Val Leu Ala Ala Leu Cys Ala Asp Gly
385                 390                 395                 400

Lys Ser Thr Ile Asn Asn Val His Met Ala Leu Arg Gly Tyr Asn Glu
                405                 410                 415

Leu Asp Lys Lys Leu Arg Leu Leu Gly Ala Asp Leu Thr Ile Arg Glu
            420                 425                 430

Gly Glu Val Pro Ser Pro
        435
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<2155>
<211> 963
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(940)
<223> RXA01268

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gctgatagtt ggaactccga aagcttcatt gctgggagtc gtg gca gca cga att 115
                                                Val Ala Ala Arg Ile
                                                  1   5

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gct cga gtg cca cga att gtc tat gtg gca cat ggg ctg cgc tct gaa   163
Ala Arg Val Pro Arg Ile Val Tyr Val Ala His Gly Leu Arg Ser Glu
                10                  15                  20

act gtt tta ggc tta aaa aag aag att cta gtg ttt ttg gaa tat ttg   211
Thr Val Leu Gly Leu Lys Lys Lys Ile Leu Val Phe Leu Glu Tyr Leu
            25                  30                  35

acc cag ttg ttt gca cat caa act ttg gct gta agt cat tct ctg aag   259
Thr Gln Leu Phe Ala His Gln Thr Leu Ala Val Ser His Ser Leu Lys
        40                  45                  50

aaa gca att gaa gat gcg cac cct cgt ttt aaa gga aga gtg caa gtc   307
Lys Ala Ile Glu Asp Ala His Pro Arg Phe Lys Gly Arg Val Gln Val
    55                  60                  65

tta ggt tat ggc agt atg aat gga gtt gag ctt gat cgc ttt aga gtt   355
Leu Gly Tyr Gly Ser Met Asn Gly Val Glu Leu Asp Arg Phe Arg Val
70                  75                  80                  85

cca tcc ctt gaa gag aaa tta tct gct cgt aat gct tta aac ctg cct   403
Pro Ser Leu Glu Glu Lys Leu Ser Ala Arg Asn Ala Leu Asn Leu Pro
                90                  95                  100

agt aaa tct gtc att gtt ggt ttt gtc ggc aga ata aat aaa gat aag   451
Ser Lys Ser Val Ile Val Gly Phe Val Gly Arg Ile Asn Lys Asp Lys
            105                 110                 115

gga gga gat ctt ctc gct gct ctt aca aaa cat gag gct ttt acc cga   499
Gly Gly Asp Leu Leu Ala Ala Leu Thr Lys His Glu Ala Phe Thr Arg
        120                 125                 130

ttg cga ctg cat ctc tta att att ggt gaa ttg gaa gac gat gac ttg   547
Leu Arg Leu His Leu Leu Ile Ile Gly Glu Leu Glu Asp Asp Asp Leu
    135                 140                 145

cga gaa gca ttc att aaa tta gtt aat gaa ggg cag gtt acg att aca   595
Arg Glu Ala Phe Ile Lys Leu Val Asn Glu Gly Gln Val Thr Ile Thr
150                 155                 160                 165

gga tgg att gat ttc cct gaa gaa cca tta gct gca gtt gat gtt ttg   643
Gly Trp Ile Asp Phe Pro Glu Glu Pro Leu Ala Ala Val Asp Val Leu
                170                 175                 180

ctt cac cca act cag cga gaa ggt tta ggt atg tct ttg ctg gaa gct   691
Leu His Pro Thr Gln Arg Glu Gly Leu Gly Met Ser Leu Leu Glu Ala
            185                 190                 195

cag gct atg gga gtg cct gta ttg acg aat gct gtg act gga aca gtt   739
Gln Ala Met Gly Val Pro Val Leu Thr Asn Ala Val Thr Gly Thr Val
        200                 205                 210

gat gca gta aca agt gga gaa ggt ggc ttt ttt gcc gat gac gat tct   787
Asp Ala Val Thr Ser Gly Glu Gly Gly Phe Phe Ala Asp Asp Asp Ser
    215                 220                 225

gtt gag tcc tgg gtt tct aag att gat tta tta gtt tcc gat cct aag   835
Val Glu Ser Trp Val Ser Lys Ile Asp Leu Leu Val Ser Asp Pro Lys
230                 235                 240                 245
```

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tta aga gac cgg atg gga cgt gct ggt cgc cag ttt gtg tca gct cgt   883
Leu Arg Asp Arg Met Gly Arg Ala Gly Arg Gln Phe Val Ser Ala Arg
                250                 255                 260

ttc aat cgt gat gat gtc gca gct cgt ttc agt cat ttc gtg gaa caa   931
Phe Asn Arg Asp Asp Val Ala Ala Arg Phe Ser His Phe Val Glu Gln
            265                 270                 275

ttc aaa aaa tagggctcat tcaatttcaa tat                            963
Phe Lys Lys
        280
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<211> 280
<212> PRT
<213> Corynebacterium glutamicum

<400> 2156

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Val Ala Ala Arg Ile Ala Arg Val Pro Arg Ile Val Tyr Val Ala His
  1               5                  10                  15

Gly Leu Arg Ser Glu Thr Val Leu Gly Leu Lys Lys Lys Ile Leu Val
             20                  25                  30

Phe Leu Glu Tyr Leu Thr Gln Leu Phe Ala His Gln Thr Leu Ala Val
         35                  40                  45

Ser His Ser Leu Lys Lys Ala Ile Glu Asp Ala His Pro Arg Phe Lys
     50                  55                  60

Gly Arg Val Gln Val Leu Gly Tyr Gly Ser Met Asn Gly Val Glu Leu
 65                  70                  75                  80

Asp Arg Phe Arg Val Pro Ser Leu Glu Glu Lys Leu Ser Ala Arg Asn
                 85                  90                  95

Ala Leu Asn Leu Pro Ser Lys Ser Val Ile Val Gly Phe Val Gly Arg
            100                 105                 110

Ile Asn Lys Asp Lys Gly Gly Asp Leu Leu Ala Ala Leu Thr Lys His
        115                 120                 125

Glu Ala Phe Thr Arg Leu Arg Leu His Leu Leu Ile Ile Gly Glu Leu
    130                 135                 140

Glu Asp Asp Asp Leu Arg Glu Ala Phe Ile Lys Leu Val Asn Glu Gly
145                 150                 155                 160

Gln Val Thr Ile Thr Gly Trp Ile Asp Phe Pro Glu Glu Pro Leu Ala
                165                 170                 175

Ala Val Asp Val Leu Leu His Pro Thr Gln Arg Glu Gly Leu Gly Met
            180                 185                 190

Ser Leu Leu Glu Ala Gln Ala Met Gly Val Pro Val Leu Thr Asn Ala
        195                 200                 205

Val Thr Gly Thr Val Asp Ala Val Thr Ser Gly Glu Gly Gly Phe Phe
    210                 215                 220
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Ala Asp Asp Asp Ser Val Glu Ser Trp Val Ser Lys Ile Asp Leu Leu
225                 230                 235                 240

Val Ser Asp Pro Lys Leu Arg Asp Arg Met Gly Arg Ala Gly Arg Gln
                245                 250                 255

Phe Val Ser Ala Arg Phe Asn Arg Asp Asp Val Ala Ala Arg Phe Ser
            260                 265                 270

His Phe Val Glu Gln Phe Lys Lys
        275                 280


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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1912)
<223> RXA01271

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ttggcgaaac ccaatttatt tcaaaagatg gtggacaaac atg gca ata agc att   115
                                              Met Ala Ile Ser Ile
                                                1               5

ggt aaa gca gga cag aac tta aaa ggg tca gtg cct atc gga aaa gtc   163
Gly Lys Ala Gly Gln Asn Leu Lys Gly Ser Val Pro Ile Gly Lys Val
                10                  15                  20

ctt ttt ctc att gat gcc ctt gcc tgg att tct gca cta ttt atc ggt   211
Leu Phe Leu Ile Asp Ala Leu Ala Trp Ile Ser Ala Leu Phe Ile Gly
            25                  30                  35

gtg gtt ttg cgg tat gaa ttc aat ctg agt tct atc aac tgg agt gcg   259
Val Val Leu Arg Tyr Glu Phe Asn Leu Ser Ser Ile Asn Trp Ser Ala
        40                  45                  50

ttt gca tgg ttc ggg ctt gct gca gtt att ttg cag ttt gtt ctc gga   307
Phe Ala Trp Phe Gly Leu Ala Ala Val Ile Leu Gln Phe Val Leu Gly
    55                  60                  65

ctt tct ctc cat ctt tac cgc aag gga tta cgt cac ctt ttc ggt agc   355
Leu Ser Leu His Leu Tyr Arg Lys Gly Leu Arg His Leu Phe Gly Ser
70                  75                  80                  85

ttc gaa gat aca cta aac gtt tct atc tcg gtc att gtt gtc ggt gtt   403
Phe Glu Asp Thr Leu Asn Val Ser Ile Ser Val Ile Val Val Gly Val
                90                  95                  100

gtc ctt tgg atc gcc tca cta ttt gtt ggt cag cgt tgg aaa atc tca   451
Val Leu Trp Ile Ala Ser Leu Phe Val Gly Gln Arg Trp Lys Ile Ser
            105                 110                 115

cgc ggt gtc atg ctg cta gtt atc ccg ctt gct ctc gta ttc gta ttg   499
Arg Gly Val Met Leu Leu Val Ile Pro Leu Ala Leu Val Phe Val Leu
        120                 125                 130
```

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gca gtg cgt tat ctc gcg cgt atg cga gtt gag cgt ttt cgt cgt ccg   547
Ala Val Arg Tyr Leu Ala Arg Met Arg Val Glu Arg Phe Arg Arg Pro
    135                 140                 145

gct gcg gat tcc aca cca gca ttg att ctt ggt ggt gga tac atc ggt   595
Ala Ala Asp Ser Thr Pro Ala Leu Ile Leu Gly Gly Gly Tyr Ile Gly
150                 155                 160                 165

acc aac ctg atc cag tgg atg atg tcc gat cct aag tcg cct ttc cgc   643
Thr Asn Leu Ile Gln Trp Met Met Ser Asp Pro Lys Ser Pro Phe Arg
                170                 175                 180

cca gtc ggc gtt att gat gat aac cct gaa tta gca tgc caa cgc gta   691
Pro Val Gly Val Ile Asp Asp Asn Pro Glu Leu Ala Cys Gln Arg Val
            185                 190                 195

cgt ggt gtg ccg gtt ctt ggc aag ttt gat gat atc gcc caa gtt gca   739
Arg Gly Val Pro Val Leu Gly Lys Phe Asp Asp Ile Ala Gln Val Ala
        200                 205                 210

tca gac act ggc gca gaa ctt ctt atc gtt gct att ggt gat gcc gac   787
Ser Asp Thr Gly Ala Glu Leu Leu Ile Val Ala Ile Gly Asp Ala Asp
    215                 220                 225

tct gca ctt tta agg cgt gtc caa gat acc gct aat aaa aat ggt ctt   835
Ser Ala Leu Leu Arg Arg Val Gln Asp Thr Ala Asn Lys Asn Gly Leu
230                 235                 240                 245

tca gta aag gta atg ccg gct att gac cgc gtc gtt tct aag ggc gtt   883
Ser Val Lys Val Met Pro Ala Ile Asp Arg Val Val Ser Lys Gly Val
                250                 255                 260

cgt gga aac gat ttg cgt gat ctc tct att gaa gat ttg ctt gga cgt   931
Arg Gly Asn Asp Leu Arg Asp Leu Ser Ile Glu Asp Leu Leu Gly Arg
            265                 270                 275

caa cct gtt gaa acc aat gtt tca gaa att act ggc tat cta aca ggt   979
Gln Pro Val Glu Thr Asn Val Ser Glu Ile Thr Gly Tyr Leu Thr Gly
        280                 285                 290

aag cgt gtt ctt gtt acc ggt gca ggt ggg tca att ggt tcc cag cta   1027
Lys Arg Val Leu Val Thr Gly Ala Gly Gly Ser Ile Gly Ser Gln Leu
    295                 300                 305

tgt acg gaa att gcc aaa tac gga cct gct gag ctt atg atg ctt gat   1075
Cys Thr Glu Ile Ala Lys Tyr Gly Pro Ala Glu Leu Met Met Leu Asp
310                 315                 320                 325

cgc gat gag act ggt ttg cag cag gtt ctg att aac gtt gct ggt aac   1123
Arg Asp Glu Thr Gly Leu Gln Gln Val Leu Ile Asn Val Ala Gly Asn
                330                 335                 340

ggt ttg ttg gat acg gat gct gtg gtt ctt gcg gat atc cgc gaa gca   1171
Gly Leu Leu Asp Thr Asp Ala Val Val Leu Ala Asp Ile Arg Glu Ala
            345                 350                 355

gac gcg atg aaa gag att ttt ctc aag cgt aaa cca gaa gtt gtc ttc   1219
Asp Ala Met Lys Glu Ile Phe Leu Lys Arg Lys Pro Glu Val Val Phe
        360                 365                 370
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cat gca gca gca tta aag cac ttg cca atg ctg gag cag tat cca gat   1267
His Ala Ala Ala Leu Lys His Leu Pro Met Leu Glu Gln Tyr Pro Asp
    375                 380                 385

gag ggc tgg aaa aca aac gtt cta gga act ctt aac gtt ctt gct gcc   1315
Glu Gly Trp Lys Thr Asn Val Leu Gly Thr Leu Asn Val Leu Ala Ala
390                 395                 400                 405

gca gaa gct gtt ggt gtt gag act ttc gtc aat att tcc acc gat aag   1363
Ala Glu Ala Val Gly Val Glu Thr Phe Val Asn Ile Ser Thr Asp Lys
                410                 415                 420

gca gct aat cca acc agc gtc tta ggg cac tca aag cga gtc gct gaa   1411
Ala Ala Asn Pro Thr Ser Val Leu Gly His Ser Lys Arg Val Ala Glu
            425                 430                 435

aag ctg act gcc tgg tat gga cag aat tcc acc agc aag tac cta tcg   1459
Lys Leu Thr Ala Trp Tyr Gly Gln Asn Ser Thr Ser Lys Tyr Leu Ser
        440                 445                 450

gtt cga ttt gga aac gtc att ggt agc cgt gga tcg atg ctc ccg act   1507
Val Arg Phe Gly Asn Val Ile Gly Ser Arg Gly Ser Met Leu Pro Thr
    455                 460                 465

ttc acc agg cta atc atg gaa gat aaa ccg cta aca gtg acg cac ccg   1555
Phe Thr Arg Leu Ile Met Glu Asp Lys Pro Leu Thr Val Thr His Pro
470                 475                 480                 485

gat gtc act agg ttc ttc atg aca att cct gaa gct tgc caa ttg gtc   1603
Asp Val Thr Arg Phe Phe Met Thr Ile Pro Glu Ala Cys Gln Leu Val
                490                 495                 500

ctg caa gcc ggt ggt att gga cgt tcc ggc gag gtt ctc atc ctt gac   1651
Leu Gln Ala Gly Gly Ile Gly Arg Ser Gly Glu Val Leu Ile Leu Asp
            505                 510                 515

atg ggt gag cct gta agc atc ctt gaa att gca cag cgc atg atc gca   1699
Met Gly Glu Pro Val Ser Ile Leu Glu Ile Ala Gln Arg Met Ile Ala
        520                 525                 530

atg tcc ggt aaa gat att gac atc gtg ttc acc ggc ctt cgc gag ggc   1747
Met Ser Gly Lys Asp Ile Asp Ile Val Phe Thr Gly Leu Arg Glu Gly
    535                 540                 545

gaa aag atg cac gaa gag ctg gtt ggt gat ggt gaa acc gaa gat cgt   1795
Glu Lys Met His Glu Glu Leu Val Gly Asp Gly Glu Thr Glu Asp Arg
550                 555                 560                 565

cca ttc cac tca aag att tcg cat gca cat gca gaa agc ctc gct cct   1843
Pro Phe His Ser Lys Ile Ser His Ala His Ala Glu Ser Leu Ala Pro
                570                 575                 580

aat aat ctc gat aga gat cga ttt atg caa cgt gct gga aaa cta gct   1891
Asn Asn Leu Asp Arg Asp Arg Phe Met Gln Arg Ala Gly Lys Leu Ala
            585                 590                 595

tca aca gat tcg gag atc atc taaatgacta atgaacgaat ttt             1935
Ser Thr Asp Ser Glu Ile Ile
        600
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<210> 2158
<211> 604
<212> PRT
<213> Corynebacterium glutamicum

<400> 2158
Met Ala Ile Ser Ile Gly Lys Ala Gly Gln Asn Leu Lys Gly Ser Val
1 5 10 15

Pro Ile Gly Lys Val Leu Phe Leu Ile Asp Ala Leu Ala Trp Ile Ser
20 25 30

Ala Leu Phe Ile Gly Val Val Leu Arg Tyr Glu Phe Asn Leu Ser Ser
35 40 45

Ile Asn Trp Ser Ala Phe Ala Trp Phe Gly Leu Ala Ala Val Ile Leu
50 55 60

Gln Phe Val Leu Gly Leu Ser Leu His Leu Tyr Arg Lys Gly Leu Arg
65 70 75 80

His Leu Phe Gly Ser Phe Glu Asp Thr Leu Asn Val Ser Ile Ser Val
85 90 95

Ile Val Val Gly Val Val Leu Trp Ile Ala Ser Leu Phe Val Gly Gln
100 105 110

Arg Trp Lys Ile Ser Arg Gly Val Met Leu Leu Val Ile Pro Leu Ala
115 120 125

Leu Val Phe Val Leu Ala Val Arg Tyr Leu Ala Arg Met Arg Val Glu
130 135 140

Arg Phe Arg Arg Pro Ala Ala Asp Ser Thr Pro Ala Leu Ile Leu Gly
145 150 155 160

Gly Gly Tyr Ile Gly Thr Asn Leu Ile Gln Trp Met Met Ser Asp Pro
165 170 175

Lys Ser Pro Phe Arg Pro Val Gly Val Ile Asp Asp Asn Pro Glu Leu
180 185 190

Ala Cys Gln Arg Val Arg Gly Val Pro Val Leu Gly Lys Phe Asp Asp
195 200 205

Ile Ala Gln Val Ala Ser Asp Thr Gly Ala Glu Leu Leu Ile Val Ala
210 215 220

Ile Gly Asp Ala Asp Ser Ala Leu Leu Arg Arg Val Gln Asp Thr Ala
225 230 235 240

Asn Lys Asn Gly Leu Ser Val Lys Val Met Pro Ala Ile Asp Arg Val
245 250 255

Val Ser Lys Gly Val Arg Gly Asn Asp Leu Arg Asp Leu Ser Ile Glu
260 265 270

Asp Leu Leu Gly Arg Gln Pro Val Glu Thr Asn Val Ser Glu Ile Thr
275 280 285

Gly Tyr Leu Thr Gly Lys Arg Val Leu Val Thr Gly Ala Gly Gly Ser

290 295 300

Ile Gly Ser Gln Leu Cys Thr Glu Ile Ala Lys Tyr Gly Pro Ala Glu
305 310 315 320

Leu Met Met Leu Asp Arg Asp Glu Thr Gly Leu Gln Gln Val Leu Ile
325 330 335

Asn Val Ala Gly Asn Gly Leu Leu Asp Thr Asp Ala Val Val Leu Ala
340 345 350

Asp Ile Arg Glu Ala Asp Ala Met Lys Glu Ile Phe Leu Lys Arg Lys
355 360 365

Pro Glu Val Val Phe His Ala Ala Ala Leu Lys His Leu Pro Met Leu
370 375 380

Glu Gln Tyr Pro Asp Glu Gly Trp Lys Thr Asn Val Leu Gly Thr Leu
385 390 395 400

Asn Val Leu Ala Ala Ala Glu Ala Val Gly Val Glu Thr Phe Val Asn
405 410 415

Ile Ser Thr Asp Lys Ala Ala Asn Pro Thr Ser Val Leu Gly His Ser
420 425 430

Lys Arg Val Ala Glu Lys Leu Thr Ala Trp Tyr Gly Gln Asn Ser Thr
435 440 445

Ser Lys Tyr Leu Ser Val Arg Phe Gly Asn Val Ile Gly Ser Arg Gly
450 455 460

Ser Met Leu Pro Thr Phe Thr Arg Leu Ile Met Glu Asp Lys Pro Leu
465 470 475 480

Thr Val Thr His Pro Asp Val Thr Arg Phe Phe Met Thr Ile Pro Glu
485 490 495

Ala Cys Gln Leu Val Leu Gln Ala Gly Gly Ile Gly Arg Ser Gly Glu
500 505 510

Val Leu Ile Leu Asp Met Gly Glu Pro Val Ser Ile Leu Glu Ile Ala
515 520 525

Gln Arg Met Ile Ala Met Ser Gly Lys Asp Ile Asp Ile Val Phe Thr
530 535 540

Gly Leu Arg Glu Gly Glu Lys Met His Glu Glu Leu Val Gly Asp Gly
545 550 555 560

Glu Thr Glu Asp Arg Pro Phe His Ser Lys Ile Ser His Ala His Ala
565 570 575

Glu Ser Leu Ala Pro Asn Asn Leu Asp Arg Asp Arg Phe Met Gln Arg
580 585 590

Ala Gly Lys Leu Ala Ser Thr Asp Ser Glu Ile Ile
595 600

<210> 2159

<211> 1557
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1534)
<223> RXA01273

<400> 2159
gacctattca gcgctggatt ttttctggca ttttcttggc agtcagtgag ttgctaacgt 60

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tctattggtt aaaaattgat ctgcaagagg actgcaaaat atg gaa tta agg gaa   115
                                              Met Glu Leu Arg Glu
                                                1               5

tac gcg aca atc ctg atg aag aat tgg gtg ttg atc gtt atc gca tcc   163
Tyr Ala Thr Ile Leu Met Lys Asn Trp Val Leu Ile Val Ile Ala Ser
                  10                  15                  20

att ctt gga att gca gcg ggc gct ggt ttt tcc ctt cta gct aca ccg   211
Ile Leu Gly Ile Ala Ala Gly Ala Gly Phe Ser Leu Leu Ala Thr Pro
              25                  30                  35

gag tat cag tca cgt act cag ttg tat gta tcg gtg cgg tcg ggg gct   259
Glu Tyr Gln Ser Arg Thr Gln Leu Tyr Val Ser Val Arg Ser Gly Ala
          40                  45                  50

ggg aca acc tct gac atg gtt cag ggt gct aac ttt tcg cgt cag att   307
Gly Thr Thr Ser Asp Met Val Gln Gly Ala Asn Phe Ser Arg Gln Ile
      55                  60                  65

gtg aat agt tat gtt gat gtc att aag acg ggt gtt gtt cta gag ccg   355
Val Asn Ser Tyr Val Asp Val Ile Lys Thr Gly Val Val Leu Glu Pro
  70                  75                  80                  85

gtt gtt gat gag ctt ggt ctg gag ttg acg gct aac cag ttg agt tct   403
Val Val Asp Glu Leu Gly Leu Glu Leu Thr Ala Asn Gln Leu Ser Ser
                  90                  95                 100

cat atc agt gcg gct tct cct gct gat act gcg ttg atc aac atc act   451
His Ile Ser Ala Ala Ser Pro Ala Asp Thr Ala Leu Ile Asn Ile Thr
             105                 110                 115

gct tct agt cct tct cct cag cag gcg gct gag atc gcc aat gca gtg   499
Ala Ser Ser Pro Ser Pro Gln Gln Ala Ala Glu Ile Ala Asn Ala Val
         120                 125                 130

ggg gag agt ttc aag aat gtg att cag act gaa ttg gaa cca gac tcc   547
Gly Glu Ser Phe Lys Asn Val Ile Gln Thr Glu Leu Glu Pro Asp Ser
     135                 140                 145

ggc gat ggc atg agc ccg att aac ctg act act act cag gtg gct ctg   595
Gly Asp Gly Met Ser Pro Ile Asn Leu Thr Thr Thr Gln Val Ala Leu
150                 155                 160                 165

gaa cca tct tct ccg gtc agt cct aat gtg atg atg aat atc ctc ctc   643
Glu Pro Ser Ser Pro Val Ser Pro Asn Val Met Met Asn Ile Leu Leu
                170                 175                 180

ggc cta ctt gta ggt ctt gca ata ggt gtt ggt att gca gtg ctt cgc   691
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```
Gly Leu Leu Val Gly Leu Ala Ile Gly Val Gly Ile Ala Val Leu Arg
            185                 190                 195

gcg gct ttg gat act cgt att cat tcc ttg cgc gat att gaa gag gtt   739
Ala Ala Leu Asp Thr Arg Ile His Ser Leu Arg Asp Ile Glu Glu Val
        200                 205                 210

act gat aag cca ctt ttg ggc gga atc att gcg gat tct gaa gtt gag   787
Thr Asp Lys Pro Leu Leu Gly Gly Ile Ile Ala Asp Ser Glu Val Glu
    215                 220                 225

aag cac ccg ttg atc att aag cac aag ccg cat agt cct att gcg gag   835
Lys His Pro Leu Ile Ile Lys His Lys Pro His Ser Pro Ile Ala Glu
230                 235                 240                 245

tcc ttt cgt gcg tta cgt act aac ctg cag ttc ctt aac gtc ggc ggc   883
Ser Phe Arg Ala Leu Arg Thr Asn Leu Gln Phe Leu Asn Val Gly Gly
                250                 255                 260

tca tct tca gta ttt gtt atc tcc tct gct aat cct ggt gag ggt aag   931
Ser Ser Ser Val Phe Val Ile Ser Ser Ala Asn Pro Gly Glu Gly Lys
            265                 270                 275

tca acc act tct gta aac cta gct ttg gcg ctt gca gag gcc ggc tcc   979
Ser Thr Thr Ser Val Asn Leu Ala Leu Ala Leu Ala Glu Ala Gly Ser
        280                 285                 290

cgt gta gcg ctg atc gaa gct gat ctt cgc ttg cca cga gtg agc aag   1027
Arg Val Ala Leu Ile Glu Ala Asp Leu Arg Leu Pro Arg Val Ser Lys
    295                 300                 305

tac ctc gga gtt gag ggc aac gca ggt ctg act gac att ctc att ggc   1075
Tyr Leu Gly Val Glu Gly Asn Ala Gly Leu Thr Asp Ile Leu Ile Gly
310                 315                 320                 325

aag gcc gag gtt aat gat gtg ttg cag cgt tgg ggt agg act cag ttg   1123
Lys Ala Glu Val Asn Asp Val Leu Gln Arg Trp Gly Arg Thr Gln Leu
                330                 335                 340

tac tat ctc ccg gca ggg cgc att ccg ccg aac ccg agt gag ttg ctt   1171
Tyr Tyr Leu Pro Ala Gly Arg Ile Pro Pro Asn Pro Ser Glu Leu Leu
            345                 350                 355

ggt tca gct gag atg gac aag gtc att gcg gag ctt gag gaa agc ttt   1219
Gly Ser Ala Glu Met Asp Lys Val Ile Ala Glu Leu Glu Glu Ser Phe
        360                 365                 370

gat tat gtg atc atc gat gcc cct ccg gcg ttg gcg gtt acc gat gct   1267
Asp Tyr Val Ile Ile Asp Ala Pro Pro Ala Leu Ala Val Thr Asp Ala
    375                 380                 385

gca gtt att ggt cat ggc aag gct ggc atc ctg att gcg gtc tcc gca   1315
Ala Val Ile Gly His Gly Lys Ala Gly Ile Leu Ile Ala Val Ser Ala
390                 395                 400                 405

ggt tct aca aag aag cct gag ttg gaa gct acg ctg tcc acg ctt gag   1363
Gly Ser Thr Lys Lys Pro Glu Leu Glu Ala Thr Leu Ser Thr Leu Glu
                410                 415                 420

aat gcg gat gcc aat gtt gtt ggc gtt gtc gct acg atg ctc ccg cct   1411
Asn Ala Asp Ala Asn Val Val Gly Val Val Ala Thr Met Leu Pro Pro
```

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            425                 430                 435

aag tct gtg gct ggt tat ggc tac gga aat tac ggc tac ggc gac acc   1459
Lys Ser Val Ala Gly Tyr Gly Tyr Gly Asn Tyr Gly Tyr Gly Asp Thr
        440                 445                 450

tcc aaa atc aat gcc cct aag ccc gac aac acc gaa cta acc acc acc   1507
Ser Lys Ile Asn Ala Pro Lys Pro Asp Asn Thr Glu Leu Thr Thr Thr
    455                 460                 465

gat gct tcc aag gcc aac aat gag caa tagcttcact attctcactg         1554
Asp Ala Ser Lys Ala Asn Asn Glu Gln
470                 475

tct                                                               1557
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<210> 2160
<211> 478
<212> PRT
<213> Corynebacterium glutamicum

<400> 2160

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Met Glu Leu Arg Glu Tyr Ala Thr Ile Leu Met Lys Asn Trp Val Leu
  1               5                  10                  15

Ile Val Ile Ala Ser Ile Leu Gly Ile Ala Ala Gly Ala Gly Phe Ser
             20                  25                  30

Leu Leu Ala Thr Pro Glu Tyr Gln Ser Arg Thr Gln Leu Tyr Val Ser
         35                  40                  45

Val Arg Ser Gly Ala Gly Thr Thr Ser Asp Met Val Gln Gly Ala Asn
     50                  55                  60

Phe Ser Arg Gln Ile Val Asn Ser Tyr Val Asp Val Ile Lys Thr Gly
 65                  70                  75                  80

Val Val Leu Glu Pro Val Val Asp Glu Leu Gly Leu Glu Leu Thr Ala
                 85                  90                  95

Asn Gln Leu Ser Ser His Ile Ser Ala Ala Ser Pro Ala Asp Thr Ala
            100                 105                 110

Leu Ile Asn Ile Thr Ala Ser Ser Pro Ser Pro Gln Gln Ala Ala Glu
        115                 120                 125

Ile Ala Asn Ala Val Gly Glu Ser Phe Lys Asn Val Ile Gln Thr Glu
    130                 135                 140

Leu Glu Pro Asp Ser Gly Asp Gly Met Ser Pro Ile Asn Leu Thr Thr
145                 150                 155                 160

Thr Gln Val Ala Leu Glu Pro Ser Ser Pro Val Ser Pro Asn Val Met
                165                 170                 175

Met Asn Ile Leu Leu Gly Leu Leu Val Gly Leu Ala Ile Gly Val Gly
            180                 185                 190

Ile Ala Val Leu Arg Ala Ala Leu Asp Thr Arg Ile His Ser Leu Arg
        195                 200                 205
```

```
Asp Ile Glu Glu Val Thr Asp Lys Pro Leu Leu Gly Gly Ile Ile Ala
    210                 215                 220

Asp Ser Glu Val Glu Lys His Pro Leu Ile Ile Lys His Lys Pro His
225                 230                 235                 240

Ser Pro Ile Ala Glu Ser Phe Arg Ala Leu Arg Thr Asn Leu Gln Phe
                245                 250                 255

Leu Asn Val Gly Gly Ser Ser Ser Val Phe Val Ile Ser Ser Ala Asn
            260                 265                 270

Pro Gly Glu Gly Lys Ser Thr Thr Ser Val Asn Leu Ala Leu Ala Leu
        275                 280                 285

Ala Glu Ala Gly Ser Arg Val Ala Leu Ile Glu Ala Asp Leu Arg Leu
    290                 295                 300

Pro Arg Val Ser Lys Tyr Leu Gly Val Glu Gly Asn Ala Gly Leu Thr
305                 310                 315                 320

Asp Ile Leu Ile Gly Lys Ala Glu Val Asn Asp Val Leu Gln Arg Trp
                325                 330                 335

Gly Arg Thr Gln Leu Tyr Tyr Leu Pro Ala Gly Arg Ile Pro Pro Asn
            340                 345                 350

Pro Ser Glu Leu Leu Gly Ser Ala Glu Met Asp Lys Val Ile Ala Glu
        355                 360                 365

Leu Glu Glu Ser Phe Asp Tyr Val Ile Ile Asp Ala Pro Pro Ala Leu
    370                 375                 380

Ala Val Thr Asp Ala Ala Val Ile Gly His Gly Lys Ala Gly Ile Leu
385                 390                 395                 400

Ile Ala Val Ser Ala Gly Ser Thr Lys Lys Pro Glu Leu Glu Ala Thr
                405                 410                 415

Leu Ser Thr Leu Glu Asn Ala Asp Ala Asn Val Val Gly Val Val Ala
            420                 425                 430

Thr Met Leu Pro Pro Lys Ser Val Ala Gly Tyr Gly Tyr Gly Asn Tyr
        435                 440                 445

Gly Tyr Gly Asp Thr Ser Lys Ile Asn Ala Pro Lys Pro Asp Asn Thr
    450                 455                 460

Glu Leu Thr Thr Thr Asp Ala Ser Lys Ala Asn Asn Glu Gln
465                 470                 475
```

<210> 2161
<211> 903
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(880)

<223> RXA01282

<400> 2161

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caggatgggt cggaacgttc gcgtcgtttg cggtgtggtt ctgggtcatt tggtgggcag 60

cggtaggaaa tacaaaaagc ccactctaag atggcagggt atg gat gag ctg ctc   115
                                              Met Asp Glu Leu Leu
                                                1               5

aaa cag gaa gtc aag gat ttc ctc acc acc agg cgt gca cgg att acg   163
Lys Gln Glu Val Lys Asp Phe Leu Thr Thr Arg Arg Ala Arg Ile Thr
                 10                  15                  20

ccg gcc gct gcg gga cta gaa acg cag ccg tgg agt gat cgt cgg gtg   211
Pro Ala Ala Ala Gly Leu Glu Thr Gln Pro Trp Ser Asp Arg Arg Val
             25                  30                  35

ccg ggg ctt cgg cgg gaa gaa gtc gcg gat ctg gcg ggc att tct ttg   259
Pro Gly Leu Arg Arg Glu Glu Val Ala Asp Leu Ala Gly Ile Ser Leu
         40                  45                  50

gag tat tac atc cgg ttt gag cgc gga aat ctc aag ggt gca tcg cct   307
Glu Tyr Tyr Ile Arg Phe Glu Arg Gly Asn Leu Lys Gly Ala Ser Pro
     55                  60                  65

gaa ata ttg caa tcg ttg gct aag gct ctc caa ctg agc cca att gag   355
Glu Ile Leu Gln Ser Leu Ala Lys Ala Leu Gln Leu Ser Pro Ile Glu
 70                  75                  80                  85

cgc gaa cac ctt cac aat ttg gct tat cgc gcc gac cat ccg cgc aac   403
Arg Glu His Leu His Asn Leu Ala Tyr Arg Ala Asp His Pro Arg Asn
                 90                  95                 100

cta cct agt gca gag acc cca acg gca ccc ctc cag gac atc gtt gat   451
Leu Pro Ser Ala Glu Thr Pro Thr Ala Pro Leu Gln Asp Ile Val Asp
             105                 110                 115

gcg gtc aca gat aaa ccg gcg tgg atc cgc aac gag cag atg gat att   499
Ala Val Thr Asp Lys Pro Ala Trp Ile Arg Asn Glu Gln Met Asp Ile
         120                 125                 130

ttg gct aca aat cgg ctc tgc gcg gaa ctt tac gcc ccg att ttc aag   547
Leu Ala Thr Asn Arg Leu Cys Ala Glu Leu Tyr Ala Pro Ile Phe Lys
     135                 140                 145

gat ctg ccc gat cgg ccc aac act gcg cgg cat tgc ttt atc ggc gca   595
Asp Leu Pro Asp Arg Pro Asn Thr Ala Arg His Cys Phe Ile Gly Ala
150                 155                 160                 165

aca gcc tcc gag ttc tgg gtg gac cgg gat cag ttc agt gcg gag ttc   643
Thr Ala Ser Glu Phe Trp Val Asp Arg Asp Gln Phe Ser Ala Glu Phe
                 170                 175                 180

gct gcc aaa cta cgc ctc gag tac gcc cgg cgc ccc agc gtg cca ggt   691
Ala Ala Lys Leu Arg Leu Glu Tyr Ala Arg Arg Pro Ser Val Pro Gly
             185                 190                 195

tta aag gag ctt atc gac gag ctc cat cag aaa agt tct gtt ttc cgc   739
Leu Lys Glu Leu Ile Asp Glu Leu His Gln Lys Ser Ser Val Phe Arg
         200                 205                 210
```

```
gat aat tgg gcg tct gct gat gtt ttg tca ttc ggc tct ggc atc aaa   787
Asp Asn Trp Ala Ser Ala Asp Val Leu Ser Phe Gly Ser Gly Ile Lys
    215                 220                 225

cgt ttc agg cac cca aca ctg ggg gag cgg gtc tat gaa tac gag acg   835
Arg Phe Arg His Pro Thr Leu Gly Glu Arg Val Tyr Glu Tyr Glu Thr
230                 235                 240                 245

ttt aat ctc aat agt gca ccg ggg tat gtg ttg agc att tac ttt       880
Phe Asn Leu Asn Ser Ala Pro Gly Tyr Val Leu Ser Ile Tyr Phe
                250                 255                 260

taggtggtgg aggggcgcgt cga                                        903
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<210> 2162
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

<400> 2162

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Met Asp Glu Leu Leu Lys Gln Glu Val Lys Asp Phe Leu Thr Thr Arg
  1               5                  10                  15

Arg Ala Arg Ile Thr Pro Ala Ala Ala Gly Leu Glu Thr Gln Pro Trp
             20                  25                  30

Ser Asp Arg Arg Val Pro Gly Leu Arg Arg Glu Glu Val Ala Asp Leu
         35                  40                  45

Ala Gly Ile Ser Leu Glu Tyr Tyr Ile Arg Phe Glu Arg Gly Asn Leu
     50                  55                  60

Lys Gly Ala Ser Pro Glu Ile Leu Gln Ser Leu Ala Lys Ala Leu Gln
 65                  70                  75                  80

Leu Ser Pro Ile Glu Arg Glu His Leu His Asn Leu Ala Tyr Arg Ala
                 85                  90                  95

Asp His Pro Arg Asn Leu Pro Ser Ala Glu Thr Pro Thr Ala Pro Leu
            100                 105                 110

Gln Asp Ile Val Asp Ala Val Thr Asp Lys Pro Ala Trp Ile Arg Asn
        115                 120                 125

Glu Gln Met Asp Ile Leu Ala Thr Asn Arg Leu Cys Ala Glu Leu Tyr
    130                 135                 140

Ala Pro Ile Phe Lys Asp Leu Pro Asp Arg Pro Asn Thr Ala Arg His
145                 150                 155                 160

Cys Phe Ile Gly Ala Thr Ala Ser Glu Phe Trp Val Asp Arg Asp Gln
                165                 170                 175

Phe Ser Ala Glu Phe Ala Ala Lys Leu Arg Leu Glu Tyr Ala Arg Arg
            180                 185                 190

Pro Ser Val Pro Gly Leu Lys Glu Leu Ile Asp Glu Leu His Gln Lys
        195                 200                 205

Ser Ser Val Phe Arg Asp Asn Trp Ala Ser Ala Asp Val Leu Ser Phe
```

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    210                 215                 220

Gly Ser Gly Ile Lys Arg Phe Arg His Pro Thr Leu Gly Glu Arg Val
225                 230                 235                 240

Tyr Glu Tyr Glu Thr Phe Asn Leu Asn Ser Ala Pro Gly Tyr Val Leu
                245                 250                 255

Ser Ile Tyr Phe
            260


<210> 2163
<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(766)
<223> RXA01294

<400> 2163
atgaagggat accgctcctt ttcgggggta cagcactcca gcaagactca ttcggctcag 60

ttagagttca ccacaacgac tcaaaaaaga aagtggcagc atg tct acg att cct   115
                                        Met Ser Thr Ile Pro
                                          1               5

gat gtt ttc acc agt gaa gtg ttc cct gaa atc agt ggc acc aaa gaa   163
Asp Val Phe Thr Ser Glu Val Phe Pro Glu Ile Ser Gly Thr Lys Glu
                 10                  15                  20

ttc cgt ggc ctg act tat atg ttc ttt gat caa ttc act ttg ccc acc   211
Phe Arg Gly Leu Thr Tyr Met Phe Phe Asp Gln Phe Thr Leu Pro Thr
             25                  30                  35

gca gaa cag ctt gag caa gct aaa gca gct ggc tgg tca ctg atc acc   259
Ala Glu Gln Leu Glu Gln Ala Lys Ala Ala Gly Trp Ser Leu Ile Thr
         40                  45                  50

tgg gga tgg tgg aat agc gac acc gat ctt gag gat gtc gaa ttg gaa   307
Trp Gly Trp Trp Asn Ser Asp Thr Asp Leu Glu Asp Val Glu Leu Glu
     55                  60                  65

gac atc act aat gaa ggc gac agc cta cca aaa ctc acg gat gaa ttc   355
Asp Ile Thr Asn Glu Gly Asp Ser Leu Pro Lys Leu Thr Asp Glu Phe
 70                  75                  80                  85

gct gtg tct tca ctg agc acc ttc gat cta aat tcc caa ggt ctg ccc   403
Ala Val Ser Ser Leu Ser Thr Phe Asp Leu Asn Ser Gln Gly Leu Pro
                 90                  95                 100

aat gat gat cgt gag ccg caa cca att gaa gaa gcc gac tca cta gat   451
Asn Asp Asp Arg Glu Pro Gln Pro Ile Glu Glu Ala Asp Ser Leu Asp
            105                 110                 115

gac atc ttc tcc gag gaa gag ggc tgg ggt cta atg gca atc aat tgc   499
Asp Ile Phe Ser Glu Glu Glu Gly Trp Gly Leu Met Ala Ile Asn Cys
        120                 125                 130
```

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ccg aat tgg caa gtc cca gca gcg tgt gaa tgg ctc ggc tgc atg aat   547
Pro Asn Trp Gln Val Pro Ala Ala Cys Glu Trp Leu Gly Cys Met Asn
    135                 140                 145

gtt ggt gaa cca ttt gaa atg tca cac gta ctt agg gtg tgg cag aac   595
Val Gly Glu Pro Phe Glu Met Ser His Val Leu Arg Val Trp Gln Asn
150                 155                 160                 165

agt tgg ggc gtc gag gcc ctg gct ttt ggt ggt gaa gaa gac gac gcg   643
Ser Trp Gly Val Glu Ala Leu Ala Phe Gly Gly Glu Glu Asp Asp Ala
                170                 175                 180

gat ctg ctg ctt cga gtc cct gaa gaa agc gaa gag cta ctg aag gct   691
Asp Leu Leu Leu Arg Val Pro Glu Glu Ser Glu Glu Leu Leu Lys Ala
            185                 190                 195

ctc gca gtc gct tct gac caa gtc act acc tac aag cat gaa gat ctg   739
Leu Ala Val Ala Ser Asp Gln Val Thr Thr Tyr Lys His Glu Asp Leu
        200                 205                 210

gga ttc tta gct agt ctt tgg ttt gac taactacaat caatgtcatg         786
Gly Phe Leu Ala Ser Leu Trp Phe Asp
    215                 220

acc                                                               789
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US20050153309A1

<210> 2164
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 2164

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Met Ser Thr Ile Pro Asp Val Phe Thr Ser Glu Val Phe Pro Glu Ile
  1               5                  10                  15

Ser Gly Thr Lys Glu Phe Arg Gly Leu Thr Tyr Met Phe Phe Asp Gln
             20                  25                  30

Phe Thr Leu Pro Thr Ala Glu Gln Leu Glu Gln Ala Lys Ala Ala Gly
         35                  40                  45

Trp Ser Leu Ile Thr Trp Gly Trp Trp Asn Ser Asp Thr Asp Leu Glu
     50                  55                  60

Asp Val Glu Leu Glu Asp Ile Thr Asn Glu Gly Asp Ser Leu Pro Lys
 65                  70                  75                  80

Leu Thr Asp Glu Phe Ala Val Ser Ser Leu Ser Thr Phe Asp Leu Asn
                 85                  90                  95

Ser Gln Gly Leu Pro Asn Asp Asp Arg Glu Pro Gln Pro Ile Glu Glu
            100                 105                 110

Ala Asp Ser Leu Asp Asp Ile Phe Ser Glu Glu Glu Gly Trp Gly Leu
        115                 120                 125

Met Ala Ile Asn Cys Pro Asn Trp Gln Val Pro Ala Ala Cys Glu Trp
    130                 135                 140

Leu Gly Cys Met Asn Val Gly Glu Pro Phe Glu Met Ser His Val Leu
```

```
145                 150                 155                 160

Arg Val Trp Gln Asn Ser Trp Gly Val Glu Ala Leu Ala Phe Gly Gly
                165                 170                 175

Glu Glu Asp Asp Ala Asp Leu Leu Leu Arg Val Pro Glu Glu Ser Glu
            180                 185                 190

Glu Leu Leu Lys Ala Leu Ala Val Ala Ser Asp Gln Val Thr Thr Tyr
        195                 200                 205

Lys His Glu Asp Leu Gly Phe Leu Ala Ser Leu Trp Phe Asp
    210                 215                 220


<210> 2165
<211> 1098
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1075)
<223> RXA01295

<400> 2165
tttctggtgt taccctcggg taattgtaaa aaattcattg attaaaaacg atcagccaat 60

tggcatgctc agactccttg tgaagaaagt gacagtttcg atg acc gaa aat ctt   115
                                              Met Thr Glu Asn Leu
                                                1               5

gat aat gcg ttg cta tcc atg cgg atg aaa cct gta caa atg gcg ctt   163
Asp Asn Ala Leu Leu Ser Met Arg Met Lys Pro Val Gln Met Ala Leu
                  10                  15                  20

atg aca ctg ggc tac aac cat gac atg gcg gtg acc gat tcc ggt atg   211
Met Thr Leu Gly Tyr Asn His Asp Met Ala Val Thr Asp Ser Gly Met
              25                  30                  35

gaa ctt ata gtg cgc cgc cca ggg ctg acc gtg aac ttc aac ttg gat   259
Glu Leu Ile Val Arg Arg Pro Gly Leu Thr Val Asn Phe Asn Leu Asp
          40                  45                  50

tcg gtc acc ttg tgc atc gtc gct gat ttc atg tgg cat ggc tgt gtc   307
Ser Val Thr Leu Cys Ile Val Ala Asp Phe Met Trp His Gly Cys Val
      55                  60                  65

cct gca aag aaa cag gca gag tac ctg cgg gcc gct aat gaa ttc aac   355
Pro Ala Lys Lys Gln Ala Glu Tyr Leu Arg Ala Ala Asn Glu Phe Asn
  70                  75                  80                  85

agg cca acc cgt gat ctg cag gtg gtt tta gat gaa gct gat tca aag   403
Arg Pro Thr Arg Asp Leu Gln Val Val Leu Asp Glu Ala Asp Ser Lys
                  90                  95                 100

aac atg act gtg cga ggt cgt gaa ttc ttc ttc tca agc gtc ggc gca   451
Asn Met Thr Val Arg Gly Arg Glu Phe Phe Phe Ser Ser Val Gly Ala
              105                 110                 115

acg tgg gaa cag tcg gca gag ttc gtg cac tac tgc atg aat gat gtg   499
```

```
Thr Trp Glu Gln Ser Ala Glu Phe Val His Tyr Cys Met Asn Asp Val
        120                 125                 130

gca acg act ttc gtg tct tgg tgc gaa caa atc tgg ccg aag ttt tcc   547
Ala Thr Thr Phe Val Ser Trp Cys Glu Gln Ile Trp Pro Lys Phe Ser
    135                 140                 145

cct gaa cgc gta gag ttc aac gca act cct cca gat gtg gat ttc gag   595
Pro Glu Arg Val Glu Phe Asn Ala Thr Pro Pro Asp Val Asp Phe Glu
150                 155                 160                 165

ttc tct gaa gat caa ctc aaa gaa ggc aat ccc ttc ggg ctg att gac   643
Phe Ser Glu Asp Gln Leu Lys Glu Gly Asn Pro Phe Gly Leu Ile Asp
                170                 175                 180

gaa ccc acc ccg ctg gtt tct ttg gat cgt atc tac caa caa tac gaa   691
Glu Pro Thr Pro Leu Val Ser Leu Asp Arg Ile Tyr Gln Gln Tyr Glu
            185                 190                 195

tta atg ggt gcg gat caa ctc aag atg ggg gag gac ttc gtt gag tat   739
Leu Met Gly Ala Asp Gln Leu Lys Met Gly Glu Asp Phe Val Glu Tyr
        200                 205                 210

ctg cat atg ggt caa cgt gtc agt gca tgg ttg acc gat ggc aac aac   787
Leu His Met Gly Gln Arg Val Ser Ala Trp Leu Thr Asp Gly Asn Asn
    215                 220                 225

ggc agc gat cga aaa acc cta gcg gtg tct tcc ggt aca ggt gtg aaa   835
Gly Ser Asp Arg Lys Thr Leu Ala Val Ser Ser Gly Thr Gly Val Lys
230                 235                 240                 245

atc aaa aac aag aag caa ctt cag gaa ctt ctt gga ctg tgc aac ctg   883
Ile Lys Asn Lys Lys Gln Leu Gln Glu Leu Leu Gly Leu Cys Asn Leu
                250                 255                 260

tac tcg aaa gaa cat gta ctg gtc aca gta ttt gcg gaa gag atc gaa   931
Tyr Ser Lys Glu His Val Leu Val Thr Val Phe Ala Glu Glu Ile Glu
            265                 270                 275

aac ggc gca agg tgg ggt att ttc gcc gaa gca cgc atc gat cta ccg   979
Asn Gly Ala Arg Trp Gly Ile Phe Ala Glu Ala Arg Ile Asp Leu Pro
        280                 285                 290

gca ggg tta aac gat cat cag ttg tgg gta ttc ctc gcc aac tcc agc   1027
Ala Gly Leu Asn Asp His Gln Leu Trp Val Phe Leu Ala Asn Ser Ser
    295                 300                 305

aaa tgg act gca gag gtg tgc ctg acc gtg gca cac cga ctg cag aac   1075
Lys Trp Thr Ala Glu Val Cys Leu Thr Val Ala His Arg Leu Gln Asn
310                 315                 320                 325

taaaggcaga acttaagcgt tca                                        1098


<210> 2166
<211> 325
<212> PRT
<213> Corynebacterium glutamicum

<400> 2166
Met Thr Glu Asn Leu Asp Asn Ala Leu Leu Ser Met Arg Met Lys Pro
```

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  1               5                  10                  15

Val Gln Met Ala Leu Met Thr Leu Gly Tyr Asn His Asp Met Ala Val
            20                  25                  30

Thr Asp Ser Gly Met Glu Leu Ile Val Arg Arg Pro Gly Leu Thr Val
        35                  40                  45

Asn Phe Asn Leu Asp Ser Val Thr Leu Cys Ile Val Ala Asp Phe Met
    50                  55                  60

Trp His Gly Cys Val Pro Ala Lys Lys Gln Ala Glu Tyr Leu Arg Ala
65                  70                  75                  80

Ala Asn Glu Phe Asn Arg Pro Thr Arg Asp Leu Gln Val Val Leu Asp
                85                  90                  95

Glu Ala Asp Ser Lys Asn Met Thr Val Arg Gly Arg Glu Phe Phe Phe
            100                 105                 110

Ser Ser Val Gly Ala Thr Trp Glu Gln Ser Ala Glu Phe Val His Tyr
        115                 120                 125

Cys Met Asn Asp Val Ala Thr Thr Phe Val Ser Trp Cys Glu Gln Ile
    130                 135                 140

Trp Pro Lys Phe Ser Pro Glu Arg Val Glu Phe Asn Ala Thr Pro Pro
145                 150                 155                 160

Asp Val Asp Phe Glu Phe Ser Glu Asp Gln Leu Lys Glu Gly Asn Pro
                165                 170                 175

Phe Gly Leu Ile Asp Glu Pro Thr Pro Leu Val Ser Leu Asp Arg Ile
            180                 185                 190

Tyr Gln Gln Tyr Glu Leu Met Gly Ala Asp Gln Leu Lys Met Gly Glu
        195                 200                 205

Asp Phe Val Glu Tyr Leu His Met Gly Gln Arg Val Ser Ala Trp Leu
    210                 215                 220

Thr Asp Gly Asn Asn Gly Ser Asp Arg Lys Thr Leu Ala Val Ser Ser
225                 230                 235                 240

Gly Thr Gly Val Lys Ile Lys Asn Lys Lys Gln Leu Gln Glu Leu Leu
                245                 250                 255

Gly Leu Cys Asn Leu Tyr Ser Lys Glu His Val Leu Val Thr Val Phe
            260                 265                 270

Ala Glu Glu Ile Glu Asn Gly Ala Arg Trp Gly Ile Phe Ala Glu Ala
        275                 280                 285

Arg Ile Asp Leu Pro Ala Gly Leu Asn Asp His Gln Leu Trp Val Phe
    290                 295                 300

Leu Ala Asn Ser Ser Lys Trp Thr Ala Glu Val Cys Leu Thr Val Ala
305                 310                 315                 320

His Arg Leu Gln Asn
                325
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<210> 2167
<211> 609
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(586)
<223> RXA01304

<400> 2167
atgcaggtaa acgaatttgt gcttatatca acattcgtga ttcggcaaaa ttaattaaac 60

tgaaaaaggg gattaattac ccccacttga ggagaaattg atg ccc gca cag aac 115
Met Pro Ala Gln Asn
1 5

aaa aac ctc cca gga tcc gtc atc gtt gtg tct gat cgg att aaa tcg 163
Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser Asp Arg Ile Lys Ser
10 15 20

gga gaa aga att gat aaa gca gga ccc gta gca gta gac ctt ctt cag 211
Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala Val Asp Leu Leu Gln
25 30 35

gaa tca ggc gtg gag att tcc aca ttc acc gtc gtg gag gag ggc ttt 259
Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val Val Glu Glu Gly Phe
40 45 50

gaa cct gtc cat caa gaa ttg gtt aag gcg ttg gcg cgc cgg gat cgc 307
Glu Pro Val His Gln Glu Leu Val Lys Ala Leu Ala Arg Arg Asp Arg
55 60 65

gtc atc atc acc atc ggc gga acg ggc gtg ggg cct aga aat cgg acg 355
Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly Pro Arg Asn Arg Thr
70 75 80 85

ccg gag gcc aca gaa ccg cac atc gat acg cta ctg ccg ggt ctg atg 403
Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu Leu Pro Gly Leu Met
90 95 100

acg cag att ttg ttc tct gga ctg tcc aat acc gcg cag gcg ggg tta 451
Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr Ala Gln Ala Gly Leu
105 110 115

tct cgg ggg ctg gtg ggc ttg agt gct cgc gat tcc acg gcc gcg ctc 499
Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp Ser Thr Ala Ala Leu
120 125 130

atc gtc aac gcg ccg agt tct tcc ggg ggc gtg cgc gac gcg ctc ggg 547
Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val Arg Asp Ala Leu Gly
135 140 145

gtg gtc tgc ccg ctt ttc ggt tcc att ttt gag cgt ctt taaaagattt 596
Val Val Cys Pro Leu Phe Gly Ser Ile Phe Glu Arg Leu
150 155 160

ttgcttatcg acg 609

<210> 2168
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 2168
Met Pro Ala Gln Asn Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser
1 5 10 15

Asp Arg Ile Lys Ser Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala
20 25 30

Val Asp Leu Leu Gln Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val
35 40 45

Val Glu Glu Gly Phe Glu Pro Val His Gln Glu Leu Val Lys Ala Leu
50 55 60

Ala Arg Arg Asp Arg Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly
65 70 75 80

Pro Arg Asn Arg Thr Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu
85 90 95

Leu Pro Gly Leu Met Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr
100 105 110

Ala Gln Ala Gly Leu Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp
115 120 125

Ser Thr Ala Ala Leu Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val
130 135 140

Arg Asp Ala Leu Gly Val Val Cys Pro Leu Phe Gly Ser Ile Phe Glu
145 150 155 160

Arg Leu

<210> 2169
<211> 450
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(427)
<223> RXA01310

<400> 2169
aaggaacgtg cgcgtgcagc tttccgaggc aaagacgact agtctttaat ccaagtaagt 60

accggttcag acagttaaac cagaaagacg agtgaacacc atg tcc tcc gcg aaa 115
Met Ser Ser Ala Lys
1 5

aag aaa ccc gca ccg gag cgt atg cac tac atc aag ggc tat gta cct 163
Lys Lys Pro Ala Pro Glu Arg Met His Tyr Ile Lys Gly Tyr Val Pro
10 15 20

```
gtg gcg tat agc tct cca cac tca tcc ctc gag cgc agc gca acc tgg   211
Val Ala Tyr Ser Ser Pro His Ser Ser Leu Glu Arg Ser Ala Thr Trp
            25                  30                  35

ttg ggc atg gga ttc ctc ctc act gct ctg gca ggc gtt ggc gca gtc   259
Leu Gly Met Gly Phe Leu Leu Thr Ala Leu Ala Gly Val Gly Ala Val
        40                  45                  50

ctc ttc gca gtc ggc gca aac agc gtt ggc cag cag cag gaa cac tgg   307
Leu Phe Ala Val Gly Ala Asn Ser Val Gly Gln Gln Gln Glu His Trp
    55                  60                  65

gtc ctc tac agc atc atc ggt gtt gta ttc gcc gtt gtc tgc aca gtt   355
Val Leu Tyr Ser Ile Ile Gly Val Val Phe Ala Val Val Cys Thr Val
70                  75                  80                  85

ttg ggc acc gtc ctg atc atc aag ggc cga gca cct tac aac cgt tac   403
Leu Gly Thr Val Leu Ile Ile Lys Gly Arg Ala Pro Tyr Asn Arg Tyr
                90                  95                  100

gtc aag gaa acc ggc cgt acg cag tagtttctgt atgcaggttc ttt         450
Val Lys Glu Thr Gly Arg Thr Gln
            105
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09/05/2005 09:50:50

<210> 2170
<211> 109
<212> PRT
<213> Corynebacterium glutamicum

<400> 2170

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Met Ser Ser Ala Lys Lys Lys Pro Ala Pro Glu Arg Met His Tyr Ile
  1               5                  10                  15

Lys Gly Tyr Val Pro Val Ala Tyr Ser Ser Pro His Ser Ser Leu Glu
            20                  25                  30

Arg Ser Ala Thr Trp Leu Gly Met Gly Phe Leu Leu Thr Ala Leu Ala
        35                  40                  45

Gly Val Gly Ala Val Leu Phe Ala Val Gly Ala Asn Ser Val Gly Gln
    50                  55                  60

Gln Gln Glu His Trp Val Leu Tyr Ser Ile Ile Gly Val Val Phe Ala
65                  70                  75                  80

Val Val Cys Thr Val Leu Gly Thr Val Leu Ile Ile Lys Gly Arg Ala
                85                  90                  95

Pro Tyr Asn Arg Tyr Val Lys Glu Thr Gly Arg Thr Gln
            100                 105
```

<210> 2171
<211> 968
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (1)..(945)
<223> RXA01313

<400> 2171

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gcc cta cgc ctc att tca cag ctg ctt gca cca tct gcg gcg ttg aat   48
Ala Leu Arg Leu Ile Ser Gln Leu Leu Ala Pro Ser Ala Ala Leu Asn
  1               5                  10                  15

ttt aag tcc gag cgc aat gcc gtc gac gtg gca aaa cac atg ctc gcc   96
Phe Lys Ser Glu Arg Asn Ala Val Asp Val Ala Lys His Met Leu Ala
             20                  25                  30

agc cag gcc caa caa cgc ggt tcc gca ctc gtt gcg cta gac acc cgc   144
Ser Gln Ala Gln Gln Arg Gly Ser Ala Leu Val Ala Leu Asp Thr Arg
         35                  40                  45

tcg gaa aac gcc gac gcc gcc acg gca tta aga aag tca ctg ctc atc   192
Ser Glu Asn Ala Asp Ala Ala Thr Ala Leu Arg Lys Ser Leu Leu Ile
     50                  55                  60

cgc agc tgg acg cag cgc ggc acc cac caa ata ctt gcc gcc gaa gac   240
Arg Ser Trp Thr Gln Arg Gly Thr His Gln Ile Leu Ala Ala Glu Asp
 65                  70                  75                  80

gtc cgc tgg atg acg cta cta tgc tcc cca cgc atc ctg gct gct tca   288
Val Arg Trp Met Thr Leu Leu Cys Ser Pro Arg Ile Leu Ala Ala Ser
                 85                  90                  95

gcc aag cgc cgc tcc agc ctt tcg ctt gat agc gcc gca gtc cag cgc   336
Ala Lys Arg Arg Ser Ser Leu Ser Leu Asp Ser Ala Ala Val Gln Arg
            100                 105                 110

gcc cgc gac gca cta aca acc gcc gcc gaa aaa tcc ccc gta tcc aga   384
Ala Arg Asp Ala Leu Thr Thr Ala Ala Glu Lys Ser Pro Val Ser Arg
        115                 120                 125

acc cag gcc tac gaa att ttc cga tcc gta gac gtt gac ccc ggc gag   432
Thr Gln Ala Tyr Glu Ile Phe Arg Ser Val Asp Val Asp Pro Gly Glu
    130                 135                 140

cac aga ggc caa cat tta ctc cgg cat ttc ggt ggc gaa ggt gac atc   480
His Arg Gly Gln His Leu Leu Arg His Phe Gly Gly Glu Gly Asp Ile
145                 150                 155                 160

gta caa ggc ccg ccc atc gga acg gaa gat tcc ttt gtg ctt ctc gat   528
Val Gln Gly Pro Pro Ile Gly Thr Glu Asp Ser Phe Val Leu Leu Asp
                165                 170                 175

tcc atc tgc ccc ctt tcc cta gca ctt aac ggc gac gaa gcg ctc aca   576
Ser Ile Cys Pro Leu Ser Leu Ala Leu Asn Gly Asp Glu Ala Leu Thr
            180                 185                 190

gag atg acc cgt cgc tac ttc cac tcc cgt ggt gct gcc act gtg aaa   624
Glu Met Thr Arg Arg Tyr Phe His Ser Arg Gly Ala Ala Thr Val Lys
        195                 200                 205

gat ctg gtg tgg tgg acc gga ctg act gtg cgt gat gta aag aaa ggc   672
Asp Leu Val Trp Trp Thr Gly Leu Thr Val Arg Asp Val Lys Lys Gly
    210                 215                 220

atc gct gcc gtg tct tcg gat gga ctg att cac tct gtt gaa ggc ccg   720
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```
Ile Ala Ala Val Ser Ser Asp Gly Leu Ile His Ser Val Glu Gly Pro
225                 230                 235                 240

aat ggt gaa gaa atg tgg atc cct acc tgg gca gat gat gtc aca gac   768
Asn Gly Glu Glu Met Trp Ile Pro Thr Trp Ala Asp Asp Val Thr Asp
                245                 250                 255

gca gag gtt tct gat gca cta gcg ttg gaa cta acc ctc ccc gcc ttt   816
Ala Glu Val Ser Asp Ala Leu Ala Leu Glu Leu Thr Leu Pro Ala Phe
            260                 265                 270

gat gaa tac cta ctt tcc tac acc gac cgc agc cac gtc atg gat ccc   864
Asp Glu Tyr Leu Leu Ser Tyr Thr Asp Arg Ser His Val Met Asp Pro
        275                 280                 285

gag cac ctt ttc agc atc ggt ccc ggc aaa aac ggt gtg ttc aaa ccc   912
Glu His Leu Phe Ser Ile Gly Pro Gly Lys Asn Gly Val Phe Lys Pro
    290                 295                 300

ttc aaa gta gtt cag ggt gag gca ctg ccg gtt tagcccagca aaatcttcac 965
Phe Lys Val Val Gln Gly Glu Ala Leu Pro Val
305                 310                 315

ttg                                                               968


<210> 2172
<211> 315
<212> PRT
<213> Corynebacterium glutamicum

<400> 2172
Ala Leu Arg Leu Ile Ser Gln Leu Leu Ala Pro Ser Ala Ala Leu Asn
  1               5                  10                  15

Phe Lys Ser Glu Arg Asn Ala Val Asp Val Ala Lys His Met Leu Ala
             20                  25                  30

Ser Gln Ala Gln Gln Arg Gly Ser Ala Leu Val Ala Leu Asp Thr Arg
         35                  40                  45

Ser Glu Asn Ala Asp Ala Ala Thr Ala Leu Arg Lys Ser Leu Leu Ile
     50                  55                  60

Arg Ser Trp Thr Gln Arg Gly Thr His Gln Ile Leu Ala Ala Glu Asp
 65                  70                  75                  80

Val Arg Trp Met Thr Leu Leu Cys Ser Pro Arg Ile Leu Ala Ala Ser
                 85                  90                  95

Ala Lys Arg Arg Ser Ser Leu Ser Leu Asp Ser Ala Ala Val Gln Arg
            100                 105                 110

Ala Arg Asp Ala Leu Thr Thr Ala Ala Glu Lys Ser Pro Val Ser Arg
        115                 120                 125

Thr Gln Ala Tyr Glu Ile Phe Arg Ser Val Asp Val Asp Pro Gly Glu
    130                 135                 140

His Arg Gly Gln His Leu Leu Arg His Phe Gly Gly Glu Gly Asp Ile
145                 150                 155                 160
```

```
Val Gln Gly Pro Pro Ile Gly Thr Glu Asp Ser Phe Val Leu Leu Asp
                165                 170                 175

Ser Ile Cys Pro Leu Ser Leu Ala Leu Asn Gly Asp Glu Ala Leu Thr
            180                 185                 190

Glu Met Thr Arg Arg Tyr Phe His Ser Arg Gly Ala Ala Thr Val Lys
        195                 200                 205

Asp Leu Val Trp Trp Thr Gly Leu Thr Val Arg Asp Val Lys Lys Gly
    210                 215                 220

Ile Ala Ala Val Ser Ser Asp Gly Leu Ile His Ser Val Glu Gly Pro
225                 230                 235                 240

Asn Gly Glu Glu Met Trp Ile Pro Thr Trp Ala Asp Asp Val Thr Asp
                245                 250                 255

Ala Glu Val Ser Asp Ala Leu Ala Leu Glu Leu Thr Leu Pro Ala Phe
            260                 265                 270

Asp Glu Tyr Leu Leu Ser Tyr Thr Asp Arg Ser His Val Met Asp Pro
        275                 280                 285

Glu His Leu Phe Ser Ile Gly Pro Gly Lys Asn Gly Val Phe Lys Pro
    290                 295                 300

Phe Lys Val Val Gln Gly Glu Ala Leu Pro Val
305                 310                 315


<210> 2173
<211> 774
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> RXA01315

<400> 2173
catgtgcggt tgtgtcctaa gtcattgatg tcacctaacg cccctaagtt cactcggtgc 60

aatattgcac tgagtgcaag tttacactag gtttacttca gtg gat att gaa gag   115
                                            Val Asp Ile Glu Glu
                                              1               5

cag ccc tcg tta aga gaa atc aag cgc caa atg acc ctg gaa gcg ata   163
Gln Pro Ser Leu Arg Glu Ile Lys Arg Gln Met Thr Leu Glu Ala Ile
                  10                  15                  20

gaa gat aac gca acc agg ctc att ctg gag cgt ggc ttc gac aat gtc   211
Glu Asp Asn Ala Thr Arg Leu Ile Leu Glu Arg Gly Phe Asp Asn Val
              25                  30                  35

aca atc gaa gac atc tgc gca gag gca ggg ata tcc aag cgc aca ttc   259
Thr Ile Glu Asp Ile Cys Ala Glu Ala Gly Ile Ser Lys Arg Thr Phe
          40                  45                  50
```

```
ttt aac tac gtg gag tcc aaa gag tct gtg gcc atc ggg cac aca gcc   307
Phe Asn Tyr Val Glu Ser Lys Glu Ser Val Ala Ile Gly His Thr Ala
     55                  60                  65

aag ctc cca acg gat gaa gaa cgt gaa gca ttc ctg gct acg cgt cat   355
Lys Leu Pro Thr Asp Glu Glu Arg Glu Ala Phe Leu Ala Thr Arg His
 70                  75                  80                  85

gaa aat att atc gat act gta ttt gac ctg gta atc aac ctc ttt ggc   403
Glu Asn Ile Ile Asp Thr Val Phe Asp Leu Val Ile Asn Leu Phe Gly
                 90                  95                 100

aac cac gac aac tcc aag tct gga gtt gca ggc gac att atg cgt cga   451
Asn His Asp Asn Ser Lys Ser Gly Val Ala Gly Asp Ile Met Arg Arg
            105                 110                 115

cgc aaa gag atc cgg gtg aag cat cca gaa ctg gca gtg caa cat ttc   499
Arg Lys Glu Ile Arg Val Lys His Pro Glu Leu Ala Val Gln His Phe
        120                 125                 130

gcc agg ttc cac caa gca cgc gaa ggg cta gaa cac cta att gtt gag   547
Ala Arg Phe His Gln Ala Arg Glu Gly Leu Glu His Leu Ile Val Glu
    135                 140                 145

tac ttc gaa aaa tgg cca ggc tcc caa cat cta gat gag cct gca gat   595
Tyr Phe Glu Lys Trp Pro Gly Ser Gln His Leu Asp Glu Pro Ala Asp
150                 155                 160                 165

cga gaa gca atc gcc ata gtt ggc ctg ctg atc tcg gtc atg ctt caa   643
Arg Glu Ala Ile Ala Ile Val Gly Leu Leu Ile Ser Val Met Leu Gln
                170                 175                 180

ggt tct cgt gaa tgg cac gac atg cca caa ggc acg caa gct gat ttc   691
Gly Ser Arg Glu Trp His Asp Met Pro Gln Gly Thr Gln Ala Asp Phe
            185                 190                 195

caa gcc tgc tgt cgc aaa gca att aaa aat act ttt ctt ctt aga ggt   739
Gln Ala Cys Cys Arg Lys Ala Ile Lys Asn Thr Phe Leu Leu Arg Gly
        200                 205                 210

gga ttt tca gaa tgacatcaca ggtcaagccg gac                        774
Gly Phe Ser Glu
    215
```

Sequence Listing

<210> 2174
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 2174

```
Val Asp Ile Glu Glu Gln Pro Ser Leu Arg Glu Ile Lys Arg Gln Met
  1               5                  10                  15

Thr Leu Glu Ala Ile Glu Asp Asn Ala Thr Arg Leu Ile Leu Glu Arg
             20                  25                  30

Gly Phe Asp Asn Val Thr Ile Glu Asp Ile Cys Ala Glu Ala Gly Ile
         35                  40                  45

Ser Lys Arg Thr Phe Phe Asn Tyr Val Glu Ser Lys Glu Ser Val Ala
```

```
     50                  55                  60

Ile Gly His Thr Ala Lys Leu Pro Thr Asp Glu Glu Arg Glu Ala Phe
 65                  70                  75                  80

Leu Ala Thr Arg His Glu Asn Ile Ile Asp Thr Val Phe Asp Leu Val
                 85                  90                  95

Ile Asn Leu Phe Gly Asn His Asp Asn Ser Lys Ser Gly Val Ala Gly
            100                 105                 110

Asp Ile Met Arg Arg Arg Lys Glu Ile Arg Val Lys His Pro Glu Leu
        115                 120                 125

Ala Val Gln His Phe Ala Arg Phe His Gln Ala Arg Glu Gly Leu Glu
    130                 135                 140

His Leu Ile Val Glu Tyr Phe Glu Lys Trp Pro Gly Ser Gln His Leu
145                 150                 155                 160

Asp Glu Pro Ala Asp Arg Glu Ala Ile Ala Ile Val Gly Leu Leu Ile
                165                 170                 175

Ser Val Met Leu Gln Gly Ser Arg Glu Trp His Asp Met Pro Gln Gly
            180                 185                 190

Thr Gln Ala Asp Phe Gln Ala Cys Cys Arg Lys Ala Ile Lys Asn Thr
        195                 200                 205

Phe Leu Leu Arg Gly Gly Phe Ser Glu
    210                 215


<210> 2175
<211> 426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(403)
<223> RXA01316

<400> 2175
aaagcgcaag gctaagaagg attccccaga accaggcgat gacgatatca tcgatggaga 60

agtaattcct ccgcagaatt aaggaagtcg gtttcacccc atg gat att tcc atg   115
                                              Met Asp Ile Ser Met
                                                1               5

ctc aac gta ata acg agc tac acc att tgg gcc att ttt gcc atc atc   163
Leu Asn Val Ile Thr Ser Tyr Thr Ile Trp Ala Ile Phe Ala Ile Ile
                10                  15                  20

ggc atc tgc gga ttc gtt ggt gcc ttc ttg gca gcc acc acc aga gaa   211
Gly Ile Cys Gly Phe Val Gly Ala Phe Leu Ala Ala Thr Thr Arg Glu
            25                  30                  35

gat gcc ttt gag gtt gct gat cgc caa aag aaa atg gtg tgg gta gca   259
Asp Ala Phe Glu Val Ala Asp Arg Gln Lys Lys Met Val Trp Val Ala
        40                  45                  50
```

```
atc ctt atc gca tcc gga ttt gtc ctc acc gcg cta ggt cca tcg att   307
Ile Leu Ile Ala Ser Gly Phe Val Leu Thr Ala Leu Gly Pro Ser Ile
     55                  60                  65

ccg atc ctg cca tgg gtc gcc atc atc atg atc ggc ctg tac tgg ttt   355
Pro Ile Leu Pro Trp Val Ala Ile Ile Met Ile Gly Leu Tyr Trp Phe
 70                  75                  80                  85

gat gtt cgc ccg caa atc aag agc atc ctt gaa ggt gcc ggc ggc tgg   403
Asp Val Arg Pro Gln Ile Lys Ser Ile Leu Glu Gly Ala Gly Gly Trp
                 90                  95                 100

taaaagctcc ctgaactgcg aaa                                        426
```

<210> 2176
<211> 101
<212> PRT
<213> Corynebacterium glutamicum

<400> 2176

```
Met Asp Ile Ser Met Leu Asn Val Ile Thr Ser Tyr Thr Ile Trp Ala
  1               5                  10                  15

Ile Phe Ala Ile Ile Gly Ile Cys Gly Phe Val Gly Ala Phe Leu Ala
             20                  25                  30

Ala Thr Thr Arg Glu Asp Ala Phe Glu Val Ala Asp Arg Gln Lys Lys
         35                  40                  45

Met Val Trp Val Ala Ile Leu Ile Ala Ser Gly Phe Val Leu Thr Ala
     50                  55                  60

Leu Gly Pro Ser Ile Pro Ile Leu Pro Trp Val Ala Ile Ile Met Ile
 65                  70                  75                  80

Gly Leu Tyr Trp Phe Asp Val Arg Pro Gln Ile Lys Ser Ile Leu Glu
                 85                  90                  95

Gly Ala Gly Gly Trp
            100
```

<210> 2177
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> RXA01317

<400> 2177

```
atacatccgc cttaatggca caattgtagg tgcattagca ggactggcca tttacgctat 60

ttcccatatc ctcttcggag cttaactagg agtaaccatc atg tcc gat gca aaa   115
                                           Met Ser Asp Ala Lys
                                             1               5
```

```
gac gat tcc atc ttg tcc aag tgg agc aat gca gct tcc gag ctc agc   163
Asp Asp Ser Ile Leu Ser Lys Trp Ser Asn Ala Ala Ser Glu Leu Ser
                 10                  15                  20

ggt gcc gtc agt gga gta gcg aag aag ctc cgt gaa gaa ctc tct gag   211
Gly Ala Val Ser Gly Val Ala Lys Lys Leu Arg Glu Glu Leu Ser Glu
             25                  30                  35

aag gaa acc ttc agc aag ctt aaa acc gaa gcc agc gaa gcc gtc gat   259
Lys Glu Thr Phe Ser Lys Leu Lys Thr Glu Ala Ser Glu Ala Val Asp
         40                  45                  50

caa gca aag tcc ggc tcc tac cta gat gcc ggt aag gaa ttc gcc cgc   307
Gln Ala Lys Ser Gly Ser Tyr Leu Asp Ala Gly Lys Glu Phe Ala Arg
     55                  60                  65

gac gcc gga tcc atc atc aaa gat gca gcc aaa acc gtc aaa ggt gcc   355
Asp Ala Gly Ser Ile Ile Lys Asp Ala Ala Lys Thr Val Lys Gly Ala
 70                  75                  80                  85

gtc agt gat tcc gat aaa aac gac gtg aaa tcc gcc ttc ggt aac gcc   403
Val Ser Asp Ser Asp Lys Asn Asp Val Lys Ser Ala Phe Gly Asn Ala
                 90                  95                 100

gtg gaa gct tcc cgc gac aag ttc gat gac acc ctc gaa aag cgc aag   451
Val Glu Ala Ser Arg Asp Lys Phe Asp Asp Thr Leu Glu Lys Arg Lys
             105                 110                 115

gct aag aag gat tcc cca gaa cca ggc gat gac gat atc atc gat gga   499
Ala Lys Lys Asp Ser Pro Glu Pro Gly Asp Asp Asp Ile Ile Asp Gly
         120                 125                 130

gaa gta att cct ccg cag aat taaggaagtc ggtttcaccc cat            543
Glu Val Ile Pro Pro Gln Asn
    135                 140
```

US20070269858A1

<210> 2178
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 2178

```
Met Ser Asp Ala Lys Asp Asp Ser Ile Leu Ser Lys Trp Ser Asn Ala
  1               5                  10                  15

Ala Ser Glu Leu Ser Gly Ala Val Ser Gly Val Ala Lys Lys Leu Arg
             20                  25                  30

Glu Glu Leu Ser Glu Lys Glu Thr Phe Ser Lys Leu Lys Thr Glu Ala
         35                  40                  45

Ser Glu Ala Val Asp Gln Ala Lys Ser Gly Ser Tyr Leu Asp Ala Gly
     50                  55                  60

Lys Glu Phe Ala Arg Asp Ala Gly Ser Ile Ile Lys Asp Ala Ala Lys
 65                  70                  75                  80

Thr Val Lys Gly Ala Val Ser Asp Ser Asp Lys Asn Asp Val Lys Ser
                 85                  90                  95
```

```
Ala Phe Gly Asn Ala Val Glu Ala Ser Arg Asp Lys Phe Asp Asp Thr
            100                 105                 110

Leu Glu Lys Arg Lys Ala Lys Lys Asp Ser Pro Glu Pro Gly Asp Asp
        115                 120                 125

Asp Ile Ile Asp Gly Glu Val Ile Pro Pro Gln Asn
    130                 135                 140


<210> 2179
<211> 1425
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1402)
<223> RXA01318

<400> 2179
ggacgcgttc cagagaaaag tgcaggcata acccctaaaa taccctgatc ttcccccgtg 60

tcctgccccc gtgtccaccc ctgcgtacat aataggacgc atg gga aaa cat gag   115
                                              Met Gly Lys His Glu
                                                1               5

gtt gct cag cag acg gtt ccg ggt cct tcg ccg gaa atg gaa gcg cag   163
Val Ala Gln Gln Thr Val Pro Gly Pro Ser Pro Glu Met Glu Ala Gln
                10                  15                  20

cgg cgt aaa gag ttg cgc aag cac aag gcc att gcc act ggc ctg ttg   211
Arg Arg Lys Glu Leu Arg Lys His Lys Ala Ile Ala Thr Gly Leu Leu
            25                  30                  35

att ttt gct gcc gct gta tat ttt ctt tgc cgt ttc gtg gag acc cgt   259
Ile Phe Ala Ala Ala Val Tyr Phe Leu Cys Arg Phe Val Glu Thr Arg
        40                  45                  50

ccg ggt gaa act gca gcg tgg gta ggt ttt gtg cgc gct gcg gca gag   307
Pro Gly Glu Thr Ala Ala Trp Val Gly Phe Val Arg Ala Ala Ala Glu
    55                  60                  65

gcc gga atg att ggc ggg ttg gcc gac tgg ttc gcg gtc acc gcg ctg   355
Ala Gly Met Ile Gly Gly Leu Ala Asp Trp Phe Ala Val Thr Ala Leu
70                  75                  80                  85

ttc cgt cat cca ttg tgg ctg cct att ccg cac act gcg att atc ccg   403
Phe Arg His Pro Leu Trp Leu Pro Ile Pro His Thr Ala Ile Ile Pro
                90                  95                  100

cgc aag aaa gac cag tta ggt gag gcc tta agc ggg ttt gtg ggg gat   451
Arg Lys Lys Asp Gln Leu Gly Glu Ala Leu Ser Gly Phe Val Gly Asp
            105                 110                 115

aac ttc cta aat gcc cag ctc att acg gaa aaa gtc tct cag gcg cgg   499
Asn Phe Leu Asn Ala Gln Leu Ile Thr Glu Lys Val Ser Gln Ala Arg
        120                 125                 130

atc cca gag cgc gcc ggg gag tgg ctc gcc cag ccg gaa aac ggg gag   547
Ile Pro Glu Arg Ala Gly Glu Trp Leu Ala Gln Pro Glu Asn Gly Glu
```

```
    135                 140                 145

aaa gtt tcg cgc gaa gtc ggc aaa ttg acc gct aat att gtg cgc gca   595
Lys Val Ser Arg Glu Val Gly Lys Leu Thr Ala Asn Ile Val Arg Ala
150                 155                 160                 165

atc gat ccg tca gat gct gaa gcg gtg att aaa tct gcg gtg atc gac   643
Ile Asp Pro Ser Asp Ala Glu Ala Val Ile Lys Ser Ala Val Ile Asp
                170                 175                 180

aag ctt gcg gaa ccc acc tgg ggc cca cca gct ggg cgg ttg ctg gaa   691
Lys Leu Ala Glu Pro Thr Trp Gly Pro Pro Ala Gly Arg Leu Leu Glu
            185                 190                 195

caa ctc ctc gcc gaa ggc aaa gcc gaa cca gtt gtc cag gaa ctc gcg   739
Gln Leu Leu Ala Glu Gly Lys Ala Glu Pro Val Val Gln Glu Leu Ala
        200                 205                 210

cag tgg ctg cac aaa aag gcg ttg ggc tcc gag ccg ctg att gat cgc   787
Gln Trp Leu His Lys Lys Ala Leu Gly Ser Glu Pro Leu Ile Asp Arg
    215                 220                 225

ctg ctc aac gag cgc cgc ccg att tgg gcg ccg aaa ttc act gcg cag   835
Leu Leu Asn Glu Arg Arg Pro Ile Trp Ala Pro Lys Phe Thr Ala Gln
230                 235                 240                 245

ctg gtc agc ggc aaa gtc tat gac gag gtc ata aaa ttc act gaa gcc   883
Leu Val Ser Gly Lys Val Tyr Asp Glu Val Ile Lys Phe Thr Glu Ala
                250                 255                 260

gtc gct gcc gat cct aac cac gag gcc cgc aaa tcg ctg cgc cga ttc   931
Val Ala Ala Asp Pro Asn His Glu Ala Arg Lys Ser Leu Arg Arg Phe
            265                 270                 275

ctt aat aaa ttg gcg caa gac ctg cag cat gac cca ggc atg att att   979
Leu Asn Lys Leu Ala Gln Asp Leu Gln His Asp Pro Gly Met Ile Ile
        280                 285                 290

aaa gtt gaa gaa atc aaa cgc gac atc atg ggc tcc ggc gcc atc gcg   1027
Lys Val Glu Glu Ile Lys Arg Asp Ile Met Gly Ser Gly Ala Ile Ala
    295                 300                 305

caa gcc gcg cca acc atc tgg gcg tca gcc tcc gag tcg ctc att gaa   1075
Gln Ala Ala Pro Thr Ile Trp Ala Ser Ala Ser Glu Ser Leu Ile Glu
310                 315                 320                 325

tcc gca gaa gat gag tca tca att ctg cgt cgc aaa att gcc gaa gca   1123
Ser Ala Glu Asp Glu Ser Ser Ile Leu Arg Arg Lys Ile Ala Glu Ala
                330                 335                 340

gct acc agc tgg ggt caa aga ttg ctt gtc gac gac tcc ctc cgg cat   1171
Ala Thr Ser Trp Gly Gln Arg Leu Leu Val Asp Asp Ser Leu Arg His
            345                 350                 355

tca ctc gac acc cgg att acc ggc gcc gct gct ttc ctc gcc gac aat   1219
Ser Leu Asp Thr Arg Ile Thr Gly Ala Ala Ala Phe Leu Ala Asp Asn
        360                 365                 370

tac gcc ccc gaa gtc acc ggc att atc tcc gaa acc att gaa cga tgg   1267
Tyr Ala Pro Glu Val Thr Gly Ile Ile Ser Glu Thr Ile Glu Arg Trp
    375                 380                 385
```

```
gac gct gaa gaa gct tca gag aaa atc gaa ctc atg gtg ggc aaa gac   1315
Asp Ala Glu Glu Ala Ser Glu Lys Ile Glu Leu Met Val Gly Lys Asp
390                 395                 400                 405

ctc caa tac atc cgc ctt aat ggc aca att gta ggt gca tta gca gga   1363
Leu Gln Tyr Ile Arg Leu Asn Gly Thr Ile Val Gly Ala Leu Ala Gly
                410                 415                 420

ctg gcc att tac gct att tcc cat atc ctc ttc gga gct taactaggag    1412
Leu Ala Ile Tyr Ala Ile Ser His Ile Leu Phe Gly Ala
            425                 430

taaccatcat gtc                                                   1425


<210> 2180
<211> 434
<212> PRT
<213> Corynebacterium glutamicum

<400> 2180
Met Gly Lys His Glu Val Ala Gln Gln Thr Val Pro Gly Pro Ser Pro
  1               5                  10                  15

Glu Met Glu Ala Gln Arg Arg Lys Glu Leu Arg Lys His Lys Ala Ile
             20                  25                  30

Ala Thr Gly Leu Leu Ile Phe Ala Ala Ala Val Tyr Phe Leu Cys Arg
         35                  40                  45

Phe Val Glu Thr Arg Pro Gly Glu Thr Ala Ala Trp Val Gly Phe Val
     50                  55                  60

Arg Ala Ala Ala Glu Ala Gly Met Ile Gly Gly Leu Ala Asp Trp Phe
 65                  70                  75                  80

Ala Val Thr Ala Leu Phe Arg His Pro Leu Trp Leu Pro Ile Pro His
                 85                  90                  95

Thr Ala Ile Ile Pro Arg Lys Lys Asp Gln Leu Gly Glu Ala Leu Ser
            100                 105                 110

Gly Phe Val Gly Asp Asn Phe Leu Asn Ala Gln Leu Ile Thr Glu Lys
        115                 120                 125

Val Ser Gln Ala Arg Ile Pro Glu Arg Ala Gly Glu Trp Leu Ala Gln
    130                 135                 140

Pro Glu Asn Gly Glu Lys Val Ser Arg Glu Val Gly Lys Leu Thr Ala
145                 150                 155                 160

Asn Ile Val Arg Ala Ile Asp Pro Ser Asp Ala Glu Ala Val Ile Lys
                165                 170                 175

Ser Ala Val Ile Asp Lys Leu Ala Glu Pro Thr Trp Gly Pro Pro Ala
            180                 185                 190

Gly Arg Leu Leu Glu Gln Leu Leu Ala Glu Gly Lys Ala Glu Pro Val
        195                 200                 205
```

```
Val Gln Glu Leu Ala Gln Trp Leu His Lys Lys Ala Leu Gly Ser Glu
    210                 215                 220

Pro Leu Ile Asp Arg Leu Leu Asn Glu Arg Arg Pro Ile Trp Ala Pro
225                 230                 235                 240

Lys Phe Thr Ala Gln Leu Val Ser Gly Lys Val Tyr Asp Glu Val Ile
                245                 250                 255

Lys Phe Thr Glu Ala Val Ala Ala Asp Pro Asn His Glu Ala Arg Lys
            260                 265                 270

Ser Leu Arg Arg Phe Leu Asn Lys Leu Ala Gln Asp Leu Gln His Asp
        275                 280                 285

Pro Gly Met Ile Ile Lys Val Glu Glu Ile Lys Arg Asp Ile Met Gly
    290                 295                 300

Ser Gly Ala Ile Ala Gln Ala Ala Pro Thr Ile Trp Ala Ser Ala Ser
305                 310                 315                 320

Glu Ser Leu Ile Glu Ser Ala Glu Asp Glu Ser Ser Ile Leu Arg Arg
                325                 330                 335

Lys Ile Ala Glu Ala Ala Thr Ser Trp Gly Gln Arg Leu Leu Val Asp
            340                 345                 350

Asp Ser Leu Arg His Ser Leu Asp Thr Arg Ile Thr Gly Ala Ala Ala
        355                 360                 365

Phe Leu Ala Asp Asn Tyr Ala Pro Glu Val Thr Gly Ile Ile Ser Glu
    370                 375                 380

Thr Ile Glu Arg Trp Asp Ala Glu Glu Ala Ser Glu Lys Ile Glu Leu
385                 390                 395                 400

Met Val Gly Lys Asp Leu Gln Tyr Ile Arg Leu Asn Gly Thr Ile Val
                405                 410                 415

Gly Ala Leu Ala Gly Leu Ala Ile Tyr Ala Ile Ser His Ile Leu Phe
            420                 425                 430

Gly Ala
```

20050130-0003-0003-0003-0003

<210> 2181
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXA01330

<400> 2181
ccgtccgttt tcctggtggg tcggccccgc atccagccct agaaatatcg gagagctgct 60

cgttgaggcc caatgaaatg cctccgaaac agaaacaggc atg tgg aaa gac tta 115
Met Trp Lys Asp Leu

```
                                                    1               5

acc gaa ccg ctg ccc gaa gct tgc gct gag ggc tta gag atc cgg gtg   163
Thr Glu Pro Leu Pro Glu Ala Cys Ala Glu Gly Leu Glu Ile Arg Val
                10                  15                  20

gtt aaa tct ccc gaa gag ctg gca gat tac gct gca gtt ctt tct gcg   211
Val Lys Ser Pro Glu Glu Leu Ala Asp Tyr Ala Ala Val Leu Ser Ala
            25                  30                  35

aat tgg aat cca ccc gcc gaa act gtg cag cgt ttc tat acc gaa gca   259
Asn Trp Asn Pro Pro Ala Glu Thr Val Gln Arg Phe Tyr Thr Glu Ala
        40                  45                  50

gct gaa tac gca ctg aga aag aac tcg ccc gca ctt tat ctg gtg ggt   307
Ala Glu Tyr Ala Leu Arg Lys Asn Ser Pro Ala Leu Tyr Leu Val Gly
    55                  60                  65

tat gcg ggc aac cgc gca gtg tgt tct gcg gaa gca ttc ata cac gcg   355
Tyr Ala Gly Asn Arg Ala Val Cys Ser Ala Glu Ala Phe Ile His Ala
70                  75                  80                  85

agc gta gtt gga atc tac aat atc tcc acc ctt gag cac aaa cgc cgg   403
Ser Val Val Gly Ile Tyr Asn Ile Ser Thr Leu Glu His Lys Arg Arg
                90                  95                  100

cgt ggc tac ggc gga gcc atc acc tta gcc acg ttg cat acc gca cgt   451
Arg Gly Tyr Gly Gly Ala Ile Thr Leu Ala Thr Leu His Thr Ala Arg
            105                 110                 115

aac gca ggg tgt gac acc gcc gtg ttg caa gct tcc gaa gat ggt gag   499
Asn Ala Gly Cys Asp Thr Ala Val Leu Gln Ala Ser Glu Asp Gly Glu
        120                 125                 130

ccc gtt tat cgc aaa cta gga ttc acc gac tgc ggt cga ttt act gaa   547
Pro Val Tyr Arg Lys Leu Gly Phe Thr Asp Cys Gly Arg Phe Thr Glu
    135                 140                 145

tac tct ttg tgattagtta gggaccgtat gcg                            579
Tyr Ser Leu
150
```

<210> 2182
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 2182

```
Met Trp Lys Asp Leu Thr Glu Pro Leu Pro Glu Ala Cys Ala Glu Gly
  1               5                  10                  15

Leu Glu Ile Arg Val Val Lys Ser Pro Glu Glu Leu Ala Asp Tyr Ala
            20                  25                  30

Ala Val Leu Ser Ala Asn Trp Asn Pro Pro Ala Glu Thr Val Gln Arg
        35                  40                  45

Phe Tyr Thr Glu Ala Ala Glu Tyr Ala Leu Arg Lys Asn Ser Pro Ala
    50                  55                  60
```

```
Leu Tyr Leu Val Gly Tyr Ala Gly Asn Arg Ala Val Cys Ser Ala Glu
 65                  70                  75                  80

Ala Phe Ile His Ala Ser Val Val Gly Ile Tyr Asn Ile Ser Thr Leu
                 85                  90                  95

Glu His Lys Arg Arg Arg Gly Tyr Gly Gly Ala Ile Thr Leu Ala Thr
            100                 105                 110

Leu His Thr Ala Arg Asn Ala Gly Cys Asp Thr Ala Val Leu Gln Ala
        115                 120                 125

Ser Glu Asp Gly Glu Pro Val Tyr Arg Lys Leu Gly Phe Thr Asp Cys
    130                 135                 140

Gly Arg Phe Thr Glu Tyr Ser Leu
145                 150


<210> 2183
<211> 1128
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1105)
<223> RXA01333

<400> 2183
cgccctttaa ggcccgtaaa gcactccaca acacttcacg gcaggccgta atttccctgt 60

gaggtacttt cttgcaagtt gtagcgcacc gccgatacca atg cct ggc ggg tgc   115
                                          Met Pro Gly Gly Cys
                                            1               5

tcc ggt aac atc gtc cgc atg ctg cct aaa tcc cgg att ttc tcc gca   163
Ser Gly Asn Ile Val Arg Met Leu Pro Lys Ser Arg Ile Phe Ser Ala
                 10                  15                  20

atc ttg ctc gga att ggt gtg gca ctt gtg gtc tgg ggt ctg gtg gct   211
Ile Leu Leu Gly Ile Gly Val Ala Leu Val Val Trp Gly Leu Val Ala
             25                  30                  35

ccg cgc ttt gtg cac gct gat ggc cgt ttg cct ctt gat ttg gag gcg   259
Pro Arg Phe Val His Ala Asp Gly Arg Leu Pro Leu Asp Leu Glu Ala
         40                  45                  50

acg acg tac gtt ctc cat gac tct gac gct cag acc act att aat tct   307
Thr Thr Tyr Val Leu His Asp Ser Asp Ala Gln Thr Thr Ile Asn Ser
     55                  60                  65

gat ccg ttg gcc ggt gtg gtg act acg ccg gtg act cgt cag ttg cat   355
Asp Pro Leu Ala Gly Val Val Thr Thr Pro Val Thr Arg Gln Leu His
 70                  75                  80                  85

ttt gag gtg atg gat cct gcg agt gct gat gat gcc act att cgt att   403
Phe Glu Val Met Asp Pro Ala Ser Ala Asp Asp Ala Thr Ile Arg Ile
                 90                  95                 100

ggt gat tcg atg ttg cgt ggt aat cct gat act cag ggt ttt gag cag   451
```

```
Gly Asp Ser Met Leu Arg Gly Asn Pro Asp Thr Gln Gly Phe Glu Gln
            105                 110                 115

gaa cgg ctc ctg tca gcg act gtg tcg agt ttc cgc att gat cgc acc   499
Glu Arg Leu Leu Ser Ala Thr Val Ser Ser Phe Arg Ile Asp Arg Thr
        120                 125                 130

tct ggt gag gtt ttg tcc gat att gcg ctg act aat cag ttg gcg agc   547
Ser Gly Glu Val Leu Ser Asp Ile Ala Leu Thr Asn Gln Leu Ala Ser
    135                 140                 145

cct acg gtg cag tat tcg gtg gat ggc att tgg ttg aag ttc cca act   595
Pro Thr Val Gln Tyr Ser Val Asp Gly Ile Trp Leu Lys Phe Pro Thr
150                 155                 160                 165

gac gcg cag gag acc act tac aac gtg gtg gat ccg gtg ctg agg tct   643
Asp Ala Gln Glu Thr Thr Tyr Asn Val Val Asp Pro Val Leu Arg Ser
                170                 175                 180

gcg ctg ccg gcg gat ttt gtg gag tcc acg gag atc gat ggc cgt gag   691
Ala Leu Pro Ala Asp Phe Val Glu Ser Thr Glu Ile Asp Gly Arg Glu
            185                 190                 195

gtg ctg cat tac cgt cag gtg att gat aac gtg aat gtg gcg gag tat   739
Val Leu His Tyr Arg Gln Val Ile Asp Asn Val Asn Val Ala Glu Tyr
        200                 205                 210

ttc gcg gat gcc aac aac acc acc acg ttg act aaa gag gat ggc ggt   787
Phe Ala Asp Ala Asn Asn Thr Thr Thr Leu Thr Lys Glu Asp Gly Gly
    215                 220                 225

acc acg acg ggc tat ttt tat cac aat gtg act cgt gat ttt tgg gtg   835
Thr Thr Thr Gly Tyr Phe Tyr His Asn Val Thr Arg Asp Phe Trp Val
230                 235                 240                 245

gat cag cgt acc ggt ttg gtt gtc gat cta gct gaa aat att gat gat   883
Asp Gln Arg Thr Gly Leu Val Val Asp Leu Ala Glu Asn Ile Asp Asp
                250                 255                 260

ttt tac ggc gac cgc agc ggc cag aag tac gaa cag aaa ttg ctt ttc   931
Phe Tyr Gly Asp Arg Ser Gly Gln Lys Tyr Glu Gln Lys Leu Leu Phe
            265                 270                 275

gac gcc tcc ctc gac gat gca gct gtc tct aag ctg gtt gca cag gcc   979
Asp Ala Ser Leu Asp Asp Ala Ala Val Ser Lys Leu Val Ala Gln Ala
        280                 285                 290

gaa agc atc cct gat gga gat gtg agc aaa atc gca aat acc gta ggt   1027
Glu Ser Ile Pro Asp Gly Asp Val Ser Lys Ile Ala Asn Thr Val Gly
    295                 300                 305

att gtg atc ggt gcg gta ttg gct ctc gtg ggc ctg gcc ggg tgt ttt   1075
Ile Val Ile Gly Ala Val Leu Ala Leu Val Gly Leu Ala Gly Cys Phe
310                 315                 320                 325

ggg gcg ttt ggg aag aaa cgt cga gaa gct taacctgctg ttcaaataga     1125
Gly Ala Phe Gly Lys Lys Arg Arg Glu Ala
                330                 335

ttt                                                               1128
```

<210> 2184
<211> 335
<212> PRT
<213> Corynebacterium glutamicum

<400> 2184

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Met Pro Gly Gly Cys Ser Gly Asn Ile Val Arg Met Leu Pro Lys Ser
  1               5                  10                  15

Arg Ile Phe Ser Ala Ile Leu Leu Gly Ile Gly Val Ala Leu Val Val
             20                  25                  30

Trp Gly Leu Val Ala Pro Arg Phe Val His Ala Asp Gly Arg Leu Pro
         35                  40                  45

Leu Asp Leu Glu Ala Thr Thr Tyr Val Leu His Asp Ser Asp Ala Gln
     50                  55                  60

Thr Thr Ile Asn Ser Asp Pro Leu Ala Gly Val Val Thr Thr Pro Val
 65                  70                  75                  80

Thr Arg Gln Leu His Phe Glu Val Met Asp Pro Ala Ser Ala Asp Asp
                 85                  90                  95

Ala Thr Ile Arg Ile Gly Asp Ser Met Leu Arg Gly Asn Pro Asp Thr
            100                 105                 110

Gln Gly Phe Glu Gln Glu Arg Leu Leu Ser Ala Thr Val Ser Ser Phe
        115                 120                 125

Arg Ile Asp Arg Thr Ser Gly Glu Val Leu Ser Asp Ile Ala Leu Thr
    130                 135                 140

Asn Gln Leu Ala Ser Pro Thr Val Gln Tyr Ser Val Asp Gly Ile Trp
145                 150                 155                 160

Leu Lys Phe Pro Thr Asp Ala Gln Glu Thr Thr Tyr Asn Val Val Asp
                165                 170                 175

Pro Val Leu Arg Ser Ala Leu Pro Ala Asp Phe Val Glu Ser Thr Glu
            180                 185                 190

Ile Asp Gly Arg Glu Val Leu His Tyr Arg Gln Val Ile Asp Asn Val
        195                 200                 205

Asn Val Ala Glu Tyr Phe Ala Asp Ala Asn Asn Thr Thr Thr Leu Thr
    210                 215                 220

Lys Glu Asp Gly Gly Thr Thr Thr Gly Tyr Phe Tyr His Asn Val Thr
225                 230                 235                 240

Arg Asp Phe Trp Val Asp Gln Arg Thr Gly Leu Val Val Asp Leu Ala
                245                 250                 255

Glu Asn Ile Asp Asp Phe Tyr Gly Asp Arg Ser Gly Gln Lys Tyr Glu
            260                 265                 270

Gln Lys Leu Leu Phe Asp Ala Ser Leu Asp Asp Ala Ala Val Ser Lys
        275                 280                 285
```

```
Leu Val Ala Gln Ala Glu Ser Ile Pro Asp Gly Asp Val Ser Lys Ile
    290                 295                 300

Ala Asn Thr Val Gly Ile Val Ile Gly Ala Val Leu Ala Leu Val Gly
305                 310                 315                 320

Leu Ala Gly Cys Phe Gly Ala Phe Gly Lys Lys Arg Arg Glu Ala
                325                 330                 335


<210> 2185
<211> 726
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> RXA01336

<400> 2185
catggcatcc gcctccaacg cgccgggcgg gggagtccac ggaatgcccg gctggtgggc 60

agcgcaagcc gttttagcag atcacaggta gaattgcgac atg gag ccc acc gta   115
                                        Met Glu Pro Thr Val
                                          1               5

aaa gcc agc gcg cgc cac acc atc cac gtc acc gcc gac acc tgg cgc   163
Lys Ala Ser Ala Arg His Thr Ile His Val Thr Ala Asp Thr Trp Arg
                  10                  15                  20

atc cgc ctg agt gcc tca gcc cac tca cac ccc aac gac gcg tac gcg   211
Ile Arg Leu Ser Ala Ser Ala His Ser His Pro Asn Asp Ala Tyr Ala
              25                  30                  35

cgc cgg gct acg gca att tcc gcc ata ggc agc gtg ctt atc gac gtc   259
Arg Arg Ala Thr Ala Ile Ser Ala Ile Gly Ser Val Leu Ile Asp Val
          40                  45                  50

ccc ctc caa ggc gaa cgc atc tct gaa tcc act gca tac gac ggc caa   307
Pro Leu Gln Gly Glu Arg Ile Ser Glu Ser Thr Ala Tyr Asp Gly Gln
      55                  60                  65

atc aac gcc gac tgg aac gca gaa gtc acc ggc acc gat gtg aac atc   355
Ile Asn Ala Asp Trp Asn Ala Glu Val Thr Gly Thr Asp Val Asn Ile
  70                  75                  80                  85

gca cgc gac atc atc tcc cgg ctc gca gcg gtg cca gac gtt caa gtc   403
Ala Arg Asp Ile Ile Ser Arg Leu Ala Ala Val Pro Asp Val Gln Val
                  90                  95                 100

gac ggc ccg ttg tgg tcc ttg agt gac agt ttg gct gca gag gct gct   451
Asp Gly Pro Leu Trp Ser Leu Ser Asp Ser Leu Ala Ala Glu Ala Ala
              105                 110                 115

gtg gag gca ttg caa ggt gct gcc gac act gcg cgg aac acc gcg acc   499
Val Glu Ala Leu Gln Gly Ala Ala Asp Thr Ala Arg Asn Thr Ala Thr
          120                 125                 130

gcc atc gca gaa tcc ctc ggc ggg cag cta ggt gca ctt ctc tac gca   547
Ala Ile Ala Glu Ser Leu Gly Gly Gln Leu Gly Ala Leu Leu Tyr Ala
```

```
    135                 140                 145

aca acc gac acc cac agc tcc aca ccg ata cca gca cgc gca gaa atg   595
Thr Thr Asp Thr His Ser Ser Thr Pro Ile Pro Ala Arg Ala Glu Met
150                 155                 160                 165

atg gca gca aaa gcc tcc ata cca ccg cgc aca ctc gac cta gaa ctc   643
Met Ala Ala Lys Ala Ser Ile Pro Pro Arg Thr Leu Asp Leu Glu Leu
                170                 175                 180

gcc ccc tct gac atc gaa gtc acc aaa gaa atc gcc gtg acc ttt gaa   691
Ala Pro Ser Asp Ile Glu Val Thr Lys Glu Ile Ala Val Thr Phe Glu
            185                 190                 195

ttc ctt gca ggc taaaccgcga tttggtattt cgg                        726
Phe Leu Ala Gly
        200


<210> 2186
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 2186
Met Glu Pro Thr Val Lys Ala Ser Ala Arg His Thr Ile His Val Thr
  1               5                  10                  15

Ala Asp Thr Trp Arg Ile Arg Leu Ser Ala Ser Ala His Ser His Pro
             20                  25                  30

Asn Asp Ala Tyr Ala Arg Arg Ala Thr Ala Ile Ser Ala Ile Gly Ser
         35                  40                  45

Val Leu Ile Asp Val Pro Leu Gln Gly Glu Arg Ile Ser Glu Ser Thr
     50                  55                  60

Ala Tyr Asp Gly Gln Ile Asn Ala Asp Trp Asn Ala Glu Val Thr Gly
 65                  70                  75                  80

Thr Asp Val Asn Ile Ala Arg Asp Ile Ile Ser Arg Leu Ala Ala Val
                 85                  90                  95

Pro Asp Val Gln Val Asp Gly Pro Leu Trp Ser Leu Ser Asp Ser Leu
            100                 105                 110

Ala Ala Glu Ala Ala Val Glu Ala Leu Gln Gly Ala Ala Asp Thr Ala
        115                 120                 125

Arg Asn Thr Ala Thr Ala Ile Ala Glu Ser Leu Gly Gly Gln Leu Gly
    130                 135                 140

Ala Leu Leu Tyr Ala Thr Thr Asp Thr His Ser Ser Thr Pro Ile Pro
145                 150                 155                 160

Ala Arg Ala Glu Met Met Ala Ala Lys Ala Ser Ile Pro Pro Arg Thr
                165                 170                 175

Leu Asp Leu Glu Leu Ala Pro Ser Asp Ile Glu Val Thr Lys Glu Ile
            180                 185                 190
```

```
Ala Val Thr Phe Glu Phe Leu Ala Gly
        195                 200


<210> 2187
<211> 1635
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1612)
<223> RXA01342

<400> 2187
gatgagtatt ctctccgagg caacgaagtt aatatgtcca tgagggcgaa gttgtagaca 60

atatttggcc catatggata attgacagga gtttaacgcc atg gaa acc cca acc   115
                                            Met Glu Thr Pro Thr
                                              1               5

caa gac atg gat gtc cgc tgg tta tac acc caa agc cag ctc aaa ctc   163
Gln Asp Met Asp Val Arg Trp Leu Tyr Thr Gln Ser Gln Leu Lys Leu
                  10                  15                  20

cgc gaa att ctc ccc aca aac aaa acc ttc gat gtc atc caa atc agc   211
Arg Glu Ile Leu Pro Thr Asn Lys Thr Phe Asp Val Ile Gln Ile Ser
              25                  30                  35

gaa ctc gtt gac ccc acc gac ttc atc agg ccc aac agc gtg gtc tta   259
Glu Leu Val Asp Pro Thr Asp Phe Ile Arg Pro Asn Ser Val Val Leu
          40                  45                  50

tcc gtt ggc atc gcc ttc gca gaa acg ccc gac ggg ctt cgc gat tgg   307
Ser Val Gly Ile Ala Phe Ala Glu Thr Pro Asp Gly Leu Arg Asp Trp
      55                  60                  65

gca cac cga ctc gcc gac gca ggg gtc atc gcg atc ggg ttc ggc tcc   355
Ala His Arg Leu Ala Asp Ala Gly Val Ile Ala Ile Gly Phe Gly Ser
  70                  75                  80                  85

ggc ctc acc ttc cca cag gtt ccg cag gcg ctt atc gac gcc tcc ctc   403
Gly Leu Thr Phe Pro Gln Val Pro Gln Ala Leu Ile Asp Ala Ser Leu
                  90                  95                 100

cac ctt ggc ctc ggc ctc ttt gaa gtc ccc cgt gaa att cca ttt atc   451
His Leu Gly Leu Gly Leu Phe Glu Val Pro Arg Glu Ile Pro Phe Ile
              105                 110                 115

tcg atc acc tcc agc gtg cgt gat gag caa acc cgc cgt gcc ggc cgc   499
Ser Ile Thr Ser Ser Val Arg Asp Glu Gln Thr Arg Arg Ala Gly Arg
          120                 125                 130

ctg caa caa gaa ctc ctc ctg gaa cag gaa cgg ctt aac tcc atc gcc   547
Leu Gln Gln Glu Leu Leu Leu Glu Gln Glu Arg Leu Asn Ser Ile Ala
      135                 140                 145

atc tcc ggt ggc atc gaa gcc ctg tgc cgt gct gcc gcc gac tat ttg   595
Ile Ser Gly Gly Ile Glu Ala Leu Cys Arg Ala Ala Ala Asp Tyr Leu
150                 155                 160                 165
```

```
ggt ggt gca gta acc atc gtg gac agc gac ggc cgc gtg gct tgc tct   643
Gly Gly Ala Val Thr Ile Val Asp Ser Asp Gly Arg Val Ala Cys Ser
                170                 175                 180

att acc acc gat gac cta gac gca ctc ccc caa gct gtc tcg cgc ctg   691
Ile Thr Thr Asp Asp Leu Asp Ala Leu Pro Gln Ala Val Ser Arg Leu
            185                 190                 195

aac gga tcc agt caa gca ctc acg gat gcc acc aac ttt gga ttc atc   739
Asn Gly Ser Ser Gln Ala Leu Thr Asp Ala Thr Asn Phe Gly Phe Ile
        200                 205                 210

cac cgc atg acc cgc tac ggc gac cgc cac cac gtg ctc tca gtc ctt   787
His Arg Met Thr Arg Tyr Gly Asp Arg His His Val Leu Ser Val Leu
    215                 220                 225

atg ccc acc cgc ccc aca gac caa cac cgc gcg ctg atc aga cac tgc   835
Met Pro Thr Arg Pro Thr Asp Gln His Arg Ala Leu Ile Arg His Cys
230                 235                 240                 245

gca ggc ctt gcc gat att ttg ctc caa cgc ccc gaa gcc atg cgc gac   883
Ala Gly Leu Ala Asp Ile Leu Leu Gln Arg Pro Glu Ala Met Arg Asp
                250                 255                 260

cga gaa atc gaa gtg cga tca ctt gcc atg tca cta ctt ctg ggt cga   931
Arg Glu Ile Glu Val Arg Ser Leu Ala Met Ser Leu Leu Leu Gly Arg
            265                 270                 275

agc gac gac ctg gcc acc att cac cgc gtg ttc gct gac atc act gat   979
Ser Asp Asp Leu Ala Thr Ile His Arg Val Phe Ala Asp Ile Thr Asp
        280                 285                 290

gct tcc gga aat atc cgc ccc atc ctc atc acc ggc aac aca ccc caa   1027
Ala Ser Gly Asn Ile Arg Pro Ile Leu Ile Thr Gly Asn Thr Pro Gln
    295                 300                 305

tca gta cga aaa gca ctc tcc agt gtc gcc acc gca ctg tac aaa cag   1075
Ser Val Arg Lys Ala Leu Ser Ser Val Ala Thr Ala Leu Tyr Lys Gln
310                 315                 320                 325

gaa cga gca cta gct cat cta cgc ctc gcc gaa tcc acc gaa ctc ctc   1123
Glu Arg Ala Leu Ala His Leu Arg Leu Ala Glu Ser Thr Glu Leu Leu
                330                 335                 340

ttc ctt cgc gga agc cgc agc gtg cac aac atc gtg caa ctt ttt ggt   1171
Phe Leu Arg Gly Ser Arg Ser Val His Asn Ile Val Gln Leu Phe Gly
            345                 350                 355

act gcc gca agc gga gtt cgc ctc tgc att ggt ctg ccc acc cga gcg   1219
Thr Ala Ala Ser Gly Val Arg Leu Cys Ile Gly Leu Pro Thr Arg Ala
        360                 365                 370

gaa aac atc gat aag aaa ctc atc cgc gaa ctc act gcc acc gca aaa   1267
Glu Asn Ile Asp Lys Lys Leu Ile Arg Glu Leu Thr Ala Thr Ala Lys
    375                 380                 385

acc cta caa ctt gga acc cac gcc gaa ccc cgt gac ggc acc ttg ctg   1315
Thr Leu Gln Leu Gly Thr His Ala Glu Pro Arg Asp Gly Thr Leu Leu
390                 395                 400                 405

tgg ctc caa aac ccc gag ctg cgc aaa atc ctt aag atc cga tcc cgc   1363
```

```
Trp Leu Gln Asn Pro Glu Leu Arg Lys Ile Leu Lys Ile Arg Ser Arg
                410                 415                 420

gac acc tac gac cgt ctc ctc gac cac gac cgc acc aac aac acc gag   1411
Asp Thr Tyr Asp Arg Leu Leu Asp His Asp Arg Thr Asn Asn Thr Glu
            425                 430                 435

ctc gcc ccc acc ttg gtg tct ttt act cag cac agc gga cat ata ggc   1459
Leu Ala Pro Thr Leu Val Ser Phe Thr Gln His Ser Gly His Ile Gly
        440                 445                 450

gac acc gcc aaa gaa ctg ggc atc cac cgc cac acc gtg cgc acc cgc   1507
Asp Thr Ala Lys Glu Leu Gly Ile His Arg His Thr Val Arg Thr Arg
    455                 460                 465

atg atc cgc att gaa gag atc tgc gaa atc gac ctc aat gat cca ctg   1555
Met Ile Arg Ile Glu Glu Ile Cys Glu Ile Asp Leu Asn Asp Pro Leu
470                 475                 480                 485

acc aga gcg gag ctg ctc tta gtg atc gca acg aag gag gga gac gtc   1603
Thr Arg Ala Glu Leu Leu Leu Val Ile Ala Thr Lys Glu Gly Asp Val
                490                 495                 500

gaa aag caa taaaaagacc ccatgcaaag cat                            1635
Glu Lys Gln
```

09550350.090550

<210> 2188
<211> 504
<212> PRT
<213> Corynebacterium glutamicum

<400> 2188

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Met Glu Thr Pro Thr Gln Asp Met Asp Val Arg Trp Leu Tyr Thr Gln
  1               5                  10                  15

Ser Gln Leu Lys Leu Arg Glu Ile Leu Pro Thr Asn Lys Thr Phe Asp
             20                  25                  30

Val Ile Gln Ile Ser Glu Leu Val Asp Pro Thr Asp Phe Ile Arg Pro
         35                  40                  45

Asn Ser Val Val Leu Ser Val Gly Ile Ala Phe Ala Glu Thr Pro Asp
     50                  55                  60

Gly Leu Arg Asp Trp Ala His Arg Leu Ala Asp Ala Gly Val Ile Ala
 65                  70                  75                  80

Ile Gly Phe Gly Ser Gly Leu Thr Phe Pro Gln Val Pro Gln Ala Leu
                 85                  90                  95

Ile Asp Ala Ser Leu His Leu Gly Leu Gly Leu Phe Glu Val Pro Arg
            100                 105                 110

Glu Ile Pro Phe Ile Ser Ile Thr Ser Ser Val Arg Asp Glu Gln Thr
        115                 120                 125

Arg Arg Ala Gly Arg Leu Gln Gln Glu Leu Leu Leu Glu Gln Glu Arg
    130                 135                 140
```

```
Leu Asn Ser Ile Ala Ile Ser Gly Gly Ile Glu Ala Leu Cys Arg Ala
145                 150                 155                 160

Ala Ala Asp Tyr Leu Gly Gly Ala Val Thr Ile Val Asp Ser Asp Gly
                165                 170                 175

Arg Val Ala Cys Ser Ile Thr Thr Asp Asp Leu Asp Ala Leu Pro Gln
            180                 185                 190

Ala Val Ser Arg Leu Asn Gly Ser Ser Gln Ala Leu Thr Asp Ala Thr
        195                 200                 205

Asn Phe Gly Phe Ile His Arg Met Thr Arg Tyr Gly Asp Arg His His
    210                 215                 220

Val Leu Ser Val Leu Met Pro Thr Arg Pro Thr Asp Gln His Arg Ala
225                 230                 235                 240

Leu Ile Arg His Cys Ala Gly Leu Ala Asp Ile Leu Leu Gln Arg Pro
                245                 250                 255

Glu Ala Met Arg Asp Arg Glu Ile Glu Val Arg Ser Leu Ala Met Ser
            260                 265                 270

Leu Leu Leu Gly Arg Ser Asp Asp Leu Ala Thr Ile His Arg Val Phe
        275                 280                 285

Ala Asp Ile Thr Asp Ala Ser Gly Asn Ile Arg Pro Ile Leu Ile Thr
    290                 295                 300

Gly Asn Thr Pro Gln Ser Val Arg Lys Ala Leu Ser Ser Val Ala Thr
305                 310                 315                 320

Ala Leu Tyr Lys Gln Glu Arg Ala Leu Ala His Leu Arg Leu Ala Glu
                325                 330                 335

Ser Thr Glu Leu Leu Phe Leu Arg Gly Ser Arg Ser Val His Asn Ile
            340                 345                 350

Val Gln Leu Phe Gly Thr Ala Ala Ser Gly Val Arg Leu Cys Ile Gly
        355                 360                 365

Leu Pro Thr Arg Ala Glu Asn Ile Asp Lys Lys Leu Ile Arg Glu Leu
    370                 375                 380

Thr Ala Thr Ala Lys Thr Leu Gln Leu Gly Thr His Ala Glu Pro Arg
385                 390                 395                 400

Asp Gly Thr Leu Leu Trp Leu Gln Asn Pro Glu Leu Arg Lys Ile Leu
                405                 410                 415

Lys Ile Arg Ser Arg Asp Thr Tyr Asp Arg Leu Leu Asp His Asp Arg
            420                 425                 430

Thr Asn Asn Thr Glu Leu Ala Pro Thr Leu Val Ser Phe Thr Gln His
        435                 440                 445

Ser Gly His Ile Gly Asp Thr Ala Lys Glu Leu Gly Ile His Arg His
    450                 455                 460

Thr Val Arg Thr Arg Met Ile Arg Ile Glu Glu Ile Cys Glu Ile Asp
```

```
465                 470                 475                 480

Leu Asn Asp Pro Leu Thr Arg Ala Glu Leu Leu Leu Val Ile Ala Thr
                485                 490                 495

Lys Glu Gly Asp Val Glu Lys Gln
            500
```

<210> 2189
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(592)
<223> RXA01348

<400> 2189

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atgggacaat gagcacgtga ctctacgatc tgcattactt gcgctactaa gttccggacc 60

attgactggg tatgacgcct cccagcgatt tggggcctcg gtg ggc ttt gtg tgg   115
                                          Val Gly Phe Val Trp
                                            1               5

agt ggt tcc gat tcg cag att tat ccc gaa ctt cga aaa atg gaa gcc   163
Ser Gly Ser Asp Ser Gln Ile Tyr Pro Glu Leu Arg Lys Met Glu Ala
                  10                  15                  20

gaa gaa ctc ctc gtg gga tcc gat gtt ccc tgg ggc tcc aaa ggc gcc   211
Glu Glu Leu Leu Val Gly Ser Asp Val Pro Trp Gly Ser Lys Gly Ala
              25                  30                  35

acc aaa acc gaa tac gcc ttg agt gaa aaa ggc tgg gaa gcg cta aga   259
Thr Lys Thr Glu Tyr Ala Leu Ser Glu Lys Gly Trp Glu Ala Leu Arg
          40                  45                  50

aaa gcg tgg tac gag cca gta acc tac ggt ccc acc aga gat cct gcc   307
Lys Ala Trp Tyr Glu Pro Val Thr Tyr Gly Pro Thr Arg Asp Pro Ala
      55                  60                  65

agg ctt aaa gcc gcc tat ttt gag gtc ggt aca aat ggc gat gca cgc   355
Arg Leu Lys Ala Ala Tyr Phe Glu Val Gly Thr Asn Gly Asp Ala Arg
  70                  75                  80                  85

cga cat tta agg gcg cac atc gct cat ttt gaa cag cag aaa att caa   403
Arg His Leu Arg Ala His Ile Ala His Phe Glu Gln Gln Lys Ile Gln
                  90                  95                 100

tca gaa tca atg att gat gag ctg aaa gca aaa act cat cca acc ttg   451
Ser Glu Ser Met Ile Asp Glu Leu Lys Ala Lys Thr His Pro Thr Leu
            105                 110                 115

gca cgg cga ctt gag cgc tcc ccg aaa aag gag cac gag cga ata gtc   499
Ala Arg Arg Leu Glu Arg Ser Pro Lys Lys Glu His Glu Arg Ile Val
        120                 125                 130

gcg ttt aaa gtg ctt gcc tat gag ggg cag att gca cgc gct cag gca   547
Ala Phe Lys Val Leu Ala Tyr Glu Gly Gln Ile Ala Arg Ala Gln Ala
    135                 140                 145
```

```
gag att gaa tgg gcg gaa aag ggc ttg aaa cta ctc gat acc ctt       592
Glu Ile Glu Trp Ala Glu Lys Gly Leu Lys Leu Leu Asp Thr Leu
150                 155                 160

tagttttcga acacgtccgt atc                                        615


<210> 2190
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 2190
Val Gly Phe Val Trp Ser Gly Ser Asp Ser Gln Ile Tyr Pro Glu Leu
  1               5                  10                  15

Arg Lys Met Glu Ala Glu Glu Leu Leu Val Gly Ser Asp Val Pro Trp
             20                  25                  30

Gly Ser Lys Gly Ala Thr Lys Thr Glu Tyr Ala Leu Ser Glu Lys Gly
         35                  40                  45

Trp Glu Ala Leu Arg Lys Ala Trp Tyr Glu Pro Val Thr Tyr Gly Pro
     50                  55                  60

Thr Arg Asp Pro Ala Arg Leu Lys Ala Ala Tyr Phe Glu Val Gly Thr
 65                  70                  75                  80

Asn Gly Asp Ala Arg Arg His Leu Arg Ala His Ile Ala His Phe Glu
                 85                  90                  95

Gln Gln Lys Ile Gln Ser Glu Ser Met Ile Asp Glu Leu Lys Ala Lys
            100                 105                 110

Thr His Pro Thr Leu Ala Arg Arg Leu Glu Arg Ser Pro Lys Lys Glu
        115                 120                 125

His Glu Arg Ile Val Ala Phe Lys Val Leu Ala Tyr Glu Gly Gln Ile
    130                 135                 140

Ala Arg Ala Gln Ala Glu Ile Glu Trp Ala Glu Lys Gly Leu Lys Leu
145                 150                 155                 160

Leu Asp Thr Leu


<210> 2191
<211> 900
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(877)
<223> RXA01349

<400> 2191
agttgtcagc tgggatttgc cgatggtgtt atctttgata tttaccttaa ccccgtttct 60
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aattcacgtt ttctcgttac ccgaaaggaa ttgatcgatt atg gcg aca tca cgt   115
                                              Met Ala Thr Ser Arg
                                                1               5

cga gat gcc gaa aac ata gac cag gcc ggt agc gaa ttc att gaa tct   163
Arg Asp Ala Glu Asn Ile Asp Gln Ala Gly Ser Glu Phe Ile Glu Ser
                10                  15                  20

gat tca gga cac acc gca acc cct gaa gag gta gta gcc acc gct ctg   211
Asp Ser Gly His Thr Ala Thr Pro Glu Glu Val Val Ala Thr Ala Leu
            25                  30                  35

aca ttt ttt gca gag gat ggt ttt agc gaa acc aaa ttg gag aaa atc   259
Thr Phe Phe Ala Glu Asp Gly Phe Ser Glu Thr Lys Leu Glu Lys Ile
        40                  45                  50

gcg aag gca tct ggc atg tcc aag cgc atg atc cac tat cac ttt ggc   307
Ala Lys Ala Ser Gly Met Ser Lys Arg Met Ile His Tyr His Phe Gly
    55                  60                  65

gat aag aaa ggc ctg tac atc aag gct gtt tcc tac gcg ttg cga ttg   355
Asp Lys Lys Gly Leu Tyr Ile Lys Ala Val Ser Tyr Ala Leu Arg Leu
70                  75                  80                  85

ctg cgc cca gag gct gaa gcg atg caa ctt gat tcc gcg gta cca gtt   403
Leu Arg Pro Glu Ala Glu Ala Met Gln Leu Asp Ser Ala Val Pro Val
                90                  95                  100

gat ggt gtc cgc aaa atc gtc gag gct tta tat acc tgc atc acc aag   451
Asp Gly Val Arg Lys Ile Val Glu Ala Leu Tyr Thr Cys Ile Thr Lys
            105                 110                 115

cac cca gaa gca gtg cgc ctg cta ttg atg gaa aac ctg cat agc caa   499
His Pro Glu Ala Val Arg Leu Leu Leu Met Glu Asn Leu His Ser Gln
        120                 125                 130

gac agc gtg gat tcc acc gcg gca tat tcc gat gaa tcc aat gtg ctg   547
Asp Ser Val Asp Ser Thr Ala Ala Tyr Ser Asp Glu Ser Asn Val Leu
    135                 140                 145

ctc aac ctg gat aag ctg ctc atg ctt ggc cag gat gcc ggc gcc ttc   595
Leu Asn Leu Asp Lys Leu Leu Met Leu Gly Gln Asp Ala Gly Ala Phe
150                 155                 160                 165

cgt cct gga atc tcc gca gaa gac gta ctg gtt ctt att agc tcc ctg   643
Arg Pro Gly Ile Ser Ala Glu Asp Val Leu Val Leu Ile Ser Ser Leu
                170                 175                 180

gcc tac ttc cgc gta tcc aac aag gtc acg ttg aag aac ctc tac tcc   691
Ala Tyr Phe Arg Val Ser Asn Lys Val Thr Leu Lys Asn Leu Tyr Ser
            185                 190                 195

ctt gat ttg gaa tca gag gcc aat att gaa ggc atg aag cgc atc gtc   739
Leu Asp Leu Glu Ser Glu Ala Asn Ile Glu Gly Met Lys Arg Ile Val
        200                 205                 210

gtt gac acg gtg ctg gca ttc ttg acc tca aat att caa aat tct ggc   787
Val Asp Thr Val Leu Ala Phe Leu Thr Ser Asn Ile Gln Asn Ser Gly
    215                 220                 225

aac tcc agc tac ctg gtt gtt ggt ggc aag act gca gaa cca gaa act   835
```

```
Asn Ser Ser Tyr Leu Val Val Gly Gly Lys Thr Ala Glu Pro Glu Thr
230                 235                 240                 245

gat gac agc gtc tac agc ttt gat acg gac gtg ttc gaa aac          877
Asp Asp Ser Val Tyr Ser Phe Asp Thr Asp Val Phe Glu Asn
                250                 255

taaagggtat cgagtagttt caa                                       900


<210> 2192
<211> 259
<212> PRT
<213> Corynebacterium glutamicum

<400> 2192
Met Ala Thr Ser Arg Arg Asp Ala Glu Asn Ile Asp Gln Ala Gly Ser
  1               5                  10                  15

Glu Phe Ile Glu Ser Asp Ser Gly His Thr Ala Thr Pro Glu Glu Val
             20                  25                  30

Val Ala Thr Ala Leu Thr Phe Phe Ala Glu Asp Gly Phe Ser Glu Thr
         35                  40                  45

Lys Leu Glu Lys Ile Ala Lys Ala Ser Gly Met Ser Lys Arg Met Ile
     50                  55                  60

His Tyr His Phe Gly Asp Lys Lys Gly Leu Tyr Ile Lys Ala Val Ser
 65                  70                  75                  80

Tyr Ala Leu Arg Leu Leu Arg Pro Glu Ala Glu Ala Met Gln Leu Asp
                 85                  90                  95

Ser Ala Val Pro Val Asp Gly Val Arg Lys Ile Val Glu Ala Leu Tyr
            100                 105                 110

Thr Cys Ile Thr Lys His Pro Glu Ala Val Arg Leu Leu Leu Met Glu
        115                 120                 125

Asn Leu His Ser Gln Asp Ser Val Asp Ser Thr Ala Ala Tyr Ser Asp
    130                 135                 140

Glu Ser Asn Val Leu Leu Asn Leu Asp Lys Leu Leu Met Leu Gly Gln
145                 150                 155                 160

Asp Ala Gly Ala Phe Arg Pro Gly Ile Ser Ala Glu Asp Val Leu Val
                165                 170                 175

Leu Ile Ser Ser Leu Ala Tyr Phe Arg Val Ser Asn Lys Val Thr Leu
            180                 185                 190

Lys Asn Leu Tyr Ser Leu Asp Leu Glu Ser Glu Ala Asn Ile Glu Gly
        195                 200                 205

Met Lys Arg Ile Val Val Asp Thr Val Leu Ala Phe Leu Thr Ser Asn
    210                 215                 220

Ile Gln Asn Ser Gly Asn Ser Ser Tyr Leu Val Val Gly Gly Lys Thr
225                 230                 235                 240
```

```
Ala Glu Pro Glu Thr Asp Asp Ser Val Tyr Ser Phe Asp Thr Asp Val
                245                 250                 255

Phe Glu Asn
```

<210> 2193
<211> 426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(403)
<223> RXA01357

<400> 2193

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acggcgcaag tcccgagcac agatatagtt atgcaaatgt ggccaaggca caccaagaat 60

ggctacacgc tgcagataat gacacgacgg aaggtggagc atg agc gct gaa gaa   115
                                           Met Ser Ala Glu Glu
                                             1               5

ctc gac aac tac gaa gca gag gtt gaa ctc tct ctt tac cgc gaa tac   163
Leu Asp Asn Tyr Glu Ala Glu Val Glu Leu Ser Leu Tyr Arg Glu Tyr
                  10                  15                  20

cgc gac gta gtc agc cag ttt tcc tat gtt gta gaa act gaa cgt cgc   211
Arg Asp Val Val Ser Gln Phe Ser Tyr Val Val Glu Thr Glu Arg Arg
              25                  30                  35

ttc tac tta gca aat gca gtg cag ctt att cca cac aac agc gga aac   259
Phe Tyr Leu Ala Asn Ala Val Gln Leu Ile Pro His Asn Ser Gly Asn
          40                  45                  50

gat gtc tac tac gaa gtc cgc atg tct gac gcc tgg gta tgg gac atg   307
Asp Val Tyr Tyr Glu Val Arg Met Ser Asp Ala Trp Val Trp Asp Met
     55                  60                  65

tac cgc tca gca cgc ttc gtt cgc tac gtc cga gtg atc acc tac aag   355
Tyr Arg Ser Ala Arg Phe Val Arg Tyr Val Arg Val Ile Thr Tyr Lys
 70                  75                  80                  85

gac gtc aac atc gaa gaa tta gat aag cct gac atc atc atg cct gag   403
Asp Val Asn Ile Glu Glu Leu Asp Lys Pro Asp Ile Ile Met Pro Glu
                  90                  95                 100

tagttcttag gtttaaaatc gct                                       426
```

<210> 2194
<211> 101
<212> PRT
<213> Corynebacterium glutamicum

<400> 2194

```
Met Ser Ala Glu Glu Leu Asp Asn Tyr Glu Ala Glu Val Glu Leu Ser
  1               5                  10                  15

Leu Tyr Arg Glu Tyr Arg Asp Val Val Ser Gln Phe Ser Tyr Val Val
```

```
            20                  25                  30

Glu Thr Glu Arg Arg Phe Tyr Leu Ala Asn Ala Val Gln Leu Ile Pro
         35                  40                  45

His Asn Ser Gly Asn Asp Val Tyr Tyr Glu Val Arg Met Ser Asp Ala
     50                  55                  60

Trp Val Trp Asp Met Tyr Arg Ser Ala Arg Phe Val Arg Tyr Val Arg
 65                  70                  75                  80

Val Ile Thr Tyr Lys Asp Val Asn Ile Glu Glu Leu Asp Lys Pro Asp
                 85                  90                  95

Ile Ile Met Pro Glu
            100


<210> 2195
<211> 1305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1282)
<223> RXA01359

<400> 2195
gttggacctt gtgcgatttg gatggggaac agcagcccaa tcttgaccat attgcgcgag 60

ccatggagct tcggggcact acatacagtg aggtagcagc atg att gac tcc cgc   115
                                           Met Ile Asp Ser Arg
                                             1               5

ttg ctg gca tgg gcg tat ctc tca aaa gtg gtg gag ggt ccc aat gca   163
Leu Leu Ala Trp Ala Tyr Leu Ser Lys Val Val Glu Gly Pro Asn Ala
            10                  15                  20

cac ctg caa aag ctc ctg aaa gaa ggt cat gat gta gag cgg atc gca   211
His Leu Gln Lys Leu Leu Lys Glu Gly His Asp Val Glu Arg Ile Ala
         25                  30                  35

ttt ggt att aaa cac cgc gaa gag tgg att ggc gaa ggt ctg ctg aaa   259
Phe Gly Ile Lys His Arg Glu Glu Trp Ile Gly Glu Gly Leu Leu Lys
      40                  45                  50

aac acc gat tcc cgg tac tcg att gat acc gcg caa act gat ctg gaa   307
Asn Thr Asp Ser Arg Tyr Ser Ile Asp Thr Ala Gln Thr Asp Leu Glu
  55                  60                  65

act atc gcc aaa ctc ggt ggg cgg ctc atc aca cct gaa gac gac gaa   355
Thr Ile Ala Lys Leu Gly Gly Arg Leu Ile Thr Pro Glu Asp Asp Glu
 70                  75                  80                  85

tgg ccg atg gaa gaa tta gac cat gct ttt gga ttt gcc gct tct ggc   403
Trp Pro Met Glu Glu Leu Asp His Ala Phe Gly Phe Ala Ala Ser Gly
                 90                  95                 100

atg agt gat cat gtg cgt acc tat caa gat gat gcg ctg cca ccg cat   451
Met Ser Asp His Val Arg Thr Tyr Gln Asp Asp Ala Leu Pro Pro His
```

```
                105                 110                 115

gcg ttg tgg att agg gga gga aat ctc aga aca ctc agt gca cag tcc   499
Ala Leu Trp Ile Arg Gly Gly Asn Leu Arg Thr Leu Ser Ala Gln Ser
        120                 125                 130

gtc aca ctc gtg ggc acc agg gca ata agc caa tat ggc acg gaa gta   547
Val Thr Leu Val Gly Thr Arg Ala Ile Ser Gln Tyr Gly Thr Glu Val
    135                 140                 145

act cgg gaa ttc acc caa aac ctt gtg tct cat cag tgg aca atc atc   595
Thr Arg Glu Phe Thr Gln Asn Leu Val Ser His Gln Trp Thr Ile Ile
150                 155                 160                 165

tca ggt ggt gcc ttg gga gtt gat agc gtc gcc cat agt gaa gcc gta   643
Ser Gly Gly Ala Leu Gly Val Asp Ser Val Ala His Ser Glu Ala Val
                170                 175                 180

cgt gca caa ggc tcc acc atc gcg atc gca gca tgc gga ttg gat cgc   691
Arg Ala Gln Gly Ser Thr Ile Ala Ile Ala Ala Cys Gly Leu Asp Arg
            185                 190                 195

tcg tac ccc agc cac aat cga gat ctg ttc aac cag att gcc aaa tcc   739
Ser Tyr Pro Ser His Asn Arg Asp Leu Phe Asn Gln Ile Ala Lys Ser
        200                 205                 210

gga aag ggg gcg ttg gtg agt gaa tat cca ccg gga act cca cct caa   787
Gly Lys Gly Ala Leu Val Ser Glu Tyr Pro Pro Gly Thr Pro Pro Gln
    215                 220                 225

cgc cac cgc ttt ctc act cgc aat cgt ctc gtt gct gct cta tct caa   835
Arg His Arg Phe Leu Thr Arg Asn Arg Leu Val Ala Ala Leu Ser Gln
230                 235                 240                 245

gga act gtc gtg gtg gag gca gcc tgg agg tca ggc gcg cta aac act   883
Gly Thr Val Val Val Glu Ala Ala Trp Arg Ser Gly Ala Leu Asn Thr
                250                 255                 260

ttg agc tgg tgt gct ggt tta ggc agg att gct atg gcg gtc cct ggg   931
Leu Ser Trp Cys Ala Gly Leu Gly Arg Ile Ala Met Ala Val Pro Gly
            265                 270                 275

ccg gta aat act gct gga tca ctt ggg tgc cac gaa agg att cga aac   979
Pro Val Asn Thr Ala Gly Ser Leu Gly Cys His Glu Arg Ile Arg Asn
        280                 285                 290

ggc agc gca caa atg gtc acc agt gcg gat gac gtt cgg tca ctt ctg   1027
Gly Ser Ala Gln Met Val Thr Ser Ala Asp Asp Val Arg Ser Leu Leu
    295                 300                 305

ggt gca gtg ggt gca atg gat agc caa act cag tat gaa tta aac ttc   1075
Gly Ala Val Gly Ala Met Asp Ser Gln Thr Gln Tyr Glu Leu Asn Phe
310                 315                 320                 325

gcg gcc act cca gta cag ggt tta acc aga aat gag ctg cga gtt ttt   1123
Ala Ala Thr Pro Val Gln Gly Leu Thr Arg Asn Glu Leu Arg Val Phe
                330                 335                 340

gat gcg tta gac gac cga gga gag ggg agg gaa gcg gcg agt atc gct   1171
Asp Ala Leu Asp Asp Arg Gly Glu Gly Arg Glu Ala Ala Ser Ile Ala
            345                 350                 355
```

```
acc gaa gcc ggg ttg acc ttg cag tta aca att ttc ctt ctc att gca   1219
Thr Glu Ala Gly Leu Thr Leu Gln Leu Thr Ile Phe Leu Leu Ile Ala
        360                 365                 370

ttg aac aag cgc gga atc gtg aaa cgc gac gga act gct tgg tcg aga   1267
Leu Asn Lys Arg Gly Ile Val Lys Arg Asp Gly Thr Ala Trp Ser Arg
    375                 380                 385

aat gcg gaa atg cca taaaacctgg gggttatata aaa                    1305
Asn Ala Glu Met Pro
390
```

<210> 2196
<211> 394
<212> PRT
<213> Corynebacterium glutamicum

<400> 2196

```
Met Ile Asp Ser Arg Leu Leu Ala Trp Ala Tyr Leu Ser Lys Val Val
  1               5                  10                  15

Glu Gly Pro Asn Ala His Leu Gln Lys Leu Leu Lys Glu Gly His Asp
             20                  25                  30

Val Glu Arg Ile Ala Phe Gly Ile Lys His Arg Glu Glu Trp Ile Gly
         35                  40                  45

Glu Gly Leu Leu Lys Asn Thr Asp Ser Arg Tyr Ser Ile Asp Thr Ala
     50                  55                  60

Gln Thr Asp Leu Glu Thr Ile Ala Lys Leu Gly Gly Arg Leu Ile Thr
 65                  70                  75                  80

Pro Glu Asp Asp Glu Trp Pro Met Glu Glu Leu Asp His Ala Phe Gly
                 85                  90                  95

Phe Ala Ala Ser Gly Met Ser Asp His Val Arg Thr Tyr Gln Asp Asp
            100                 105                 110

Ala Leu Pro Pro His Ala Leu Trp Ile Arg Gly Gly Asn Leu Arg Thr
        115                 120                 125

Leu Ser Ala Gln Ser Val Thr Leu Val Gly Thr Arg Ala Ile Ser Gln
    130                 135                 140

Tyr Gly Thr Glu Val Thr Arg Glu Phe Thr Gln Asn Leu Val Ser His
145                 150                 155                 160

Gln Trp Thr Ile Ile Ser Gly Gly Ala Leu Gly Val Asp Ser Val Ala
                165                 170                 175

His Ser Glu Ala Val Arg Ala Gln Gly Ser Thr Ile Ala Ile Ala Ala
            180                 185                 190

Cys Gly Leu Asp Arg Ser Tyr Pro Ser His Asn Arg Asp Leu Phe Asn
        195                 200                 205

Gln Ile Ala Lys Ser Gly Lys Gly Ala Leu Val Ser Glu Tyr Pro Pro
    210                 215                 220
```

```
Gly Thr Pro Pro Gln Arg His Arg Phe Leu Thr Arg Asn Arg Leu Val
225                 230                 235                 240

Ala Ala Leu Ser Gln Gly Thr Val Val Val Glu Ala Ala Trp Arg Ser
                245                 250                 255

Gly Ala Leu Asn Thr Leu Ser Trp Cys Ala Gly Leu Gly Arg Ile Ala
            260                 265                 270

Met Ala Val Pro Gly Pro Val Asn Thr Ala Gly Ser Leu Gly Cys His
        275                 280                 285

Glu Arg Ile Arg Asn Gly Ser Ala Gln Met Val Thr Ser Ala Asp Asp
    290                 295                 300

Val Arg Ser Leu Leu Gly Ala Val Gly Ala Met Asp Ser Gln Thr Gln
305                 310                 315                 320

Tyr Glu Leu Asn Phe Ala Ala Thr Pro Val Gln Gly Leu Thr Arg Asn
                325                 330                 335

Glu Leu Arg Val Phe Asp Ala Leu Asp Asp Arg Gly Glu Gly Arg Glu
            340                 345                 350

Ala Ala Ser Ile Ala Thr Glu Ala Gly Leu Thr Leu Gln Leu Thr Ile
        355                 360                 365

Phe Leu Leu Ile Ala Leu Asn Lys Arg Gly Ile Val Lys Arg Asp Gly
    370                 375                 380

Thr Ala Trp Ser Arg Asn Ala Glu Met Pro
385                 390


<210> 2197
<211> 513
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(490)
<223> RXA01366

<400> 2197
atgcatgaaa acaaattcta tgtgtgttga gctgccaaaa ggggttggcg cgccgatgat 60

gactgtccaa acctaaacca aaggtctaaa ctttggcttc gtg agt cag ttt cgt   115
                                        Val Ser Gln Phe Arg
                                          1               5

cgt tgt tcc cgc cct ggt tgt ggc aag cct gcc gtc gca acc ctc acc   163
Arg Cys Ser Arg Pro Gly Cys Gly Lys Pro Ala Val Ala Thr Leu Thr
                 10                  15                  20

tac gca tat tcg gat tcc act gcg gtg gtt ggt cct ttg gcg cct gca   211
Tyr Ala Tyr Ser Asp Ser Thr Ala Val Val Gly Pro Leu Ala Pro Ala
             25                  30                  35

gca gag ccc cat agt tgg gat ctg tgt gag cat cat gcc gag cgt att   259
```

```
Ala Glu Pro His Ser Trp Asp Leu Cys Glu His His Ala Glu Arg Ile
         40                  45                  50

act gcg ccc ctt ggt tgg gag atg ctg cgg gtg aac gac atc aaa gtc   307
Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val Asn Asp Ile Lys Val
     55                  60                  65

gat gac gat gag gat ctg acg gct ctt gct cag gct gtt cgt gag gct   355
Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln Ala Val Arg Glu Ala
 70                  75                  80                  85

gga cgc act gtg agt ggt ctg gtt cct gaa gac gaa gtg ggc ggc aac   403
Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp Glu Val Gly Gly Asn
                 90                  95                 100

cat ccg gtg aac cgg agt gcg cgg atc gcg gaa cag aag gtt cac cgc   451
His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu Gln Lys Val His Arg
            105                 110                 115

agg ggt cat ctc tat gtt gtg cct gat cag gac gaa tca taaggtttgc    500
Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp Glu Ser
        120                 125                 130

tattcggatt gga                                                   513


<210> 2198
<211> 130
<212> PRT
<213> Corynebacterium glutamicum

<400> 2198
Val Ser Gln Phe Arg Arg Cys Ser Arg Pro Gly Cys Gly Lys Pro Ala
  1               5                  10                  15

Val Ala Thr Leu Thr Tyr Ala Tyr Ser Asp Ser Thr Ala Val Val Gly
             20                  25                  30

Pro Leu Ala Pro Ala Ala Glu Pro His Ser Trp Asp Leu Cys Glu His
         35                  40                  45

His Ala Glu Arg Ile Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val
     50                  55                  60

Asn Asp Ile Lys Val Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln
 65                  70                  75                  80

Ala Val Arg Glu Ala Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp
                 85                  90                  95

Glu Val Gly Gly Asn His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu
            100                 105                 110

Gln Lys Val His Arg Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp
        115                 120                 125

Glu Ser
    130


<210> 2199
```

<211> 525
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(502)
<223> RXA01367

<400> 2199
cgcgccaacc ccttttggca gctcaacaca catagaattt gttttcatgc atacgagaac 60

tttccgcaat cggcacggac gcggtctccg cggcccactc atg ccc gtc gaa gtt 115
Met Pro Val Glu Val
1 5

ccc cgc cac gcc tct aga cgc caa gcc ttc gac cgc gca gtc tta gag 163
Pro Arg His Ala Ser Arg Arg Gln Ala Phe Asp Arg Ala Val Leu Glu
10 15 20

gcc tac tcc cct ctt tac ggg att tac caa aaa gag ctc agc aat cta 211
Ala Tyr Ser Pro Leu Tyr Gly Ile Tyr Gln Lys Glu Leu Ser Asn Leu
25 30 35

gac atc gct gtc gat acc gtt cct cgc atg cga ctc agc gcc gac ctt 259
Asp Ile Ala Val Asp Thr Val Pro Arg Met Arg Leu Ser Ala Asp Leu
40 45 50

gcc att ctc ccc gat gaa atc acc gcc gac ggc ccc gtt cca ctt ggt 307
Ala Ile Leu Pro Asp Glu Ile Thr Ala Asp Gly Pro Val Pro Leu Gly
55 60 65

cgc gtc atc cca ccg gcg atc gat acc aag gga aac ccc acg aga gcg 355
Arg Val Ile Pro Pro Ala Ile Asp Thr Lys Gly Asn Pro Thr Arg Ala
70 75 80 85

cgc atc gtt att ttc aga atg ccg atc gag caa cga gtc acc aac gct 403
Arg Ile Val Ile Phe Arg Met Pro Ile Glu Gln Arg Val Thr Asn Ala
90 95 100

gtg gaa cgc cac gag cta ttg act cat gtt ctc acc tct ttg gtg gcg 451
Val Glu Arg His Glu Leu Leu Thr His Val Leu Thr Ser Leu Val Ala
105 110 115

aac tat ctg aat att gat cca cga gac atc gat ccg gga ttc cag gat 499
Asn Tyr Leu Asn Ile Asp Pro Arg Asp Ile Asp Pro Gly Phe Gln Asp
120 125 130

ctc tagcgtggcc ggtgcaccat ggg 525
Leu

<210> 2200
<211> 134
<212> PRT
<213> Corynebacterium glutamicum

<400> 2200
Met Pro Val Glu Val Pro Arg His Ala Ser Arg Arg Gln Ala Phe Asp
1 5 10 15

```
Arg Ala Val Leu Glu Ala Tyr Ser Pro Leu Tyr Gly Ile Tyr Gln Lys
            20                  25                  30

Glu Leu Ser Asn Leu Asp Ile Ala Val Asp Thr Val Pro Arg Met Arg
        35                  40                  45

Leu Ser Ala Asp Leu Ala Ile Leu Pro Asp Glu Ile Thr Ala Asp Gly
    50                  55                  60

Pro Val Pro Leu Gly Arg Val Ile Pro Pro Ala Ile Asp Thr Lys Gly
65                  70                  75                  80

Asn Pro Thr Arg Ala Arg Ile Val Ile Phe Arg Met Pro Ile Glu Gln
                85                  90                  95

Arg Val Thr Asn Ala Val Glu Arg His Glu Leu Leu Thr His Val Leu
            100                 105                 110

Thr Ser Leu Val Ala Asn Tyr Leu Asn Ile Asp Pro Arg Asp Ile Asp
        115                 120                 125

Pro Gly Phe Gln Asp Leu
    130
```

<210> 2201
<211> 474
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(451)
<223> RXA01370

<400> 2201

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ctgtctgaat cgtgtgggcg ttagatgaat tgttataaac cggatgttta acggaattta 60

atacgtgtct tattacgcgg actagaaagg ttttagggac atg ggt gca tgg gac   115
                                            Met Gly Ala Trp Asp
                                              1               5

gat gca atc ttg act gag gaa gtc aac gtt gat ttt ctc gac gag atc   163
Asp Ala Ile Leu Thr Glu Glu Val Asn Val Asp Phe Leu Asp Glu Ile
                  10                  15                  20

tca gaa tta gat act caa gac att ctt gag gcg ttg gaa gac gca tgt   211
Ser Glu Leu Asp Thr Gln Asp Ile Leu Glu Ala Leu Glu Asp Ala Cys
              25                  30                  35

ttg ctg gtg gtt aac cag gac aac gcc act gaa gac gaa cac ctc aac   259
Leu Leu Val Val Asn Gln Asp Asn Ala Thr Glu Asp Glu His Leu Asn
          40                  45                  50

ggt cag gcg gct gcg acg atc gcg gcc atc atg ttt ggc gct cca tat   307
Gly Gln Ala Ala Ala Thr Ile Ala Ala Ile Met Phe Gly Ala Pro Tyr
      55                  60                  65

tct gcg ggc cag gtg ctg gag aat tac cca ttt atc cgc gaa ctc gtc   355
Ser Ala Gly Gln Val Leu Glu Asn Tyr Pro Phe Ile Arg Glu Leu Val
```

```
 70                  75                  80                  85

ggt gag ggc tct gaa gct ctt cgc ggt gct gca gcg cag gtt ttg gaa   403
Gly Glu Gly Ser Glu Ala Leu Arg Gly Ala Ala Ala Gln Val Leu Glu
                90                  95                 100

gag gca gat gtg gaa tat gac ctc gaa gct tat tta gag gcc ctc aac   451
Glu Ala Asp Val Glu Tyr Asp Leu Glu Ala Tyr Leu Glu Ala Leu Asn
            105                 110                 115

tagccctcca ctaaacagct tca                                        474


<210> 2202
<211> 117
<212> PRT
<213> Corynebacterium glutamicum

<400> 2202
Met Gly Ala Trp Asp Asp Ala Ile Leu Thr Glu Glu Val Asn Val Asp
  1               5                  10                  15

Phe Leu Asp Glu Ile Ser Glu Leu Asp Thr Gln Asp Ile Leu Glu Ala
             20                  25                  30

Leu Glu Asp Ala Cys Leu Leu Val Val Asn Gln Asp Asn Ala Thr Glu
         35                  40                  45

Asp Glu His Leu Asn Gly Gln Ala Ala Ala Thr Ile Ala Ala Ile Met
     50                  55                  60

Phe Gly Ala Pro Tyr Ser Ala Gly Gln Val Leu Glu Asn Tyr Pro Phe
 65                  70                  75                  80

Ile Arg Glu Leu Val Gly Glu Gly Ser Glu Ala Leu Arg Gly Ala Ala
                 85                  90                  95

Ala Gln Val Leu Glu Glu Ala Asp Val Glu Tyr Asp Leu Glu Ala Tyr
            100                 105                 110

Leu Glu Ala Leu Asn
        115


<210> 2203
<211> 614
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(591)
<223> RXA01372

<400> 2203
cag gac acc ttc gtc ctt ccc acc ttg ccc acg gcc gca ggc ttg tcg    48
Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser
  1               5                  10                  15

cct gcc cgc atc gtg gcg tcg ata agc act ctt tta gat ctt tta gaa    96
Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu
```

```
                20                  25                  30

gca gac ccc agc att att tcc gac cgc ttg gaa cac ctc gcc gac tgc   144
Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys
         35                  40                  45

att gat gag gaa gtg gaa tcg cta tcg ccg gaa cgt gac gaa cta gtc   192
Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val
     50                  55                  60

aat ccc ggc cga aaa ctg cgc gca tac gta gat cac gca cgg atc gtg   240
Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val
 65                  70                  75                  80

cat acc ggc cga act gat gtg gga ctc gcg att gcc aac gtt atc gcc   288
His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala
                 85                  90                  95

cca atc tgg acc cga cga ggc ctg gta tca gcc gtg ctg gat ttt ccc   336
Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro
            100                 105                 110

gag ctc atg gaa tca ttg ccg gaa ctc cgc gga ccc gag cca att acc   384
Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr
        115                 120                 125

gac gat ata ttc cat gac cca ttc ata gat gac gaa ccc ggg gtg gta   432
Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val
    130                 135                 140

ccg ttt agg gct gtt gtc tgg gcc gaa gag gaa ccc gga atc ccc gat   480
Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp
145                 150                 155                 160

gcc atg gcg caa agc tgc gac gga cct agc aaa ggg gcg ctg aca caa   528
Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln
                165                 170                 175

gca ctg cgt ttg ctg gtg cgc gga cag tca gcc acg acc tat tcc att   576
Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile
            180                 185                 190

gaa gaa aag gac ttg taaatggagc tattggaagg ctc                    614
Glu Glu Lys Asp Leu
        195
```

<210> 2204
<211> 197
<212> PRT
<213> Corynebacterium glutamicum

<400> 2204

```
Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser
  1               5                  10                  15

Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu
             20                  25                  30

Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys
         35                  40                  45
```

```
Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val
     50                  55                  60

Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val
 65                  70                  75                  80

His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala
                 85                  90                  95

Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro
            100                 105                 110

Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr
        115                 120                 125

Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val
    130                 135                 140

Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp
145                 150                 155                 160

Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln
                165                 170                 175

Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile
            180                 185                 190

Glu Glu Lys Asp Leu
        195
```

<210> 2205
<211> 1278
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1278)
<223> RXA01378

<400> 2205

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cat gtg tgg att tca cca ggt gcg agc aat ccg atc aag gat cgc ctc   48
His Val Trp Ile Ser Pro Gly Ala Ser Asn Pro Ile Lys Asp Arg Leu
  1               5                  10                  15

ttc cct tgg aca ttg gtg aag gct ttt ctc tcc tcc cct gca gcc ttg   96
Phe Pro Trp Thr Leu Val Lys Ala Phe Leu Ser Ser Pro Ala Ala Leu
             20                  25                  30

ggc gaa aca gtg tcc aat cgc ctc aaa aag gcc tct gca cca gaa gaa   144
Gly Glu Thr Val Ser Asn Arg Leu Lys Lys Ala Ser Ala Pro Glu Glu
         35                  40                  45

aaa cgc gcc cta gaa acc ctt tca caa ctt aat tct gcg atc acc ccg   192
Lys Arg Ala Leu Glu Thr Leu Ser Gln Leu Asn Ser Ala Ile Thr Pro
     50                  55                  60

cag acc tca cag aag tac caa tct cta ctg agc tac ctc ggt gac atc   240
Gln Thr Ser Gln Lys Tyr Gln Ser Leu Leu Ser Tyr Leu Gly Asp Ile
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65                  70                  75                  80

gga gtg aag aag aac tcc gat acc cgc gtg gtg att ttc tct gag cgt   288
Gly Val Lys Lys Asn Ser Asp Thr Arg Val Val Ile Phe Ser Glu Arg
                 85                  90                  95

gtc gct act ttg cac tgg ctg cag gaa aac ctc atc cgt gat ctc aag   336
Val Ala Thr Leu His Trp Leu Gln Glu Asn Leu Ile Arg Asp Leu Lys
            100                 105                 110

atg cca ccc aac tct att gct gtt atg cac ggc ggt ctc ccc gac cag   384
Met Pro Pro Asn Ser Ile Ala Val Met His Gly Gly Leu Pro Asp Gln
        115                 120                 125

gag caa atg cgc ctg gtg gat gag ttt aaa aag acg gat tct ccc atc   432
Glu Gln Met Arg Leu Val Asp Glu Phe Lys Lys Thr Asp Ser Pro Ile
    130                 135                 140

cgc atc atg atc acc ggc gat gtt gcc tca gaa ggt gtg aac ctg cat   480
Arg Ile Met Ile Thr Gly Asp Val Ala Ser Glu Gly Val Asn Leu His
145                 150                 155                 160

act ctc tgc cac aac ttg gtg cac tat gac atc ccg tgg tca ctg atc   528
Thr Leu Cys His Asn Leu Val His Tyr Asp Ile Pro Trp Ser Leu Ile
                165                 170                 175

cgc att cag cag cgc aat ggc cgt att gat cgt tat ggt caa acc cac   576
Arg Ile Gln Gln Arg Asn Gly Arg Ile Asp Arg Tyr Gly Gln Thr His
            180                 185                 190

aac cct tcc atc gtt acc ttc ttg ctc gat ccc gcc gag gat tcc aaa   624
Asn Pro Ser Ile Val Thr Phe Leu Leu Asp Pro Ala Glu Asp Ser Lys
        195                 200                 205

gta ggt gaa gtc cat gtg ctg gag agg ctc atg gag cgc gaa cat gag   672
Val Gly Glu Val His Val Leu Glu Arg Leu Met Glu Arg Glu His Glu
    210                 215                 220

gcg cac tct ttg ctc ggt gat gcc gca tct ctc atg ggc aag cac tct   720
Ala His Ser Leu Leu Gly Asp Ala Ala Ser Leu Met Gly Lys His Ser
225                 230                 235                 240

gag cgt ttg gaa gaa gaa acc atc cgc gaa gtc ctg cgc ggt gcc caa   768
Glu Arg Leu Glu Glu Glu Thr Ile Arg Glu Val Leu Arg Gly Ala Gln
                245                 250                 255

aac ttt aat gat gca gtg gct gat cca gcg gaa gtc cta gaa aac cca   816
Asn Phe Asn Asp Ala Val Ala Asp Pro Ala Glu Val Leu Glu Asn Pro
            260                 265                 270

gca ggc cta gat gat att gat tgg ttg cta gcc caa atc gcc caa gcc   864
Ala Gly Leu Asp Asp Ile Asp Trp Leu Leu Ala Gln Ile Ala Gln Ala
        275                 280                 285

gat gcc aag gca gaa aca gaa gca gaa gca gaa aca gaa aac caa aca   912
Asp Ala Lys Ala Glu Thr Glu Ala Glu Ala Glu Thr Glu Asn Gln Thr
    290                 295                 300

gca cca gat gca gct tcc aat agc acg cag cat gca caa cgc cgg ttg   960
Ala Pro Asp Ala Ala Ser Asn Ser Thr Gln His Ala Gln Arg Arg Leu
305                 310                 315                 320
```

```
tat gca cag gaa agc tct ttc ctc tat gac tgc ctc ctc gaa ggt ttc   1008
Tyr Ala Gln Glu Ser Ser Phe Leu Tyr Asp Cys Leu Leu Glu Gly Phe
                325                 330                 335

aat aac gta ccg gag gat tcc atc aac cgc ggt ggc gtg ggg ttc aaa   1056
Asn Asn Val Pro Glu Asp Ser Ile Asn Arg Gly Gly Val Gly Phe Lys
            340                 345                 350

aaa cac gat aat gac atc gtg gag ctc acc ccc acc gat gat ctg cgc   1104
Lys His Asp Asn Asp Ile Val Glu Leu Thr Pro Thr Asp Asp Leu Arg
        355                 360                 365

cgt cgt cta gat ttc ctc ccg cag gat tat gtg gct gct cgg aaa gtt   1152
Arg Arg Leu Asp Phe Leu Pro Gln Asp Tyr Val Ala Ala Arg Lys Val
    370                 375                 380

aag gaa gat ctc cta cta gct tcc aca ctg atg cgt ggc caa gaa cgc   1200
Lys Glu Asp Leu Leu Leu Ala Ser Thr Leu Met Arg Gly Gln Glu Arg
385                 390                 395                 400

ctc aac gct gcg cgc act ggt gaa gat ggc agt acc tgg cca agt gcc   1248
Leu Asn Ala Ala Arg Thr Gly Glu Asp Gly Ser Thr Trp Pro Ser Ala
                405                 410                 415

cac tat cta ggc ccc ctg cac cca gtc act                          1278
His Tyr Leu Gly Pro Leu His Pro Val Thr
            420                 425
```

<210> 2206
<211> 426
<212> PRT
<213> Corynebacterium glutamicum

<400> 2206

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His Val Trp Ile Ser Pro Gly Ala Ser Asn Pro Ile Lys Asp Arg Leu
  1               5                  10                  15

Phe Pro Trp Thr Leu Val Lys Ala Phe Leu Ser Ser Pro Ala Ala Leu
             20                  25                  30

Gly Glu Thr Val Ser Asn Arg Leu Lys Lys Ala Ser Ala Pro Glu Glu
         35                  40                  45

Lys Arg Ala Leu Glu Thr Leu Ser Gln Leu Asn Ser Ala Ile Thr Pro
     50                  55                  60

Gln Thr Ser Gln Lys Tyr Gln Ser Leu Leu Ser Tyr Leu Gly Asp Ile
 65                  70                  75                  80

Gly Val Lys Lys Asn Ser Asp Thr Arg Val Val Ile Phe Ser Glu Arg
                 85                  90                  95

Val Ala Thr Leu His Trp Leu Gln Glu Asn Leu Ile Arg Asp Leu Lys
            100                 105                 110

Met Pro Pro Asn Ser Ile Ala Val Met His Gly Gly Leu Pro Asp Gln
        115                 120                 125

Glu Gln Met Arg Leu Val Asp Glu Phe Lys Lys Thr Asp Ser Pro Ile
```

```
    130                 135                 140

Arg Ile Met Ile Thr Gly Asp Val Ala Ser Glu Gly Val Asn Leu His
145                 150                 155                 160

Thr Leu Cys His Asn Leu Val His Tyr Asp Ile Pro Trp Ser Leu Ile
                165                 170                 175

Arg Ile Gln Gln Arg Asn Gly Arg Ile Asp Arg Tyr Gly Gln Thr His
            180                 185                 190

Asn Pro Ser Ile Val Thr Phe Leu Leu Asp Pro Ala Glu Asp Ser Lys
        195                 200                 205

Val Gly Glu Val His Val Leu Glu Arg Leu Met Glu Arg Glu His Glu
    210                 215                 220

Ala His Ser Leu Leu Gly Asp Ala Ala Ser Leu Met Gly Lys His Ser
225                 230                 235                 240

Glu Arg Leu Glu Glu Glu Thr Ile Arg Glu Val Leu Arg Gly Ala Gln
                245                 250                 255

Asn Phe Asn Asp Ala Val Ala Asp Pro Ala Glu Val Leu Glu Asn Pro
            260                 265                 270

Ala Gly Leu Asp Asp Ile Asp Trp Leu Leu Ala Gln Ile Ala Gln Ala
        275                 280                 285

Asp Ala Lys Ala Glu Thr Glu Ala Glu Ala Glu Thr Glu Asn Gln Thr
    290                 295                 300

Ala Pro Asp Ala Ala Ser Asn Ser Thr Gln His Ala Gln Arg Arg Leu
305                 310                 315                 320

Tyr Ala Gln Glu Ser Ser Phe Leu Tyr Asp Cys Leu Leu Glu Gly Phe
                325                 330                 335

Asn Asn Val Pro Glu Asp Ser Ile Asn Arg Gly Gly Val Gly Phe Lys
            340                 345                 350

Lys His Asp Asn Asp Ile Val Glu Leu Thr Pro Thr Asp Asp Leu Arg
        355                 360                 365

Arg Arg Leu Asp Phe Leu Pro Gln Asp Tyr Val Ala Ala Arg Lys Val
    370                 375                 380

Lys Glu Asp Leu Leu Leu Ala Ser Thr Leu Met Arg Gly Gln Glu Arg
385                 390                 395                 400

Leu Asn Ala Ala Arg Thr Gly Glu Asp Gly Ser Thr Trp Pro Ser Ala
                405                 410                 415

His Tyr Leu Gly Pro Leu His Pro Val Thr
            420                 425
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<210> 2207
<211> 2039
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(2016)
<223> RXA01380

<400> 2207

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tcg ctg att ttg gga tgc gac acc aag gct cgc ctg gag gat ctg tac   48
Ser Leu Ile Leu Gly Cys Asp Thr Lys Ala Arg Leu Glu Asp Leu Tyr
  1               5                  10                  15

ctg ccg ttc aaa aaa cgg cgc aag acg aag gcc gat atc gct agg gag   96
Leu Pro Phe Lys Lys Arg Arg Lys Thr Lys Ala Asp Ile Ala Arg Glu
            20                  25                  30

gcg ggc ctg gag ggg ctc gtc gat aag ctt atc gac gcc ccg tcc ctc  144
Ala Gly Leu Glu Gly Leu Val Asp Lys Leu Ile Asp Ala Pro Ser Leu
        35                  40                  45

gac gcc gca gcg cag gca gct gca ttt acg act gag ggc ttt gag gat  192
Asp Ala Ala Ala Gln Ala Ala Ala Phe Thr Thr Glu Gly Phe Glu Asp
    50                  55                  60

tcc aaa aaa gtt ttg gat ggc gct cgc gcc att ttg att gac cgc ttc  240
Ser Lys Lys Val Leu Asp Gly Ala Arg Ala Ile Leu Ile Asp Arg Phe
65                  70                  75                  80

gcg ctc gat gcc gat ttg gtg ggc gag gtg cgt gag caa atg tat cgc  288
Ala Leu Asp Ala Asp Leu Val Gly Glu Val Arg Glu Gln Met Tyr Arg
                85                  90                  95

gcg ggt tcc atg gcg gca tcg gtg gtg gcg ggc aag gag cag gaa ggc  336
Ala Gly Ser Met Ala Ala Ser Val Val Ala Gly Lys Glu Gln Glu Gly
            100                 105                 110

gca aag ttc aag gac tac ttt gag ttt tcc gaa cct ttt gac aag ctt  384
Ala Lys Phe Lys Asp Tyr Phe Glu Phe Ser Glu Pro Phe Asp Lys Leu
        115                 120                 125

cca tct cac cga att ttg gcg ctg ctg cgc ggt gaa aac gaa ggt gtg  432
Pro Ser His Arg Ile Leu Ala Leu Leu Arg Gly Glu Asn Glu Gly Val
    130                 135                 140

ctg agc ctc aac ctc gat gcg ggc gac gac ata atc tac gaa ggt ttg  480
Leu Ser Leu Asn Leu Asp Ala Gly Asp Asp Ile Ile Tyr Glu Gly Leu
145                 150                 155                 160

atc gcc gac cga ttc tcc ctg gac acc cac act tct agc tgg ctg gct  528
Ile Ala Asp Arg Phe Ser Leu Asp Thr His Thr Ser Ser Trp Leu Ala
                165                 170                 175

gag gct gtg cgc tgg ggt tgg cgc acc aaa ctg tat gtg tcc tcc gga  576
Glu Ala Val Arg Trp Gly Trp Arg Thr Lys Leu Tyr Val Ser Ser Gly
            180                 185                 190

ttg gat gtg cgc atg cgt ctg aaa gaa aaa gca gag gaa ggc gca ctc  624
Leu Asp Val Arg Met Arg Leu Lys Glu Lys Ala Glu Glu Gly Ala Leu
        195                 200                 205

gat gtg ttt gcc acc aac ctc cgc gac gtt ctc ctt gca gct ccc gct  672
Asp Val Phe Ala Thr Asn Leu Arg Asp Val Leu Leu Ala Ala Pro Ala
```

```
    210                 215                 220

ggt cag cgc tcc aca att ggc ctt gac ccg gga ttc cgc aac ggt gtg   720
Gly Gln Arg Ser Thr Ile Gly Leu Asp Pro Gly Phe Arg Asn Gly Val
225                 230                 235                 240

aaa gta gct gtc gtg gat tcc acc ggt aag gat gtt gcc acc acg atc   768
Lys Val Ala Val Val Asp Ser Thr Gly Lys Asp Val Ala Thr Thr Ile
                245                 250                 255

gtc tac cca cac cag ccc caa aac cgc tgg aag gaa gcc gta tcc gaa   816
Val Tyr Pro His Gln Pro Gln Asn Arg Trp Lys Glu Ala Val Ser Glu
            260                 265                 270

ctg gct aac ctg tgc gcg acc cac ggt gtg gaa ctc atg gcg atc ggc   864
Leu Ala Asn Leu Cys Ala Thr His Gly Val Glu Leu Met Ala Ile Gly
        275                 280                 285

aac gga acc gcc tcg agg gaa acg gaa aaa ctc gcc ggc gaa gta gct   912
Asn Gly Thr Ala Ser Arg Glu Thr Glu Lys Leu Ala Gly Glu Val Ala
    290                 295                 300

gac atg atc aaa gcc gca ggt ggc acg cga cca acc ccc gtg gtg gtc   960
Asp Met Ile Lys Ala Ala Gly Gly Thr Arg Pro Thr Pro Val Val Val
305                 310                 315                 320

tcc gaa tcg ggc gca tcc gtg tac tcg gca tca ccg atc gca gcc gaa  1008
Ser Glu Ser Gly Ala Ser Val Tyr Ser Ala Ser Pro Ile Ala Ala Glu
                325                 330                 335

gaa ttc ccc gac atg gac gtc tcc ctc cgc ggt gca gtt tct atc gcg  1056
Glu Phe Pro Asp Met Asp Val Ser Leu Arg Gly Ala Val Ser Ile Ala
            340                 345                 350

agg cga ctc cag gat cca ctg gcg gag ctc gtc aag att gag ccc aaa  1104
Arg Arg Leu Gln Asp Pro Leu Ala Glu Leu Val Lys Ile Glu Pro Lys
        355                 360                 365

gcc atc gga gtc ggc cag tac caa cac gat gtc aac cag gtt gca ctt  1152
Ala Ile Gly Val Gly Gln Tyr Gln His Asp Val Asn Gln Val Ala Leu
    370                 375                 380

gcc aaa acc ctt gat ggt gtc gtc gaa gac gca gta aac gca gtc gga  1200
Ala Lys Thr Leu Asp Gly Val Val Glu Asp Ala Val Asn Ala Val Gly
385                 390                 395                 400

gtt aac ctc aac acc gca tcc gca cca ctt ctt acc cga gtt gcc gga  1248
Val Asn Leu Asn Thr Ala Ser Ala Pro Leu Leu Thr Arg Val Ala Gly
                405                 410                 415

gtg acc tcc acc ttg gca aac aat atc gtg gcc tac cgc aac gaa aac  1296
Val Thr Ser Thr Leu Ala Asn Asn Ile Val Ala Tyr Arg Asn Glu Asn
            420                 425                 430

ggt gga ttc tcc tcc cga aaa gaa ctg aac aaa gtt cct cgc ctg gga  1344
Gly Gly Phe Ser Ser Arg Lys Glu Leu Asn Lys Val Pro Arg Leu Gly
        435                 440                 445

ccc aaa gcc ttt gaa cag tgt gct ggc ttc ctc cgc att tct gga tcc  1392
Pro Lys Ala Phe Glu Gln Cys Ala Gly Phe Leu Arg Ile Ser Gly Ser
    450                 455                 460
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acc gac cct ctc gac gcc tcc gct gtt cac ccc gag gcg tac cca gtt   1440
Thr Asp Pro Leu Asp Ala Ser Ala Val His Pro Glu Ala Tyr Pro Val
465                 470                 475                 480

gtt cgc aac att gcg aaa gcc aca gga ttg gat gtc tcg gga ctg atc   1488
Val Arg Asn Ile Ala Lys Ala Thr Gly Leu Asp Val Ser Gly Leu Ile
                485                 490                 495

gga aac tct gcg gtg ctc acc aaa ttg aag ccc gct gat ttc gct gat   1536
Gly Asn Ser Ala Val Leu Thr Lys Leu Lys Pro Ala Asp Phe Ala Asp
            500                 505                 510

gaa cga ttc ggc atc ccc acc gtc acc gac atc atc gcc gag ctg gat   1584
Glu Arg Phe Gly Ile Pro Thr Val Thr Asp Ile Ile Ala Glu Leu Asp
        515                 520                 525

aaa ccc gga cgt gac ccc cgc cca gaa ttc aaa acc gcc agc ttc aaa   1632
Lys Pro Gly Arg Asp Pro Arg Pro Glu Phe Lys Thr Ala Ser Phe Lys
    530                 535                 540

gaa ggc gtg gag aaa atc tcc gac ctc aca ccc ggc atg atc ctg gaa   1680
Glu Gly Val Glu Lys Ile Ser Asp Leu Thr Pro Gly Met Ile Leu Glu
545                 550                 555                 560

gga act gtc acc aac gtt gcg gcg ttc ggc gca ttc gtt gac gtg gga   1728
Gly Thr Val Thr Asn Val Ala Ala Phe Gly Ala Phe Val Asp Val Gly
                565                 570                 575

gtg cac cga gat ggc ctc gtt cac gtt tcc gcg atg agc gac aaa ttc   1776
Val His Arg Asp Gly Leu Val His Val Ser Ala Met Ser Asp Lys Phe
            580                 585                 590

atc tcc aac ccc cac gaa gtt gtt cgc tct ggt gag gtc gtg aag gta   1824
Ile Ser Asn Pro His Glu Val Val Arg Ser Gly Glu Val Val Lys Val
        595                 600                 605

aag gtc atg gaa gtt gac gtc gac cgc aaa cgc atc ggc ctt tcc ctc   1872
Lys Val Met Glu Val Asp Val Asp Arg Lys Arg Ile Gly Leu Ser Leu
    610                 615                 620

cgc ttg acc gat gaa ccc ggt gcc cca gct ccg caa aag cgc gga aac   1920
Arg Leu Thr Asp Glu Pro Gly Ala Pro Ala Pro Gln Lys Arg Gly Asn
625                 630                 635                 640

cga cca gcc aaa cag cag cga gct ccg caa aaa cag tcc gct aag ccc   1968
Arg Pro Ala Lys Gln Gln Arg Ala Pro Gln Lys Gln Ser Ala Lys Pro
                645                 650                 655

gcc aca ggt tcc atg gca gat gct tta cga cgc gcc ggc ctc ggt ggc   2016
Ala Thr Gly Ser Met Ala Asp Ala Leu Arg Arg Ala Gly Leu Gly Gly
            660                 665                 670

taaggcaact ttcaaaccaa gcg                                        2039
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<210> 2208
<211> 672
<212> PRT
<213> Corynebacterium glutamicum

<400> 2208

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Ser Leu Ile Leu Gly Cys Asp Thr Lys Ala Arg Leu Glu Asp Leu Tyr
  1               5                  10                  15

Leu Pro Phe Lys Lys Arg Arg Lys Thr Lys Ala Asp Ile Ala Arg Glu
             20                  25                  30

Ala Gly Leu Glu Gly Leu Val Asp Lys Leu Ile Asp Ala Pro Ser Leu
         35                  40                  45

Asp Ala Ala Ala Gln Ala Ala Ala Phe Thr Thr Glu Gly Phe Glu Asp
     50                  55                  60

Ser Lys Lys Val Leu Asp Gly Ala Arg Ala Ile Leu Ile Asp Arg Phe
 65                  70                  75                  80

Ala Leu Asp Ala Asp Leu Val Gly Glu Val Arg Glu Gln Met Tyr Arg
                 85                  90                  95

Ala Gly Ser Met Ala Ala Ser Val Val Ala Gly Lys Glu Gln Glu Gly
            100                 105                 110

Ala Lys Phe Lys Asp Tyr Phe Glu Phe Ser Glu Pro Phe Asp Lys Leu
        115                 120                 125

Pro Ser His Arg Ile Leu Ala Leu Leu Arg Gly Glu Asn Glu Gly Val
    130                 135                 140

Leu Ser Leu Asn Leu Asp Ala Gly Asp Asp Ile Ile Tyr Glu Gly Leu
145                 150                 155                 160

Ile Ala Asp Arg Phe Ser Leu Asp Thr His Thr Ser Ser Trp Leu Ala
                165                 170                 175

Glu Ala Val Arg Trp Gly Trp Arg Thr Lys Leu Tyr Val Ser Ser Gly
            180                 185                 190

Leu Asp Val Arg Met Arg Leu Lys Glu Lys Ala Glu Glu Gly Ala Leu
        195                 200                 205

Asp Val Phe Ala Thr Asn Leu Arg Asp Val Leu Leu Ala Ala Pro Ala
    210                 215                 220

Gly Gln Arg Ser Thr Ile Gly Leu Asp Pro Gly Phe Arg Asn Gly Val
225                 230                 235                 240

Lys Val Ala Val Val Asp Ser Thr Gly Lys Asp Val Ala Thr Thr Ile
                245                 250                 255

Val Tyr Pro His Gln Pro Gln Asn Arg Trp Lys Glu Ala Val Ser Glu
            260                 265                 270

Leu Ala Asn Leu Cys Ala Thr His Gly Val Glu Leu Met Ala Ile Gly
        275                 280                 285

Asn Gly Thr Ala Ser Arg Glu Thr Glu Lys Leu Ala Gly Glu Val Ala
    290                 295                 300

Asp Met Ile Lys Ala Ala Gly Gly Thr Arg Pro Thr Pro Val Val Val
305                 310                 315                 320
```

```
Ser Glu Ser Gly Ala Ser Val Tyr Ser Ala Ser Pro Ile Ala Ala Glu
                325                 330                 335

Glu Phe Pro Asp Met Asp Val Ser Leu Arg Gly Ala Val Ser Ile Ala
            340                 345                 350

Arg Arg Leu Gln Asp Pro Leu Ala Glu Leu Val Lys Ile Glu Pro Lys
        355                 360                 365

Ala Ile Gly Val Gly Gln Tyr Gln His Asp Val Asn Gln Val Ala Leu
    370                 375                 380

Ala Lys Thr Leu Asp Gly Val Val Glu Asp Ala Val Asn Ala Val Gly
385                 390                 395                 400

Val Asn Leu Asn Thr Ala Ser Ala Pro Leu Leu Thr Arg Val Ala Gly
                405                 410                 415

Val Thr Ser Thr Leu Ala Asn Asn Ile Val Ala Tyr Arg Asn Glu Asn
            420                 425                 430

Gly Gly Phe Ser Ser Arg Lys Glu Leu Asn Lys Val Pro Arg Leu Gly
        435                 440                 445

Pro Lys Ala Phe Glu Gln Cys Ala Gly Phe Leu Arg Ile Ser Gly Ser
    450                 455                 460

Thr Asp Pro Leu Asp Ala Ser Ala Val His Pro Glu Ala Tyr Pro Val
465                 470                 475                 480

Val Arg Asn Ile Ala Lys Ala Thr Gly Leu Asp Val Ser Gly Leu Ile
                485                 490                 495

Gly Asn Ser Ala Val Leu Thr Lys Leu Lys Pro Ala Asp Phe Ala Asp
            500                 505                 510

Glu Arg Phe Gly Ile Pro Thr Val Thr Asp Ile Ile Ala Glu Leu Asp
        515                 520                 525

Lys Pro Gly Arg Asp Pro Arg Pro Glu Phe Lys Thr Ala Ser Phe Lys
    530                 535                 540

Glu Gly Val Glu Lys Ile Ser Asp Leu Thr Pro Gly Met Ile Leu Glu
545                 550                 555                 560

Gly Thr Val Thr Asn Val Ala Ala Phe Gly Ala Phe Val Asp Val Gly
                565                 570                 575

Val His Arg Asp Gly Leu Val His Val Ser Ala Met Ser Asp Lys Phe
            580                 585                 590

Ile Ser Asn Pro His Glu Val Val Arg Ser Gly Glu Val Val Lys Val
        595                 600                 605

Lys Val Met Glu Val Asp Val Asp Arg Lys Arg Ile Gly Leu Ser Leu
    610                 615                 620

Arg Leu Thr Asp Glu Pro Gly Ala Pro Ala Pro Gln Lys Arg Gly Asn
625                 630                 635                 640

Arg Pro Ala Lys Gln Gln Arg Ala Pro Gln Lys Gln Ser Ala Lys Pro
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645 650 655

Ala Thr Gly Ser Met Ala Asp Ala Leu Arg Arg Ala Gly Leu Gly Gly
660 665 670

<210> 2209
<211> 1839
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1816)
<223> RXA01384

<400> 2209
actgtccctc actctgcgag cagccattgc gctatcggca gctacctgca aggtgcgctg 60

gtgggaagcg tcgacaagca tctttaagta gcgttgatgt atg cgc tca ctt caa 115
Met Arg Ser Leu Gln
1 5

tcg gtc ctt gac ctg ctg act tct aag tcc aaa gtg gct acc aaa att 163
Ser Val Leu Asp Leu Leu Thr Ser Lys Ser Lys Val Ala Thr Lys Ile
10 15 20

gtg gtg gaa cga att gaa aag cat cct gtt cat gga ttg gga tgg atg 211
Val Val Glu Arg Ile Glu Lys His Pro Val His Gly Leu Gly Trp Met
25 30 35

atg tat ccg cca ttt cat cca tgg act gat gct tcg acc ttg acg att 259
Met Tyr Pro Pro Phe His Pro Trp Thr Asp Ala Ser Thr Leu Thr Ile
40 45 50

gag cga aac gga acc agt cgg cgc gcg agt cag aat ggc gtt gcg gtt 307
Glu Arg Asn Gly Thr Ser Arg Arg Ala Ser Gln Asn Gly Val Ala Val
55 60 65

ctt cat cag cat gag caa gtt caa act atc ggt cta gcc agc tat ttt 355
Leu His Gln His Glu Gln Val Gln Thr Ile Gly Leu Ala Ser Tyr Phe
70 75 80 85

atc gac tcc aag att tgg gta aac gag ctg gct ggc ctt gat cgt atc 403
Ile Asp Ser Lys Ile Trp Val Asn Glu Leu Ala Gly Leu Asp Arg Ile
90 95 100

aac att tct gag agt gaa gtt gct ggt cgt gac gta tta gtt ctg ccg 451
Asn Ile Ser Glu Ser Glu Val Ala Gly Arg Asp Val Leu Val Leu Pro
105 110 115

tta tct gat ctg act tta agc atc gat gcg aaa tac ggc gtg gtt ttg 499
Leu Ser Asp Leu Thr Leu Ser Ile Asp Ala Lys Tyr Gly Val Val Leu
120 125 130

gct gcg gaa gac agc gat gaa tca gtg cgc gcg gta tcc gtg gag ttc 547
Ala Ala Glu Asp Ser Asp Glu Ser Val Arg Ala Val Ser Val Glu Phe
135 140 145

```
ctg gac cag tgg gta gat gaa gaa gaa ccc cca gcg gaa gaa gtg cct   595
Leu Asp Gln Trp Val Asp Glu Glu Glu Pro Pro Ala Glu Glu Val Pro
150                 155                 160                 165

aaa tat acg gaa acc agg gag gaa ctt cct cca ctt gag att cct ccg   643
Lys Tyr Thr Glu Thr Arg Glu Glu Leu Pro Pro Leu Glu Ile Pro Pro
                170                 175                 180

gct cct tcc gga aat cgt aat ctc cga gtt ctg tgc acg tgg gga gcg   691
Ala Pro Ser Gly Asn Arg Asn Leu Arg Val Leu Cys Thr Trp Gly Ala
            185                 190                 195

atg gaa gga att att cct gag tgg aaa ccc ggc gat caa gtt tca ctg   739
Met Glu Gly Ile Ile Pro Glu Trp Lys Pro Gly Asp Gln Val Ser Leu
        200                 205                 210

ttt ttg tct ttc gac ctc gac gat ccg ccg ttc gaa cag ctc aaa acc   787
Phe Leu Ser Phe Asp Leu Asp Asp Pro Pro Phe Glu Gln Leu Lys Thr
    215                 220                 225

act cgt cgc ggg tac acc gaa cct ggc gag att tat gga aac cag cgc   835
Thr Arg Arg Gly Tyr Thr Glu Pro Gly Glu Ile Tyr Gly Asn Gln Arg
230                 235                 240                 245

agc tat aaa ttt cac gct gat ggt tgg aac gct gtt att tcc gcc aaa   883
Ser Tyr Lys Phe His Ala Asp Gly Trp Asn Ala Val Ile Ser Ala Lys
                250                 255                 260

gtg cca ctg cgc acc gaa gaa aac ctc acc ggc tac ttc acc cac agc   931
Val Pro Leu Arg Thr Glu Glu Asn Leu Thr Gly Tyr Phe Thr His Ser
            265                 270                 275

tcc tac gcg gac acg agc cgc cgc acg tca gcg gtc atc acc gca gtc   979
Ser Tyr Ala Asp Thr Ser Arg Arg Thr Ser Ala Val Ile Thr Ala Val
        280                 285                 290

tac cgc cac ggt aag gac gca att atc gac gtg acc ctc gac ggt gcg   1027
Tyr Arg His Gly Lys Asp Ala Ile Ile Asp Val Thr Leu Asp Gly Ala
    295                 300                 305

aaa cct cct aga tat caa gaa tcc ttg gat tgg agc agc acc agt acc   1075
Lys Pro Pro Arg Tyr Gln Glu Ser Leu Asp Trp Ser Ser Thr Ser Thr
310                 315                 320                 325

tgt gac ggt gaa aca atc tgg ctg tcc gat aag agc ttg ccc ttc gtc   1123
Cys Asp Gly Glu Thr Ile Trp Leu Ser Asp Lys Ser Leu Pro Phe Val
                330                 335                 340

cgc ggt ttc aat gtc tcc aca ggc aag cta gta cac gag atc tcc ata   1171
Arg Gly Phe Asn Val Ser Thr Gly Lys Leu Val His Glu Ile Ser Ile
            345                 350                 355

ccc acc ttc aat gag atc gcc ctc gaa tcc ggc aat aga gcc cgc gca   1219
Pro Thr Phe Asn Glu Ile Ala Leu Glu Ser Gly Asn Arg Ala Arg Ala
        360                 365                 370

gcg aaa aaa ctt tgg gaa ctt cca gat ctt aaa gag gca acc gac cct   1267
Ala Lys Lys Leu Trp Glu Leu Pro Asp Leu Lys Glu Ala Thr Asp Pro
    375                 380                 385
```

```
gtc cca gcg atc ccc gcg ggc tgg aaa cta cac aaa aga ttc ggg aaa   1315
Val Pro Ala Ile Pro Ala Gly Trp Lys Leu His Lys Arg Phe Gly Lys
390                 395                 400                 405

aac ttc cat atc gta agc gct gac aac gga acc tgg aaa caa acc atc   1363
Asn Phe His Ile Val Ser Ala Asp Asn Gly Thr Trp Lys Gln Thr Ile
                410                 415                 420

ctt agg atc aaa ccc ttc aaa gca att gag ctt gat ctt gga tac gcc   1411
Leu Arg Ile Lys Pro Phe Lys Ala Ile Glu Leu Asp Leu Gly Tyr Ala
            425                 430                 435

aag att tcg acg att tac caa tac ggt gaa cga att tat ctg cgt tcc   1459
Lys Ile Ser Thr Ile Tyr Gln Tyr Gly Glu Arg Ile Tyr Leu Arg Ser
        440                 445                 450

gat ctt cac cag atc acg ttt aat cag gat ctt gaa atc ctc agt gta   1507
Asp Leu His Gln Ile Thr Phe Asn Gln Asp Leu Glu Ile Leu Ser Val
    455                 460                 465

gag gtc cac gga aat ccc gat gca ggt tat tgg cca ctt tcc gat ctt   1555
Glu Val His Gly Asn Pro Asp Ala Gly Tyr Trp Pro Leu Ser Asp Leu
470                 475                 480                 485

cca cca ggg gat tct cca acg ctg gga ttt cct atc gga tca ctc atg   1603
Pro Pro Gly Asp Ser Pro Thr Leu Gly Phe Pro Ile Gly Ser Leu Met
                490                 495                 500

atg ttc cac gaa caa caa gat atc tac gct ttc cac gat cct aaa aca   1651
Met Phe His Glu Gln Gln Asp Ile Tyr Ala Phe His Asp Pro Lys Thr
            505                 510                 515

aca aag caa cta aca act gtg aac ttg ccc aaa agg cag ttt gaa gtg   1699
Thr Lys Gln Leu Thr Thr Val Asn Leu Pro Lys Arg Gln Phe Glu Val
        520                 525                 530

gaa tat gct tct cag aac aga att gtt att tcg ctg aaa aat cca gaa   1747
Glu Tyr Ala Ser Gln Asn Arg Ile Val Ile Ser Leu Lys Asn Pro Glu
    535                 540                 545

agc cgc ctc att gac aaa ctg ttg gtg tgg gaa cca caa acc agg tgg   1795
Ser Arg Leu Ile Asp Lys Leu Leu Val Trp Glu Pro Gln Thr Arg Trp
550                 555                 560                 565

cgg gaa caa aac ctg gag agc tgagcacggt ttgattaacg tcg             1839
Arg Glu Gln Asn Leu Glu Ser
                570
```

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<210> 2210
<211> 572
<212> PRT
<213> Corynebacterium glutamicum

<400> 2210

```
Met Arg Ser Leu Gln Ser Val Leu Asp Leu Leu Thr Ser Lys Ser Lys
  1               5                  10                  15

Val Ala Thr Lys Ile Val Val Glu Arg Ile Glu Lys His Pro Val His
             20                  25                  30
```

```
Gly Leu Gly Trp Met Met Tyr Pro Pro Phe His Pro Trp Thr Asp Ala
          35                  40                  45

Ser Thr Leu Thr Ile Glu Arg Asn Gly Thr Ser Arg Arg Ala Ser Gln
      50                  55                  60

Asn Gly Val Ala Val Leu His Gln His Glu Gln Val Gln Thr Ile Gly
 65                  70                  75                  80

Leu Ala Ser Tyr Phe Ile Asp Ser Lys Ile Trp Val Asn Glu Leu Ala
                 85                  90                  95

Gly Leu Asp Arg Ile Asn Ile Ser Glu Ser Glu Val Ala Gly Arg Asp
            100                 105                 110

Val Leu Val Leu Pro Leu Ser Asp Leu Thr Leu Ser Ile Asp Ala Lys
        115                 120                 125

Tyr Gly Val Val Leu Ala Ala Glu Asp Ser Asp Glu Ser Val Arg Ala
    130                 135                 140

Val Ser Val Glu Phe Leu Asp Gln Trp Val Asp Glu Glu Glu Pro Pro
145                 150                 155                 160

Ala Glu Glu Val Pro Lys Tyr Thr Glu Thr Arg Glu Glu Leu Pro Pro
                165                 170                 175

Leu Glu Ile Pro Pro Ala Pro Ser Gly Asn Arg Asn Leu Arg Val Leu
            180                 185                 190

Cys Thr Trp Gly Ala Met Glu Gly Ile Ile Pro Glu Trp Lys Pro Gly
        195                 200                 205

Asp Gln Val Ser Leu Phe Leu Ser Phe Asp Leu Asp Asp Pro Pro Phe
    210                 215                 220

Glu Gln Leu Lys Thr Thr Arg Arg Gly Tyr Thr Glu Pro Gly Glu Ile
225                 230                 235                 240

Tyr Gly Asn Gln Arg Ser Tyr Lys Phe His Ala Asp Gly Trp Asn Ala
                245                 250                 255

Val Ile Ser Ala Lys Val Pro Leu Arg Thr Glu Glu Asn Leu Thr Gly
            260                 265                 270

Tyr Phe Thr His Ser Ser Tyr Ala Asp Thr Ser Arg Arg Thr Ser Ala
        275                 280                 285

Val Ile Thr Ala Val Tyr Arg His Gly Lys Asp Ala Ile Ile Asp Val
    290                 295                 300

Thr Leu Asp Gly Ala Lys Pro Pro Arg Tyr Gln Glu Ser Leu Asp Trp
305                 310                 315                 320

Ser Ser Thr Ser Thr Cys Asp Gly Glu Thr Ile Trp Leu Ser Asp Lys
                325                 330                 335

Ser Leu Pro Phe Val Arg Gly Phe Asn Val Ser Thr Gly Lys Leu Val
            340                 345                 350

His Glu Ile Ser Ile Pro Thr Phe Asn Glu Ile Ala Leu Glu Ser Gly
```

```
        355                 360                 365

Asn Arg Ala Arg Ala Ala Lys Lys Leu Trp Glu Leu Pro Asp Leu Lys
    370                 375                 380

Glu Ala Thr Asp Pro Val Pro Ala Ile Pro Ala Gly Trp Lys Leu His
385                 390                 395                 400

Lys Arg Phe Gly Lys Asn Phe His Ile Val Ser Ala Asp Asn Gly Thr
                405                 410                 415

Trp Lys Gln Thr Ile Leu Arg Ile Lys Pro Phe Lys Ala Ile Glu Leu
            420                 425                 430

Asp Leu Gly Tyr Ala Lys Ile Ser Thr Ile Tyr Gln Tyr Gly Glu Arg
        435                 440                 445

Ile Tyr Leu Arg Ser Asp Leu His Gln Ile Thr Phe Asn Gln Asp Leu
    450                 455                 460

Glu Ile Leu Ser Val Glu Val His Gly Asn Pro Asp Ala Gly Tyr Trp
465                 470                 475                 480

Pro Leu Ser Asp Leu Pro Pro Gly Asp Ser Pro Thr Leu Gly Phe Pro
                485                 490                 495

Ile Gly Ser Leu Met Met Phe His Glu Gln Gln Asp Ile Tyr Ala Phe
            500                 505                 510

His Asp Pro Lys Thr Thr Lys Gln Leu Thr Thr Val Asn Leu Pro Lys
        515                 520                 525

Arg Gln Phe Glu Val Glu Tyr Ala Ser Gln Asn Arg Ile Val Ile Ser
    530                 535                 540

Leu Lys Asn Pro Glu Ser Arg Leu Ile Asp Lys Leu Leu Val Trp Glu
545                 550                 555                 560

Pro Gln Thr Arg Trp Arg Glu Gln Asn Leu Glu Ser
                565                 570
```

<210> 2211
<211> 381
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(358)
<223> RXA01396

<400> 2211
tcaccaaccc acttaacttc gagaccttcg attccctcgt cgttccagtt ggttcttctg 60

caaccgctga gatccaggct cagcttcaac ctcccgcgtt ttg aag gct ttc aac 115
                                              Leu Lys Ala Phe Asn
                                                1   5

acc aac ttc gca gcc act ttg gct acc gga aag gtt ggc gat atc acc 163
Thr Asn Phe Ala Ala Thr Leu Ala Thr Gly Lys Val Gly Asp Ile Thr

```
                10                  15                  20

acc acc gtt tta gtt gca ggc gat gat gaa gac gca aag aac gct ctt   211
Thr Thr Val Leu Val Ala Gly Asp Asp Glu Asp Ala Lys Asn Ala Leu
            25                  30                  35

atc acc gac gtc aac gct ggc ggc ctc gac gcc ctt gac gct ggt tcc   259
Ile Thr Asp Val Asn Ala Gly Gly Leu Asp Ala Leu Asp Ala Gly Ser
        40                  45                  50

ctc aag cgt gca cac gag ctt gaa gca gtt ggt ttc ctg cag ctc acc   307
Leu Lys Arg Ala His Glu Leu Glu Ala Val Gly Phe Leu Gln Leu Thr
    55                  60                  65

ctt gca ggt tcc gag aag att gga tgg acc ggc gga ttc ggc ctg gtc   355
Leu Ala Gly Ser Glu Lys Ile Gly Trp Thr Gly Gly Phe Gly Leu Val
70                  75                  80                  85

aag taacacccag cctcaaaagc act                                     381
Lys
```

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<210> 2212
<211> 86
<212> PRT
<213> Corynebacterium glutamicum

<400> 2212
Leu Lys Ala Phe Asn Thr Asn Phe Ala Ala Thr Leu Ala Thr Gly Lys
  1   5   10   15

Val Gly Asp Ile Thr Thr Thr Val Leu Val Ala Gly Asp Asp Glu Asp
            20   25   30

Ala Lys Asn Ala Leu Ile Thr Asp Val Asn Ala Gly Gly Leu Asp Ala
        35   40   45

Leu Asp Ala Gly Ser Leu Lys Arg Ala His Glu Leu Glu Ala Val Gly
    50   55   60

Phe Leu Gln Leu Thr Leu Ala Gly Ser Glu Lys Ile Gly Trp Thr Gly
65   70   75   80

Gly Phe Gly Leu Val Lys
                85

<210> 2213
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> RXA01397

<400> 2213
tgagctgcta aaagtctcgc attaaaggac tgcttccctt cgggggagca tttcttttta 60

```
actaattact tgacacgtca agtaattagg gtctagtgtt gtg ttc atg atc aaa   115
                                           Val Phe Met Ile Lys
                                             1               5

gaa ctg ctc aac aag ctc ttc gga aac aag aag gct tcc ccg gca atg   163
Glu Leu Leu Asn Lys Leu Phe Gly Asn Lys Lys Ala Ser Pro Ala Met
                 10                  15                  20

aca caa tct gaa acc att tca cac aag gag aac aac aca atg acc act   211
Thr Gln Ser Glu Thr Ile Ser His Lys Glu Asn Asn Thr Met Thr Thr
             25                  30                  35

tac acc atc ttc ggc cgc ggc aac atg ggc acc gca atc gca ggc gtc   259
Tyr Thr Ile Phe Gly Arg Gly Asn Met Gly Thr Ala Ile Ala Gly Val
         40                  45                  50

ctc acc aag ggt ggt gca act gta gaa cac atc ggt tct gca gat tct   307
Leu Thr Lys Gly Gly Ala Thr Val Glu His Ile Gly Ser Ala Asp Ser
     55                  60                  65

gac atc gca acc atc aac ggt gac gtt gtt atc ctt gct gtt cct tac   355
Asp Ile Ala Thr Ile Asn Gly Asp Val Val Ile Leu Ala Val Pro Tyr
 70                  75                  80                  85

cca gca gta gag tcc atc att gca agc cac aag gat gct ctc gca ggc   403
Pro Ala Val Glu Ser Ile Ile Ala Ser His Lys Asp Ala Leu Ala Gly
                 90                  95                 100

aag acc gtt atc gat atc acc aac cca ctt aac ttc gag acc ttc gat   451
Lys Thr Val Ile Asp Ile Thr Asn Pro Leu Asn Phe Glu Thr Phe Asp
             105                 110                 115

tcc ctc gtc gtt cca gtt ggt tct tct gca acc gct gag atc cag gct   499
Ser Leu Val Val Pro Val Gly Ser Ser Ala Thr Ala Glu Ile Gln Ala
         120                 125                 130

cag ctt caa cct ccc gcg ttt tgaaggcttt caacaccaac ttc            543
Gln Leu Gln Pro Pro Ala Phe
    135                 140
```

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<210> 2214
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 2214

```
Val Phe Met Ile Lys Glu Leu Leu Asn Lys Leu Phe Gly Asn Lys Lys
  1               5                  10                  15

Ala Ser Pro Ala Met Thr Gln Ser Glu Thr Ile Ser His Lys Glu Asn
             20                  25                  30

Asn Thr Met Thr Thr Tyr Thr Ile Phe Gly Arg Gly Asn Met Gly Thr
         35                  40                  45

Ala Ile Ala Gly Val Leu Thr Lys Gly Gly Ala Thr Val Glu His Ile
     50                  55                  60

Gly Ser Ala Asp Ser Asp Ile Ala Thr Ile Asn Gly Asp Val Val Ile
 65                  70                  75                  80
```

```
Leu Ala Val Pro Tyr Pro Ala Val Glu Ser Ile Ile Ala Ser His Lys
                 85                  90                  95

Asp Ala Leu Ala Gly Lys Thr Val Ile Asp Ile Thr Asn Pro Leu Asn
            100                 105                 110

Phe Glu Thr Phe Asp Ser Leu Val Val Pro Val Gly Ser Ser Ala Thr
        115                 120                 125

Ala Glu Ile Gln Ala Gln Leu Gln Pro Pro Ala Phe
    130                 135                 140


<210> 2215
<211> 384
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(361)
<223> RXA01401

<400> 2215
tgccaaacgg aaggtttaat tggtctacat gtgtcagtct catggcacta taatagacct 60

agtatctata gattgataga aaataattta ggaagtttcc atg aac tct ccc cta   115
                                            Met Asn Ser Pro Leu
                                              1               5

caa cac agc gcc ttc ccc gtc ccc ggc gcg caa ctc tcc acc tca tac   163
Gln His Ser Ala Phe Pro Val Pro Gly Ala Gln Leu Ser Thr Ser Tyr
                 10                  15                  20

agc gac gaa cac ggc caa gcc gtc atc caa ctt cac ggc ctc acc tcc   211
Ser Asp Glu His Gly Gln Ala Val Ile Gln Leu His Gly Leu Thr Ser
             25                  30                  35

tcc cgc caa cgc gac cgc ctc ctc gac ctc gac ctc ggc cgt ggc ctt   259
Ser Arg Gln Arg Asp Arg Leu Leu Asp Leu Asp Leu Gly Arg Gly Leu
         40                  45                  50

tcc ggc acg cgc ctt ttg cgt tac gac gcc cgc ggc cac ggc acc tcc   307
Ser Gly Thr Arg Leu Leu Arg Tyr Asp Ala Arg Gly His Gly Thr Ser
     55                  60                  65

acc ggc cgc gct gcc tcc acc gat tat cag tgg gac acc cta gcg ggt   355
Thr Gly Arg Ala Ala Ser Thr Asp Tyr Gln Trp Asp Thr Leu Ala Gly
 70                  75                  80                  85

gac ctt taatgcttct cgacgcccac ttc                                384
Asp Leu


<210> 2216
<211> 87
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 2216
Met Asn Ser Pro Leu Gln His Ser Ala Phe Pro Val Pro Gly Ala Gln
1 5 10 15

Leu Ser Thr Ser Tyr Ser Asp Glu His Gly Gln Ala Val Ile Gln Leu
20 25 30

His Gly Leu Thr Ser Ser Arg Gln Arg Asp Arg Leu Leu Asp Leu Asp
35 40 45

Leu Gly Arg Gly Leu Ser Gly Thr Arg Leu Leu Arg Tyr Asp Ala Arg
50 55 60

Gly His Gly Thr Ser Thr Gly Arg Ala Ala Ser Thr Asp Tyr Gln Trp
65 70 75 80

Asp Thr Leu Ala Gly Asp Leu
85

<210> 2217
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> RXA01402

<400> 2217
cgctgcctcc accgattatc agtgggacac cctagcgggt gacctttaat gcttctcgac 60

gcccacttcc ccacgaacaa gtccacggcg tcggcccctc atg ggt tgc gcc acc 115
Met Gly Cys Ala Thr
1 5

ctc ctc aaa gcc gcg gtg tta aac ccc gac cgc ttc agt gga ttc aca 163
Leu Leu Lys Ala Ala Val Leu Asn Pro Asp Arg Phe Ser Gly Phe Thr
10 15 20

ctc atg ctc cca ccc acc gcc tgg gaa tcc cga aaa gcc caa gcc tcc 211
Leu Met Leu Pro Pro Thr Ala Trp Glu Ser Arg Lys Ala Gln Ala Ser
25 30 35

gaa tac cta tcc cga gca gaa ttc cta gaa acc cac ggc atg gac gcc 259
Glu Tyr Leu Ser Arg Ala Glu Phe Leu Glu Thr His Gly Met Asp Ala
40 45 50

ttc ctc aac gcc gaa aaa ctc cac gcc caa cca cca gca acc gta gga 307
Phe Leu Asn Ala Glu Lys Leu His Ala Gln Pro Pro Ala Thr Val Gly
55 60 65

acc ccc gac aca gtc ccc gac att tcc gcc gaa ctc ctc ccc tgg gct 355
Thr Pro Asp Thr Val Pro Asp Ile Ser Ala Glu Leu Leu Pro Trp Ala
70 75 80 85

tac cga ggc gcc gcc caa agc gac ctc ccc tca aag aaa gaa atc gcc 403
Tyr Arg Gly Ala Ala Gln Ser Asp Leu Pro Ser Lys Lys Glu Ile Ala
90 95 100

```
aaa ata aca gcc ccc acc act att ctg agc tgg acc gac gat ccc gga   451
Lys Ile Thr Ala Pro Thr Thr Ile Leu Ser Trp Thr Asp Asp Pro Gly
            105                 110                 115

cac ccc gta tcc acg gca atc gag cta acc cgc ctc atg cca aac gcc   499
His Pro Val Ser Thr Ala Ile Glu Leu Thr Arg Leu Met Pro Asn Ala
        120                 125                 130

caa ctg cgc att gcc act acc cca gcg gaa gtc gcg cgg tgg cca caa   547
Gln Leu Arg Ile Ala Thr Thr Pro Ala Glu Val Ala Arg Trp Pro Gln
    135                 140                 145

cac ctt cgc gat gac ctg cag ttg gac taaaaacctt cattatctgg         594
His Leu Arg Asp Asp Leu Gln Leu Asp
150                 155

ttt                                                               597
```

<210> 2218
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 2218

```
Met Gly Cys Ala Thr Leu Leu Lys Ala Ala Val Leu Asn Pro Asp Arg
  1               5                  10                  15

Phe Ser Gly Phe Thr Leu Met Leu Pro Pro Thr Ala Trp Glu Ser Arg
             20                  25                  30

Lys Ala Gln Ala Ser Glu Tyr Leu Ser Arg Ala Glu Phe Leu Glu Thr
         35                  40                  45

His Gly Met Asp Ala Phe Leu Asn Ala Glu Lys Leu His Ala Gln Pro
     50                  55                  60

Pro Ala Thr Val Gly Thr Pro Asp Thr Val Pro Asp Ile Ser Ala Glu
 65                  70                  75                  80

Leu Leu Pro Trp Ala Tyr Arg Gly Ala Ala Gln Ser Asp Leu Pro Ser
                 85                  90                  95

Lys Lys Glu Ile Ala Lys Ile Thr Ala Pro Thr Thr Ile Leu Ser Trp
            100                 105                 110

Thr Asp Asp Pro Gly His Pro Val Ser Thr Ala Ile Glu Leu Thr Arg
        115                 120                 125

Leu Met Pro Asn Ala Gln Leu Arg Ile Ala Thr Thr Pro Ala Glu Val
    130                 135                 140

Ala Arg Trp Pro Gln His Leu Arg Asp Asp Leu Gln Leu Asp
145                 150                 155
```

<210> 2219
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXA01405

<400> 2219
aattagacgt ctgtctctag ggatgccgca tcccgccggc gctcctagag tccgtttgta 60

aaacctagaa ttccgaatac gttccgaata gggtgggggt atg agt aag ata gtt 115
Met Ser Lys Ile Val
1 5

gat ctg cgc tat ggg acc cgg cgt tcc tcg gag ttg agc aaa cgc tct 163
Asp Leu Arg Tyr Gly Thr Arg Arg Ser Ser Glu Leu Ser Lys Arg Ser
10 15 20

gct gaa gtc ttt gcc gaa gct gaa gaa cat ccc att act gtg aca cgt 211
Ala Glu Val Phe Ala Glu Ala Glu Glu His Pro Ile Thr Val Thr Arg
25 30 35

cgt gat ggt gaa gcg ttg gta ttg atg tcg cag cgc gaa gct gac ggg 259
Arg Asp Gly Glu Ala Leu Val Leu Met Ser Gln Arg Glu Ala Asp Gly
40 45 50

cga gcc cgc ctg ctg gag ttg gct gca cag tta att act gtg gcc act 307
Arg Ala Arg Leu Leu Glu Leu Ala Ala Gln Leu Ile Thr Val Ala Thr
55 60 65

gat cat cag ggc acg tta gcc gaa cgt atg gcg aaa gta ttc ccg tgg 355
Asp His Gln Gly Thr Leu Ala Glu Arg Met Ala Lys Val Phe Pro Trp
70 75 80 85

atg ctg gcc ctg tca gtg gcg gat cgt gag gcg tgt gcc cgt gag att 403
Met Leu Ala Leu Ser Val Ala Asp Arg Glu Ala Cys Ala Arg Glu Ile
90 95 100

ctt gac gct gca cga gca tcg ttt gca acc gaa caa cct cac ctc gct 451
Leu Asp Ala Ala Arg Ala Ser Phe Ala Thr Glu Gln Pro His Leu Ala
105 110 115

ctt act gaa ctg acc tca tgg aaa gaa aca gca gca gct gtt gct gct 499
Leu Thr Glu Leu Thr Ser Trp Lys Glu Thr Ala Ala Ala Val Ala Ala
120 125 130

gga ttg agt aac act gat ctg cag tgg tac gac gat ccg cat ctg gtg 547
Gly Leu Ser Asn Thr Asp Leu Gln Trp Tyr Asp Asp Pro His Leu Val
135 140 145

gag cgt ccc taagcgtggc tggaaagaaa agc 579
Glu Arg Pro
150

<210> 2220
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 2220
Met Ser Lys Ile Val Asp Leu Arg Tyr Gly Thr Arg Arg Ser Ser Glu
1 5 10 15

```
Leu Ser Lys Arg Ser Ala Glu Val Phe Ala Glu Ala Glu Glu His Pro
            20                  25                  30

Ile Thr Val Thr Arg Arg Asp Gly Glu Ala Leu Val Leu Met Ser Gln
        35                  40                  45

Arg Glu Ala Asp Gly Arg Ala Arg Leu Leu Glu Leu Ala Ala Gln Leu
    50                  55                  60

Ile Thr Val Ala Thr Asp His Gln Gly Thr Leu Ala Glu Arg Met Ala
65                  70                  75                  80

Lys Val Phe Pro Trp Met Leu Ala Leu Ser Val Ala Asp Arg Glu Ala
                85                  90                  95

Cys Ala Arg Glu Ile Leu Asp Ala Ala Arg Ala Ser Phe Ala Thr Glu
            100                 105                 110

Gln Pro His Leu Ala Leu Thr Glu Leu Thr Ser Trp Lys Glu Thr Ala
        115                 120                 125

Ala Ala Val Ala Ala Gly Leu Ser Asn Thr Asp Leu Gln Trp Tyr Asp
    130                 135                 140

Asp Pro His Leu Val Glu Arg Pro
145                 150


<210> 2221
<211> 723
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(700)
<223> RXA01413

<400> 2221
tttgccctat tggaagaagt aaattccaca ccttcacttt ccaatacttc ttttggtgag 60

cgggtttcct cagcgtttaa ccatctgaaa ccatctgaga ttg acc cat ctg ttc   115
                                              Leu Thr His Leu Phe
                                                1               5

tta gaa ctc gat gag cgt tta gta ctg ggt gtt cag caa gat ggt tac   163
Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val Gln Gln Asp Gly Tyr
                10                  15                  20

caa tgg act gag cat ttg ttc cgg ctg cca ctg caa cat ctc cgt aac   211
Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu Gln His Leu Arg Asn
            25                  30                  35

tcg ccc aat gac ctg cag gga ttg aag ata cga tgg tgt gaa ctt tat   259
Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg Trp Cys Glu Leu Tyr
        40                  45                  50

tcc aca acg ggg aaa gat caa ggg gta gaa ctt ctg cct caa gca acc   307
Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu Leu Pro Gln Ala Thr
    55                  60                  65
```

```
gtc gtt acc cca aat aac ttc gag gct tcc acc ctc tcc ggc ctt gag   355
Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr Leu Ser Gly Leu Glu
 70                  75                  80                  85

aag ctt gag acc gtc gag gac ctc aag gag gct gcc cgc ctc att tat   403
Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala Ala Arg Leu Ile Tyr
                 90                  95                 100

gag caa ggc ccc cag tac gta gtc gtc aag ggt ggc atg gac ttc ccc   451
Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly Gly Met Asp Phe Pro
            105                 110                 115

ggc gag aac gcc gtg gat gtg ctt ttc gac gga tcc tcc tac cac gtc   499
Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly Ser Ser Tyr His Val
        120                 125                 130

ttc tct gag cca aag att ggt gaa gag cgc gtt tcc ggc gca gtc tgc   547
Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val Ser Gly Ala Val Cys
    135                 140                 145

acc ttc gca gct gtt atc acc gca gag cta gca aag ggt gct gag gtt   595
Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Ala Glu Val
150                 155                 160                 165

gta gac cca gtg gca acc gca aag cgt gtg gtc acc cgt gcg gtt caa   643
Val Asp Pro Val Ala Thr Ala Lys Arg Val Val Thr Arg Ala Val Gln
                170                 175                 180

gat gct gtt gca tcc aac gca cct ttt acc tcc gta tgg ctt gct gag   691
Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu
            185                 190                 195

gac aac aag tagagtttta aaataccgat caa                            723
Asp Asn Lys
        200
```

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<210> 2222
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 2222

```
Leu Thr His Leu Phe Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val
  1               5                  10                  15

Gln Gln Asp Gly Tyr Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu
             20                  25                  30

Gln His Leu Arg Asn Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg
         35                  40                  45

Trp Cys Glu Leu Tyr Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu
     50                  55                  60

Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr
 65                  70                  75                  80

Leu Ser Gly Leu Glu Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala
                 85                  90                  95
```

```
Ala Arg Leu Ile Tyr Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly
            100                 105                 110

Gly Met Asp Phe Pro Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly
        115                 120                 125

Ser Ser Tyr His Val Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val
    130                 135                 140

Ser Gly Ala Val Cys Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala
145                 150                 155                 160

Lys Gly Ala Glu Val Val Asp Pro Val Ala Thr Ala Lys Arg Val Val
                165                 170                 175

Thr Arg Ala Val Gln Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser
            180                 185                 190

Val Trp Leu Ala Glu Asp Asn Lys
        195                 200
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US20070269862A1

<210> 2223
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(607)
<223> RXA01414

<400> 2223

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tattgcctaa gtagaccaat aggtctatgc ttcatagaac aactagttca taagtgatta 60

gttttaagaa tttattacct ctctacagga gaacccagcg atg gcc gtt ttt gat   115
                                              Met Ala Val Phe Asp
                                                1               5

ttc cct aac ccc gtt aac gaa tat gca gct cgc tgc act gcg ggt ttg   163
Phe Pro Asn Pro Val Asn Glu Tyr Ala Ala Arg Cys Thr Ala Gly Leu
                10                  15                  20

gtt gtt ttg ctg agc gcc gcc acg ctt ttt gcc tct ggt gac ctt cgt   211
Val Val Leu Leu Ser Ala Ala Thr Leu Phe Ala Ser Gly Asp Leu Arg
            25                  30                  35

att att ttg gca agc atc ttg acc ttc ggc ttc gca ttg cgc gtg gcc   259
Ile Ile Leu Ala Ser Ile Leu Thr Phe Gly Phe Ala Leu Arg Val Ala
        40                  45                  50

ggc gga ccc cgt tac tcc ccc ttt gga cgt ctt tca gta cac gta ctt   307
Gly Gly Pro Arg Tyr Ser Pro Phe Gly Arg Leu Ser Val His Val Leu
    55                  60                  65

gta cca ctg ctg aag aaa gca ccg atc ctg acc cct ggc cca cca aag   355
Val Pro Leu Leu Lys Lys Ala Pro Ile Leu Thr Pro Gly Pro Pro Lys
70                  75                  80                  85

cgc ttc gcg cag acc atc ggc ctg ggc ttt agc ggt act tcc ctt atc   403
```

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Arg Phe Ala Gln Thr Ile Gly Leu Gly Phe Ser Gly Thr Ser Leu Ile
                 90                  95                 100

ctt atg gcc ttt gga ttt aac gtt gca gct tcc gta gtc cta gtc atg   451
Leu Met Ala Phe Gly Phe Asn Val Ala Ala Ser Val Val Leu Val Met
            105                 110                 115

ctc atc gca gca gcc acc tta gaa tcc gtc ttt ggt atc tgc ctc ggt   499
Leu Ile Ala Ala Ala Thr Leu Glu Ser Val Phe Gly Ile Cys Leu Gly
        120                 125                 130

tgc tgg gga ttc ggc aag ctc atg cgc tac ggc gtc atc cca gaa gac   547
Cys Trp Gly Phe Gly Lys Leu Met Arg Tyr Gly Val Ile Pro Glu Asp
    135                 140                 145

gtt tgc gag cag tgc ttc cag aag gaa tcc tcc cgc acc ggc tgg ctc   595
Val Cys Glu Gln Cys Phe Gln Lys Glu Ser Ser Arg Thr Gly Trp Leu
150                 155                 160                 165

gtt agc ctg aag tagcacttcg aatctaagac cac                        630
Val Ser Leu Lys
```

<210> 2224
<211> 169
<212> PRT
<213> Corynebacterium glutamicum

<400> 2224

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Met Ala Val Phe Asp Phe Pro Asn Pro Val Asn Glu Tyr Ala Ala Arg
  1               5                  10                  15

Cys Thr Ala Gly Leu Val Val Leu Leu Ser Ala Ala Thr Leu Phe Ala
             20                  25                  30

Ser Gly Asp Leu Arg Ile Ile Leu Ala Ser Ile Leu Thr Phe Gly Phe
         35                  40                  45

Ala Leu Arg Val Ala Gly Gly Pro Arg Tyr Ser Pro Phe Gly Arg Leu
     50                  55                  60

Ser Val His Val Leu Val Pro Leu Leu Lys Lys Ala Pro Ile Leu Thr
 65                  70                  75                  80

Pro Gly Pro Pro Lys Arg Phe Ala Gln Thr Ile Gly Leu Gly Phe Ser
                 85                  90                  95

Gly Thr Ser Leu Ile Leu Met Ala Phe Gly Phe Asn Val Ala Ala Ser
            100                 105                 110

Val Val Leu Val Met Leu Ile Ala Ala Ala Thr Leu Glu Ser Val Phe
        115                 120                 125

Gly Ile Cys Leu Gly Cys Trp Gly Phe Gly Lys Leu Met Arg Tyr Gly
    130                 135                 140

Val Ile Pro Glu Asp Val Cys Glu Gln Cys Phe Gln Lys Glu Ser Ser
145                 150                 155                 160

Arg Thr Gly Trp Leu Val Ser Leu Lys
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165

<210> 2225
<211> 720
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(697)
<223> RXA01417

<400> 2225
agcctcccca aggctggtta gtcccactat cctctcagag agaagcaaaa ctgaaataac 60

ttcagcctca gctatccccg caatttaagg aaaataggat atg act gac aag ttt 115
Met Thr Asp Lys Phe
1 5

gac aga gtc ctt gct gta gag gtg tgc att cag gag tgg atc gac gag 163
Asp Arg Val Leu Ala Val Glu Val Cys Ile Gln Glu Trp Ile Asp Glu
10 15 20

caa aac ctc acg cta gag gtg cca tta atg att gca cgt ttg cag ctt 211
Gln Asn Leu Thr Leu Glu Val Pro Leu Met Ile Ala Arg Leu Gln Leu
25 30 35

aga gac gtc gcg aag gat atc act gct gtt cac gaa gaa aaa ttc tac 259
Arg Asp Val Ala Lys Asp Ile Thr Ala Val His Glu Glu Lys Phe Tyr
40 45 50

gac ctc act gat atc gat act gat gcc ttt gtg aaa aac atc aaa ctg 307
Asp Leu Thr Asp Ile Asp Thr Asp Ala Phe Val Lys Asn Ile Lys Leu
55 60 65

gga tgg aat gaa cgc ttg atc aag aaa agc ctc ttt cca caa ccg gac 355
Gly Trp Asn Glu Arg Leu Ile Lys Lys Ser Leu Phe Pro Gln Pro Asp
70 75 80 85

gtg cat aaa caa cat ttc aca gaa act gaa cat ggc att gac gcg act 403
Val His Lys Gln His Phe Thr Glu Thr Glu His Gly Ile Asp Ala Thr
90 95 100

gtg acg gtc tgg tcg aag ggc ttc gat ccg gaa agt ggc ccc gac ttc 451
Val Thr Val Trp Ser Lys Gly Phe Asp Pro Glu Ser Gly Pro Asp Phe
105 110 115

ttg gtt tcc tat gtg gat ggt ctt tgg tca gcc gat att aga aac cgc 499
Leu Val Ser Tyr Val Asp Gly Leu Trp Ser Ala Asp Ile Arg Asn Arg
120 125 130

atc acg aaa ttt cag aat aga gaa atc gtt agc aaa ttc tat ttt act 547
Ile Thr Lys Phe Gln Asn Arg Glu Ile Val Ser Lys Phe Tyr Phe Thr
135 140 145

cca gaa cat att aag gag gat gga gat ttc tcc gca gag att ttt att 595
Pro Glu His Ile Lys Glu Asp Gly Asp Phe Ser Ala Glu Ile Phe Ile
150 155 160 165

aac cga cca gaa aat gac gac gac tca caa gat ttg gtc gag gtg tgg 643

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Asn Arg Pro Glu Asn Asp Asp Asp Ser Gln Asp Leu Val Glu Val Trp
                170                 175                 180

act gat caa gac acc aga tac tgc ggt gaa atg atc atc tat ttc aaa   691
Thr Asp Gln Asp Thr Arg Tyr Cys Gly Glu Met Ile Ile Tyr Phe Lys
            185                 190                 195

tgg ctc taaattccac ttttctgcat cag                                 720
Trp Leu
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<210> 2226
<211> 199
<212> PRT
<213> Corynebacterium glutamicum

<400> 2226

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Met Thr Asp Lys Phe Asp Arg Val Leu Ala Val Glu Val Cys Ile Gln
  1               5                  10                  15

Glu Trp Ile Asp Glu Gln Asn Leu Thr Leu Glu Val Pro Leu Met Ile
             20                  25                  30

Ala Arg Leu Gln Leu Arg Asp Val Ala Lys Asp Ile Thr Ala Val His
         35                  40                  45

Glu Glu Lys Phe Tyr Asp Leu Thr Asp Ile Asp Thr Asp Ala Phe Val
     50                  55                  60

Lys Asn Ile Lys Leu Gly Trp Asn Glu Arg Leu Ile Lys Lys Ser Leu
 65                  70                  75                  80

Phe Pro Gln Pro Asp Val His Lys Gln His Phe Thr Glu Thr Glu His
                 85                  90                  95

Gly Ile Asp Ala Thr Val Thr Val Trp Ser Lys Gly Phe Asp Pro Glu
            100                 105                 110

Ser Gly Pro Asp Phe Leu Val Ser Tyr Val Asp Gly Leu Trp Ser Ala
        115                 120                 125

Asp Ile Arg Asn Arg Ile Thr Lys Phe Gln Asn Arg Glu Ile Val Ser
    130                 135                 140

Lys Phe Tyr Phe Thr Pro Glu His Ile Lys Glu Asp Gly Asp Phe Ser
145                 150                 155                 160

Ala Glu Ile Phe Ile Asn Arg Pro Glu Asn Asp Asp Asp Ser Gln Asp
                165                 170                 175

Leu Val Glu Val Trp Thr Asp Gln Asp Thr Arg Tyr Cys Gly Glu Met
            180                 185                 190

Ile Ile Tyr Phe Lys Trp Leu
        195
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<210> 2227
<211> 510
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(487)
<223> RXA01421

<400> 2227
ttgatgcacg tgcagaaatc gtcggcggtc cgtggcaccc atctgttaag ggagactcgg 60

ttactgcagg gatcctgcga gatcgagtaa acgcctaaag atg acg tcg aaa agc 115
Met Thr Ser Lys Ser
1 5

att agc ggc aag cgc ccg aat ctg ccg tcg ctc act gga gcg cgg tgg 163
Ile Ser Gly Lys Arg Pro Asn Leu Pro Ser Leu Thr Gly Ala Arg Trp
10 15 20

ctc gcg gcg ctc gct gtt tat ttt ttg cat gcg ttg gtg ttt ttg tcg 211
Leu Ala Ala Leu Ala Val Tyr Phe Leu His Ala Leu Val Phe Leu Ser
25 30 35

gtg tat ccg ttc cag cag tcg gaa ctg ttt gcc aca atc cat aaa ttt 259
Val Tyr Pro Phe Gln Gln Ser Glu Leu Phe Ala Thr Ile His Lys Phe
40 45 50

gtc ccc atg cag ctg ggt tca gct ggt gta acc ttc ttc ttt atc ttg 307
Val Pro Met Gln Leu Gly Ser Ala Gly Val Thr Phe Phe Phe Ile Leu
55 60 65

tcc gga ttt ttg atc tat tgg tca aat agc cag ctc aag ggc atg aag 355
Ser Gly Phe Leu Ile Tyr Trp Ser Asn Ser Gln Leu Lys Gly Met Lys
70 75 80 85

aat gtg ctg tat tac tgc aag cgc cgc atc acc aag att tat ccc atg 403
Asn Val Leu Tyr Tyr Cys Lys Arg Arg Ile Thr Lys Ile Tyr Pro Met
90 95 100

cac ttg att gcg ttg ccg atg ttt att gag gcg tcg gcg aag ttc acg 451
His Leu Ile Ala Leu Pro Met Phe Ile Glu Ala Ser Ala Lys Phe Thr
105 110 115

act aca ggc att acc tgg gtg ctg att ttg cgc gag taaagctgtg 497
Thr Thr Gly Ile Thr Trp Val Leu Ile Leu Arg Glu
120 125

gctgcggaat gcg 510

<210> 2228
<211> 129
<212> PRT
<213> Corynebacterium glutamicum

<400> 2228
Met Thr Ser Lys Ser Ile Ser Gly Lys Arg Pro Asn Leu Pro Ser Leu
1 5 10 15

Thr Gly Ala Arg Trp Leu Ala Ala Leu Ala Val Tyr Phe Leu His Ala
20 25 30

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Leu Val Phe Leu Ser Val Tyr Pro Phe Gln Gln Ser Glu Leu Phe Ala
          35                  40                  45

Thr Ile His Lys Phe Val Pro Met Gln Leu Gly Ser Ala Gly Val Thr
     50                  55                  60

Phe Phe Phe Ile Leu Ser Gly Phe Leu Ile Tyr Trp Ser Asn Ser Gln
 65                  70                  75                  80

Leu Lys Gly Met Lys Asn Val Leu Tyr Tyr Cys Lys Arg Arg Ile Thr
                 85                  90                  95

Lys Ile Tyr Pro Met His Leu Ile Ala Leu Pro Met Phe Ile Glu Ala
            100                 105                 110

Ser Ala Lys Phe Thr Thr Thr Gly Ile Thr Trp Val Leu Ile Leu Arg
        115                 120                 125

Glu
```

<210> 2229
<211> 1008
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(985)
<223> RXA01425

<400> 2229

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agtccctatt aatcccaagg agtttcgact cacagtgctc aatttcattt attggccaat 60

ttcggccatt ctgtggttct ggcataaagc gttcagcttt gtg ctg agc cca gat   115
                                              Val Leu Ser Pro Asp
                                                1               5

tcc gga att acc tgg gcc ttg tcg atc atg ttc ttg acc ttc acc gtg   163
Ser Gly Ile Thr Trp Ala Leu Ser Ile Met Phe Leu Thr Phe Thr Val
                10                  15                  20

cgt atg gtt ctg gtc aag ccg atg gtc aac acc atg cgt tca cag cgc   211
Arg Met Val Leu Val Lys Pro Met Val Asn Thr Met Arg Ser Gln Arg
            25                  30                  35

aag atg caa gac atg gct cca aag atg cag gcc atc cgc gag aag tac   259
Lys Met Gln Asp Met Ala Pro Lys Met Gln Ala Ile Arg Glu Lys Tyr
        40                  45                  50

aaa aat gac cag cag aag atg atg gag gag acc cgc aaa ctt caa aaa   307
Lys Asn Asp Gln Gln Lys Met Met Glu Glu Thr Arg Lys Leu Gln Lys
    55                  60                  65

gaa gtg ggc gtt aac ccc atc gca ggc tgt ttg cca atg ttg gtg cag   355
Glu Val Gly Val Asn Pro Ile Ala Gly Cys Leu Pro Met Leu Val Gln
70                  75                  80                  85

atc cca gtg ttc ctg ggt ctg ttc cac gtg ctg cgc tcc ttc aac cgc   403
Ile Pro Val Phe Leu Gly Leu Phe His Val Leu Arg Ser Phe Asn Arg
```

```
                    90                  95                  100

acc ggt tct ggc gtt ggc cag ctg gaa atg acc gtt gag caa aac gcg   451
Thr Gly Ser Gly Val Gly Gln Leu Glu Met Thr Val Glu Gln Asn Ala
            105                 110                 115

aac acc ccg aac tac atc ttc ggt gtc gac gag gtt cag tcc ttc ctg   499
Asn Thr Pro Asn Tyr Ile Phe Gly Val Asp Glu Val Gln Ser Phe Leu
        120                 125                 130

cgt gca gac ctg ttc ggt gcg cca ctg tcg tcc tac atc acc atg cct   547
Arg Ala Asp Leu Phe Gly Ala Pro Leu Ser Ser Tyr Ile Thr Met Pro
    135                 140                 145

gct gac gcg ttc gac gcg ttc ctt ggc ctg gat gtc tcc cgc ctc aac   595
Ala Asp Ala Phe Asp Ala Phe Leu Gly Leu Asp Val Ser Arg Leu Asn
150                 155                 160                 165

atc gcg ctg gtt gca gct cca atg att ttg atc att gtc gtg gca act   643
Ile Ala Leu Val Ala Ala Pro Met Ile Leu Ile Ile Val Val Ala Thr
                170                 175                 180

cac atg aac gcg cgt ctg tcc gtc aac cgc cag gaa gct cgc aag gca   691
His Met Asn Ala Arg Leu Ser Val Asn Arg Gln Glu Ala Arg Lys Ala
            185                 190                 195

gcc ggc aag cag cag gcc gct tcc agc gat cag atg gcc atg cag atg   739
Ala Gly Lys Gln Gln Ala Ala Ser Ser Asp Gln Met Ala Met Gln Met
        200                 205                 210

caa atg atg aac aag atg atg ctc tgg ttc atg cca gcc acc att ttg   787
Gln Met Met Asn Lys Met Met Leu Trp Phe Met Pro Ala Thr Ile Leu
    215                 220                 225

ttc acc ggc ttc atc tgg acc atc ggt ctt ctt gtc tac atg atg tcc   835
Phe Thr Gly Phe Ile Trp Thr Ile Gly Leu Leu Val Tyr Met Met Ser
230                 235                 240                 245

aac aac gtg tgg acc ttc ttc cag cag cgc tac atc ttc gcc aag atg   883
Asn Asn Val Trp Thr Phe Phe Gln Gln Arg Tyr Ile Phe Ala Lys Met
                250                 255                 260

gac gct gag gaa gca gct gag gag gag gaa aag cgc gca gca aag cgc   931
Asp Ala Glu Glu Ala Ala Glu Glu Glu Glu Lys Arg Ala Ala Lys Arg
            265                 270                 275

act acc gct cca aag cct ggc gtg aag cca gaa aac ccc aag aag cgt   979
Thr Thr Ala Pro Lys Pro Gly Val Lys Pro Glu Asn Pro Lys Lys Arg
        280                 285                 290

aag aag taaaacttca ctaaaaaccg cca                                1008
Lys Lys
    295
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<210> 2230
<211> 295
<212> PRT
<213> Corynebacterium glutamicum

<400> 2230

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Val Leu Ser Pro Asp Ser Gly Ile Thr Trp Ala Leu Ser Ile Met Phe
  1               5                  10                  15

Leu Thr Phe Thr Val Arg Met Val Leu Val Lys Pro Met Val Asn Thr
             20                  25                  30

Met Arg Ser Gln Arg Lys Met Gln Asp Met Ala Pro Lys Met Gln Ala
         35                  40                  45

Ile Arg Glu Lys Tyr Lys Asn Asp Gln Gln Lys Met Met Glu Glu Thr
     50                  55                  60

Arg Lys Leu Gln Lys Glu Val Gly Val Asn Pro Ile Ala Gly Cys Leu
 65                  70                  75                  80

Pro Met Leu Val Gln Ile Pro Val Phe Leu Gly Leu Phe His Val Leu
                 85                  90                  95

Arg Ser Phe Asn Arg Thr Gly Ser Gly Val Gly Gln Leu Glu Met Thr
            100                 105                 110

Val Glu Gln Asn Ala Asn Thr Pro Asn Tyr Ile Phe Gly Val Asp Glu
        115                 120                 125

Val Gln Ser Phe Leu Arg Ala Asp Leu Phe Gly Ala Pro Leu Ser Ser
    130                 135                 140

Tyr Ile Thr Met Pro Ala Asp Ala Phe Asp Ala Phe Leu Gly Leu Asp
145                 150                 155                 160

Val Ser Arg Leu Asn Ile Ala Leu Val Ala Ala Pro Met Ile Leu Ile
                165                 170                 175

Ile Val Val Ala Thr His Met Asn Ala Arg Leu Ser Val Asn Arg Gln
            180                 185                 190

Glu Ala Arg Lys Ala Ala Gly Lys Gln Gln Ala Ala Ser Ser Asp Gln
        195                 200                 205

Met Ala Met Gln Met Gln Met Met Asn Lys Met Met Leu Trp Phe Met
    210                 215                 220

Pro Ala Thr Ile Leu Phe Thr Gly Phe Ile Trp Thr Ile Gly Leu Leu
225                 230                 235                 240

Val Tyr Met Met Ser Asn Asn Val Trp Thr Phe Phe Gln Gln Arg Tyr
                245                 250                 255

Ile Phe Ala Lys Met Asp Ala Glu Glu Ala Ala Glu Glu Glu Glu Lys
            260                 265                 270

Arg Ala Ala Lys Arg Thr Thr Ala Pro Lys Pro Gly Val Lys Pro Glu
        275                 280                 285

Asn Pro Lys Lys Arg Lys Lys
    290                 295
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<210> 2231
<211> 741
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(718)
<223> RXA01429

<400> 2231
ggtaagaaga agggcaagct cgtggtggaa ttcggcgaca aggatgattt cgagcgcatc 60

atgtccttga tccagggcca ataattttaa gtttggcgcc atg ctc cag gct tcc 115
Met Leu Gln Ala Ser
1 5

ctt ttc ccg atc gtg cag gaa cac ata gat ttc ctg cac ccc cag gcc 163
Leu Phe Pro Ile Val Gln Glu His Ile Asp Phe Leu His Pro Gln Ala
10 15 20

cgc aag tcg gtg ttt tgg gag ctc gca cct gag gtt gca gct aaa gct 211
Arg Lys Ser Val Phe Trp Glu Leu Ala Pro Glu Val Ala Ala Lys Ala
25 30 35

gat ccg gtg ttt gag aag gaa gcc tgg ctg tcc acc acg ctg ctg gaa 259
Asp Pro Val Phe Glu Lys Glu Ala Trp Leu Ser Thr Thr Leu Leu Glu
40 45 50

tat gaa tcc tgc ggt ttc aac att ggt tac cgc aat gga act ccg gcg 307
Tyr Glu Ser Cys Gly Phe Asn Ile Gly Tyr Arg Asn Gly Thr Pro Ala
55 60 65

ttg gcg tcg gtc att ttc tgc gag cgc gat gcc gcc ccg ggc gcg aag 355
Leu Ala Ser Val Ile Phe Cys Glu Arg Asp Ala Ala Pro Gly Ala Lys
70 75 80 85

gcg ctg cct acg gca ccg gtg tct agc gac gct gcg atc atc agc agc 403
Ala Leu Pro Thr Ala Pro Val Ser Ser Asp Ala Ala Ile Ile Ser Ser
90 95 100

ctg ttc atc gac gag gtt ttc cgg ggc acg ggc atg gaa tcg gcg ctt 451
Leu Phe Ile Asp Glu Val Phe Arg Gly Thr Gly Met Glu Ser Ala Leu
105 110 115

ctc gac gct tcc ctc atg gaa ctc att cgg cgc gac tac cca gcc gtt 499
Leu Asp Ala Ser Leu Met Glu Leu Ile Arg Arg Asp Tyr Pro Ala Val
120 125 130

gag gcg ttt gga tac cgc tcg gaa aac aca gaa gcg gat gcg atc gca 547
Glu Ala Phe Gly Tyr Arg Ser Glu Asn Thr Glu Ala Asp Ala Ile Ala
135 140 145

gct agg cgt tta gaa atc ggc ctg att gat gtg gag gcg tta gaa tca 595
Ala Arg Arg Leu Glu Ile Gly Leu Ile Asp Val Glu Ala Leu Glu Ser
150 155 160 165

gcc ggt ttc gaa gtg gtt gct gac cat ccc gtg tta ccc cgt ctg cgg 643
Ala Gly Phe Glu Val Val Ala Asp His Pro Val Leu Pro Arg Leu Arg
170 175 180

atg gaa tta cca ccc gca acg gtg ctg ctc aca gct aag gat gcc cag 691
Met Glu Leu Pro Pro Ala Thr Val Leu Leu Thr Ala Lys Asp Ala Gln
185 190 195

```
cga ctc ctt caa gag atg ggc gcg att tagccagcct gctctgattg          738
Arg Leu Leu Gln Glu Met Gly Ala Ile
        200                 205

caa                                                                741
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<210> 2232
<211> 206
<212> PRT
<213> Corynebacterium glutamicum

<400> 2232

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Met Leu Gln Ala Ser Leu Phe Pro Ile Val Gln Glu His Ile Asp Phe
  1               5                  10                  15

Leu His Pro Gln Ala Arg Lys Ser Val Phe Trp Glu Leu Ala Pro Glu
             20                  25                  30

Val Ala Ala Lys Ala Asp Pro Val Phe Glu Lys Glu Ala Trp Leu Ser
         35                  40                  45

Thr Thr Leu Leu Glu Tyr Glu Ser Cys Gly Phe Asn Ile Gly Tyr Arg
     50                  55                  60

Asn Gly Thr Pro Ala Leu Ala Ser Val Ile Phe Cys Glu Arg Asp Ala
 65                  70                  75                  80

Ala Pro Gly Ala Lys Ala Leu Pro Thr Ala Pro Val Ser Ser Asp Ala
                 85                  90                  95

Ala Ile Ile Ser Ser Leu Phe Ile Asp Glu Val Phe Arg Gly Thr Gly
            100                 105                 110

Met Glu Ser Ala Leu Leu Asp Ala Ser Leu Met Glu Leu Ile Arg Arg
        115                 120                 125

Asp Tyr Pro Ala Val Glu Ala Phe Gly Tyr Arg Ser Glu Asn Thr Glu
    130                 135                 140

Ala Asp Ala Ile Ala Ala Arg Arg Leu Glu Ile Gly Leu Ile Asp Val
145                 150                 155                 160

Glu Ala Leu Glu Ser Ala Gly Phe Glu Val Val Ala Asp His Pro Val
                165                 170                 175

Leu Pro Arg Leu Arg Met Glu Leu Pro Pro Ala Thr Val Leu Leu Thr
            180                 185                 190

Ala Lys Asp Ala Gln Arg Leu Leu Gln Glu Met Gly Ala Ile
        195                 200                 205
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<210> 2233
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(646)
<223> RXA01439

<400> 2233
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cgactgtcta cttagtaggt ttgcaggcta gtcttttgtc atg acc cga tac ttt 115
Met Thr Arg Tyr Phe
1 5

gca gtt tcc aat ctt cag gag ctt ggc tcc ctc gaa gta cac aaa ttg 163
Ala Val Ser Asn Leu Gln Glu Leu Gly Ser Leu Glu Val His Lys Leu
10 15 20

tac aaa ctt cgt gta gat att ttc gtc cac gag cag cag act ccg tac 211
Tyr Lys Leu Arg Val Asp Ile Phe Val His Glu Gln Gln Thr Pro Tyr
25 30 35

gcg gag atc gat gac acc gat gct gcc cca acc acc aat cac atc ctg 259
Ala Glu Ile Asp Asp Thr Asp Ala Ala Pro Thr Thr Asn His Ile Leu
40 45 50

gtt tgg gag cgc gcc gac gcc acc cca acc aac ctc atc ggc tgc gca 307
Val Trp Glu Arg Ala Asp Ala Thr Pro Thr Asn Leu Ile Gly Cys Ala
55 60 65

cgc ctc gcg ccc atc acc gcc gcc gag ctt aag gcg tac acc ggc aag 355
Arg Leu Ala Pro Ile Thr Ala Ala Glu Leu Lys Ala Tyr Thr Gly Lys
70 75 80 85

ggc att tcg ctt gac gac gcc acc ccg ctc tca caa ctc ggc cgc gta 403
Gly Ile Ser Leu Asp Asp Ala Thr Pro Leu Ser Gln Leu Gly Arg Val
90 95 100

gcg gtg gca cag gaa ggg cgg ggc tcg ggg ctc tca ggt gag ctc atg 451
Ala Val Ala Gln Glu Gly Arg Gly Ser Gly Leu Ser Gly Glu Leu Met
105 110 115

cgc aac gcg ctg cgt ctt gca tat gag cag tac ccc gac cgc gat gtt 499
Arg Asn Ala Leu Arg Leu Ala Tyr Glu Gln Tyr Pro Asp Arg Asp Val
120 125 130

gtc ctg acc gcg cag aag cct ttg gta gat ttc tac gca gaa tac ggc 547
Val Leu Thr Ala Gln Lys Pro Leu Val Asp Phe Tyr Ala Glu Tyr Gly
135 140 145

ttt gag gtc ttg ggt gag gaa tac ctt gac tcg ggt gtt cct cac ctt 595
Phe Glu Val Leu Gly Glu Glu Tyr Leu Asp Ser Gly Val Pro His Leu
150 155 160 165

ccg atg ttg ctc aag gct gat gag ctt gaa agg ttc tca gac cta gac 643
Pro Met Leu Leu Lys Ala Asp Glu Leu Glu Arg Phe Ser Asp Leu Asp
170 175 180

gcc taatccgtag tcactggaac tca 669
Ala

<210> 2234
<211> 182

<212> PRT
<213> Corynebacterium glutamicum

<400> 2234

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Met Thr Arg Tyr Phe Ala Val Ser Asn Leu Gln Glu Leu Gly Ser Leu
  1               5                  10                  15

Glu Val His Lys Leu Tyr Lys Leu Arg Val Asp Ile Phe Val His Glu
             20                  25                  30

Gln Gln Thr Pro Tyr Ala Glu Ile Asp Asp Thr Asp Ala Ala Pro Thr
         35                  40                  45

Thr Asn His Ile Leu Val Trp Glu Arg Ala Asp Ala Thr Pro Thr Asn
     50                  55                  60

Leu Ile Gly Cys Ala Arg Leu Ala Pro Ile Thr Ala Ala Glu Leu Lys
 65                  70                  75                  80

Ala Tyr Thr Gly Lys Gly Ile Ser Leu Asp Asp Ala Thr Pro Leu Ser
                 85                  90                  95

Gln Leu Gly Arg Val Ala Val Ala Gln Glu Gly Arg Gly Ser Gly Leu
            100                 105                 110

Ser Gly Glu Leu Met Arg Asn Ala Leu Arg Leu Ala Tyr Glu Gln Tyr
        115                 120                 125

Pro Asp Arg Asp Val Val Leu Thr Ala Gln Lys Pro Leu Val Asp Phe
    130                 135                 140

Tyr Ala Glu Tyr Gly Phe Glu Val Leu Gly Glu Glu Tyr Leu Asp Ser
145                 150                 155                 160

Gly Val Pro His Leu Pro Met Leu Leu Lys Ala Asp Glu Leu Glu Arg
                165                 170                 175

Phe Ser Asp Leu Asp Ala
            180
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<210> 2235
<211> 1131
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1108)
<223> RXA01440

<400> 2235

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ttgatggaac caccctcacg ctgaccacgc ctcaggggaa tcagtattgg gcaaacacac 60

acgattttgg agccggcaca cactaatttt aggagcactg atg aaa acc aag tgg   115
                                               Met Lys Thr Lys Trp
                                                 1               5

tta gcg atc att cca ttc gtg gcg ctt gcg gtg gtt gca tgc tct gat   163
Leu Ala Ile Ile Pro Phe Val Ala Leu Ala Val Val Ala Cys Ser Asp
                 10                  15                  20
```

```
acg cag ccg ccg gtt aca gaa aca gtg aca gaa acc gcc ccg caa cct   211
Thr Gln Pro Pro Val Thr Glu Thr Val Thr Glu Thr Ala Pro Gln Pro
            25                  30                  35

act tct gaa acg gca gcg cag cca cca caa ccc acg aca cct gcg gaa   259
Thr Ser Glu Thr Ala Ala Gln Pro Pro Gln Pro Thr Thr Pro Ala Glu
        40                  45                  50

acg acc acg cag cag gca gaa ggt atc aac ttg acg cct cgc tac act   307
Thr Thr Thr Gln Gln Ala Glu Gly Ile Asn Leu Thr Pro Arg Tyr Thr
    55                  60                  65

cgc caa aat gtg ggg cac ttt tcc agt ggt tat cag cct gga cag gtg   355
Arg Gln Asn Val Gly His Phe Ser Ser Gly Tyr Gln Pro Gly Gln Val
70                  75                  80                  85

agt ttt tcc tca gct gat gga acc att aaa tgt gag ttt cgc ccc atg   403
Ser Phe Ser Ser Ala Asp Gly Thr Ile Lys Cys Glu Phe Arg Pro Met
                90                  95                  100

gaa cag gac gca cct atc aac cgg gag ccc tcc acc gat tgg cgg ttg   451
Glu Gln Asp Ala Pro Ile Asn Arg Glu Pro Ser Thr Asp Trp Arg Leu
            105                 110                 115

agt ttc gtg cag ggt gcg tgc caa ttc gac gat ggt tac gta gtg gcg   499
Ser Phe Val Gln Gly Ala Cys Gln Phe Asp Asp Gly Tyr Val Val Ala
        120                 125                 130

gat aca aat gtg gaa aac aga cca ggt ttt gct gag tac acc acg gcg   547
Asp Thr Asn Val Glu Asn Arg Pro Gly Phe Ala Glu Tyr Thr Thr Ala
    135                 140                 145

att tct cat gtc atg ccg gaa aat tac acc acg ttg ccg ccg gga acc   595
Ile Ser His Val Met Pro Glu Asn Tyr Thr Thr Leu Pro Pro Gly Thr
150                 155                 160                 165

tac atc gat tta cac acc atg gct tgt ttc acc gag tct gcc gat gaa   643
Tyr Ile Asp Leu His Thr Met Ala Cys Phe Thr Glu Ser Ala Asp Glu
                170                 175                 180

att tcc tgc att aag tac gcg acc aat gaa aca ttc cgc atc agc gcg   691
Ile Ser Cys Ile Lys Tyr Ala Thr Asn Glu Thr Phe Arg Ile Ser Ala
            185                 190                 195

cag ggt ttt gag atg ctc tca aat gcc cag cgc gac gcg gaa cta acc   739
Gln Gly Phe Glu Met Leu Ser Asn Ala Gln Arg Asp Ala Glu Leu Thr
        200                 205                 210

aca caa ggt ggc ttg tac cag gca ttt tcc aac atc gcg gaa tta cgg   787
Thr Gln Gly Gly Leu Tyr Gln Ala Phe Ser Asn Ile Ala Glu Leu Arg
    215                 220                 225

ttc agt gac ggc aac gcc atg tca tgt ttc ttt gac gcg ccg gga tcg   835
Phe Ser Asp Gly Asn Ala Met Ser Cys Phe Phe Asp Ala Pro Gly Ser
230                 235                 240                 245

caa gat ttc tgg tgc caa aca ctc agc acc ccc ggc tgg gac gac ggc   883
Gln Asp Phe Trp Cys Gln Thr Leu Ser Thr Pro Gly Trp Asp Asp Gly
                250                 255                 260
```

```
agc aac ctc att cat ttg acg gtc acc ggc gga aaa ctc agc ctg atg   931
Ser Asn Leu Ile His Leu Thr Val Thr Gly Gly Lys Leu Ser Leu Met
            265                 270                 275

ggc acc caa gtg ggc aac ccc ggc ctc gac tat ttc cgc ggc cgc cag   979
Gly Thr Gln Val Gly Asn Pro Gly Leu Asp Tyr Phe Arg Gly Arg Gln
        280                 285                 290

ctc att gag gcg cca aat tcg ctt ctc gac gcc tcc ctc tcc gta aca   1027
Leu Ile Glu Ala Pro Asn Ser Leu Leu Asp Ala Ser Leu Ser Val Thr
    295                 300                 305

ctc gac ggc gat cgg gtg cgt ttc cgc acc gcg acc ggc gag gag atg   1075
Leu Asp Gly Asp Arg Val Arg Phe Arg Thr Ala Thr Gly Glu Glu Met
310                 315                 320                 325

tgg gtg agt tcc agt gac tac gga tta ggc gtc taggtctgag aacctttcaa 1128
Trp Val Ser Ser Ser Asp Tyr Gly Leu Gly Val
                330                 335

gct                                                               1131
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20050170900

<210> 2236
<211> 336
<212> PRT
<213> Corynebacterium glutamicum

<400> 2236

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Met Lys Thr Lys Trp Leu Ala Ile Ile Pro Phe Val Ala Leu Ala Val
  1               5                  10                  15

Val Ala Cys Ser Asp Thr Gln Pro Pro Val Thr Glu Thr Val Thr Glu
             20                  25                  30

Thr Ala Pro Gln Pro Thr Ser Glu Thr Ala Ala Gln Pro Pro Gln Pro
         35                  40                  45

Thr Thr Pro Ala Glu Thr Thr Thr Gln Gln Ala Glu Gly Ile Asn Leu
     50                  55                  60

Thr Pro Arg Tyr Thr Arg Gln Asn Val Gly His Phe Ser Ser Gly Tyr
 65                  70                  75                  80

Gln Pro Gly Gln Val Ser Phe Ser Ser Ala Asp Gly Thr Ile Lys Cys
                 85                  90                  95

Glu Phe Arg Pro Met Glu Gln Asp Ala Pro Ile Asn Arg Glu Pro Ser
            100                 105                 110

Thr Asp Trp Arg Leu Ser Phe Val Gln Gly Ala Cys Gln Phe Asp Asp
        115                 120                 125

Gly Tyr Val Val Ala Asp Thr Asn Val Glu Asn Arg Pro Gly Phe Ala
    130                 135                 140

Glu Tyr Thr Thr Ala Ile Ser His Val Met Pro Glu Asn Tyr Thr Thr
145                 150                 155                 160

Leu Pro Pro Gly Thr Tyr Ile Asp Leu His Thr Met Ala Cys Phe Thr
                165                 170                 175
```

```
Glu Ser Ala Asp Glu Ile Ser Cys Ile Lys Tyr Ala Thr Asn Glu Thr
            180                 185                 190

Phe Arg Ile Ser Ala Gln Gly Phe Glu Met Leu Ser Asn Ala Gln Arg
        195                 200                 205

Asp Ala Glu Leu Thr Thr Gln Gly Gly Leu Tyr Gln Ala Phe Ser Asn
    210                 215                 220

Ile Ala Glu Leu Arg Phe Ser Asp Gly Asn Ala Met Ser Cys Phe Phe
225                 230                 235                 240

Asp Ala Pro Gly Ser Gln Asp Phe Trp Cys Gln Thr Leu Ser Thr Pro
                245                 250                 255

Gly Trp Asp Asp Gly Ser Asn Leu Ile His Leu Thr Val Thr Gly Gly
            260                 265                 270

Lys Leu Ser Leu Met Gly Thr Gln Val Gly Asn Pro Gly Leu Asp Tyr
        275                 280                 285

Phe Arg Gly Arg Gln Leu Ile Glu Ala Pro Asn Ser Leu Leu Asp Ala
    290                 295                 300

Ser Leu Ser Val Thr Leu Asp Gly Asp Arg Val Arg Phe Arg Thr Ala
305                 310                 315                 320

Thr Gly Glu Glu Met Trp Val Ser Ser Ser Asp Tyr Gly Leu Gly Val
                325                 330                 335
```

US 20050250190 A1

<210> 2237
<211> 1152
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1129)
<223> RXA01441

<400> 2237

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ttataacaat tagccgtgag ggtattaatc aaggtttcgg gagactaacg ttttagaaac 60

aagtggactc cagcacacct cgtgagatgg caggttcatc atg gct aga acg aca   115
                                            Met Ala Arg Thr Thr
                                              1               5

aca gcg cac gca gtt ctc atg gcg ctt agt tca gtc ggg ctt ttg atg   163
Thr Ala His Ala Val Leu Met Ala Leu Ser Ser Val Gly Leu Leu Met
                 10                  15                  20

ctc cag gcc tgc tcc gaa cag gaa caa acc cca gaa caa acg cca gcg   211
Leu Gln Ala Cys Ser Glu Gln Glu Gln Thr Pro Glu Gln Thr Pro Ala
            25                  30                  35

ccc acc ctg act tcg cag gct ccc gag act cct caa gcc tca aca acc   259
```

```
Pro Thr Leu Thr Ser Gln Ala Pro Glu Thr Pro Gln Ala Ser Thr Thr
          40                  45                  50

tcc tca gca agc tcc aca gca act ccc ata gca act ccc ata gca gcc   307
Ser Ser Ala Ser Ser Thr Ala Thr Pro Ile Ala Thr Pro Ile Ala Ala
     55                  60                  65

acc gag ttg gat tat ctc cac atc gat cca gca acg tat gac atc ggt   355
Thr Glu Leu Asp Tyr Leu His Ile Asp Pro Ala Thr Tyr Asp Ile Gly
 70                  75                  80                  85

gtc caa gac caa gaa act gcc gta ttt acc act ggc gat ggg atc aca   403
Val Gln Asp Gln Glu Thr Ala Val Phe Thr Thr Gly Asp Gly Ile Thr
                 90                  95                 100

gcg cag tgt ttc ttc gag gca aca ccg ggg gag acc agc tat cag atc   451
Ala Gln Cys Phe Phe Glu Ala Thr Pro Gly Glu Thr Ser Tyr Gln Ile
            105                 110                 115

aag gag ttt gat ttc gac gaa act gcg gga acg tgc gct ttt ggt gat   499
Lys Glu Phe Asp Phe Asp Glu Thr Ala Gly Thr Cys Ala Phe Gly Asp
        120                 125                 130

caa cac atc agc gtc acc acg gat gaa aat gtc cgg gaa cgc ttt gcc   547
Gln His Ile Ser Val Thr Thr Asp Glu Asn Val Arg Glu Arg Phe Ala
    135                 140                 145

gaa ttg agt gaa acc gaa gaa gaa tta cca gaa gcg caa gcg act ctc   595
Glu Leu Ser Glu Thr Glu Glu Glu Leu Pro Glu Ala Gln Ala Thr Leu
150                 155                 160                 165

gat gtt ggt gag atg gtg cat ctt ggt cac atg ggt tgt tgg gcg ccg   643
Asp Val Gly Glu Met Val His Leu Gly His Met Gly Cys Trp Ala Pro
                170                 175                 180

agt gta tcg gag ttt agt tgt ctc gat ttc gcc tcc aac cag gcg ttc   691
Ser Val Ser Glu Phe Ser Cys Leu Asp Phe Ala Ser Asn Gln Ala Phe
            185                 190                 195

acc atg aat gaa cag ggc ttc cat gag ctt gat cct gca aaa gcc act   739
Thr Met Asn Glu Gln Gly Phe His Glu Leu Asp Pro Ala Lys Ala Thr
        200                 205                 210

gag cag cta att aat tcg agt ggc cag gtt caa acg tta tcg aaa atg   787
Glu Gln Leu Ile Asn Ser Ser Gly Gln Val Gln Thr Leu Ser Lys Met
    215                 220                 225

acg aat ttc cag ttc acc gat ggc acc agc atc acc tgt gtc agt gag   835
Thr Asn Phe Gln Phe Thr Asp Gly Thr Ser Ile Thr Cys Val Ser Glu
230                 235                 240                 245

ttg cag gcg gaa gag ttc ttg tgc cac aac agt ggt cct gga ggc tgg   883
Leu Gln Ala Glu Glu Phe Leu Cys His Asn Ser Gly Pro Gly Gly Trp
                250                 255                 260

tca act tca gct ggc cct gcc aac acc ctg tgg tgg aat ctg aac cag   931
Ser Thr Ser Ala Gly Pro Ala Asn Thr Leu Trp Trp Asn Leu Asn Gln
            265                 270                 275

gcc gac tcc gag ttt gag ggt gct cgc ccc acg aat cca acg caa agc   979
Ala Asp Ser Glu Phe Glu Gly Ala Arg Pro Thr Asn Pro Thr Gln Ser
```

```
        280                 285                 290

gtt tat aaa tct caa caa ata ttc ggt ccg gga tcg tat ctc ctc gcg   1027
Val Tyr Lys Ser Gln Gln Ile Phe Gly Pro Gly Ser Tyr Leu Leu Ala
    295                 300                 305

aac ggt gtg agt gca gaa ttt gat gga acc acc ctc acg ctg acc acg   1075
Asn Gly Val Ser Ala Glu Phe Asp Gly Thr Thr Leu Thr Leu Thr Thr
310                 315                 320                 325

cct cag ggg aat cag tat tgg gca aac aca cac gat ttt gga gcc ggc   1123
Pro Gln Gly Asn Gln Tyr Trp Ala Asn Thr His Asp Phe Gly Ala Gly
                330                 335                 340

aca cac taattttagg agcactgatg aaa                                1152
Thr His
```

<210> 2238
<211> 343
<212> PRT
<213> Corynebacterium glutamicum

<400> 2238

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Met Ala Arg Thr Thr Thr Ala His Ala Val Leu Met Ala Leu Ser Ser
  1               5                  10                  15

Val Gly Leu Leu Met Leu Gln Ala Cys Ser Glu Gln Glu Gln Thr Pro
             20                  25                  30

Glu Gln Thr Pro Ala Pro Thr Leu Thr Ser Gln Ala Pro Glu Thr Pro
         35                  40                  45

Gln Ala Ser Thr Thr Ser Ser Ala Ser Ser Thr Ala Thr Pro Ile Ala
     50                  55                  60

Thr Pro Ile Ala Ala Thr Glu Leu Asp Tyr Leu His Ile Asp Pro Ala
 65                  70                  75                  80

Thr Tyr Asp Ile Gly Val Gln Asp Gln Glu Thr Ala Val Phe Thr Thr
                 85                  90                  95

Gly Asp Gly Ile Thr Ala Gln Cys Phe Phe Glu Ala Thr Pro Gly Glu
            100                 105                 110

Thr Ser Tyr Gln Ile Lys Glu Phe Asp Phe Asp Glu Thr Ala Gly Thr
        115                 120                 125

Cys Ala Phe Gly Asp Gln His Ile Ser Val Thr Thr Asp Glu Asn Val
    130                 135                 140

Arg Glu Arg Phe Ala Glu Leu Ser Glu Thr Glu Glu Glu Leu Pro Glu
145                 150                 155                 160

Ala Gln Ala Thr Leu Asp Val Gly Glu Met Val His Leu Gly His Met
                165                 170                 175

Gly Cys Trp Ala Pro Ser Val Ser Glu Phe Ser Cys Leu Asp Phe Ala
            180                 185                 190
```

```
Ser Asn Gln Ala Phe Thr Met Asn Glu Gln Gly Phe His Glu Leu Asp
        195                 200                 205

Pro Ala Lys Ala Thr Glu Gln Leu Ile Asn Ser Ser Gly Gln Val Gln
    210                 215                 220

Thr Leu Ser Lys Met Thr Asn Phe Gln Phe Thr Asp Gly Thr Ser Ile
225                 230                 235                 240

Thr Cys Val Ser Glu Leu Gln Ala Glu Glu Phe Leu Cys His Asn Ser
                245                 250                 255

Gly Pro Gly Gly Trp Ser Thr Ser Ala Gly Pro Ala Asn Thr Leu Trp
            260                 265                 270

Trp Asn Leu Asn Gln Ala Asp Ser Glu Phe Glu Gly Ala Arg Pro Thr
        275                 280                 285

Asn Pro Thr Gln Ser Val Tyr Lys Ser Gln Gln Ile Phe Gly Pro Gly
    290                 295                 300

Ser Tyr Leu Leu Ala Asn Gly Val Ser Ala Glu Phe Asp Gly Thr Thr
305                 310                 315                 320

Leu Thr Leu Thr Thr Pro Gln Gly Asn Gln Tyr Trp Ala Asn Thr His
                325                 330                 335

Asp Phe Gly Ala Gly Thr His
            340


<210> 2239
<211> 1116
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1093)
<223> RXA01445

<400> 2239
gagtctcgaa tgtataacga gtttgttcct aataacttta tcattaacta tgcctgcaat 60

aggcttggga aattttggca tccaggtaat cgcgctgtca atg atc cca ctt att   115
                                              Met Ile Pro Leu Ile
                                                1               5

aat gta cgt ttt ccc gtt gcc gcc tta cct ctc gca tta gtg gcg act   163
Asn Val Arg Phe Pro Val Ala Ala Leu Pro Leu Ala Leu Val Ala Thr
                10                  15                  20

gta tgg ctt aat gct tgg gca gac cat ctt ctc cta act ggt ttt att   211
Val Trp Leu Asn Ala Trp Ala Asp His Leu Leu Leu Thr Gly Phe Ile
            25                  30                  35

gtt tat ctt gct gtg gaa tac gca aca agc cgt ggg cgc ttc gct ctc   259
Val Tyr Leu Ala Val Glu Tyr Ala Thr Ser Arg Gly Arg Phe Ala Leu
        40                  45                  50

gca ttg att ttg gga gtt gaa tgg atc tta att gct tat ggg gta gct   307
```

```
Ala Leu Ile Leu Gly Val Glu Trp Ile Leu Ile Ala Tyr Gly Val Ala
     55                  60                  65

ttg gaa agg cct ctt gag gct aaa gac tct cca tct ctc att acc gaa   355
Leu Glu Arg Pro Leu Glu Ala Lys Asp Ser Pro Ser Leu Ile Thr Glu
 70                  75                  80                  85

att ttg ctc ata ctt gta gca gct ggc aca ggg gca ggt cgg tgg aaa   403
Ile Leu Leu Ile Leu Val Ala Ala Gly Thr Gly Ala Gly Arg Trp Lys
                 90                  95                 100

att ttg agt gaa cgc aag caa cgt gca att act cag cag gaa atc atc   451
Ile Leu Ser Glu Arg Lys Gln Arg Ala Ile Thr Gln Gln Glu Ile Ile
            105                 110                 115

aaa aaa atc cgt act gat ata gcg cac tat ttg cat gac agt atg gca   499
Lys Lys Ile Arg Thr Asp Ile Ala His Tyr Leu His Asp Ser Met Ala
        120                 125                 130

aga tcg ttg gca ata atg ata gtt caa tca aag ctg act gaa cta gag   547
Arg Ser Leu Ala Ile Met Ile Val Gln Ser Lys Leu Thr Glu Leu Glu
    135                 140                 145

cct gat cca aaa aag att caa gaa aaa cta aac agt att gcc aaa att   595
Pro Asp Pro Lys Lys Ile Gln Glu Lys Leu Asn Ser Ile Ala Lys Ile
150                 155                 160                 165

gga caa gag gca gtg gct gat ttg cat caa tta gtt aga cac ctc gtg   643
Gly Gln Glu Ala Val Ala Asp Leu His Gln Leu Val Arg His Leu Val
                170                 175                 180

gtc gag gag tct gct gaa aaa gcc aca gcg ttt gga gca tgg gct gca   691
Val Glu Glu Ser Ala Glu Lys Ala Thr Ala Phe Gly Ala Trp Ala Ala
            185                 190                 195

gtt tct att cat gac acg gtt aat tct gcc att cag tta tta gta gat   739
Val Ser Ile His Asp Thr Val Asn Ser Ala Ile Gln Leu Leu Val Asp
        200                 205                 210

gca gga cat gtc gtt tcc ttt gac agt aga aaa aag aac tat aag ctg   787
Ala Gly His Val Val Ser Phe Asp Ser Arg Lys Lys Asn Tyr Lys Leu
    215                 220                 225

gac cat att gct gaa acg gcg ttt gct tta gcc ttc aat gag gca gtc   835
Asp His Ile Ala Glu Thr Ala Phe Ala Leu Ala Phe Asn Glu Ala Val
230                 235                 240                 245

tgt aat gca att aaa cat tct ccg ccc aag gca aac gtt act att cgc   883
Cys Asn Ala Ile Lys His Ser Pro Pro Lys Ala Asn Val Thr Ile Arg
                250                 255                 260

ata aca gaa aaa gca cag tct ctt cag att cta gta atg aat cct att   931
Ile Thr Glu Lys Ala Gln Ser Leu Gln Ile Leu Val Met Asn Pro Ile
            265                 270                 275

gga gat tgg cat gca aat ggg gag tcc gca att cca ggt gtg ggc att   979
Gly Asp Trp His Ala Asn Gly Glu Ser Ala Ile Pro Gly Val Gly Ile
        280                 285                 290

ggc gta gaa agc tta acc aga agg ata cgt aat att aaa gga cag gtc   1027
Gly Val Glu Ser Leu Thr Arg Arg Ile Arg Asn Ile Lys Gly Gln Val
```

```
    295                 300                 305

tgt gtg act tca ctg caa gga tac tgg aaa gta gtt att tca cta cct   1075
Cys Val Thr Ser Leu Gln Gly Tyr Trp Lys Val Val Ile Ser Leu Pro
310                 315                 320                 325

ttg aaa tgt gag gat tct taaattgtct ctatttgttg aac               1116
Leu Lys Cys Glu Asp Ser
                330
```

<210> 2240
<211> 331
<212> PRT
<213> Corynebacterium glutamicum

<400> 2240

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Met Ile Pro Leu Ile Asn Val Arg Phe Pro Val Ala Ala Leu Pro Leu
  1               5                  10                  15

Ala Leu Val Ala Thr Val Trp Leu Asn Ala Trp Ala Asp His Leu Leu
             20                  25                  30

Leu Thr Gly Phe Ile Val Tyr Leu Ala Val Glu Tyr Ala Thr Ser Arg
         35                  40                  45

Gly Arg Phe Ala Leu Ala Leu Ile Leu Gly Val Glu Trp Ile Leu Ile
     50                  55                  60

Ala Tyr Gly Val Ala Leu Glu Arg Pro Leu Glu Ala Lys Asp Ser Pro
 65                  70                  75                  80

Ser Leu Ile Thr Glu Ile Leu Leu Ile Leu Val Ala Ala Gly Thr Gly
                 85                  90                  95

Ala Gly Arg Trp Lys Ile Leu Ser Glu Arg Lys Gln Arg Ala Ile Thr
            100                 105                 110

Gln Gln Glu Ile Ile Lys Lys Ile Arg Thr Asp Ile Ala His Tyr Leu
        115                 120                 125

His Asp Ser Met Ala Arg Ser Leu Ala Ile Met Ile Val Gln Ser Lys
    130                 135                 140

Leu Thr Glu Leu Glu Pro Asp Pro Lys Lys Ile Gln Glu Lys Leu Asn
145                 150                 155                 160

Ser Ile Ala Lys Ile Gly Gln Glu Ala Val Ala Asp Leu His Gln Leu
                165                 170                 175

Val Arg His Leu Val Val Glu Glu Ser Ala Glu Lys Ala Thr Ala Phe
            180                 185                 190

Gly Ala Trp Ala Ala Val Ser Ile His Asp Thr Val Asn Ser Ala Ile
        195                 200                 205

Gln Leu Leu Val Asp Ala Gly His Val Val Ser Phe Asp Ser Arg Lys
    210                 215                 220

Lys Asn Tyr Lys Leu Asp His Ile Ala Glu Thr Ala Phe Ala Leu Ala
225                 230                 235                 240
```

```
Phe Asn Glu Ala Val Cys Asn Ala Ile Lys His Ser Pro Pro Lys Ala
                245                 250                 255

Asn Val Thr Ile Arg Ile Thr Glu Lys Ala Gln Ser Leu Gln Ile Leu
            260                 265                 270

Val Met Asn Pro Ile Gly Asp Trp His Ala Asn Gly Glu Ser Ala Ile
        275                 280                 285

Pro Gly Val Gly Ile Gly Val Glu Ser Leu Thr Arg Arg Ile Arg Asn
    290                 295                 300

Ile Lys Gly Gln Val Cys Val Thr Ser Leu Gln Gly Tyr Trp Lys Val
305                 310                 315                 320

Val Ile Ser Leu Pro Leu Lys Cys Glu Asp Ser
                325                 330
```

<210> 2241
<211> 972
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(949)
<223> RXA01447

<400> 2241

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tccatgaagt tggagtatgc acgcgtgtgc gcacacagac gttatttcat cttactatcc 60

catgtgaggt ttttaatcat cgcgatacta agcttgcggt atg cgt ctt ctg gtt   115
                                            Met Arg Leu Leu Val
                                              1               5

ttg cgg tgc gat gcc cca cac atc aac gaa ttc cct gcc ctt tcc acc   163
Leu Arg Cys Asp Ala Pro His Ile Asn Glu Phe Pro Ala Leu Ser Thr
                  10                  15                  20

tct gtg gag atc cac gat ttg cct gcg gtg ccc acc cga aaa gac ctc   211
Ser Val Glu Ile His Asp Leu Pro Ala Val Pro Thr Arg Lys Asp Leu
              25                  30                  35

aaa att ctt gat gat gtg gcc ttt gat gtg ctc cct cag gat ccc acg   259
Lys Ile Leu Asp Asp Val Ala Phe Asp Val Leu Pro Gln Asp Pro Thr
          40                  45                  50

cct tct ctc gat gag atc gcc aag cag cct gat gtc gag cat ttg agc   307
Pro Ser Leu Asp Glu Ile Ala Lys Gln Pro Asp Val Glu His Leu Ser
      55                  60                  65

agc cct aag ttt gcg cca caa cag cct gaa acc cgt ttg cgc atc gtg   355
Ser Pro Lys Phe Ala Pro Gln Gln Pro Glu Thr Arg Leu Arg Ile Val
  70                  75                  80                  85

gtg atc ggt tcg gat gca gcg ctg tct gcg gtc ctg act cgt ctc atg   403
Val Ile Gly Ser Asp Ala Ala Leu Ser Ala Val Leu Thr Arg Leu Met
                  90                  95                 100
```

```
cgc gcc gat aat ttg tgg gcg gag att gga ttc gtg ccc gtt ggt cct   451
Arg Ala Asp Asn Leu Trp Ala Glu Ile Gly Phe Val Pro Val Gly Pro
            105                 110                 115

tca acg gct gcg aag aac tgg ggt ctg ccc gcc gat gag gct gcc gcg   499
Ser Thr Ala Ala Lys Asn Trp Gly Leu Pro Ala Asp Glu Ala Ala Ala
        120                 125                 130

ctt gag ctc gca ctg acc gga ttg gtc aat cct gcc ccg ctc atc cgc   547
Leu Glu Leu Ala Leu Thr Gly Leu Val Asn Pro Ala Pro Leu Ile Arg
    135                 140                 145

gat gac gtt gcg gtc gcc gtc gcc ggt tca gcc acc atc acc aac tgg   595
Asp Asp Val Ala Val Ala Val Ala Gly Ser Ala Thr Ile Thr Asn Trp
150                 155                 160                 165

gag ccg ggt gag atc acc ggc gaa gtc atc gtc gat gat cat gtt ctc   643
Glu Pro Gly Glu Ile Thr Gly Glu Val Ile Val Asp Asp His Val Leu
                170                 175                 180

atc cgc cac gag gct gcc tcg aag gcc cca cgc cgt ggc gtc tac ggt   691
Ile Arg His Glu Ala Ala Ser Lys Ala Pro Arg Arg Gly Val Tyr Gly
            185                 190                 195

gcc cgc ttg gtg ccg atg ctt gac gcc cca ggc atc gct gcg gtc atc   739
Ala Arg Leu Val Pro Met Leu Asp Ala Pro Gly Ile Ala Ala Val Ile
        200                 205                 210

atg gac act ccc ctg ccc ggc gag gtg ccc tcc cgc agc ctg ttc cct   787
Met Asp Thr Pro Leu Pro Gly Glu Val Pro Ser Arg Ser Leu Phe Pro
    215                 220                 225

cgc ccc tcg ggc tcg gtt att cca gag agc ttt tcg acg ggc cgt gcc   835
Arg Pro Ser Gly Ser Val Ile Pro Glu Ser Phe Ser Thr Gly Arg Ala
230                 235                 240                 245

atg caa gcc ggc ggc ccc tcg cta caa atc cgg gtt gac gga att tcc   883
Met Gln Ala Gly Gly Pro Ser Leu Gln Ile Arg Val Asp Gly Ile Ser
                250                 255                 260

cgc aaa cgt aaa gtg gag cgc gtt acc ttc tat cga cat ttg cgc gat   931
Arg Lys Arg Lys Val Glu Arg Val Thr Phe Tyr Arg His Leu Arg Asp
            265                 270                 275

ctc caa atc gtg cgg ccg taaaacaagg agccagcatg gca                972
Leu Gln Ile Val Arg Pro
        280
```

<210> 2242
<211> 283
<212> PRT
<213> Corynebacterium glutamicum

<400> 2242

```
Met Arg Leu Leu Val Leu Arg Cys Asp Ala Pro His Ile Asn Glu Phe
  1               5                  10                  15

Pro Ala Leu Ser Thr Ser Val Glu Ile His Asp Leu Pro Ala Val Pro
             20                  25                  30
```

```
Thr Arg Lys Asp Leu Lys Ile Leu Asp Asp Val Ala Phe Asp Val Leu
          35                  40                  45

Pro Gln Asp Pro Thr Pro Ser Leu Asp Glu Ile Ala Lys Gln Pro Asp
      50                  55                  60

Val Glu His Leu Ser Ser Pro Lys Phe Ala Pro Gln Gln Pro Glu Thr
 65                  70                  75                  80

Arg Leu Arg Ile Val Val Ile Gly Ser Asp Ala Ala Leu Ser Ala Val
                 85                  90                  95

Leu Thr Arg Leu Met Arg Ala Asp Asn Leu Trp Ala Glu Ile Gly Phe
            100                 105                 110

Val Pro Val Gly Pro Ser Thr Ala Ala Lys Asn Trp Gly Leu Pro Ala
        115                 120                 125

Asp Glu Ala Ala Ala Leu Glu Leu Ala Leu Thr Gly Leu Val Asn Pro
    130                 135                 140

Ala Pro Leu Ile Arg Asp Asp Val Ala Val Ala Val Ala Gly Ser Ala
145                 150                 155                 160

Thr Ile Thr Asn Trp Glu Pro Gly Glu Ile Thr Gly Glu Val Ile Val
                165                 170                 175

Asp Asp His Val Leu Ile Arg His Glu Ala Ala Ser Lys Ala Pro Arg
            180                 185                 190

Arg Gly Val Tyr Gly Ala Arg Leu Val Pro Met Leu Asp Ala Pro Gly
        195                 200                 205

Ile Ala Ala Val Ile Met Asp Thr Pro Leu Pro Gly Glu Val Pro Ser
    210                 215                 220

Arg Ser Leu Phe Pro Arg Pro Ser Gly Ser Val Ile Pro Glu Ser Phe
225                 230                 235                 240

Ser Thr Gly Arg Ala Met Gln Ala Gly Gly Pro Ser Leu Gln Ile Arg
                245                 250                 255

Val Asp Gly Ile Ser Arg Lys Arg Lys Val Glu Arg Val Thr Phe Tyr
            260                 265                 270

Arg His Leu Arg Asp Leu Gln Ile Val Arg Pro
        275                 280
```

<210> 2243
<211> 402
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(379)
<223> RXA01452

<400> 2243
ccgccaagaa ggtaaggact acgtgatggt cgatggcgac gttgtggagt tccggtttaa 60

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cgtctagcgt tattgacgct cctcgttata cgctggtctc gtg atc aga tcg ttc   115
                                             Val Ile Arg Ser Phe
                                               1               5

gcc gac cgc gac acc gag ttg gtc tgg ttg cgt gaa ggt gcg aaa cgc   163
Ala Asp Arg Asp Thr Glu Leu Val Trp Leu Arg Glu Gly Ala Lys Arg
                 10                  15                  20

gtc gat ccg cga ata cac aaa gtg gcg aat cgg aag ctg cat ctg ctg   211
Val Asp Pro Arg Ile His Lys Val Ala Asn Arg Lys Leu His Leu Leu
             25                  30                  35

gac gcg gcg acg acc ctc gat gct ctg cgt gtg act ccg ggg aat cgc   259
Asp Ala Ala Thr Thr Leu Asp Ala Leu Arg Val Thr Pro Gly Asn Arg
         40                  45                  50

ctg gaa acg ctc gag ggt gat cga gtc ggt cag tac agc att cga gtc   307
Leu Glu Thr Leu Glu Gly Asp Arg Val Gly Gln Tyr Ser Ile Arg Val
     55                  60                  65

aac gac cag tgg cgg atc tgc ttc cgt tgg aac gac tcg ggc ccc gaa   355
Asn Asp Gln Trp Arg Ile Cys Phe Arg Trp Asn Asp Ser Gly Pro Glu
 70                  75                  80                  85

aac gtc gag atc gtg gat tat cac tgaggaggag acgatggctc aga         402
Asn Val Glu Ile Val Asp Tyr His
                 90
```

<210> 2244
<211> 93
<212> PRT
<213> Corynebacterium glutamicum

<400> 2244

```
Val Ile Arg Ser Phe Ala Asp Arg Asp Thr Glu Leu Val Trp Leu Arg
  1               5                  10                  15

Glu Gly Ala Lys Arg Val Asp Pro Arg Ile His Lys Val Ala Asn Arg
             20                  25                  30

Lys Leu His Leu Leu Asp Ala Ala Thr Thr Leu Asp Ala Leu Arg Val
         35                  40                  45

Thr Pro Gly Asn Arg Leu Glu Thr Leu Glu Gly Asp Arg Val Gly Gln
     50                  55                  60

Tyr Ser Ile Arg Val Asn Asp Gln Trp Arg Ile Cys Phe Arg Trp Asn
 65                  70                  75                  80

Asp Ser Gly Pro Glu Asn Val Glu Ile Val Asp Tyr His
                 85                  90
```

<210> 2245
<211> 645
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(622)
<223> RXA01456

<400> 2245
aagacaatat ccttatatgt acgtgattat gcgtttctcc cccactctac ggtttaatca 60

cctataaagg ccaacaagta gttcacaaaa ggaaaaaatt atg aac gat tcc att 115
Met Asn Asp Ser Ile
1 5

ttt agt ccc caa gca ctg aat aaa gcg atg ctc gaa gcc gtc gag ttt 163
Phe Ser Pro Gln Ala Leu Asn Lys Ala Met Leu Glu Ala Val Glu Phe
10 15 20

atc cac gcc gaa ggt tgg gac gcc ggc cct acc ctg ttc gca ttg gtc 211
Ile His Ala Glu Gly Trp Asp Ala Gly Pro Thr Leu Phe Ala Leu Val
25 30 35

ccc act gaa atg ctg gtg gat act ctt gat gag gca gct gac gac tcc 259
Pro Thr Glu Met Leu Val Asp Thr Leu Asp Glu Ala Ala Asp Asp Ser
40 45 50

cca cta acc ctt gtt gta cag gac aac ctc cct gac aac ttg ctg cca 307
Pro Leu Thr Leu Val Val Gln Asp Asn Leu Pro Asp Asn Leu Leu Pro
55 60 65

ggt tcc gaa gcg tta ggt gac tat gtg tcc cgt ttg gcg tgg cca gca 355
Gly Ser Glu Ala Leu Gly Asp Tyr Val Ser Arg Leu Ala Trp Pro Ala
70 75 80 85

gag att gcc ggc gcg gtg ttg gct cag gaa att atg ttc acc gat gct 403
Glu Ile Ala Gly Ala Val Leu Ala Gln Glu Ile Met Phe Thr Asp Ala
90 95 100

gcc gtt gca ggc tca gaa cca cga ccc gct cgt ctt ttt tcc ggc gtt 451
Ala Val Ala Gly Ser Glu Pro Arg Pro Ala Arg Leu Phe Ser Gly Val
105 110 115

ttg cgc ggc gaa gca gaa ctc acc ctt ctg cag ctt cgc ccc acc gaa 499
Leu Arg Gly Glu Ala Glu Leu Thr Leu Leu Gln Leu Arg Pro Thr Glu
120 125 130

gag gaa ttg gca gaa cgc gga ccg ttt gct gaa gat gaa atc gaa ctg 547
Glu Glu Leu Ala Glu Arg Gly Pro Phe Ala Glu Asp Glu Ile Glu Leu
135 140 145

cgc ggc ggc cca ggg gtt gca ccg ggt gta atc gca gca ctg cgc tac 595
Arg Gly Gly Pro Gly Val Ala Pro Gly Val Ile Ala Ala Leu Arg Tyr
150 155 160 165

acc ctc gaa gcg gac cca gac gaa atc taaaaactga cttttcgtcc 642
Thr Leu Glu Ala Asp Pro Asp Glu Ile
170

agg 645

<210> 2246
<211> 174
<212> PRT

<213> Corynebacterium glutamicum

<400> 2246

```
Met Asn Asp Ser Ile Phe Ser Pro Gln Ala Leu Asn Lys Ala Met Leu
  1               5                  10                  15

Glu Ala Val Glu Phe Ile His Ala Glu Gly Trp Asp Ala Gly Pro Thr
             20                  25                  30

Leu Phe Ala Leu Val Pro Thr Glu Met Leu Val Asp Thr Leu Asp Glu
         35                  40                  45

Ala Ala Asp Asp Ser Pro Leu Thr Leu Val Val Gln Asp Asn Leu Pro
     50                  55                  60

Asp Asn Leu Leu Pro Gly Ser Glu Ala Leu Gly Asp Tyr Val Ser Arg
 65                  70                  75                  80

Leu Ala Trp Pro Ala Glu Ile Ala Gly Ala Val Leu Ala Gln Glu Ile
                 85                  90                  95

Met Phe Thr Asp Ala Ala Val Ala Gly Ser Glu Pro Arg Pro Ala Arg
            100                 105                 110

Leu Phe Ser Gly Val Leu Arg Gly Glu Ala Glu Leu Thr Leu Leu Gln
        115                 120                 125

Leu Arg Pro Thr Glu Glu Glu Leu Ala Glu Arg Gly Pro Phe Ala Glu
    130                 135                 140

Asp Glu Ile Glu Leu Arg Gly Gly Pro Gly Val Ala Pro Gly Val Ile
145                 150                 155                 160

Ala Ala Leu Arg Tyr Thr Leu Glu Ala Asp Pro Asp Glu Ile
                165                 170
```

<210> 2247
<211> 798
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> RXA01457

<400> 2247

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gaagcggacc cagacgaaat ctaaaaactg acttttcgtc caggttcgct aggataaatt 60

aagttaaccc cgcccacaat ttatttgagg agttcacact gtg gcg tcc acc ccg   115
                                              Val Ala Ser Thr Pro
                                                1               5

cac aag cat gtc cgc gtt gca ctg gga tta gtg gcg ctc att cct ctt   163
His Lys His Val Arg Val Ala Leu Gly Leu Val Ala Leu Ile Pro Leu
                10                  15                  20

tta gct gca tgt acg ggc ggc gga tcc acc gaa act tcc act gaa tcc   211
Leu Ala Ala Cys Thr Gly Gly Gly Ser Thr Glu Thr Ser Thr Glu Ser
            25                  30                  35
```

```
acg gca gaa aca act cct gcg aca aca acg gaa gca acg aca act cct   259
Thr Ala Glu Thr Thr Pro Ala Thr Thr Thr Glu Ala Thr Thr Thr Pro
         40                  45                  50

gct acc act gct tcg tct tca gta att gaa acg aca gag tca agc act   307
Ala Thr Thr Ala Ser Ser Ser Val Ile Glu Thr Thr Glu Ser Ser Thr
     55                  60                  65

gcc gaa acg tcg acg aaa gag agt ggg gag acg tcg aca agc aaa cct   355
Ala Glu Thr Ser Thr Lys Glu Ser Gly Glu Thr Ser Thr Ser Lys Pro
 70                  75                  80                  85

cgt atg acc aag gac gtt gaa gtc gcc tat aaa gct ttc tcc tcg ctc   403
Arg Met Thr Lys Asp Val Glu Val Ala Tyr Lys Ala Phe Ser Ser Leu
                 90                  95                 100

gcg ccc gtc gag ctt ttt gag caa ttc gaa acc tgc gac ccg tca ggg   451
Ala Pro Val Glu Leu Phe Glu Gln Phe Glu Thr Cys Asp Pro Ser Gly
            105                 110                 115

gtc gag gat tcc ttc gcg tgc aac ggg ccg gaa gtt ggc caa ttc caa   499
Val Glu Asp Ser Phe Ala Cys Asn Gly Pro Glu Val Gly Gln Phe Gln
        120                 125                 130

ttc ttt gac aat gcg tcg aag gcc acg agc acg acg cag ctg ctc acg   547
Phe Phe Asp Asn Ala Ser Lys Ala Thr Ser Thr Thr Gln Leu Leu Thr
    135                 140                 145

gaa ctg cgc agc tca cgc gtg gtt gag gat tcc gga tcc aag gtt gtg   595
Glu Leu Arg Ser Ser Arg Val Val Glu Asp Ser Gly Ser Lys Val Val
150                 155                 160                 165

ggc tgg acc acg att ggc acg atg tcg att atc acg gtc gtt gat aat   643
Gly Trp Thr Thr Ile Gly Thr Met Ser Ile Ile Thr Val Val Asp Asn
                170                 175                 180

gac caa ggc cta gtg ctg cag caa atg gtg tcc tcc gac aaa atc gat   691
Asp Gln Gly Leu Val Leu Gln Gln Met Val Ser Ser Asp Lys Ile Asp
            185                 190                 195

ccg gag gaa cgc atc tac gaa ctt ggg ctg tcg aca ccg aag gac act   739
Pro Glu Glu Arg Ile Tyr Glu Leu Gly Leu Ser Thr Pro Lys Asp Thr
        200                 205                 210

gaa gag tcc tcg gaa gaa acc tca gcg tct aaa aac tagccacacg        785
Glu Glu Ser Ser Glu Glu Thr Ser Ala Ser Lys Asn
    215                 220                 225

tctggaaatc aga                                                   798
```

<210> 2248
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 2248

```
Val Ala Ser Thr Pro His Lys His Val Arg Val Ala Leu Gly Leu Val
  1               5                  10                  15
```

```
Ala Leu Ile Pro Leu Leu Ala Ala Cys Thr Gly Gly Gly Ser Thr Glu
             20                  25                  30

Thr Ser Thr Glu Ser Thr Ala Glu Thr Thr Pro Ala Thr Thr Thr Glu
         35                  40                  45

Ala Thr Thr Thr Pro Ala Thr Thr Ala Ser Ser Ser Val Ile Glu Thr
     50                  55                  60

Thr Glu Ser Ser Thr Ala Glu Thr Ser Thr Lys Glu Ser Gly Glu Thr
 65                  70                  75                  80

Ser Thr Ser Lys Pro Arg Met Thr Lys Asp Val Glu Val Ala Tyr Lys
                 85                  90                  95

Ala Phe Ser Ser Leu Ala Pro Val Glu Leu Phe Glu Gln Phe Glu Thr
            100                 105                 110

Cys Asp Pro Ser Gly Val Glu Asp Ser Phe Ala Cys Asn Gly Pro Glu
        115                 120                 125

Val Gly Gln Phe Gln Phe Phe Asp Asn Ala Ser Lys Ala Thr Ser Thr
    130                 135                 140

Thr Gln Leu Leu Thr Glu Leu Arg Ser Ser Arg Val Val Glu Asp Ser
145                 150                 155                 160

Gly Ser Lys Val Val Gly Trp Thr Thr Ile Gly Thr Met Ser Ile Ile
                165                 170                 175

Thr Val Val Asp Asn Asp Gln Gly Leu Val Leu Gln Gln Met Val Ser
            180                 185                 190

Ser Asp Lys Ile Asp Pro Glu Glu Arg Ile Tyr Glu Leu Gly Leu Ser
        195                 200                 205

Thr Pro Lys Asp Thr Glu Glu Ser Ser Glu Glu Thr Ser Ala Ser Lys
    210                 215                 220

Asn
225
```

US 6,962,809 B2

<2210> 2249
<211> 1287
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1264)
<223> RXA01463

<400> 2249
attagaacaa atattcgtta gaacacttgt ttgttttgat ttgtgtggtt agggtgggtg 60

ctaatgagtt aaaaagggga aatttaaacc attaggggc atg gaa atg tca tac 115
Met Glu Met Ser Tyr
1 5

ttc agc cat cag gac cca aat aat cca gag agt cac atc aac ttc acc 163

```
Phe Ser His Gln Asp Pro Asn Asn Pro Glu Ser His Ile Asn Phe Thr
                10                  15                  20

atg gcg caa atg gag atc cag cgc tgg act ttg ctg atc tca aac cca   211
Met Ala Gln Met Glu Ile Gln Arg Trp Thr Leu Leu Ile Ser Asn Pro
            25                  30                  35

gag gcg gac gct agc act ctt gtc atg gag ttg aaa acc gtc acg ggg   259
Glu Ala Asp Ala Ser Thr Leu Val Met Glu Leu Lys Thr Val Thr Gly
        40                  45                  50

gaa tcc aag cat ttt atc aac cag gct att aac gcc atg tgg gct tta   307
Glu Ser Lys His Phe Ile Asn Gln Ala Ile Asn Ala Met Trp Ala Leu
    55                  60                  65

atg aag ctg ccc att tta aga gtg gtg gta gaa act cac ttc cac gtt   355
Met Lys Leu Pro Ile Leu Arg Val Val Val Glu Thr His Phe His Val
70                  75                  80                  85

cgg att ccg tac ctg gcc cgc att atg cag gca gtc aag cag gct aaa   403
Arg Ile Pro Tyr Leu Ala Arg Ile Met Gln Ala Val Lys Gln Ala Lys
                90                  95                  100

ccg gag ttg tgg gat gag ttg gac cat cgc att gcc gaa aag ctg aca   451
Pro Glu Leu Trp Asp Glu Leu Asp His Arg Ile Ala Glu Lys Leu Thr
            105                 110                 115

ccg cgc att gct ggc cag gca ctg atg gaa gcc tcc gca ctt gca ggg   499
Pro Arg Ile Ala Gly Gln Ala Leu Met Glu Ala Ser Ala Leu Ala Gly
        120                 125                 130

ctg att act cgc tgg atc aag gaa ctg gat cca acc ttc aca gga aag   547
Leu Ile Thr Arg Trp Ile Lys Glu Leu Asp Pro Thr Phe Thr Gly Lys
    135                 140                 145

aag cgt ggg cca aag ggg agt gat ggc acc ttg act ttc cgc cac gtg   595
Lys Arg Gly Pro Lys Gly Ser Asp Gly Thr Leu Thr Phe Arg His Val
150                 155                 160                 165

gac ggg cgt acg tac atc agt gga aat att gac ggt gtc acc ggc aag   643
Asp Gly Arg Thr Tyr Ile Ser Gly Asn Ile Asp Gly Val Thr Gly Lys
                170                 175                 180

ctg ttc caa aaa gct ctg gaa aaa gtg aaa cag aag ggc gag gac ctc   691
Leu Phe Gln Lys Ala Leu Glu Lys Val Lys Gln Lys Gly Glu Asp Leu
            185                 190                 195

gcg cgg gcc ctg gtc acc ttc ctg gcg ggg cgg acc aaa gtg aaa atc   739
Ala Arg Ala Leu Val Thr Phe Leu Ala Gly Arg Thr Lys Val Lys Ile
        200                 205                 210

gtc agc gcg gta tac acg ccc ctg gtg ggt ggc gtg tcc tgg att ccg   787
Val Ser Ala Val Tyr Thr Pro Leu Val Gly Gly Val Ser Trp Ile Pro
    215                 220                 225

ggg gtg gga ttc ctg agt caa gag gag tcc cgg aag ctg ggt aag act   835
Gly Val Gly Phe Leu Ser Gln Glu Glu Ser Arg Lys Leu Gly Lys Thr
230                 235                 240                 245

gcc tcg aag gtc att gac ctg gat acg atc gcc act cgt gtg gaa aat   883
Ala Ser Lys Val Ile Asp Leu Asp Thr Ile Ala Thr Arg Val Glu Asn
```

```
                  250                 255                 260

ggc tac acc cca agt ccc gag cta cgc ctt tat gtg atg ggg cgg gac   931
Gly Tyr Thr Pro Ser Pro Glu Leu Arg Leu Tyr Val Met Gly Arg Asp
            265                 270                 275

ggc acc tgt agg cat ccg ggc tgc acg gtg tct gcc gac aac tgc cag   979
Gly Thr Cys Arg His Pro Gly Cys Thr Val Ser Ala Asp Asn Cys Gln
        280                 285                 290

atc gat cac gtg atc ccg ttc ggt gag ggt ggg ttg act gtg gcc tgg   1027
Ile Asp His Val Ile Pro Phe Gly Glu Gly Gly Leu Thr Val Ala Trp
    295                 300                 305

aac ttg cag tgc ctc tgc gcg cat cat cac aat atg aag act gat ggg   1075
Asn Leu Gln Cys Leu Cys Ala His His His Asn Met Lys Thr Asp Gly
310                 315                 320                 325

cgc atc cag gcg gcg att gat tcc atg ggt cgg gtc gcc tgg att ggg   1123
Arg Ile Gln Ala Ala Ile Asp Ser Met Gly Arg Val Ala Trp Ile Gly
                330                 335                 340

ccg tgc aat cgc aca gtg gta acc gaa cct gtc gga ccg ttg gcg caa   1171
Pro Cys Asn Arg Thr Val Val Thr Glu Pro Val Gly Pro Leu Ala Gln
            345                 350                 355

gag atg ccc acg ggg cag tgg ggg cag act ctg gaa gca cgg atg gag   1219
Glu Met Pro Thr Gly Gln Trp Gly Gln Thr Leu Glu Ala Arg Met Glu
        360                 365                 370

aag act ttt gaa aag ctc cgc agt tca ctc gag gta ttg gat gac       1264
Lys Thr Phe Glu Lys Leu Arg Ser Ser Leu Glu Val Leu Asp Asp
    375                 380                 385

taaaccctta tgcacacccc tag                                        1287


<210> 2250
<211> 388
<212> PRT
<213> Corynebacterium glutamicum

<400> 2250
Met Glu Met Ser Tyr Phe Ser His Gln Asp Pro Asn Asn Pro Glu Ser
  1               5                  10                  15

His Ile Asn Phe Thr Met Ala Gln Met Glu Ile Gln Arg Trp Thr Leu
            20                  25                  30

Leu Ile Ser Asn Pro Glu Ala Asp Ala Ser Thr Leu Val Met Glu Leu
        35                  40                  45

Lys Thr Val Thr Gly Glu Ser Lys His Phe Ile Asn Gln Ala Ile Asn
    50                  55                  60

Ala Met Trp Ala Leu Met Lys Leu Pro Ile Leu Arg Val Val Val Glu
65                  70                  75                  80

Thr His Phe His Val Arg Ile Pro Tyr Leu Ala Arg Ile Met Gln Ala
                85                  90                  95
```

```
Val Lys Gln Ala Lys Pro Glu Leu Trp Asp Glu Leu Asp His Arg Ile
            100                 105                 110

Ala Glu Lys Leu Thr Pro Arg Ile Ala Gly Gln Ala Leu Met Glu Ala
        115                 120                 125

Ser Ala Leu Ala Gly Leu Ile Thr Arg Trp Ile Lys Glu Leu Asp Pro
    130                 135                 140

Thr Phe Thr Gly Lys Lys Arg Gly Pro Lys Gly Ser Asp Gly Thr Leu
145                 150                 155                 160

Thr Phe Arg His Val Asp Gly Arg Thr Tyr Ile Ser Gly Asn Ile Asp
                165                 170                 175

Gly Val Thr Gly Lys Leu Phe Gln Lys Ala Leu Glu Lys Val Lys Gln
            180                 185                 190

Lys Gly Glu Asp Leu Ala Arg Ala Leu Val Thr Phe Leu Ala Gly Arg
        195                 200                 205

Thr Lys Val Lys Ile Val Ser Ala Val Tyr Thr Pro Leu Val Gly Gly
    210                 215                 220

Val Ser Trp Ile Pro Gly Val Gly Phe Leu Ser Gln Glu Glu Ser Arg
225                 230                 235                 240

Lys Leu Gly Lys Thr Ala Ser Lys Val Ile Asp Leu Asp Thr Ile Ala
                245                 250                 255

Thr Arg Val Glu Asn Gly Tyr Thr Pro Ser Pro Glu Leu Arg Leu Tyr
            260                 265                 270

Val Met Gly Arg Asp Gly Thr Cys Arg His Pro Gly Cys Thr Val Ser
        275                 280                 285

Ala Asp Asn Cys Gln Ile Asp His Val Ile Pro Phe Gly Glu Gly Gly
    290                 295                 300

Leu Thr Val Ala Trp Asn Leu Gln Cys Leu Cys Ala His His His Asn
305                 310                 315                 320

Met Lys Thr Asp Gly Arg Ile Gln Ala Ala Ile Asp Ser Met Gly Arg
                325                 330                 335

Val Ala Trp Ile Gly Pro Cys Asn Arg Thr Val Val Thr Glu Pro Val
            340                 345                 350

Gly Pro Leu Ala Gln Glu Met Pro Thr Gly Gln Trp Gly Gln Thr Leu
        355                 360                 365

Glu Ala Arg Met Glu Lys Thr Phe Glu Lys Leu Arg Ser Ser Leu Glu
    370                 375                 380

Val Leu Asp Asp
385
```

<210> 2251
<211> 1155
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1132)
<223> RXA01469

<400> 2251
tccatcgccg atcttgccga ttgctgggac gatcctttcg gtgacggtgc atttcacgta 60

ccagatgagc agcagttcac tgactagtat tctgtaggtc atg gca ttt gca gac 115
Met Ala Phe Ala Asp
1 5

att gtg cgc agc gtc gaa aac cgc acc aac gca gcg acc ctc aac tgg 163
Ile Val Arg Ser Val Glu Asn Arg Thr Asn Ala Ala Thr Leu Asn Trp
10 15 20

tcc atc aaa aat ggc tgg aag ccc gaa gtc acc gga ttt tcc ggg tac 211
Ser Ile Lys Asn Gly Trp Lys Pro Glu Val Thr Gly Phe Ser Gly Tyr
25 30 35

ggc tcc ggg cgt cga gtg cgc gtc ctt gcg cgc gtg ctc atg tcc aac 259
Gly Ser Gly Arg Arg Val Arg Val Leu Ala Arg Val Leu Met Ser Asn
40 45 50

ccc gaa aat ttg ctt gtc gac gcc ccc tcc caa tca att acc caa caa 307
Pro Glu Asn Leu Leu Val Asp Ala Pro Ser Gln Ser Ile Thr Gln Gln
55 60 65

gca cag cgc ggt tgg cgc cag ttc ttc acc atc caa gtg ccc aac ctg 355
Ala Gln Arg Gly Trp Arg Gln Phe Phe Thr Ile Gln Val Pro Asn Leu
70 75 80 85

cca gta act gtc acc gtt ggt ggg aaa aca gtt acc tca tcc acc aac 403
Pro Val Thr Val Thr Val Gly Gly Lys Thr Val Thr Ser Ser Thr Asn
90 95 100

gac aac ggc tac gtt gac ctc ctg gtg gaa gac cac aac ctt gac ccc 451
Asp Asn Gly Tyr Val Asp Leu Leu Val Glu Asp His Asn Leu Asp Pro
105 110 115

ggc tgg cac acc atc cag atc caa gcc gaa ggt tcc acc ccc gcc gaa 499
Gly Trp His Thr Ile Gln Ile Gln Ala Glu Gly Ser Thr Pro Ala Glu
120 125 130

gcc cgc gtc ctc atc gtg gaa aac acc gcc cga atc gga ctc atc tcc 547
Ala Arg Val Leu Ile Val Glu Asn Thr Ala Arg Ile Gly Leu Ile Ser
135 140 145

gac atc gac gac acc atc atg gtc acc tgg ctt ccc cga gca ctc ctc 595
Asp Ile Asp Asp Thr Ile Met Val Thr Trp Leu Pro Arg Ala Leu Leu
150 155 160 165

gcc gca tgg aac tcg tgg gtt ttg cac acc aac acc cgc aaa cca gtc 643
Ala Ala Trp Asn Ser Trp Val Leu His Thr Asn Thr Arg Lys Pro Val
170 175 180

ccc gga atg aac cgc ttc tac gaa gaa ctc ctc aaa gac cac ccc gac 691
Pro Gly Met Asn Arg Phe Tyr Glu Glu Leu Leu Lys Asp His Pro Asp
185 190 195

```
gca ccc gtg ttc tac ctc tcc acc ggc gca tgg aac acc ttt gaa acc   739
Ala Pro Val Phe Tyr Leu Ser Thr Gly Ala Trp Asn Thr Phe Glu Thr
        200                 205                 210

ctc caa gag ttc atc aac aaa cac gca ctc ccc gac ggc ccc atg ctg   787
Leu Gln Glu Phe Ile Asn Lys His Ala Leu Pro Asp Gly Pro Met Leu
    215                 220                 225

ctc acc gac tgg gga cca acc ccc aca gga cta ttc cgc tca ggt caa   835
Leu Thr Asp Trp Gly Pro Thr Pro Thr Gly Leu Phe Arg Ser Gly Gln
230                 235                 240                 245

gag cac aag aaa gtc caa ctg cgc aac ctg ttt atc gaa tac ccc gac   883
Glu His Lys Lys Val Gln Leu Arg Asn Leu Phe Ile Glu Tyr Pro Asp
                250                 255                 260

atg aaa tgg atc ctc gtc ggc gac gat ggc caa cac gat ccc ctc atc   931
Met Lys Trp Ile Leu Val Gly Asp Asp Gly Gln His Asp Pro Leu Ile
            265                 270                 275

tac ggc gaa gca gtc gaa gaa cac ccc aac cgc atc gca ggc gtt gca   979
Tyr Gly Glu Ala Val Glu Glu His Pro Asn Arg Ile Ala Gly Val Ala
        280                 285                 290

atc cgt gag ctc tcc ccc ggc gaa cat gtg ctc tcc cac gga aca act  1027
Ile Arg Glu Leu Ser Pro Gly Glu His Val Leu Ser His Gly Thr Thr
    295                 300                 305

gcg tca ctg tcc acc atc acg acc aac ggg ggc caa gga gtc cca gta  1075
Ala Ser Leu Ser Thr Ile Thr Thr Asn Gly Gly Gln Gly Val Pro Val
310                 315                 320                 325

gtt cac ggc cgc gat gga tat gag ttg ctg cag cgc tac gag acg aag  1123
Val His Gly Arg Asp Gly Tyr Glu Leu Leu Gln Arg Tyr Glu Thr Lys
                330                 335                 340

ccg ttc gcc tgagtcctac tgggtgtctc atg                           1155
Pro Phe Ala
```

<210> 2252
<211> 344
<212> PRT
<213> Corynebacterium glutamicum

<400> 2252

```
Met Ala Phe Ala Asp Ile Val Arg Ser Val Glu Asn Arg Thr Asn Ala
  1               5                  10                  15

Ala Thr Leu Asn Trp Ser Ile Lys Asn Gly Trp Lys Pro Glu Val Thr
             20                  25                  30

Gly Phe Ser Gly Tyr Gly Ser Gly Arg Arg Val Arg Val Leu Ala Arg
         35                  40                  45

Val Leu Met Ser Asn Pro Glu Asn Leu Leu Val Asp Ala Pro Ser Gln
     50                  55                  60

Ser Ile Thr Gln Gln Ala Gln Arg Gly Trp Arg Gln Phe Phe Thr Ile
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 65                  70                  75                  80

Gln Val Pro Asn Leu Pro Val Thr Val Thr Val Gly Gly Lys Thr Val
                 85                  90                  95

Thr Ser Ser Thr Asn Asp Asn Gly Tyr Val Asp Leu Leu Val Glu Asp
            100                 105                 110

His Asn Leu Asp Pro Gly Trp His Thr Ile Gln Ile Gln Ala Glu Gly
        115                 120                 125

Ser Thr Pro Ala Glu Ala Arg Val Leu Ile Val Glu Asn Thr Ala Arg
    130                 135                 140

Ile Gly Leu Ile Ser Asp Ile Asp Asp Thr Ile Met Val Thr Trp Leu
145                 150                 155                 160

Pro Arg Ala Leu Leu Ala Ala Trp Asn Ser Trp Val Leu His Thr Asn
                165                 170                 175

Thr Arg Lys Pro Val Pro Gly Met Asn Arg Phe Tyr Glu Glu Leu Leu
            180                 185                 190

Lys Asp His Pro Asp Ala Pro Val Phe Tyr Leu Ser Thr Gly Ala Trp
        195                 200                 205

Asn Thr Phe Glu Thr Leu Gln Glu Phe Ile Asn Lys His Ala Leu Pro
    210                 215                 220

Asp Gly Pro Met Leu Leu Thr Asp Trp Gly Pro Thr Pro Thr Gly Leu
225                 230                 235                 240

Phe Arg Ser Gly Gln Glu His Lys Lys Val Gln Leu Arg Asn Leu Phe
                245                 250                 255

Ile Glu Tyr Pro Asp Met Lys Trp Ile Leu Val Gly Asp Asp Gly Gln
            260                 265                 270

His Asp Pro Leu Ile Tyr Gly Glu Ala Val Glu Glu His Pro Asn Arg
        275                 280                 285

Ile Ala Gly Val Ala Ile Arg Glu Leu Ser Pro Gly Glu His Val Leu
    290                 295                 300

Ser His Gly Thr Thr Ala Ser Leu Ser Thr Ile Thr Thr Asn Gly Gly
305                 310                 315                 320

Gln Gly Val Pro Val Val His Gly Arg Asp Gly Tyr Glu Leu Leu Gln
                325                 330                 335

Arg Tyr Glu Thr Lys Pro Phe Ala
            340
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<210> 2253
<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(526)
<223> RXA01470

<400> 2253
aagacgaacc tcgtcttact tcctttagta actgcacata tctacttgta tatgtgtgcg 60

ggaattgaag gcagttaagt gttgccgaag gaaaccgaac atg acg aac aat gca 115
Met Thr Asn Asn Ala
1 5

tta acc gtg cca acc cgg acc cgt cat cag gcg gat ttg ctc acg gca 163
Leu Thr Val Pro Thr Arg Thr Arg His Gln Ala Asp Leu Leu Thr Ala
10 15 20

gac ttc tgg gaa gac atg ggg ttg ccc caa ctg aaa act acc atc gaa 211
Asp Phe Trp Glu Asp Met Gly Leu Pro Gln Leu Lys Thr Thr Ile Glu
25 30 35

gaa tcc atc gac gat gta gcc ctc cca atg cat acc gct gtt cta gaa 259
Glu Ser Ile Asp Asp Val Ala Leu Pro Met His Thr Ala Val Leu Glu
40 45 50

atc agc gga atg cca aag gaa ctg cgt cag acc gtg gaa tcc gca atg 307
Ile Ser Gly Met Pro Lys Glu Leu Arg Gln Thr Val Glu Ser Ala Met
55 60 65

gtt gtg tgt att ccg agt cct tcg gag ctg tcc ggc tcc aac agg gac 355
Val Val Cys Ile Pro Ser Pro Ser Glu Leu Ser Gly Ser Asn Arg Asp
70 75 80 85

ccg ctc acc gca cga tgg ttc act gca tgg cgc cgt gac cca ttc gaa 403
Pro Leu Thr Ala Arg Trp Phe Thr Ala Trp Arg Arg Asp Pro Phe Glu
90 95 100

ctt ggc ctc act gag tgt cga gag gtg atc acc gga act cca cgc gaa 451
Leu Gly Leu Thr Glu Cys Arg Glu Val Ile Thr Gly Thr Pro Arg Glu
105 110 115

ctc gac aaa ctt cga gga gtg ctg gaa tct ctg gct gat gaa tac cgt 499
Leu Asp Lys Leu Arg Gly Val Leu Glu Ser Leu Ala Asp Glu Tyr Arg
120 125 130

ttt gaa gtt gag ctg cga atc gtt gac tagaaagcca gtgattcttt 546
Phe Glu Val Glu Leu Arg Ile Val Asp
135 140

agc 549

<210> 2254
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 2254
Met Thr Asn Asn Ala Leu Thr Val Pro Thr Arg Thr Arg His Gln Ala
1 5 10 15

Asp Leu Leu Thr Ala Asp Phe Trp Glu Asp Met Gly Leu Pro Gln Leu
20 25 30

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Lys Thr Thr Ile Glu Glu Ser Ile Asp Asp Val Ala Leu Pro Met His
          35                  40                  45

Thr Ala Val Leu Glu Ile Ser Gly Met Pro Lys Glu Leu Arg Gln Thr
      50                  55                  60

Val Glu Ser Ala Met Val Val Cys Ile Pro Ser Pro Ser Glu Leu Ser
 65                  70                  75                  80

Gly Ser Asn Arg Asp Pro Leu Thr Ala Arg Trp Phe Thr Ala Trp Arg
                 85                  90                  95

Arg Asp Pro Phe Glu Leu Gly Leu Thr Glu Cys Arg Glu Val Ile Thr
            100                 105                 110

Gly Thr Pro Arg Glu Leu Asp Lys Leu Arg Gly Val Leu Glu Ser Leu
        115                 120                 125

Ala Asp Glu Tyr Arg Phe Glu Val Glu Leu Arg Ile Val Asp
    130                 135                 140
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<210> 2255
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXA01472

<400> 2255

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gcacgtccac gcgccggact tgcgcgccta tttacaagca cgcttatcga cgtaattaca 60

ctcggtggaa accgtcgcgg aaaaatggag gatcctcgcc atg aac caa gca aac   115
                                            Met Asn Gln Ala Asn
                                              1               5

ctg cct gcc gaa atc gcg gac ctc tcc gat gaa acc gca ctg tgg gaa   163
Leu Pro Ala Glu Ile Ala Asp Leu Ser Asp Glu Thr Ala Leu Trp Glu
                 10                  15                  20

atc atc aac gaa tac aac tgg gac gac ggc ttc gcg gtt ccc ctt gca   211
Ile Ile Asn Glu Tyr Asn Trp Asp Asp Gly Phe Ala Val Pro Leu Ala
             25                  30                  35

gta gtc cga cac ccc aaa tgc gac cga gcg cta gcc ctt cgc ctg ttt   259
Val Val Arg His Pro Lys Cys Asp Arg Ala Leu Ala Leu Arg Leu Phe
         40                  45                  50

tgg gac atc gat gaa acc gcc caa atc cac cac tcc gac gaa gaa tca   307
Trp Asp Ile Asp Glu Thr Ala Gln Ile His His Ser Asp Glu Glu Ser
     55                  60                  65

gcg atc gcc gag ttg tac gcc agc acc gca gaa aac gac cca gca gaa   355
Ala Ile Ala Glu Leu Tyr Ala Ser Thr Ala Glu Asn Asp Pro Ala Glu
 70                  75                  80                  85

ttc gac aga atc atg gac tac tgc acc aca ctg gtc gaa ggg ctc cgc   403
Phe Asp Arg Ile Met Asp Tyr Cys Thr Thr Leu Val Glu Gly Leu Arg
```

```
                  90                  95                 100

aag cag acc tat cct cgg ggc gcc aac cgt ttc gac acg gga ttt ttc   451
Lys Gln Thr Tyr Pro Arg Gly Ala Asn Arg Phe Asp Thr Gly Phe Phe
            105                 110                 115

aac ctc gag gac cct tct ttg acc gac cgt cag cgc aaa atc cgc gcc   499
Asn Leu Glu Asp Pro Ser Leu Thr Asp Arg Gln Arg Lys Ile Arg Ala
        120                 125                 130

ggg aaa acc aaa ttt gcg ctc aag aat ttc gag gaa gct ttc ctc caa   547
Gly Lys Thr Lys Phe Ala Leu Lys Asn Phe Glu Glu Ala Phe Leu Gln
    135                 140                 145

cca gag cta taaaaaaggt tgtagaagaa att                            579
Pro Glu Leu
150
```

<210> 2256
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 2256

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Met Asn Gln Ala Asn Leu Pro Ala Glu Ile Ala Asp Leu Ser Asp Glu
  1               5                  10                  15

Thr Ala Leu Trp Glu Ile Ile Asn Glu Tyr Asn Trp Asp Asp Gly Phe
             20                  25                  30

Ala Val Pro Leu Ala Val Val Arg His Pro Lys Cys Asp Arg Ala Leu
         35                  40                  45

Ala Leu Arg Leu Phe Trp Asp Ile Asp Glu Thr Ala Gln Ile His His
     50                  55                  60

Ser Asp Glu Glu Ser Ala Ile Ala Glu Leu Tyr Ala Ser Thr Ala Glu
 65                  70                  75                  80

Asn Asp Pro Ala Glu Phe Asp Arg Ile Met Asp Tyr Cys Thr Thr Leu
                85                  90                  95

Val Glu Gly Leu Arg Lys Gln Thr Tyr Pro Arg Gly Ala Asn Arg Phe
            100                 105                 110

Asp Thr Gly Phe Phe Asn Leu Glu Asp Pro Ser Leu Thr Asp Arg Gln
        115                 120                 125

Arg Lys Ile Arg Ala Gly Lys Thr Lys Phe Ala Leu Lys Asn Phe Glu
    130                 135                 140

Glu Ala Phe Leu Gln Pro Glu Leu
145                 150
```

<210> 2257
<211> 888
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(865)
<223> RXA01473

<400> 2257
cgtaagcaat tcccaccaat gcagtttcct cggtgcgtta tagtgtcgag tagggccaaa 60

aaccaacaat atcctggtag ccaagaataa gatcgtgctt atg act gac atc ggt 115
Met Thr Asp Ile Gly
1 5

gat gtc gat caa ata gtc tgg gaa ttc atc cat ttc cac gat gac tcg 163
Asp Val Asp Gln Ile Val Trp Glu Phe Ile His Phe His Asp Asp Ser
10 15 20

ata aat cca ttc ttt gag ttc atc aag agt gat tgc atc aac gat gag 211
Ile Asn Pro Phe Phe Glu Phe Ile Lys Ser Asp Cys Ile Asn Asp Glu
25 30 35

gca atc gaa cgc aaa acc cag atc ctc gga atc atc ttg ggt aac gag 259
Ala Ile Glu Arg Lys Thr Gln Ile Leu Gly Ile Ile Leu Gly Asn Glu
40 45 50

cca tgc ggg agt gtt att cac gcc cgc cag aat aca ata aag ccc atg 307
Pro Cys Gly Ser Val Ile His Ala Arg Gln Asn Thr Ile Lys Pro Met
55 60 65

agc cat acg gtc tct ttt ggc gac ggc tgg atc caa gtc ctt gag gat 355
Ser His Thr Val Ser Phe Gly Asp Gly Trp Ile Gln Val Leu Glu Asp
70 75 80 85

gct gca gaa acc gtg tcg atc acc gac acg ttg gat gcc ctc cga ttt 403
Ala Ala Glu Thr Val Ser Ile Thr Asp Thr Leu Asp Ala Leu Arg Phe
90 95 100

tct ccc gag caa gcg gaa tgg gct gca gaa ttc gga cca cta ctg tgc 451
Ser Pro Glu Gln Ala Glu Trp Ala Ala Glu Phe Gly Pro Leu Leu Cys
105 110 115

ggc cca gcg aac caa ccg ccg gcg tat ctc acg gct tta gac ggg cac 499
Gly Pro Ala Asn Gln Pro Pro Ala Tyr Leu Thr Ala Leu Asp Gly His
120 125 130

aca aag cta ccg ctt agc ccg cag ctg acg gag ttc tat agc tac gcc 547
Thr Lys Leu Pro Leu Ser Pro Gln Leu Thr Glu Phe Tyr Ser Tyr Ala
135 140 145

cga tcc tgg aca aac agt gag gcc ttg gga aac gtc att gat ccc gat 595
Arg Ser Trp Thr Asn Ser Glu Ala Leu Gly Asn Val Ile Asp Pro Asp
150 155 160 165

gac tac ctc gat cat ctc acc gac cct cgc ctt cat ttg cag gat ctt 643
Asp Tyr Leu Asp His Leu Thr Asp Pro Arg Leu His Leu Gln Asp Leu
170 175 180

ctg gat aat gag ttt gaa cgg gtg ggg gtg ctc gtc gat aag caa aat 691
Leu Asp Asn Glu Phe Glu Arg Val Gly Val Leu Val Asp Lys Gln Asn
185 190 195

cgc ccg ctc gac cct gcc cgg tgc gcg ctg ttc tcg ctc gac gca ctt 739

```
Arg Pro Leu Asp Pro Ala Arg Cys Ala Leu Phe Ser Leu Asp Ala Leu
        200                 205                 210

gca cgc gcg ccc tac aac cgc gcc tac ttc gtc ttc gcc gcg ccc gag   787
Ala Arg Ala Pro Tyr Asn Arg Ala Tyr Phe Val Phe Ala Ala Pro Glu
    215                 220                 225

cct gag atc tgg gcg ttt gag aac gag cac gtc cac gcg ccg gac ttg   835
Pro Glu Ile Trp Ala Phe Glu Asn Glu His Val His Ala Pro Asp Leu
230                 235                 240                 245

cgc gcc tat tta caa gca cgc tta tcg acg taattacact cggtggaaac     885
Arg Ala Tyr Leu Gln Ala Arg Leu Ser Thr
                250                 255

cgt                                                               888


<210> 2258
<211> 255
<212> PRT
<213> Corynebacterium glutamicum

<400> 2258
Met Thr Asp Ile Gly Asp Val Asp Gln Ile Val Trp Glu Phe Ile His
  1               5                  10                  15

Phe His Asp Asp Ser Ile Asn Pro Phe Phe Glu Phe Ile Lys Ser Asp
             20                  25                  30

Cys Ile Asn Asp Glu Ala Ile Glu Arg Lys Thr Gln Ile Leu Gly Ile
         35                  40                  45

Ile Leu Gly Asn Glu Pro Cys Gly Ser Val Ile His Ala Arg Gln Asn
     50                  55                  60

Thr Ile Lys Pro Met Ser His Thr Val Ser Phe Gly Asp Gly Trp Ile
 65                  70                  75                  80

Gln Val Leu Glu Asp Ala Ala Glu Thr Val Ser Ile Thr Asp Thr Leu
                 85                  90                  95

Asp Ala Leu Arg Phe Ser Pro Glu Gln Ala Glu Trp Ala Ala Glu Phe
            100                 105                 110

Gly Pro Leu Leu Cys Gly Pro Ala Asn Gln Pro Pro Ala Tyr Leu Thr
        115                 120                 125

Ala Leu Asp Gly His Thr Lys Leu Pro Leu Ser Pro Gln Leu Thr Glu
    130                 135                 140

Phe Tyr Ser Tyr Ala Arg Ser Trp Thr Asn Ser Glu Ala Leu Gly Asn
145                 150                 155                 160

Val Ile Asp Pro Asp Asp Tyr Leu Asp His Leu Thr Asp Pro Arg Leu
                165                 170                 175

His Leu Gln Asp Leu Leu Asp Asn Glu Phe Glu Arg Val Gly Val Leu
            180                 185                 190

Val Asp Lys Gln Asn Arg Pro Leu Asp Pro Ala Arg Cys Ala Leu Phe
```

```
        195                 200                 205

Ser Leu Asp Ala Leu Ala Arg Ala Pro Tyr Asn Arg Ala Tyr Phe Val
    210                 215                 220

Phe Ala Ala Pro Glu Pro Glu Ile Trp Ala Phe Glu Asn Glu His Val
225                 230                 235                 240

His Ala Pro Asp Leu Arg Ala Tyr Leu Gln Ala Arg Leu Ser Thr
                245                 250                 255


<210> 2259
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(646)
<223> RXA01474

<400> 2259
catcaccgat gtcagtcata agcacgatct tattcttggc taccaggata ttgttggttt 60

ttggccctac tcgacactat aacgcaccga ggaaactgca ttg gtg gga att gct   115
                                              Leu Val Gly Ile Ala
                                                1               5

tac gcc cgt ttc cct gat acc cgc gac gat tcc atc agc cgc ggc aaa   163
Tyr Ala Arg Phe Pro Asp Thr Arg Asp Asp Ser Ile Ser Arg Gly Lys
                10                  15                  20

gca cga tca gcg ttg gag aaa tcc acg ggc ctt aaa gag cgt ttc gcg   211
Ala Arg Ser Ala Leu Glu Lys Ser Thr Gly Leu Lys Glu Arg Phe Ala
            25                  30                  35

cgt cat ttt cct gca att tcc ata cct gtc gat acg ggt gat gct gca   259
Arg His Phe Pro Ala Ile Ser Ile Pro Val Asp Thr Gly Asp Ala Ala
        40                  45                  50

gat att ctc gta tcg ggt tgg tgg ctt tca ggt tct aaa aag aag atc   307
Asp Ile Leu Val Ser Gly Trp Trp Leu Ser Gly Ser Lys Lys Lys Ile
    55                  60                  65

ctg act gca gcg gaa atc cag acc tta ttt atc aac cga ttg gcc aca   355
Leu Thr Ala Ala Glu Ile Gln Thr Leu Phe Ile Asn Arg Leu Ala Thr
70                  75                  80                  85

ggt cca ttg agc act caa ttg gaa act gct acc ggg ttg aaa ctg cag   403
Gly Pro Leu Ser Thr Gln Leu Glu Thr Ala Thr Gly Leu Lys Leu Gln
                90                  95                  100

gtg gtg acc aat cga gag cgt atg aag atc act ctc att gaa ccc aaa   451
Val Val Thr Asn Arg Glu Arg Met Lys Ile Thr Leu Ile Glu Pro Lys
            105                 110                 115

ggc aca tca gga cat gcc atc gac ccc caa gct ggc aag ggt tca agg   499
Gly Thr Ser Gly His Ala Ile Asp Pro Gln Ala Gly Lys Gly Ser Arg
        120                 125                 130
```

```
ggt ggc ttc ctc ctg gac aat ggc caa gaa gat gaa tac gac gat gtc   547
Gly Gly Phe Leu Leu Asp Asn Gly Gln Glu Asp Glu Tyr Asp Asp Val
    135                 140                 145

gac acc gtc aca atc ccc gat gca ctc aat gtc atc ggt tac att ctt   595
Asp Thr Val Thr Ile Pro Asp Ala Leu Asn Val Ile Gly Tyr Ile Leu
150                 155                 160                 165

acc cat gga act cca cct caa gaa ggc tgg aag gta gac gtg ttg gag   643
Thr His Gly Thr Pro Pro Gln Glu Gly Trp Lys Val Asp Val Leu Glu
                170                 175                 180

cgt tagtcctcga tgaattcttc tcc                                    669
Arg
```

<210> 2260
<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 2260

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Leu Val Gly Ile Ala Tyr Ala Arg Phe Pro Asp Thr Arg Asp Asp Ser
  1               5                  10                  15

Ile Ser Arg Gly Lys Ala Arg Ser Ala Leu Glu Lys Ser Thr Gly Leu
             20                  25                  30

Lys Glu Arg Phe Ala Arg His Phe Pro Ala Ile Ser Ile Pro Val Asp
         35                  40                  45

Thr Gly Asp Ala Ala Asp Ile Leu Val Ser Gly Trp Trp Leu Ser Gly
     50                  55                  60

Ser Lys Lys Lys Ile Leu Thr Ala Ala Glu Ile Gln Thr Leu Phe Ile
 65                  70                  75                  80

Asn Arg Leu Ala Thr Gly Pro Leu Ser Thr Gln Leu Glu Thr Ala Thr
                 85                  90                  95

Gly Leu Lys Leu Gln Val Val Thr Asn Arg Glu Arg Met Lys Ile Thr
            100                 105                 110

Leu Ile Glu Pro Lys Gly Thr Ser Gly His Ala Ile Asp Pro Gln Ala
        115                 120                 125

Gly Lys Gly Ser Arg Gly Gly Phe Leu Leu Asp Asn Gly Gln Glu Asp
    130                 135                 140

Glu Tyr Asp Asp Val Asp Thr Val Thr Ile Pro Asp Ala Leu Asn Val
145                 150                 155                 160

Ile Gly Tyr Ile Leu Thr His Gly Thr Pro Pro Gln Glu Gly Trp Lys
                165                 170                 175

Val Asp Val Leu Glu Arg
            180
```

<210> 2261

<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(526)
<223> RXA01475

<400> 2261
tggatctcaa tgtagtcgca atacggcttt tattcgtcag gcagttctgc gaatagtatt 60

cgtgcacatt ggattcacac ccgtagtagt ttttgggggа atg agc atc caa ggg 115
Met Ser Ile Gln Gly
1 5

ttt tcc gca ggt gac tat tct gca tgt ttt gaa ccg cgc atc gat gcg 163
Phe Ser Ala Gly Asp Tyr Ser Ala Cys Phe Glu Pro Arg Ile Asp Ala
10 15 20

tgg gtt gat att cgc ggt ccg cgg aag ccc gag tgg ttg gcg gaa aat 211
Trp Val Asp Ile Arg Gly Pro Arg Lys Pro Glu Trp Leu Ala Glu Asn
25 30 35

atc gat aat ccg ctg aga cac tgg ggc gat aat cct cat atc ccg gtg 259
Ile Asp Asn Pro Leu Arg His Trp Gly Asp Asn Pro His Ile Pro Val
40 45 50

tct gct gcg aaa aag gct gga aat att tac aaa gag acc ctt cga acc 307
Ser Ala Ala Lys Lys Ala Gly Asn Ile Tyr Lys Glu Thr Leu Arg Thr
55 60 65

atg aga gcc tca aca aag acc cca gac cag gat ccc tta aaa gaa acc 355
Met Arg Ala Ser Thr Lys Thr Pro Asp Gln Asp Pro Leu Lys Glu Thr
70 75 80 85

ctg cgc agc ttc atc gca agc atc aac cag ctc gcc gca aag aag aat 403
Leu Arg Ser Phe Ile Ala Ser Ile Asn Gln Leu Ala Ala Lys Lys Asn
90 95 100

ttc att gat gcc ggg gtg cgc gaa gat atc gtt gtt gcg ctg gaa aaa 451
Phe Ile Asp Ala Gly Val Arg Glu Asp Ile Val Val Ala Leu Glu Lys
105 110 115

cta tgc gaa gca gca gaa gct agc cca gaa gaa att cag cag gcg atc 499
Leu Cys Glu Ala Ala Glu Ala Ser Pro Glu Glu Ile Gln Gln Ala Ile
120 125 130

gtg atg gga gaa gaa ttc atc gag gac taacgctcca acacgtctac 546
Val Met Gly Glu Glu Phe Ile Glu Asp
135 140

ctt 549

<210> 2262
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 2262

```
Met Ser Ile Gln Gly Phe Ser Ala Gly Asp Tyr Ser Ala Cys Phe Glu
  1               5                  10                  15

Pro Arg Ile Asp Ala Trp Val Asp Ile Arg Gly Pro Arg Lys Pro Glu
             20                  25                  30

Trp Leu Ala Glu Asn Ile Asp Asn Pro Leu Arg His Trp Gly Asp Asn
         35                  40                  45

Pro His Ile Pro Val Ser Ala Ala Lys Lys Ala Gly Asn Ile Tyr Lys
     50                  55                  60

Glu Thr Leu Arg Thr Met Arg Ala Ser Thr Lys Thr Pro Asp Gln Asp
 65                  70                  75                  80

Pro Leu Lys Glu Thr Leu Arg Ser Phe Ile Ala Ser Ile Asn Gln Leu
                 85                  90                  95

Ala Ala Lys Lys Asn Phe Ile Asp Ala Gly Val Arg Glu Asp Ile Val
            100                 105                 110

Val Ala Leu Glu Lys Leu Cys Glu Ala Ala Glu Ala Ser Pro Glu Glu
        115                 120                 125

Ile Gln Gln Ala Ile Val Met Gly Glu Glu Phe Ile Glu Asp
    130                 135                 140


<210> 2263
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXA01476

<400> 2263
atccaagaaa tttcgcacct caggagtagc gatacttcgt aaatttggga agaaggagta 60

gccacatgac gttgatcgac ctcactgctg gagtgagcgc atg agc gat tca ccg   115
                                            Met Ser Asp Ser Pro
                                              1               5

tgc acc gtc gtc atc ctg aac cgc aca gct act gcg act tcc atc ctg   163
Cys Thr Val Val Ile Leu Asn Arg Thr Ala Thr Ala Thr Ser Ile Leu
                 10                  15                  20

aga gat att aaa gcc ctc acc ggt tac ggc ctg tct gag atc agg tcg   211
Arg Asp Ile Lys Ala Leu Thr Gly Tyr Gly Leu Ser Glu Ile Arg Ser
             25                  30                  35

cgc atc gtt gcg gga ctt ccc gtc gtg atc gag gag atg ttc tca aac   259
Arg Ile Val Ala Gly Leu Pro Val Val Ile Glu Glu Met Phe Ser Asn
         40                  45                  50

gcc tgg tac gac gaa cgc gca caa ctg ttg ctg gca ctg ctg acc aaa   307
Ala Trp Tyr Asp Glu Arg Ala Gln Leu Leu Leu Ala Leu Leu Thr Lys
     55                  60                  65
```

```
tgg cag aac gaa gga atc aca ttc gag att cgg gaa gtc gct gag gat   355
Trp Gln Asn Glu Gly Ile Thr Phe Glu Ile Arg Glu Val Ala Glu Asp
 70                  75                  80                  85

gat ccc atc gaa gca ggg gca ttg atc tct cta gaa gtg ctg cga aac   403
Asp Pro Ile Glu Ala Gly Ala Leu Ile Ser Leu Glu Val Leu Arg Asn
                 90                  95                 100

atc att gag cca gac gat aat gaa tcg agg gac ggt atc tagtggtgaa    452
Ile Ile Glu Pro Asp Asp Asn Glu Ser Arg Asp Gly Ile
            105                 110

cgtaaacccc cgg                                                   465


<210> 2264
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 2264
Met Ser Asp Ser Pro Cys Thr Val Val Ile Leu Asn Arg Thr Ala Thr
  1               5                  10                  15

Ala Thr Ser Ile Leu Arg Asp Ile Lys Ala Leu Thr Gly Tyr Gly Leu
             20                  25                  30

Ser Glu Ile Arg Ser Arg Ile Val Ala Gly Leu Pro Val Val Ile Glu
         35                  40                  45

Glu Met Phe Ser Asn Ala Trp Tyr Asp Glu Arg Ala Gln Leu Leu Leu
     50                  55                  60

Ala Leu Leu Thr Lys Trp Gln Asn Glu Gly Ile Thr Phe Glu Ile Arg
 65                  70                  75                  80

Glu Val Ala Glu Asp Asp Pro Ile Glu Ala Gly Ala Leu Ile Ser Leu
                 85                  90                  95

Glu Val Leu Arg Asn Ile Ile Glu Pro Asp Asp Asn Glu Ser Arg Asp
            100                 105                 110

Gly Ile



<210> 2265
<211> 954
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(931)
<223> RXA01488

<400> 2265
ccttgatatc gccaccggca tcgatgatgc cctcgcactt gcctacgcac tgggctcacc 60

tgaactagag ctcattggtg tcaccaccac ctacggtaac gtg cta ctc gaa acc   115
                                            Val Leu Leu Glu Thr
```

```
                                                        1               5

ggt gca gtc aat gac ctg gca ctg ctt gat ctg ttc ggt gca cca gaa   163
Gly Ala Val Asn Asp Leu Ala Leu Leu Asp Leu Phe Gly Ala Pro Glu
                 10                  15                  20

gta cct gtg tac ttg ggt gag cca cac gca cag acc aag gat ggc ttt   211
Val Pro Val Tyr Leu Gly Glu Pro His Ala Gln Thr Lys Asp Gly Phe
             25                  30                  35

gaa gtt ctt gag atc tcc gcg ttc att cac gga caa aac ggc atc ggc   259
Glu Val Leu Glu Ile Ser Ala Phe Ile His Gly Gln Asn Gly Ile Gly
         40                  45                  50

gaa gtc gag ctg cca gca agc gag tca aag gca ctc ccc ggc gca gtg   307
Glu Val Glu Leu Pro Ala Ser Glu Ser Lys Ala Leu Pro Gly Ala Val
     55                  60                  65

gat ttc ctc att gat tcc gtc aac acc cac ggc gat gac ctg gtg atc   355
Asp Phe Leu Ile Asp Ser Val Asn Thr His Gly Asp Asp Leu Val Ile
 70                  75                  80                  85

atc gca act ggt ccc atg acc aac ctg tct gcg gca atc gca aag gat   403
Ile Ala Thr Gly Pro Met Thr Asn Leu Ser Ala Ala Ile Ala Lys Asp
                 90                  95                 100

cca agc ttt gct tcc aag gct cac gtg gtc atc atg ggt ggc gcc ttg   451
Pro Ser Phe Ala Ser Lys Ala His Val Val Ile Met Gly Gly Ala Leu
            105                 110                 115

act gtc cca ggc aac gtc agc aca tgg gca gaa gca aac atc aac cag   499
Thr Val Pro Gly Asn Val Ser Thr Trp Ala Glu Ala Asn Ile Asn Gln
        120                 125                 130

gac cca gat gca gca aac gat ctg ttc cgt tcc ggt gca gat gtc acc   547
Asp Pro Asp Ala Ala Asn Asp Leu Phe Arg Ser Gly Ala Asp Val Thr
    135                 140                 145

atg atc ggt ctt gat gtc acc ctg cag acc ctt ctt acc aag aag cac   595
Met Ile Gly Leu Asp Val Thr Leu Gln Thr Leu Leu Thr Lys Lys His
150                 155                 160                 165

act gcg cag tgg cgc gaa ctg ggc act cca gct gct atc gca ctg gcc   643
Thr Ala Gln Trp Arg Glu Leu Gly Thr Pro Ala Ala Ile Ala Leu Ala
                170                 175                 180

gac atg act gat tac tac atc aag gca tat gag acc acc gca cca cac   691
Asp Met Thr Asp Tyr Tyr Ile Lys Ala Tyr Glu Thr Thr Ala Pro His
            185                 190                 195

ctg ggc ggt tgc ggc ctg cac gac cca ctg gca gta ggc gtt gca gtg   739
Leu Gly Gly Cys Gly Leu His Asp Pro Leu Ala Val Gly Val Ala Val
        200                 205                 210

gac cca agc ctg gtc act ttg ctc ccc atc aac ctc aag gta gac att   787
Asp Pro Ser Leu Val Thr Leu Leu Pro Ile Asn Leu Lys Val Asp Ile
    215                 220                 225

gag ggc gag acc cgt gga cgc acc att ggc gat gaa gtc cgc ctc aac   835
Glu Gly Glu Thr Arg Gly Arg Thr Ile Gly Asp Glu Val Arg Leu Asn
230                 235                 240                 245
```

```
gat cca gtg cgc acc tcc cgc gca gct gtc gcc gta gac gtg gat cgt   883
Asp Pro Val Arg Thr Ser Arg Ala Ala Val Ala Val Asp Val Asp Arg
                250                 255                 260

ttc ctt tct gaa ttc atg acc cgc atc ggc cga gtc gca gca cag cag   931
Phe Leu Ser Glu Phe Met Thr Arg Ile Gly Arg Val Ala Ala Gln Gln
            265                 270                 275

taaaagcagc tctggtgaag gtt                                        954
```

<210> 2266
<211> 277
<212> PRT
<213> Corynebacterium glutamicum

<400> 2266

```
Val Leu Leu Glu Thr Gly Ala Val Asn Asp Leu Ala Leu Leu Asp Leu
  1               5                  10                  15

Phe Gly Ala Pro Glu Val Pro Val Tyr Leu Gly Glu Pro His Ala Gln
             20                  25                  30

Thr Lys Asp Gly Phe Glu Val Leu Glu Ile Ser Ala Phe Ile His Gly
         35                  40                  45

Gln Asn Gly Ile Gly Glu Val Glu Leu Pro Ala Ser Glu Ser Lys Ala
     50                  55                  60

Leu Pro Gly Ala Val Asp Phe Leu Ile Asp Ser Val Asn Thr His Gly
 65                  70                  75                  80

Asp Asp Leu Val Ile Ile Ala Thr Gly Pro Met Thr Asn Leu Ser Ala
                 85                  90                  95

Ala Ile Ala Lys Asp Pro Ser Phe Ala Ser Lys Ala His Val Val Ile
            100                 105                 110

Met Gly Gly Ala Leu Thr Val Pro Gly Asn Val Ser Thr Trp Ala Glu
        115                 120                 125

Ala Asn Ile Asn Gln Asp Pro Asp Ala Ala Asn Asp Leu Phe Arg Ser
    130                 135                 140

Gly Ala Asp Val Thr Met Ile Gly Leu Asp Val Thr Leu Gln Thr Leu
145                 150                 155                 160

Leu Thr Lys Lys His Thr Ala Gln Trp Arg Glu Leu Gly Thr Pro Ala
                165                 170                 175

Ala Ile Ala Leu Ala Asp Met Thr Asp Tyr Tyr Ile Lys Ala Tyr Glu
            180                 185                 190

Thr Thr Ala Pro His Leu Gly Gly Cys Gly Leu His Asp Pro Leu Ala
        195                 200                 205

Val Gly Val Ala Val Asp Pro Ser Leu Val Thr Leu Leu Pro Ile Asn
    210                 215                 220

Leu Lys Val Asp Ile Glu Gly Glu Thr Arg Gly Arg Thr Ile Gly Asp
```

```
225                 230                 235                 240

Glu Val Arg Leu Asn Asp Pro Val Arg Thr Ser Arg Ala Ala Val Ala
                245                 250                 255

Val Asp Val Asp Arg Phe Leu Ser Glu Phe Met Thr Arg Ile Gly Arg
            260                 265                 270

Val Ala Ala Gln Gln
        275
```

<210> 2267
<211> 1119
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1096)
<223> RXA01494

<400> 2267

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gcgatgagga gctggctaaa ttgcgcgaag gtgcagcgcc tgcaggtgat gcagatcctt 60

acaagacttc atccaagtct gaatctgagg aataacacca gtg acg gat aat agt   115
                                              Val Thr Asp Asn Ser
                                                1               5

cag ttt cat gct gct tca gca tta gtc cag gca gct cac acg gtt agc   163
Gln Phe His Ala Ala Ser Ala Leu Val Gln Ala Ala His Thr Val Ser
                10                  15                  20

gtt gtg ggg cat ctg cga ccc gat gct gat gca atc ggc agt gta gct   211
Val Val Gly His Leu Arg Pro Asp Ala Asp Ala Ile Gly Ser Val Ala
            25                  30                  35

gcc aca gtg gcg gca cta cag caa ctt ggt aaa gac gcc gta ggt gca   259
Ala Thr Val Ala Ala Leu Gln Gln Leu Gly Lys Asp Ala Val Gly Ala
        40                  45                  50

atc ggc cag cta gat tcg atg ccc gag aac ttg tac acc att cct ggg   307
Ile Gly Gln Leu Asp Ser Met Pro Glu Asn Leu Tyr Thr Ile Pro Gly
    55                  60                  65

gca tca aac att aag ttt ggc gat tca ctg ccg gaa tct gac ctc atc   355
Ala Ser Asn Ile Lys Phe Gly Asp Ser Leu Pro Glu Ser Asp Leu Ile
70                  75                  80                  85

att gtt gtt gat tgt ggg tca atc gaa cgc acc ggt gcg ttt gaa agc   403
Ile Val Val Asp Cys Gly Ser Ile Glu Arg Thr Gly Ala Phe Glu Ser
                90                  95                  100

atc atc gtc aac aat cct gac aaa gta ttg gtg gtt gat cac cac gcc   451
Ile Ile Val Asn Asn Pro Asp Lys Val Leu Val Val Asp His His Ala
            105                 110                 115

acc aat cct ggg ttt ggt gcc gtc aac tta atc gat gtg gag gca gaa   499
Thr Asn Pro Gly Phe Gly Ala Val Asn Leu Ile Asp Val Glu Ala Glu
        120                 125                 130
```

```
tcc acc acc acg att tta tat gac tgg ttt gat gcg atg tcg gtg caa   547
Ser Thr Thr Thr Ile Leu Tyr Asp Trp Phe Asp Ala Met Ser Val Gln
    135                 140                 145

att act ccc gat atc gcc cac ggc ctt tat gct gga ctg ctc acc gat   595
Ile Thr Pro Asp Ile Ala His Gly Leu Tyr Ala Gly Leu Leu Thr Asp
150                 155                 160                 165

acc ggg tgc ttc agg tgg ggt cga cca gtc atg cat gac atg gct aaa   643
Thr Gly Cys Phe Arg Trp Gly Arg Pro Val Met His Asp Met Ala Lys
                170                 175                 180

gaa ctc atg gag ttc ggt cta gac att cgt gcc att tca tca gca ttg   691
Glu Leu Met Glu Phe Gly Leu Asp Ile Arg Ala Ile Ser Ser Ala Leu
            185                 190                 195

ctt gat caa acc tcc gtg gat gat ttg cgt ctt gtt ggc cag att gtc   739
Leu Asp Gln Thr Ser Val Asp Asp Leu Arg Leu Val Gly Gln Ile Val
        200                 205                 210

tct cgg atc gag ctg cgg gaa gca ggg cca tat act ctt gct gtt ctc   787
Ser Arg Ile Glu Leu Arg Glu Ala Gly Pro Tyr Thr Leu Ala Val Leu
    215                 220                 225

gtg gca gac ttc gat acc atc aac ggc cgt tca cgc gcc gtt gtg gaa   835
Val Ala Asp Phe Asp Thr Ile Asn Gly Arg Ser Arg Ala Val Val Glu
230                 235                 240                 245

ggc ttg atc gaa atg gtt cgc gct gtg gaa ggc gca gac ttc gga gca   883
Gly Leu Ile Glu Met Val Arg Ala Val Glu Gly Ala Asp Phe Gly Ala
                250                 255                 260

gta ttc aaa gaa tat gaa cgt ggc gtc tat acc gtg tca ctg cgt tcc   931
Val Phe Lys Glu Tyr Glu Arg Gly Val Tyr Thr Val Ser Leu Arg Ser
            265                 270                 275

tcc aat ttg agt gtc gct tcc ttg gca gtg cat ctt ggc ggt ggc gga   979
Ser Asn Leu Ser Val Ala Ser Leu Ala Val His Leu Gly Gly Gly Gly
        280                 285                 290

cac att cct gct gca ggc tat acc gct cgt ggt acg gaa atc gaa gcc   1027
His Ile Pro Ala Ala Gly Tyr Thr Ala Arg Gly Thr Glu Ile Glu Ala
    295                 300                 305

ctc gat acg ttg att gaa gca acc gtt acc ttg ggg gag tct ttg cga   1075
Leu Asp Thr Leu Ile Glu Ala Thr Val Thr Leu Gly Glu Ser Leu Arg
310                 315                 320                 325

agc tcg gcg cat gtc gat gtc taacaacgac tttgagcatg agt             1119
Ser Ser Ala His Val Asp Val
                330
```

<210> 2268
<211> 332
<212> PRT
<213> Corynebacterium glutamicum

<400> 2268

```
Val Thr Asp Asn Ser Gln Phe His Ala Ala Ser Ala Leu Val Gln Ala
  1               5                  10                  15
```

```
Ala His Thr Val Ser Val Val Gly His Leu Arg Pro Asp Ala Asp Ala
            20                  25                  30

Ile Gly Ser Val Ala Ala Thr Val Ala Ala Leu Gln Gln Leu Gly Lys
        35                  40                  45

Asp Ala Val Gly Ala Ile Gly Gln Leu Asp Ser Met Pro Glu Asn Leu
    50                  55                  60

Tyr Thr Ile Pro Gly Ala Ser Asn Ile Lys Phe Gly Asp Ser Leu Pro
65                  70                  75                  80

Glu Ser Asp Leu Ile Ile Val Val Asp Cys Gly Ser Ile Glu Arg Thr
                85                  90                  95

Gly Ala Phe Glu Ser Ile Ile Val Asn Asn Pro Asp Lys Val Leu Val
            100                 105                 110

Val Asp His His Ala Thr Asn Pro Gly Phe Gly Ala Val Asn Leu Ile
        115                 120                 125

Asp Val Glu Ala Glu Ser Thr Thr Thr Ile Leu Tyr Asp Trp Phe Asp
    130                 135                 140

Ala Met Ser Val Gln Ile Thr Pro Asp Ile Ala His Gly Leu Tyr Ala
145                 150                 155                 160

Gly Leu Leu Thr Asp Thr Gly Cys Phe Arg Trp Gly Arg Pro Val Met
                165                 170                 175

His Asp Met Ala Lys Glu Leu Met Glu Phe Gly Leu Asp Ile Arg Ala
            180                 185                 190

Ile Ser Ser Ala Leu Leu Asp Gln Thr Ser Val Asp Asp Leu Arg Leu
        195                 200                 205

Val Gly Gln Ile Val Ser Arg Ile Glu Leu Arg Glu Ala Gly Pro Tyr
    210                 215                 220

Thr Leu Ala Val Leu Val Ala Asp Phe Asp Thr Ile Asn Gly Arg Ser
225                 230                 235                 240

Arg Ala Val Val Glu Gly Leu Ile Glu Met Val Arg Ala Val Glu Gly
                245                 250                 255

Ala Asp Phe Gly Ala Val Phe Lys Glu Tyr Glu Arg Gly Val Tyr Thr
            260                 265                 270

Val Ser Leu Arg Ser Ser Asn Leu Ser Val Ala Ser Leu Ala Val His
        275                 280                 285

Leu Gly Gly Gly Gly His Ile Pro Ala Ala Gly Tyr Thr Ala Arg Gly
    290                 295                 300

Thr Glu Ile Glu Ala Leu Asp Thr Leu Ile Glu Ala Thr Val Thr Leu
305                 310                 315                 320

Gly Glu Ser Leu Arg Ser Ser Ala His Val Asp Val
                325                 330
```

<210> 2269
<211> 1041
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1018)
<223> RXA01497

<400> 2269
cgcccacggg caaagttttc aaaaactctg atccatatgg atcagagttt tttcgtatct 60

gccaccagaa agacgcccct ttggcacgcc gaattagtca atg gtg ggt aaa ctt 115
Met Val Gly Lys Leu
1 5

ccc atc atg gct gaa acc aac gaa aat gat ctt cca gtt atc gac ctt 163
Pro Ile Met Ala Glu Thr Asn Glu Asn Asp Leu Pro Val Ile Asp Leu
10 15 20

gcc caa atc gaa ggc tat gtt gta gat gac tcg gat gaa gat gat cca 211
Ala Gln Ile Glu Gly Tyr Val Val Asp Asp Ser Asp Glu Asp Asp Pro
25 30 35

gta ctt ctg cgt cca gat gga acc ccc att gaa acc tgg cgc gaa gac 259
Val Leu Leu Arg Pro Asp Gly Thr Pro Ile Glu Thr Trp Arg Glu Asp
40 45 50

ttc cct tat gaa gag cgc gtc acc cgc gaa gac tat gag aag gtc aag 307
Phe Pro Tyr Glu Glu Arg Val Thr Arg Glu Asp Tyr Glu Lys Val Lys
55 60 65

cgc tcc ctc cag atc gag ctg ctg aag tgg cag aac tgg acc aag gaa 355
Arg Ser Leu Gln Ile Glu Leu Leu Lys Trp Gln Asn Trp Thr Lys Glu
70 75 80 85

act ggc cag cgc cac atc att ttg ttc gaa ggg cgt gac gcc gct ggt 403
Thr Gly Gln Arg His Ile Ile Leu Phe Glu Gly Arg Asp Ala Ala Gly
90 95 100

aag ggt ggc acc att aag cgc ttc aac gaa cac ctg aac cct cgt ggt 451
Lys Gly Gly Thr Ile Lys Arg Phe Asn Glu His Leu Asn Pro Arg Gly
105 110 115

gcc cgt act gtt gcg ttg gag aag cca tca cca cgc gaa tcc acc tca 499
Ala Arg Thr Val Ala Leu Glu Lys Pro Ser Pro Arg Glu Ser Thr Ser
120 125 130

tgg tac ttc cag cgc tat att cag cac ttc cca gct gct ggc gag atc 547
Trp Tyr Phe Gln Arg Tyr Ile Gln His Phe Pro Ala Ala Gly Glu Ile
135 140 145

gtt ttc ttt gac cgc tct tgg tac aac cgt tcc ggc gtg gag cgc gtc 595
Val Phe Phe Asp Arg Ser Trp Tyr Asn Arg Ser Gly Val Glu Arg Val
150 155 160 165

atg ggt ttc tgc acc gaa tca cag cat gca gag ttc ctg cgt gag gtt 643
Met Gly Phe Cys Thr Glu Ser Gln His Ala Glu Phe Leu Arg Glu Val
170 175 180

```
cca atg ctg gaa aac atg atc ctg ggc tct ggt atc agc ttg acc aag   691
Pro Met Leu Glu Asn Met Ile Leu Gly Ser Gly Ile Ser Leu Thr Lys
            185                 190                 195

ttc tgg ttc tcg gtg acc cgt aaa gag cag cgc acc cgt ttt gct atc   739
Phe Trp Phe Ser Val Thr Arg Lys Glu Gln Arg Thr Arg Phe Ala Ile
        200                 205                 210

cgc cag gtt gat cct gtg cgt cag tgg aag ctt tcc cca atg gac ttg   787
Arg Gln Val Asp Pro Val Arg Gln Trp Lys Leu Ser Pro Met Asp Leu
    215                 220                 225

gct tca ctt gat cgc tgg gat gat tac acc cgc gct aag gaa gag cag   835
Ala Ser Leu Asp Arg Trp Asp Asp Tyr Thr Arg Ala Lys Glu Glu Gln
230                 235                 240                 245

ttc cgt tac acc gac act gat gag tcc ccg tgg atc acc atc aag tcg   883
Phe Arg Tyr Thr Asp Thr Asp Glu Ser Pro Trp Ile Thr Ile Lys Ser
                250                 255                 260

aat gac aag aag cgt gcg cgt atc aac gcg atg cgt tat gta ttg tcc   931
Asn Asp Lys Lys Arg Ala Arg Ile Asn Ala Met Arg Tyr Val Leu Ser
            265                 270                 275

aag ttt gat tac acc gac aag gat tac gag ctc gtt ggt gag cct gac   979
Lys Phe Asp Tyr Thr Asp Lys Asp Tyr Glu Leu Val Gly Glu Pro Asp
        280                 285                 290

cct aag gtt gtg ctt cgt ggg cgc gac cag atc ggt gac tagtcactag   1028
Pro Lys Val Val Leu Arg Gly Arg Asp Gln Ile Gly Asp
    295                 300                 305

gcgggcatga aaa                                                  1041
```

Sequence Listing - 09/10/2007

<210> 2270
<211> 306
<212> PRT
<213> Corynebacterium glutamicum

<400> 2270

```
Met Val Gly Lys Leu Pro Ile Met Ala Glu Thr Asn Glu Asn Asp Leu
  1               5                  10                  15

Pro Val Ile Asp Leu Ala Gln Ile Glu Gly Tyr Val Val Asp Asp Ser
             20                  25                  30

Asp Glu Asp Asp Pro Val Leu Leu Arg Pro Asp Gly Thr Pro Ile Glu
         35                  40                  45

Thr Trp Arg Glu Asp Phe Pro Tyr Glu Glu Arg Val Thr Arg Glu Asp
     50                  55                  60

Tyr Glu Lys Val Lys Arg Ser Leu Gln Ile Glu Leu Leu Lys Trp Gln
 65                  70                  75                  80

Asn Trp Thr Lys Glu Thr Gly Gln Arg His Ile Ile Leu Phe Glu Gly
                 85                  90                  95

Arg Asp Ala Ala Gly Lys Gly Gly Thr Ile Lys Arg Phe Asn Glu His
```

```
            100                 105                 110

Leu Asn Pro Arg Gly Ala Arg Thr Val Ala Leu Glu Lys Pro Ser Pro
        115                 120                 125

Arg Glu Ser Thr Ser Trp Tyr Phe Gln Arg Tyr Ile Gln His Phe Pro
    130                 135                 140

Ala Ala Gly Glu Ile Val Phe Phe Asp Arg Ser Trp Tyr Asn Arg Ser
145                 150                 155                 160

Gly Val Glu Arg Val Met Gly Phe Cys Thr Glu Ser Gln His Ala Glu
                165                 170                 175

Phe Leu Arg Glu Val Pro Met Leu Glu Asn Met Ile Leu Gly Ser Gly
            180                 185                 190

Ile Ser Leu Thr Lys Phe Trp Phe Ser Val Thr Arg Lys Glu Gln Arg
        195                 200                 205

Thr Arg Phe Ala Ile Arg Gln Val Asp Pro Val Arg Gln Trp Lys Leu
    210                 215                 220

Ser Pro Met Asp Leu Ala Ser Leu Asp Arg Trp Asp Asp Tyr Thr Arg
225                 230                 235                 240

Ala Lys Glu Glu Gln Phe Arg Tyr Thr Asp Thr Asp Glu Ser Pro Trp
                245                 250                 255

Ile Thr Ile Lys Ser Asn Asp Lys Lys Arg Ala Arg Ile Asn Ala Met
            260                 265                 270

Arg Tyr Val Leu Ser Lys Phe Asp Tyr Thr Asp Lys Asp Tyr Glu Leu
        275                 280                 285

Val Gly Glu Pro Asp Pro Lys Val Val Leu Arg Gly Arg Asp Gln Ile
    290                 295                 300

Gly Asp
305
```

<210> 2271
<211> 411
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(388)
<223> RXA01501

<400> 2271
ctaacgaaat cgccggactc ctcgcaatca caagaagcga cgactagcct gtggggacaa 60

actatttcaa gaatttattc aacaaaggag ttcttcacaa atg aag gaa gta gca 115
                                                Met Lys Glu Val Ala
                                                  1   5

gtc aac gaa gtc cca gca ggc gca cag ttg atc gat gtc cgc gag acc 163
Val Asn Glu Val Pro Ala Gly Ala Gln Leu Ile Asp Val Arg Glu Thr

```
                  10                  15                  20

gat gaa tac gca gag gtt cga gca cag ggt gcc gtc aac att cct atg   211
Asp Glu Tyr Ala Glu Val Arg Ala Gln Gly Ala Val Asn Ile Pro Met
             25                  30                  35

agc gag ttc gtt ggc cgc atc gat gag atc gat ctg gac cgc gac att   259
Ser Glu Phe Val Gly Arg Ile Asp Glu Ile Asp Leu Asp Arg Asp Ile
         40                  45                  50

tat gtc att tgc aag ctg ggt gga cgc tca gct cag gtt gcc gaa tac   307
Tyr Val Ile Cys Lys Leu Gly Gly Arg Ser Ala Gln Val Ala Glu Tyr
     55                  60                  65

ctt gag cag cgc gga att gaa gcc atc aac gta aac ggt ggc acc gac   355
Leu Glu Gln Arg Gly Ile Glu Ala Ile Asn Val Asn Gly Gly Thr Asp
 70                  75                  80                  85

ggc tgg gtt gct gca gga ttg cca acc gag gca taagaacccg ccgcaaaaga 408
Gly Trp Val Ala Ala Gly Leu Pro Thr Glu Ala
                 90                  95

tcc                                                               411
```

20050070080

<210> 2272
<211> 96
<212> PRT
<213> Corynebacterium glutamicum

<400> 2272

```
Met Lys Glu Val Ala Val Asn Glu Val Pro Ala Gly Ala Gln Leu Ile
  1               5                  10                  15

Asp Val Arg Glu Thr Asp Glu Tyr Ala Glu Val Arg Ala Gln Gly Ala
             20                  25                  30

Val Asn Ile Pro Met Ser Glu Phe Val Gly Arg Ile Asp Glu Ile Asp
         35                  40                  45

Leu Asp Arg Asp Ile Tyr Val Ile Cys Lys Leu Gly Gly Arg Ser Ala
     50                  55                  60

Gln Val Ala Glu Tyr Leu Glu Gln Arg Gly Ile Glu Ala Ile Asn Val
 65                  70                  75                  80

Asn Gly Gly Thr Asp Gly Trp Val Ala Ala Gly Leu Pro Thr Glu Ala
                 85                  90                  95
```

<210> 2273
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)

<223> RXA01504

<400> 2273

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gcatgtagcg agtttgatga agttgtcgcg ataagaggag gggcgtgtcg gtctgtagga 60

ttggctcgta ccgaacttag aaaactcatg ggagtttcgc atg aat atc acg tgg   115
                                          Met Asn Ile Thr Trp
                                            1               5

ctt atc ctg gcc ggt gtt tta gcc atc atc gct gtc gtg ttc ttt tat   163
Leu Ile Leu Ala Gly Val Leu Ala Ile Ile Ala Val Val Phe Phe Tyr
                 10                  15                  20

ctt tca gca cag aag aaa aag agc gaa ccg cag cct cct cgt cag cgt   211
Leu Ser Ala Gln Lys Lys Lys Ser Glu Pro Gln Pro Pro Arg Gln Arg
             25                  30                  35

caa gat cct ctg aaa ttt gcc gac gga tcc gac act ttt aat gcc cgc   259
Gln Asp Pro Leu Lys Phe Ala Asp Gly Ser Asp Thr Phe Asn Ala Arg
         40                  45                  50

att ttg ggt cct gga gca att att tcc cgc ggt ggc gtg gat tat gtc   307
Ile Leu Gly Pro Gly Ala Ile Ile Ser Arg Gly Gly Val Asp Tyr Val
     55                  60                  65

tgc cgc gga gcc atc cag ttc cgt caa ggc caa tac att tgg cac gag   355
Cys Arg Gly Ala Ile Gln Phe Arg Gln Gly Gln Tyr Ile Trp His Glu
 70                  75                  80                  85

tat cta ctc gac ggt ggc aaa ggc agt gag tac ctg agc gtg gaa tac   403
Tyr Leu Leu Asp Gly Gly Lys Gly Ser Glu Tyr Leu Ser Val Glu Tyr
                 90                  95                 100

gat gag ggc caa ctc aac ctc gga tgg tgg att acc cgc cct gac ctg   451
Asp Glu Gly Gln Leu Asn Leu Gly Trp Trp Ile Thr Arg Pro Asp Leu
            105                 110                 115

gca caa cag ccc gca cat gat gtc acc gtg gag ggc gtt cgc tac cgt   499
Ala Gln Gln Pro Ala His Asp Val Thr Val Glu Gly Val Arg Tyr Arg
        120                 125                 130

aaa acc gaa tct ggc gtg ggc acc ttc acc tcc gaa ggc acc acc ggc   547
Lys Thr Glu Ser Gly Val Gly Thr Phe Thr Ser Glu Gly Thr Thr Gly
    135                 140                 145

gtg gct gat caa ggt gaa ttt gaa tac tgg gat ctc gcc gaa gtt ggc   595
Val Ala Asp Gln Gly Glu Phe Glu Tyr Trp Asp Leu Ala Glu Val Gly
150                 155                 160                 165

gga aac agg ttg ctc agt ttt gaa cgc tac ggc aaa gac agt cca ttt   643
Gly Asn Arg Leu Leu Ser Phe Glu Arg Tyr Gly Lys Asp Ser Pro Phe
                170                 175                 180

gaa gta tcg ctc ggg tgg acg gtg ctg ccc ggc gaa ctc acc gtt tac   691
Glu Val Ser Leu Gly Trp Thr Val Leu Pro Gly Glu Leu Thr Val Tyr
            185                 190                 195

cca gca cca gag gcc tca tgattcatca catcgattgc atg                732
Pro Ala Pro Glu Ala Ser
        200
```

<210> 2274
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 2274
Met Asn Ile Thr Trp Leu Ile Leu Ala Gly Val Leu Ala Ile Ile Ala
1 5 10 15

Val Val Phe Phe Tyr Leu Ser Ala Gln Lys Lys Lys Ser Glu Pro Gln
20 25 30

Pro Pro Arg Gln Arg Gln Asp Pro Leu Lys Phe Ala Asp Gly Ser Asp
35 40 45

Thr Phe Asn Ala Arg Ile Leu Gly Pro Gly Ala Ile Ile Ser Arg Gly
50 55 60

Gly Val Asp Tyr Val Cys Arg Gly Ala Ile Gln Phe Arg Gln Gly Gln
65 70 75 80

Tyr Ile Trp His Glu Tyr Leu Leu Asp Gly Gly Lys Gly Ser Glu Tyr
85 90 95

Leu Ser Val Glu Tyr Asp Glu Gly Gln Leu Asn Leu Gly Trp Trp Ile
100 105 110

Thr Arg Pro Asp Leu Ala Gln Gln Pro Ala His Asp Val Thr Val Glu
115 120 125

Gly Val Arg Tyr Arg Lys Thr Glu Ser Gly Val Gly Thr Phe Thr Ser
130 135 140

Glu Gly Thr Thr Gly Val Ala Asp Gln Gly Glu Phe Glu Tyr Trp Asp
145 150 155 160

Leu Ala Glu Val Gly Gly Asn Arg Leu Leu Ser Phe Glu Arg Tyr Gly
165 170 175

Lys Asp Ser Pro Phe Glu Val Ser Leu Gly Trp Thr Val Leu Pro Gly
180 185 190

Glu Leu Thr Val Tyr Pro Ala Pro Glu Ala Ser
195 200

<210> 2275
<211> 621
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(598)
<223> RXA01505

<400> 2275
tcagttttga acgctacggc aaagacagtc catttgaagt atcgctcggg tggacggtgc 60

tgcccggcga actcaccgtt tacccagcac cagaggcctc atg att cat cac atc 115

```
                                                    Met Ile His His Ile
                                                      1               5

gat tgc atg cct aca gat gtc tcc gcc gaa gcg ctc ggc gtg agc tgg   163
Asp Cys Met Pro Thr Asp Val Ser Ala Glu Ala Leu Gly Val Ser Trp
                 10                  15                  20

aat ggg gaa tcg ccg gag gtg ctc gtc gat aag ctt atc gac gca tcc   211
Asn Gly Glu Ser Pro Glu Val Leu Val Asp Lys Leu Ile Asp Ala Ser
             25                  30                  35

cca cac ccc agc acc tgc cat tta gcg gtg att ggc ggc tcg cat gtg   259
Pro His Pro Ser Thr Cys His Leu Ala Val Ile Gly Gly Ser His Val
         40                  45                  50

gtt acc gtt gaa acg ccc gat ggg cgt ttc cgg gaa gaa att tcc tgc   307
Val Thr Val Glu Thr Pro Asp Gly Arg Phe Arg Glu Glu Ile Ser Cys
     55                  60                  65

cat gca caa gaa gcg gaa gat tcc cgc tgg ccg ctg ccc gac agc atc   355
His Ala Gln Glu Ala Glu Asp Ser Arg Trp Pro Leu Pro Asp Ser Ile
 70                  75                  80                  85

acg cgg gaa aac tac ctg ctg caa acc aac gtc gcc gtg ctg tct gag   403
Thr Arg Glu Asn Tyr Leu Leu Gln Thr Asn Val Ala Val Leu Ser Glu
                 90                  95                 100

gaa gat ttt gcc cgc gca gcc gaa gaa atc tcc aac ggc gac gac gac   451
Glu Asp Phe Ala Arg Ala Ala Glu Glu Ile Ser Asn Gly Asp Asp Asp
             105                 110                 115

tgg ttg atc gcc agt ttc ccc ggc gcc ggc gaa cac cac ctc acc gcg   499
Trp Leu Ile Ala Ser Phe Pro Gly Ala Gly Glu His His Leu Thr Ala
         120                 125                 130

ctg acc gca gaa ttt ctg gaa gac gta tgg gaa tgg ttt agc cac cac   547
Leu Thr Ala Glu Phe Leu Glu Asp Val Trp Glu Trp Phe Ser His His
     135                 140                 145

ctc tac cca gaa gag ctc acc atc gtg agc acg agg agc att tac aaa   595
Leu Tyr Pro Glu Glu Leu Thr Ile Val Ser Thr Arg Ser Ile Tyr Lys
150                 155                 160                 165

cca tgagctcccg aaactaccga agc                                    621
Pro
```

US-09-975-070-2276

<210> 2276
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

<400> 2276

```
Met Ile His His Ile Asp Cys Met Pro Thr Asp Val Ser Ala Glu Ala
  1               5                  10                  15

Leu Gly Val Ser Trp Asn Gly Glu Ser Pro Glu Val Leu Val Asp Lys
             20                  25                  30

Leu Ile Asp Ala Ser Pro His Pro Ser Thr Cys His Leu Ala Val Ile
```

```
          35                  40                  45

Gly Gly Ser His Val Val Thr Val Glu Thr Pro Asp Gly Arg Phe Arg
     50                  55                  60

Glu Glu Ile Ser Cys His Ala Gln Glu Ala Glu Asp Ser Arg Trp Pro
 65                  70                  75                  80

Leu Pro Asp Ser Ile Thr Arg Glu Asn Tyr Leu Leu Gln Thr Asn Val
                 85                  90                  95

Ala Val Leu Ser Glu Glu Asp Phe Ala Arg Ala Ala Glu Glu Ile Ser
            100                 105                 110

Asn Gly Asp Asp Asp Trp Leu Ile Ala Ser Phe Pro Gly Ala Gly Glu
        115                 120                 125

His His Leu Thr Ala Leu Thr Ala Glu Phe Leu Glu Asp Val Trp Glu
    130                 135                 140

Trp Phe Ser His His Leu Tyr Pro Glu Glu Leu Thr Ile Val Ser Thr
145                 150                 155                 160

Arg Ser Ile Tyr Lys Pro
                165


<210> 2277
<211> 534
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> RXA01506

<400> 2277
cgctgaccgc agaatttctg gaagacgtat gggaatggtt tagccaccac ctctacccag 60

aagagctcac catcgtgagc acgaggagca tttacaaacc atg agc tcc cga aac   115
                                        Met Ser Ser Arg Asn
                                          1               5

tac cga agc ata gga ttc atc ctg ctg ttt tta gca gtg ttg tgc ctg   163
Tyr Arg Ser Ile Gly Phe Ile Leu Leu Phe Leu Ala Val Leu Cys Leu
                 10                  15                  20

ttc gct gcg gtt ttt gcc aag cct gcg gtg gga agc caa gtc tcc gac   211
Phe Ala Ala Val Phe Ala Lys Pro Ala Val Gly Ser Gln Val Ser Asp
            25                  30                  35

cgc tgg ccc gga aac aac ggc acc tac tca tgc gct ggc gaa agt ggg   259
Arg Trp Pro Gly Asn Asn Gly Thr Tyr Ser Cys Ala Gly Glu Ser Gly
        40                  45                  50

gtg gtg gat gaa atc gtg aac atg tcc acc cca acc gac cgc gcc acc   307
Val Val Asp Glu Ile Val Asn Met Ser Thr Pro Thr Asp Arg Ala Thr
    55                  60                  65

gac ccc gca act ggc gat act tac ctg cga tac agc aaa aac ctg atc   355
```

```
Asp Pro Ala Thr Gly Asp Thr Tyr Leu Arg Tyr Ser Lys Asn Leu Ile
 70                  75                  80                  85

atc atc tca ggt gaa ggc acg ccg gaa tgc acc atc acc gtc gaa ggc   403
Ile Ile Ser Gly Glu Gly Thr Pro Glu Cys Thr Ile Thr Val Glu Gly
                 90                  95                 100

ctt gac cgc gtc aac agt ggt gcg ttc atc tgg ctc ggc ggc ggt ttc   451
Leu Asp Arg Val Asn Ser Gly Ala Phe Ile Trp Leu Gly Gly Gly Phe
            105                 110                 115

ggc cca tcc tca cca agc agt tcc agc ggc gga tcc tcc ggt tcc ggc   499
Gly Pro Ser Ser Pro Ser Ser Ser Ser Gly Gly Ser Ser Gly Ser Gly
        120                 125                 130

ggt ggc gtg aaa tagaaagaac actatgagtc aat                         534
Gly Gly Val Lys
    135
```

<210> 2278
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 2278

```
Met Ser Ser Arg Asn Tyr Arg Ser Ile Gly Phe Ile Leu Leu Phe Leu
  1               5                  10                  15

Ala Val Leu Cys Leu Phe Ala Ala Val Phe Ala Lys Pro Ala Val Gly
             20                  25                  30

Ser Gln Val Ser Asp Arg Trp Pro Gly Asn Asn Gly Thr Tyr Ser Cys
         35                  40                  45

Ala Gly Glu Ser Gly Val Val Asp Glu Ile Val Asn Met Ser Thr Pro
     50                  55                  60

Thr Asp Arg Ala Thr Asp Pro Ala Thr Gly Asp Thr Tyr Leu Arg Tyr
 65                  70                  75                  80

Ser Lys Asn Leu Ile Ile Ile Ser Gly Glu Gly Thr Pro Glu Cys Thr
                 85                  90                  95

Ile Thr Val Glu Gly Leu Asp Arg Val Asn Ser Gly Ala Phe Ile Trp
            100                 105                 110

Leu Gly Gly Gly Phe Gly Pro Ser Ser Pro Ser Ser Ser Ser Gly Gly
        115                 120                 125

Ser Ser Gly Ser Gly Gly Gly Val Lys
    130                 135
```

<210> 2279
<211> 546
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(523)
<223> RXA01507

<400> 2279
gcgttcatct ggctcggcgg cggtttcggc ccatcctcac caagcagttc cagcggcgga 60

tcctccggtt ccggcggtgg cgtgaaatag aaagaacact atg agt caa tat ctt 115
Met Ser Gln Tyr Leu
1 5

gtc gac gga gtg ctc ggc acc ctt tca tat ttc gtg ttg gcc gca gtg 163
Val Asp Gly Val Leu Gly Thr Leu Ser Tyr Phe Val Leu Ala Ala Val
10 15 20

atc ctc gtg gtc ggt ttt gtg att ttg gac ttg atc acc cca ggt aaa 211
Ile Leu Val Val Gly Phe Val Ile Leu Asp Leu Ile Thr Pro Gly Lys
25 30 35

ctg cat gaa ctc gtg ttt gtg cac cat ctg ccc aac gcc gct gtg atc 259
Leu His Glu Leu Val Phe Val His His Leu Pro Asn Ala Ala Val Ile
40 45 50

acc gtg gcg cag cag gtt tcc atc gga atc atc gtg gtc act gct gtg 307
Thr Val Ala Gln Gln Val Ser Ile Gly Ile Ile Val Val Thr Ala Val
55 60 65

ctg acc tcc tca gat att ttg agt gaa ggt ttg ctg gag act gca gtg 355
Leu Thr Ser Ser Asp Ile Leu Ser Glu Gly Leu Leu Glu Thr Ala Val
70 75 80 85

ttc ggt gcc ctt ggt ctg gtt atc caa gtg gtg gtc atg gcg gtg ttg 403
Phe Gly Ala Leu Gly Leu Val Ile Gln Val Val Val Met Ala Val Leu
90 95 100

gaa gct gtc att ccg gga cgt ttc cgt gat ctc gtg gaa gat ccc aaa 451
Glu Ala Val Ile Pro Gly Arg Phe Arg Asp Leu Val Glu Asp Pro Lys
105 110 115

ctc cgt tcc ggt gcc gtc gtg gcc gcc gtc atc ttg atc gtg gtg gga 499
Leu Arg Ser Gly Ala Val Val Ala Ala Val Ile Leu Ile Val Val Gly
120 125 130

acc gta aac gct gca tgt ctg att taggacccat ctggcgctgg ctg 546
Thr Val Asn Ala Ala Cys Leu Ile
135 140

<210> 2280
<211> 141
<212> PRT
<213> Corynebacterium glutamicum

<400> 2280
Met Ser Gln Tyr Leu Val Asp Gly Val Leu Gly Thr Leu Ser Tyr Phe
1 5 10 15

Val Leu Ala Ala Val Ile Leu Val Val Gly Phe Val Ile Leu Asp Leu
20 25 30

Ile Thr Pro Gly Lys Leu His Glu Leu Val Phe Val His His Leu Pro
35 40 45

```
Asn Ala Ala Val Ile Thr Val Ala Gln Gln Val Ser Ile Gly Ile Ile
     50                  55                  60

Val Val Thr Ala Val Leu Thr Ser Ser Asp Ile Leu Ser Glu Gly Leu
 65                  70                  75                  80

Leu Glu Thr Ala Val Phe Gly Ala Leu Gly Leu Val Ile Gln Val Val
                 85                  90                  95

Val Met Ala Val Leu Glu Ala Val Ile Pro Gly Arg Phe Arg Asp Leu
            100                 105                 110

Val Glu Asp Pro Lys Leu Arg Ser Gly Ala Val Val Ala Ala Val Ile
        115                 120                 125

Leu Ile Val Val Gly Thr Val Asn Ala Ala Cys Leu Ile
    130                 135                 140
```

<210> 2281
<211> 870
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(847)
<223> RXA01519

<400> 2281

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ctgggcggaa tcgcactctc agctgccgga ctttatttag agcgaagctg tgaggctccg 60

cctccccaat ctggcgaagc gatcagctag attggaattc atg aat caa gac ctg   115
                                          Met Asn Gln Asp Leu
                                            1               5

tca cac gag gat tcc ggc gac ggc aat tct gtc gac cgt gga cag att   163
Ser His Glu Asp Ser Gly Asp Gly Asn Ser Val Asp Arg Gly Gln Ile
                 10                  15                  20

ctg cta gca gta ctc att gga ctt gcc ctg att gcc agc gtc atc atg   211
Leu Leu Ala Val Leu Ile Gly Leu Ala Leu Ile Ala Ser Val Ile Met
             25                  30                  35

ctg ctg gcc aac agt gac ggc gcc atg aaa ata gca ctt ctt gca gcg   259
Leu Leu Ala Asn Ser Asp Gly Ala Met Lys Ile Ala Leu Leu Ala Ala
         40                  45                  50

ctg tgg gcg gca atc atc gga ttc ttc ctt gtt tat cgg tcc cgc aaa   307
Leu Trp Ala Ala Ile Ile Gly Phe Phe Leu Val Tyr Arg Ser Arg Lys
     55                  60                  65

caa gtc gaa gct gct gcg cgg gag aag gaa acc ctc gaa tac gca cac   355
Gln Val Glu Ala Ala Ala Arg Glu Lys Glu Thr Leu Glu Tyr Ala His
 70                  75                  80                  85

caa tct gaa ctc aac cga cta gaa gct gaa ctc gtc caa gaa aaa atg   403
Gln Ser Glu Leu Asn Arg Leu Glu Ala Glu Leu Val Gln Glu Lys Met
                 90                  95                 100
```

```
gag att tct gaa tcc cgt cgt gca cgc gat cag gaa acc ctt gag gaa   451
Glu Ile Ser Glu Ser Arg Arg Ala Arg Asp Gln Glu Thr Leu Glu Glu
            105                 110                 115

atc aaa ctt caa ctg gag gaa atg cgc acc cag ctg tct gag ctt tct   499
Ile Lys Leu Gln Leu Glu Glu Met Arg Thr Gln Leu Ser Glu Leu Ser
        120                 125                 130

ggc cgt gaa tgg ggc tat gag cca acc atg ctg cgt gcc gaa gcc cga   547
Gly Arg Glu Trp Gly Tyr Glu Pro Thr Met Leu Arg Ala Glu Ala Arg
    135                 140                 145

cga atc ctt gag ttg gaa tcc cag cag ctt tcc cag cag ttc cag gca   595
Arg Ile Leu Glu Leu Glu Ser Gln Gln Leu Ser Gln Gln Phe Gln Ala
150                 155                 160                 165

ccg cag cca gaa gtc ccg gag cct gtt gca gtt cca gag cca atg ccg   643
Pro Gln Pro Glu Val Pro Glu Pro Val Ala Val Pro Glu Pro Met Pro
            170                 175                 180

gaa cct gca ccg gtg ccg gaa cca gta cca gaa cct gag cca gtt gaa   691
Glu Pro Ala Pro Val Pro Glu Pro Val Pro Glu Pro Glu Pro Val Glu
            185                 190                 195

gtt gct gtc gaa gct gag gaa gaa cca gca cca ggt cgc aga agg cgt   739
Val Ala Val Glu Ala Glu Glu Glu Pro Ala Pro Gly Arg Arg Arg Arg
        200                 205                 210

agg cac gca gct ccc gaa gaa act ggc gga cgc cga cgc aaa gat gaa   787
Arg His Ala Ala Pro Glu Glu Thr Gly Gly Arg Arg Arg Lys Asp Glu
    215                 220                 225

cgc caa ggc ggt ttg agc gtg gct gat ctt ctg gca gca gca agg aaa   835
Arg Gln Gly Gly Leu Ser Val Ala Asp Leu Leu Ala Ala Ala Arg Lys
230                 235                 240                 245

aag gaa aac aac taatgcaggc tcctcgcctt cgc                        870
Lys Glu Asn Asn
```

Sequence Listing

<210> 2282
<211> 249
<212> PRT
<213> Corynebacterium glutamicum

<400> 2282

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Met Asn Gln Asp Leu Ser His Glu Asp Ser Gly Asp Gly Asn Ser Val
  1               5                  10                  15

Asp Arg Gly Gln Ile Leu Leu Ala Val Leu Ile Gly Leu Ala Leu Ile
             20                  25                  30

Ala Ser Val Ile Met Leu Leu Ala Asn Ser Asp Gly Ala Met Lys Ile
         35                  40                  45

Ala Leu Leu Ala Ala Leu Trp Ala Ala Ile Ile Gly Phe Phe Leu Val
     50                  55                  60

Tyr Arg Ser Arg Lys Gln Val Glu Ala Ala Ala Arg Glu Lys Glu Thr
 65                  70                  75                  80
```

```
Leu Glu Tyr Ala His Gln Ser Glu Leu Asn Arg Leu Glu Ala Glu Leu
                 85                  90                  95

Val Gln Glu Lys Met Glu Ile Ser Glu Ser Arg Arg Ala Arg Asp Gln
            100                 105                 110

Glu Thr Leu Glu Glu Ile Lys Leu Gln Leu Glu Glu Met Arg Thr Gln
        115                 120                 125

Leu Ser Glu Leu Ser Gly Arg Glu Trp Gly Tyr Glu Pro Thr Met Leu
    130                 135                 140

Arg Ala Glu Ala Arg Arg Ile Leu Glu Leu Glu Ser Gln Gln Leu Ser
145                 150                 155                 160

Gln Gln Phe Gln Ala Pro Gln Pro Glu Val Pro Glu Pro Val Ala Val
                165                 170                 175

Pro Glu Pro Met Pro Glu Pro Ala Pro Val Pro Glu Pro Val Pro Glu
            180                 185                 190

Pro Glu Pro Val Glu Val Ala Val Glu Ala Glu Glu Glu Pro Ala Pro
        195                 200                 205

Gly Arg Arg Arg Arg Arg His Ala Ala Pro Glu Glu Thr Gly Gly Arg
    210                 215                 220

Arg Arg Lys Asp Glu Arg Gln Gly Gly Leu Ser Val Ala Asp Leu Leu
225                 230                 235                 240

Ala Ala Ala Arg Lys Lys Glu Asn Asn
                245
```

<210> 2283
<211> 507
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(484)
<223> RXA01520

<400> 2283

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ctgcatacct cgctcacgca cggcatcact gtgatggatc cgctgcagac gtccggcagg 60

catcgtgatg tctgcgcacc cgattggtca ggaccggtgg gtg gcg tcc gcg ttg   115
                                              Val Ala Ser Ala Leu
                                                1               5

gat gag ttg ggg gag acc atc gtg ggg ctt ttg gtg ggg gag ctc ggt   163
Asp Glu Leu Gly Glu Thr Ile Val Gly Leu Leu Val Gly Glu Leu Gly
                10                  15                  20

ggc tcg att gtc gag atc gcc gat gac aag cgc gca cag ttg gct gca   211
Gly Ser Ile Val Glu Ile Ala Asp Asp Lys Arg Ala Gln Leu Ala Ala
            25                  30                  35

gcg ctg acc tat gcc gga ttt tta agc acc ttg cag cgc gat gcg tcg   259
```

```
Ala Leu Thr Tyr Ala Gly Phe Leu Ser Thr Leu Gln Arg Asp Ala Ser
         40                  45                  50

tat ttc ctg gat gaa ttt ctt ggc gat ccc gat gtg acc tct gac atc   307
Tyr Phe Leu Asp Glu Phe Leu Gly Asp Pro Asp Val Thr Ser Asp Ile
     55                  60                  65

gtt atg gat tcc gca cag caa ttc cag gca ctg cct tcg ttg gat gag   355
Val Met Asp Ser Ala Gln Gln Phe Gln Ala Leu Pro Ser Leu Asp Glu
 70                  75                  80                  85

gtc att gcc cag tac gat tcg att aac aac ccc ggc agg caa cgc ctt   403
Val Ile Ala Gln Tyr Asp Ser Ile Asn Asn Pro Gly Arg Gln Arg Leu
                 90                  95                 100

ttc cgg gat ttg gcg cgc agg cag gca gag att tcc cgc gcg caa gat   451
Phe Arg Asp Leu Ala Arg Arg Gln Ala Glu Ile Ser Arg Ala Gln Asp
            105                 110                 115

att gag ctg tgg gca att cag aag gag gac cgt tgagtttcac gcatggtcag 504
Ile Glu Leu Trp Ala Ile Gln Lys Glu Asp Arg
        120                 125

ggc                                                               507


<210> 2284
<211> 128
<212> PRT
<213> Corynebacterium glutamicum

<400> 2284
Val Ala Ser Ala Leu Asp Glu Leu Gly Glu Thr Ile Val Gly Leu Leu
  1               5                  10                  15

Val Gly Glu Leu Gly Gly Ser Ile Val Glu Ile Ala Asp Asp Lys Arg
             20                  25                  30

Ala Gln Leu Ala Ala Ala Leu Thr Tyr Ala Gly Phe Leu Ser Thr Leu
         35                  40                  45

Gln Arg Asp Ala Ser Tyr Phe Leu Asp Glu Phe Leu Gly Asp Pro Asp
     50                  55                  60

Val Thr Ser Asp Ile Val Met Asp Ser Ala Gln Gln Phe Gln Ala Leu
 65                  70                  75                  80

Pro Ser Leu Asp Glu Val Ile Ala Gln Tyr Asp Ser Ile Asn Asn Pro
                 85                  90                  95

Gly Arg Gln Arg Leu Phe Arg Asp Leu Ala Arg Arg Gln Ala Glu Ile
            100                 105                 110

Ser Arg Ala Gln Asp Ile Glu Leu Trp Ala Ile Gln Lys Glu Asp Arg
        115                 120                 125


<210> 2285
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<211> 1074
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1051)
<223> RXA01523

<400> 2285
aatcctccaa acctgtggat agaacaatct atccacaggt tttcagtttt ctgcaaagtt 60

catccttggc ttcttatgcc ttcggatcca tagtggggtc atg aaa aac tgg caa 115
Met Lys Asn Trp Gln
1 5

gaa gaa ttc caa cta gtc aat ctc acg aaa ctt ctg cat agc gat acc 163
Glu Glu Phe Gln Leu Val Asn Leu Thr Lys Leu Leu His Ser Asp Thr
10 15 20

gag act tct gcg gca atc agt aat ggt caa atg att aaa ctc act cat 211
Glu Thr Ser Ala Ala Ile Ser Asn Gly Gln Met Ile Lys Leu Thr His
25 30 35

gaa gtc gca atc aat gct gaa aag tac cga agc ctt cct gca tgg gat 259
Glu Val Ala Ile Asn Ala Glu Lys Tyr Arg Ser Leu Pro Ala Trp Asp
40 45 50

aaa gca gcc gcc cga gct ttt gca gtg ggt atg act gtg gac aaa gca 307
Lys Ala Ala Ala Arg Ala Phe Ala Val Gly Met Thr Val Asp Lys Ala
55 60 65

gtg gta gcg ggg cag tct gcg gcg agg tta tgg gga tac caa act ttg 355
Val Val Ala Gly Gln Ser Ala Ala Arg Leu Trp Gly Tyr Gln Thr Leu
70 75 80 85

act gtt gag aaa acc gtg ttg tgt ctg ttg ccg gaa agg cta cgt tca 403
Thr Val Glu Lys Thr Val Leu Cys Leu Leu Pro Glu Arg Leu Arg Ser
90 95 100

aaa tcc tcc aag cat tgg ccg tcc ggg atg cga tat aaa gat cgt tac 451
Lys Ser Ser Lys His Trp Pro Ser Gly Met Arg Tyr Lys Asp Arg Tyr
105 110 115

ctc tcg tcg cgt gat att cga gag gtt cat ggg atc cga gtt acg gga 499
Leu Ser Ser Arg Asp Ile Arg Glu Val His Gly Ile Arg Val Thr Gly
120 125 130

gcg ttc cgc aca ttt ttg gac atc gct ttg gat gat ggg gtg gtg gcg 547
Ala Phe Arg Thr Phe Leu Asp Ile Ala Leu Asp Asp Gly Val Val Ala
135 140 145

gct gtg gtc act att gat tca gct cga aga cag aat cca tcg ctt acg 595
Ala Val Val Thr Ile Asp Ser Ala Arg Arg Gln Asn Pro Ser Leu Thr
150 155 160 165

cgt gag aag tta atg cac agt gcg gaa agt ttc ccg agg cat cgg ggt 643
Arg Glu Lys Leu Met His Ser Ala Glu Ser Phe Pro Arg His Arg Gly
170 175 180

gtg aag gcg tat cgg cag gcg att gag ttg tcg att ccc aat tcg gat 691

```
Val Lys Ala Tyr Arg Gln Ala Ile Glu Leu Ser Ile Pro Asn Ser Asp
            185                 190                 195

agt gct cag gag acg agg gct cgg tta atc ctt cgg gag gcc aag ctc   739
Ser Ala Gln Glu Thr Arg Ala Arg Leu Ile Leu Arg Glu Ala Lys Leu
        200                 205                 210

ccg gaa atc cag tca gtg aag gtg cag gcc cgt ttc gat caa tcg cac   787
Pro Glu Ile Gln Ser Val Lys Val Gln Ala Arg Phe Asp Gln Ser His
    215                 220                 225

aac aag tat ttc ctc gtc gat ttc ttg atc aat gag tgg atc atc gtg   835
Asn Lys Tyr Phe Leu Val Asp Phe Leu Ile Asn Glu Trp Ile Ile Val
230                 235                 240                 245

gag att gat gga cgt tcg aaa tat gat tcc ccg gag ctc aat gag gtg   883
Glu Ile Asp Gly Arg Ser Lys Tyr Asp Ser Pro Glu Leu Asn Glu Val
                250                 255                 260

ctc atg gct gaa cgc gat cgg gag aaa ttc ttc ctc aat cag ggc tat   931
Leu Met Ala Glu Arg Asp Arg Glu Lys Phe Phe Leu Asn Gln Gly Tyr
            265                 270                 275

gcg gtc tta aga atc gat ccg aaa cag tta gac ctc aac caa gat ggg   979
Ala Val Leu Arg Ile Asp Pro Lys Gln Leu Asp Leu Asn Gln Asp Gly
        280                 285                 290

gag tgt gag ttc atc gga atc ctc aaa aac act ttg cag aag acc cca   1027
Glu Cys Glu Phe Ile Gly Ile Leu Lys Asn Thr Leu Gln Lys Thr Pro
    295                 300                 305

cct gag cac ctc aag caa gcc gcc taaacactcc aagaaccacc att         1074
Pro Glu His Leu Lys Gln Ala Ala
310                 315


<210> 2286
<211> 317
<212> PRT
<213> Corynebacterium glutamicum

<400> 2286
Met Lys Asn Trp Gln Glu Glu Phe Gln Leu Val Asn Leu Thr Lys Leu
  1               5                  10                  15

Leu His Ser Asp Thr Glu Thr Ser Ala Ala Ile Ser Asn Gly Gln Met
             20                  25                  30

Ile Lys Leu Thr His Glu Val Ala Ile Asn Ala Glu Lys Tyr Arg Ser
         35                  40                  45

Leu Pro Ala Trp Asp Lys Ala Ala Ala Arg Ala Phe Ala Val Gly Met
     50                  55                  60

Thr Val Asp Lys Ala Val Val Ala Gly Gln Ser Ala Ala Arg Leu Trp
 65                  70                  75                  80

Gly Tyr Gln Thr Leu Thr Val Glu Lys Thr Val Leu Cys Leu Leu Pro
                 85                  90                  95

Glu Arg Leu Arg Ser Lys Ser Ser Lys His Trp Pro Ser Gly Met Arg
```

```
            100                 105                 110

Tyr Lys Asp Arg Tyr Leu Ser Ser Arg Asp Ile Arg Glu Val His Gly
        115                 120                 125

Ile Arg Val Thr Gly Ala Phe Arg Thr Phe Leu Asp Ile Ala Leu Asp
    130                 135                 140

Asp Gly Val Val Ala Ala Val Val Thr Ile Asp Ser Ala Arg Arg Gln
145                 150                 155                 160

Asn Pro Ser Leu Thr Arg Glu Lys Leu Met His Ser Ala Glu Ser Phe
                165                 170                 175

Pro Arg His Arg Gly Val Lys Ala Tyr Arg Gln Ala Ile Glu Leu Ser
            180                 185                 190

Ile Pro Asn Ser Asp Ser Ala Gln Glu Thr Arg Ala Arg Leu Ile Leu
        195                 200                 205

Arg Glu Ala Lys Leu Pro Glu Ile Gln Ser Val Lys Val Gln Ala Arg
    210                 215                 220

Phe Asp Gln Ser His Asn Lys Tyr Phe Leu Val Asp Phe Leu Ile Asn
225                 230                 235                 240

Glu Trp Ile Ile Val Glu Ile Asp Gly Arg Ser Lys Tyr Asp Ser Pro
                245                 250                 255

Glu Leu Asn Glu Val Leu Met Ala Glu Arg Asp Arg Glu Lys Phe Phe
            260                 265                 270

Leu Asn Gln Gly Tyr Ala Val Leu Arg Ile Asp Pro Lys Gln Leu Asp
        275                 280                 285

Leu Asn Gln Asp Gly Glu Cys Glu Phe Ile Gly Ile Leu Lys Asn Thr
    290                 295                 300

Leu Gln Lys Thr Pro Pro Glu His Leu Lys Gln Ala Ala
305                 310                 315
```

<210> 2287
<211> 1845
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1822)
<223> RXA01525

<400> 2287

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gtctctgtag aaatctaggg ctttcgacgc ttgagccccg cgcacctgca aggtgcgctg 60

tagggaggcg tcgacaagca tctttaagta gctttgaagc atg cgt tcc ttt caa   115
                                            Met Arg Ser Phe Gln
                                              1               5

tcg atc ctt gac ctg gta aat tca gca tcc gag gtg gct acc aaa att   163
Ser Ile Leu Asp Leu Val Asn Ser Ala Ser Glu Val Ala Thr Lys Ile
```

```
                    10                  15                  20

gtg ttg aag cgc ttc gaa aaa cgg ata acc agc gaa act gac tgg gta   211
Val Leu Lys Arg Phe Glu Lys Arg Ile Thr Ser Glu Thr Asp Trp Val
            25                  30                  35

ccg tat cag cgg ttt agt ctt tgg tcg gtt ggt tct ccg cta acg atc   259
Pro Tyr Gln Arg Phe Ser Leu Trp Ser Val Gly Ser Pro Leu Thr Ile
        40                  45                  50

gaa cgc aaa ggc ccc gat gtg cgt gtg agc aag gac aac act gcc gtt   307
Glu Arg Lys Gly Pro Asp Val Arg Val Ser Lys Asp Asn Thr Ala Val
    55                  60                  65

ctt cag cgc tat caa aga ccg gaa gca gaa gga ctg atc agc tac ttc   355
Leu Gln Arg Tyr Gln Arg Pro Glu Ala Glu Gly Leu Ile Ser Tyr Phe
70                  75                  80                  85

atg gat cca aag cca tgg ata act gaa ttg gca ggc ctg aat ctg gac   403
Met Asp Pro Lys Pro Trp Ile Thr Glu Leu Ala Gly Leu Asn Leu Asp
                90                  95                  100

gat gtt tcc gaa gat aca gtt gca ggt cgg aca gta tta gtg gtt ccc   451
Asp Val Ser Glu Asp Thr Val Ala Gly Arg Thr Val Leu Val Val Pro
            105                 110                 115

cta tcc aat gtc att ctc agc atc gat gcg gaa ttt ggg atg att cta   499
Leu Ser Asn Val Ile Leu Ser Ile Asp Ala Glu Phe Gly Met Ile Leu
        120                 125                 130

act gcg gaa aac gac ata gaa aag atc cac gca ata tct gtc gaa ctc   547
Thr Ala Glu Asn Asp Ile Glu Lys Ile His Ala Ile Ser Val Glu Leu
    135                 140                 145

tta gaa aaa tgg aga tca tcc cat tac cct gag ccg cat ttt cct gca   595
Leu Glu Lys Trp Arg Ser Ser His Tyr Pro Glu Pro His Phe Pro Ala
150                 155                 160                 165

gcg gtt ctc cca cct gcg tcg act gga aac cgc aac ctc cga gtt cta   643
Ala Val Leu Pro Pro Ala Ser Thr Gly Asn Arg Asn Leu Arg Val Leu
                170                 175                 180

tgc cct gag ttt tcc att cca agt gtc aac gtt ggt gat cag gtt tta   691
Cys Pro Glu Phe Ser Ile Pro Ser Val Asn Val Gly Asp Gln Val Leu
            185                 190                 195

cta ttt tta aca ttt gat caa acc ctg cca cca gta gat cag ctt gaa   739
Leu Phe Leu Thr Phe Asp Gln Thr Leu Pro Pro Val Asp Gln Leu Glu
        200                 205                 210

act act cgc cgc gga tac act gat cca atc cag ctt gac tac gac cac   787
Thr Thr Arg Arg Gly Tyr Thr Asp Pro Ile Gln Leu Asp Tyr Asp His
    215                 220                 225

cgc caa tac agg ttt cac gcc gac ggt tgg gat gcc atc atc tcc acg   835
Arg Gln Tyr Arg Phe His Ala Asp Gly Trp Asp Ala Ile Ile Ser Thr
230                 235                 240                 245

gtg gag cca cta cac gac gaa gaa gaa ctc aca ggt tac ttc ctg cac   883
Val Glu Pro Leu His Asp Glu Glu Glu Leu Thr Gly Tyr Phe Leu His
                250                 255                 260
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```
cgc ctt gac cca gat agc gcg tac cca acc att gca gtc gtt aca gca   931
Arg Leu Asp Pro Asp Ser Ala Tyr Pro Thr Ile Ala Val Val Thr Ala
            265                 270                 275

gcg cac tac cac ggt acg gac gca att atc gac gtg acc cta gat ggt   979
Ala His Tyr His Gly Thr Asp Ala Ile Ile Asp Val Thr Leu Asp Gly
        280                 285                 290

gtg cat cca ccc aaa aac caa gaa act ctt gaa ggc atc agc act agt   1027
Val His Pro Pro Lys Asn Gln Glu Thr Leu Glu Gly Ile Ser Thr Ser
    295                 300                 305

acc agt gac ggt gac ata ttt tgg ctc tcc gat gaa agc ttg cct ttc   1075
Thr Ser Asp Gly Asp Ile Phe Trp Leu Ser Asp Glu Ser Leu Pro Phe
310                 315                 320                 325

gtc cgt gga ttc agc gtg tca aca ggc gaa cta tta cac gag atc tcc   1123
Val Arg Gly Phe Ser Val Ser Thr Gly Glu Leu Leu His Glu Ile Ser
                330                 335                 340

atc ccc acg ttc caa gag atc gtc ctc gat tcc gct aat aga gcc cgc   1171
Ile Pro Thr Phe Gln Glu Ile Val Leu Asp Ser Ala Asn Arg Ala Arg
            345                 350                 355

gta aaa caa aag caa tgg cct cac gat ttc agt gat tgc aag gga aaa   1219
Val Lys Gln Lys Gln Trp Pro His Asp Phe Ser Asp Cys Lys Gly Lys
        360                 365                 370

aca tgg gag ctt ccg gat ctt aaa gaa gta ttc gaa gct gtc cct tcg   1267
Thr Trp Glu Leu Pro Asp Leu Lys Glu Val Phe Glu Ala Val Pro Ser
    375                 380                 385

att cca gca ggt tgg aga ttg tta gac agc ttc ggg aaa aac ttg cac   1315
Ile Pro Ala Gly Trp Arg Leu Leu Asp Ser Phe Gly Lys Asn Leu His
390                 395                 400                 405

aat gtc aca cgc gaa aac cct cgt ctt aat gac aac ttt tgg ctt caa   1363
Asn Val Thr Arg Glu Asn Pro Arg Leu Asn Asp Asn Phe Trp Leu Gln
                410                 415                 420

aca atc ctt agg ctt aaa cca ttt aaa gca gta gat ctt gat atc ggc   1411
Thr Ile Leu Arg Leu Lys Pro Phe Lys Ala Val Asp Leu Asp Ile Gly
            425                 430                 435

cga tcg ata atc aca gca att tac cca tac ggt gat cga att tac tta   1459
Arg Ser Ile Ile Thr Ala Ile Tyr Pro Tyr Gly Asp Arg Ile Tyr Leu
        440                 445                 450

cgc gct agt aac cac cac atc acg ttt aac cag gac ctc gag att ctc   1507
Arg Ala Ser Asn His His Ile Thr Phe Asn Gln Asp Leu Glu Ile Leu
    455                 460                 465

aac gta gaa gtc ttt ggc gac cct gag gtt ccc gaa tct ggt cta att   1555
Asn Val Glu Val Phe Gly Asp Pro Glu Val Pro Glu Ser Gly Leu Ile
470                 475                 480                 485

tat ctt cca cct ggg gat tct cca aca ctc ggt ttt ccc acc gga aca   1603
Tyr Leu Pro Pro Gly Asp Ser Pro Thr Leu Gly Phe Pro Thr Gly Thr
                490                 495                 500
```

```
ctc atg atg ttt cat gag caa gaa ggc aca tat gct ttc cac gac cct   1651
Leu Met Met Phe His Glu Gln Glu Gly Thr Tyr Ala Phe His Asp Pro
            505                 510                 515

gaa aca aca gaa caa ata aca act gtg aac tta gac agg aat agt ttt   1699
Glu Thr Thr Glu Gln Ile Thr Thr Val Asn Leu Asp Arg Asn Ser Phe
        520                 525                 530

tca gtg gca tat tct tcc cga acc aaa att gtt att tca ctg aaa aac   1747
Ser Val Ala Tyr Ser Ser Arg Thr Lys Ile Val Ile Ser Leu Lys Asn
    535                 540                 545

cca gaa agc cga cct acc aac aag ctg ttg gtg tgg gaa cca caa acc   1795
Pro Glu Ser Arg Pro Thr Asn Lys Leu Leu Val Trp Glu Pro Gln Thr
550                 555                 560                 565

ggg tgg cga gaa cag aac ctg gag cgc tgagcacgct taaggtgagg         1842
Gly Trp Arg Glu Gln Asn Leu Glu Arg
                570

tgg                                                              1845
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US 20050153417 A1

<210> 2288
<211> 574
<212> PRT
<213> Corynebacterium glutamicum

<400> 2288

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Met Arg Ser Phe Gln Ser Ile Leu Asp Leu Val Asn Ser Ala Ser Glu
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Val Ala Thr Lys Ile Val Leu Lys Arg Phe Glu Lys Arg Ile Thr Ser
             20                  25                  30

Glu Thr Asp Trp Val Pro Tyr Gln Arg Phe Ser Leu Trp Ser Val Gly
         35                  40                  45

Ser Pro Leu Thr Ile Glu Arg Lys Gly Pro Asp Val Arg Val Ser Lys
     50                  55                  60

Asp Asn Thr Ala Val Leu Gln Arg Tyr Gln Arg Pro Glu Ala Glu Gly
 65                  70                  75                  80

Leu Ile Ser Tyr Phe Met Asp Pro Lys Pro Trp Ile Thr Glu Leu Ala
                 85                  90                  95

Gly Leu Asn Leu Asp Asp Val Ser Glu Asp Thr Val Ala Gly Arg Thr
            100                 105                 110

Val Leu Val Val Pro Leu Ser Asn Val Ile Leu Ser Ile Asp Ala Glu
        115                 120                 125

Phe Gly Met Ile Leu Thr Ala Glu Asn Asp Ile Glu Lys Ile His Ala
    130                 135                 140

Ile Ser Val Glu Leu Leu Glu Lys Trp Arg Ser Ser His Tyr Pro Glu
145                 150                 155                 160

Pro His Phe Pro Ala Ala Val Leu Pro Pro Ala Ser Thr Gly Asn Arg
                165                 170                 175
```

```
Asn Leu Arg Val Leu Cys Pro Glu Phe Ser Ile Pro Ser Val Asn Val
            180                 185                 190

Gly Asp Gln Val Leu Leu Phe Leu Thr Phe Asp Gln Thr Leu Pro Pro
        195                 200                 205

Val Asp Gln Leu Glu Thr Thr Arg Arg Gly Tyr Thr Asp Pro Ile Gln
    210                 215                 220

Leu Asp Tyr Asp His Arg Gln Tyr Arg Phe His Ala Asp Gly Trp Asp
225                 230                 235                 240

Ala Ile Ile Ser Thr Val Glu Pro Leu His Asp Glu Glu Glu Leu Thr
                245                 250                 255

Gly Tyr Phe Leu His Arg Leu Asp Pro Asp Ser Ala Tyr Pro Thr Ile
            260                 265                 270

Ala Val Val Thr Ala Ala His Tyr His Gly Thr Asp Ala Ile Ile Asp
        275                 280                 285

Val Thr Leu Asp Gly Val His Pro Pro Lys Asn Gln Glu Thr Leu Glu
    290                 295                 300

Gly Ile Ser Thr Ser Thr Ser Asp Gly Asp Ile Phe Trp Leu Ser Asp
305                 310                 315                 320

Glu Ser Leu Pro Phe Val Arg Gly Phe Ser Val Ser Thr Gly Glu Leu
                325                 330                 335

Leu His Glu Ile Ser Ile Pro Thr Phe Gln Glu Ile Val Leu Asp Ser
            340                 345                 350

Ala Asn Arg Ala Arg Val Lys Gln Lys Gln Trp Pro His Asp Phe Ser
        355                 360                 365

Asp Cys Lys Gly Lys Thr Trp Glu Leu Pro Asp Leu Lys Glu Val Phe
    370                 375                 380

Glu Ala Val Pro Ser Ile Pro Ala Gly Trp Arg Leu Leu Asp Ser Phe
385                 390                 395                 400

Gly Lys Asn Leu His Asn Val Thr Arg Glu Asn Pro Arg Leu Asn Asp
                405                 410                 415

Asn Phe Trp Leu Gln Thr Ile Leu Arg Leu Lys Pro Phe Lys Ala Val
            420                 425                 430

Asp Leu Asp Ile Gly Arg Ser Ile Ile Thr Ala Ile Tyr Pro Tyr Gly
        435                 440                 445

Asp Arg Ile Tyr Leu Arg Ala Ser Asn His His Ile Thr Phe Asn Gln
    450                 455                 460

Asp Leu Glu Ile Leu Asn Val Glu Val Phe Gly Asp Pro Glu Val Pro
465                 470                 475                 480

Glu Ser Gly Leu Ile Tyr Leu Pro Pro Gly Asp Ser Pro Thr Leu Gly
                485                 490                 495
```

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Phe Pro Thr Gly Thr Leu Met Met Phe His Glu Gln Glu Gly Thr Tyr
            500                 505                 510

Ala Phe His Asp Pro Glu Thr Thr Glu Gln Ile Thr Thr Val Asn Leu
        515                 520                 525

Asp Arg Asn Ser Phe Ser Val Ala Tyr Ser Ser Arg Thr Lys Ile Val
    530                 535                 540

Ile Ser Leu Lys Asn Pro Glu Ser Arg Pro Thr Asn Lys Leu Leu Val
545                 550                 555                 560

Trp Glu Pro Gln Thr Gly Trp Arg Glu Gln Asn Leu Glu Arg
                565                 570


<210> 2289
<211> 2634
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2611)
<223> RXA01527

<400> 2289
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ttgctttgaa ggaaaaggcg gagggaaggt ccaccccaag gtg att ccg aac ccc   115
                                        Val Ile Pro Asn Pro
                                          1               5

aac ccg aac ccc aaa gcc aaa act ctt cgc ctc gtt tca gcg ctg acc   163
Asn Pro Asn Pro Lys Ala Lys Thr Leu Arg Leu Val Ser Ala Leu Thr
                10                  15                  20

gcc atc act gtg gtg ggt ttt agc gct tca cct gtt cat gcg ttg ccg   211
Ala Ile Thr Val Val Gly Phe Ser Ala Ser Pro Val His Ala Leu Pro
            25                  30                  35

att ccg ttg gat cct tct gat ccg gcg gtg tcg gag ttg tgg gtg aat   259
Ile Pro Leu Asp Pro Ser Asp Pro Ala Val Ser Glu Leu Trp Val Asn
        40                  45                  50

ccg aat gcg cgg gct gat gat gag ctt tct ggt gtg gat gta gag atc   307
Pro Asn Ala Arg Ala Asp Asp Glu Leu Ser Gly Val Asp Val Glu Ile
    55                  60                  65

tcg gat ttt gtc atg ccg aat agc aat cta act gtg cag gtg ggg gag   355
Ser Asp Phe Val Met Pro Asn Ser Asn Leu Thr Val Gln Val Gly Glu
70                  75                  80                  85

tct ttt aag gcg cag gtt cgg gtg act aat cgt tcg tcg gag acg ttg   403
Ser Phe Lys Ala Gln Val Arg Val Thr Asn Arg Ser Ser Glu Thr Leu
                90                  95                  100

agc aat att acg ttg cag gcg cgt cgt gcg gag gcg tcg ttt gat atg   451
Ser Asn Ile Thr Leu Gln Ala Arg Arg Ala Glu Ala Ser Phe Asp Met
            105                 110                 115
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gcg agt gct cgg gtg gcg gcg acg gat aat aat tat ggc tac ttc ggc   499
Ala Ser Ala Arg Val Ala Ala Thr Asp Asn Asn Tyr Gly Tyr Phe Gly
        120                 125                 130

gcg atg gtg act ctt gat gat gag ttg gag ccg ggg gag agt gtt gag   547
Ala Met Val Thr Leu Asp Asp Glu Leu Glu Pro Gly Glu Ser Val Glu
    135                 140                 145

act gag gtg gag att tct acc gat agt ttg tcg att tct cag ccg ggt   595
Thr Glu Val Glu Ile Ser Thr Asp Ser Leu Ser Ile Ser Gln Pro Gly
150                 155                 160                 165

tct tat ccg acg atg ttg gcg ttg tcg ggg cag ctt gat ggg gtg gcg   643
Ser Tyr Pro Thr Met Leu Ala Leu Ser Gly Gln Leu Asp Gly Val Ala
                170                 175                 180

cag cat ttg gat tcg cag cgt ttc ctt ctg cca gtc ctc agc gat aca   691
Gln His Leu Asp Ser Gln Arg Phe Leu Leu Pro Val Leu Ser Asp Thr
            185                 190                 195

act gat aca gaa gac acc gcc acc ccc acg acg atg att tac ccg ata   739
Thr Asp Thr Glu Asp Thr Ala Thr Pro Thr Thr Met Ile Tyr Pro Ile
        200                 205                 210

tca gcc cag acg aat gtg ttg ggt ggt gag acc ggc gag gcg ccg gaa   787
Ser Ala Gln Thr Asn Val Leu Gly Gly Glu Thr Gly Glu Ala Pro Glu
    215                 220                 225

gag ccg cct ttg ctg gtc agt tcc gac gcg ctt gcg ggc gag ttg gat   835
Glu Pro Pro Leu Leu Val Ser Ser Asp Ala Leu Ala Gly Glu Leu Asp
230                 235                 240                 245

gag ggc ggt cgt ttg caa aag ctt atc gac gcc tac ctc cag tct tca   883
Glu Gly Gly Arg Leu Gln Lys Leu Ile Asp Ala Tyr Leu Gln Ser Ser
                250                 255                 260

ccc gcc gtg cag caa gcc acg tgc ctt gct att gat ccg cag ctt ctt   931
Pro Ala Val Gln Gln Ala Thr Cys Leu Ala Ile Asp Pro Gln Leu Leu
            265                 270                 275

gat gtg gtg gat cgc atg acc ggc ggt tac acc gtg acc gat act cgt   979
Asp Val Val Asp Arg Met Thr Gly Gly Tyr Thr Val Thr Asp Thr Arg
        280                 285                 290

ccc agt acg gtg cgg cag aat cag cgg ctt cgt gag ttg tgg act gcc   1027
Pro Ser Thr Val Arg Gln Asn Gln Arg Leu Arg Glu Leu Trp Thr Ala
    295                 300                 305

gat aat caa ccc acc aat ggt gtc gcg ggc acg ggt gcg gaa aac gct   1075
Asp Asn Gln Pro Thr Asn Gly Val Ala Gly Thr Gly Ala Glu Asn Ala
310                 315                 320                 325

gcc att ttc ttg gag aaa ctc cga cag gcc aca gcc acc tcg tgc acc   1123
Ala Ile Phe Leu Glu Lys Leu Arg Gln Ala Thr Ala Thr Ser Cys Thr
                330                 335                 340

gtg gcg ttg ccg tgg gcg aat gct gat cta aat gca gtg agc caa acc   1171
Val Ala Leu Pro Trp Ala Asn Ala Asp Leu Asn Ala Val Ser Gln Thr
            345                 350                 355

ggt aat cag tgg ttg atg cgc gag gcg cta cag cga ggt gtc acc acc   1219
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Gly Asn Gln Trp Leu Met Arg Glu Ala Leu Gln Arg Gly Val Thr Thr
        360                 365                 370

ttt gaa gaa gtg ttg ggt gtt att ccg gaa tcc aat gtg gtg att cct   1267
Phe Glu Glu Val Leu Gly Val Ile Pro Glu Ser Asn Val Val Ile Pro
    375                 380                 385

gga aat ggt ttt gtg gag ccc tcc acc gtg ggt gat ctc gga tgg gcg   1315
Gly Asn Gly Phe Val Glu Pro Ser Thr Val Gly Asp Leu Gly Trp Ala
390                 395                 400                 405

gaa gta acg ctt aat ccg gat cag gcg tgg gag gtg cag tca gag gag   1363
Glu Val Thr Leu Asn Pro Asp Gln Ala Trp Glu Val Gln Ser Glu Glu
                410                 415                 420

ttg gtt gct gcc cct gat gcc aca gag caa agc gca ttg gat aac cct   1411
Leu Val Ala Ala Pro Asp Ala Thr Glu Gln Ser Ala Leu Asp Asn Pro
            425                 430                 435

aag cca acg cca ggc acg gtg acg ccg cca acc cct atg tca acg gtg   1459
Lys Pro Thr Pro Gly Thr Val Thr Pro Pro Thr Pro Met Ser Thr Val
        440                 445                 450

tcc gtg ttg gtt tct gat aac acg gtg tgg cgc aca acg agc gcg gat   1507
Ser Val Leu Val Ser Asp Asn Thr Val Trp Arg Thr Thr Ser Ala Asp
    455                 460                 465

cgg ttc cac tct ttg gct ccg gga ata act ggg gtg tcg tat cag gga   1555
Arg Phe His Ser Leu Ala Pro Gly Ile Thr Gly Val Ser Tyr Gln Gly
470                 475                 480                 485

tcg tta tcg gca acc ttg gct acc ttg gga caa aac cct gag act gtg   1603
Ser Leu Ser Ala Thr Leu Ala Thr Leu Gly Gln Asn Pro Glu Thr Val
                490                 495                 500

ggc tat tcc aat ccg gat tcg cgt tat gac tac gcc atg gat tct gag   1651
Gly Tyr Ser Asn Pro Asp Ser Arg Tyr Asp Tyr Ala Met Asp Ser Glu
            505                 510                 515

agc gcc cgc aat ctc acc ggc cag gcg gcg ctg cgc ttg acg gtg gac   1699
Ser Ala Arg Asn Leu Thr Gly Gln Ala Ala Leu Arg Leu Thr Val Asp
        520                 525                 530

aac ggc gat gaa gac tct ccc gtg ttg atc atg ccg agc gcg gtg ctg   1747
Asn Gly Asp Glu Asp Ser Pro Val Leu Ile Met Pro Ser Ala Val Leu
    535                 540                 545

ggc gcc gaa gac ggc gcg atg ttg ctt gag acc acc ggg gct ttg ctt   1795
Gly Ala Glu Asp Gly Ala Met Leu Leu Glu Thr Thr Gly Ala Leu Leu
550                 555                 560                 565

gcc gac ggc tcc gcc cga cct ttt tcc ctg cag caa tat gtc act gcc   1843
Ala Asp Gly Ser Ala Arg Pro Phe Ser Leu Gln Gln Tyr Val Thr Ala
                570                 575                 580

aat gcg gaa caa aga aat act ttg gcc aca gca aca act cca ccg gat   1891
Asn Ala Glu Gln Arg Asn Thr Leu Ala Thr Ala Thr Thr Pro Pro Asp
            585                 590                 595

gac act gct ttt ggt gca ccc tac gac gat cct gcg tca ttg acg gaa   1939
Asp Thr Ala Phe Gly Ala Pro Tyr Asp Asp Pro Ala Ser Leu Thr Glu
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        600                 605                 610

acc gaa att ctg cga acc act cag cag gcg gag tac atc gat gat ctc   1987
Thr Glu Ile Leu Arg Thr Thr Gln Gln Ala Glu Tyr Ile Asp Asp Leu
    615                 620                 625

act ggc atc atg tcc aat gat ccc agc att gca ctg acc cgt tat ggg   2035
Thr Gly Ile Met Ser Asn Asp Pro Ser Ile Ala Leu Thr Arg Tyr Gly
630                 635                 640                 645

ttt aca gca ccg ctg cgg caa gat ctg ctg cgc gcg ttg agt atc agt   2083
Phe Thr Ala Pro Leu Arg Gln Asp Leu Leu Arg Ala Leu Ser Ile Ser
                650                 655                 660

gag cgt cgt tcg tta gct cgc cac acc cag gca acc tct gct gcc gat   2131
Glu Arg Arg Ser Leu Ala Arg His Thr Gln Ala Thr Ser Ala Ala Asp
            665                 670                 675

aaa tta ctt aat cgc aac cgc gat act ctg cag aag ctg cgt agc tct   2179
Lys Leu Leu Asn Arg Asn Arg Asp Thr Leu Gln Lys Leu Arg Ser Ser
        680                 685                 690

gtg gcg ttg ttg ccg ccg gga aat gtg tat acc cga acc tcg gaa tcg   2227
Val Ala Leu Leu Pro Pro Gly Asn Val Tyr Thr Arg Thr Ser Glu Ser
    695                 700                 705

tct ccg ttg ttg att gtg gcg caa aac ggt ttg cca ttg ccc gcg gag   2275
Ser Pro Leu Leu Ile Val Ala Gln Asn Gly Leu Pro Leu Pro Ala Glu
710                 715                 720                 725

act cag att ttg tat tcc gga aat cag gat gcg cac atc aat act ccg   2323
Thr Gln Ile Leu Tyr Ser Gly Asn Gln Asp Ala His Ile Asn Thr Pro
                730                 735                 740

ggt gtg gtt cgt att ccg gcg cag ggt tcc atc acc ttg cag atg act   2371
Gly Val Val Arg Ile Pro Ala Gln Gly Ser Ile Thr Leu Gln Met Thr
            745                 750                 755

gcg gat ttg ccc gat gac aat ctg cgc act gat ctc acg ttg tgg ttg   2419
Ala Asp Leu Pro Asp Asp Asn Leu Arg Thr Asp Leu Thr Leu Trp Leu
        760                 765                 770

gca tcc cca gat ggg gcc acc att agt gaa cct gtg gaa att act gtc   2467
Ala Ser Pro Asp Gly Ala Thr Ile Ser Glu Pro Val Glu Ile Thr Val
    775                 780                 785

cag cct cgc ccg aat ttg ggc acc acg ctg ttt ttc gtg gca gcg ggc   2515
Gln Pro Arg Pro Asn Leu Gly Thr Thr Leu Phe Phe Val Ala Ala Gly
790                 795                 800                 805

att ctg gca gta gga ggg ttg ttg ttt ata cgg aag aaa cga aac gtc   2563
Ile Leu Ala Val Gly Gly Leu Leu Phe Ile Arg Lys Lys Arg Asn Val
                810                 815                 820

gaa aag cgc tcg ccc ggt acg gga tcg ccc aaa ccg cca cca acc cac   2611
Glu Lys Arg Ser Pro Gly Thr Gly Ser Pro Lys Pro Pro Pro Thr His
            825                 830                 835

taacgtatcg catagttatt ttc                                        2634
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<211> 837
<212> PRT
<213> Corynebacterium glutamicum

<400> 2290

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Val Ile Pro Asn Pro Asn Pro Asn Pro Lys Ala Lys Thr Leu Arg Leu
  1               5                  10                  15

Val Ser Ala Leu Thr Ala Ile Thr Val Val Gly Phe Ser Ala Ser Pro
             20                  25                  30

Val His Ala Leu Pro Ile Pro Leu Asp Pro Ser Asp Pro Ala Val Ser
         35                  40                  45

Glu Leu Trp Val Asn Pro Asn Ala Arg Ala Asp Asp Glu Leu Ser Gly
     50                  55                  60

Val Asp Val Glu Ile Ser Asp Phe Val Met Pro Asn Ser Asn Leu Thr
 65                  70                  75                  80

Val Gln Val Gly Glu Ser Phe Lys Ala Gln Val Arg Val Thr Asn Arg
                 85                  90                  95

Ser Ser Glu Thr Leu Ser Asn Ile Thr Leu Gln Ala Arg Arg Ala Glu
            100                 105                 110

Ala Ser Phe Asp Met Ala Ser Ala Arg Val Ala Ala Thr Asp Asn Asn
        115                 120                 125

Tyr Gly Tyr Phe Gly Ala Met Val Thr Leu Asp Asp Glu Leu Glu Pro
    130                 135                 140

Gly Glu Ser Val Glu Thr Glu Val Glu Ile Ser Thr Asp Ser Leu Ser
145                 150                 155                 160

Ile Ser Gln Pro Gly Ser Tyr Pro Thr Met Leu Ala Leu Ser Gly Gln
                165                 170                 175

Leu Asp Gly Val Ala Gln His Leu Asp Ser Gln Arg Phe Leu Leu Pro
            180                 185                 190

Val Leu Ser Asp Thr Thr Asp Thr Glu Asp Thr Ala Thr Pro Thr Thr
        195                 200                 205

Met Ile Tyr Pro Ile Ser Ala Gln Thr Asn Val Leu Gly Gly Glu Thr
    210                 215                 220

Gly Glu Ala Pro Glu Glu Pro Pro Leu Leu Val Ser Ser Asp Ala Leu
225                 230                 235                 240

Ala Gly Glu Leu Asp Glu Gly Gly Arg Leu Gln Lys Leu Ile Asp Ala
                245                 250                 255

Tyr Leu Gln Ser Ser Pro Ala Val Gln Gln Ala Thr Cys Leu Ala Ile
            260                 265                 270

Asp Pro Gln Leu Leu Asp Val Val Asp Arg Met Thr Gly Gly Tyr Thr
        275                 280                 285

Val Thr Asp Thr Arg Pro Ser Thr Val Arg Gln Asn Gln Arg Leu Arg
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    290                 295                 300

Glu Leu Trp Thr Ala Asp Asn Gln Pro Thr Asn Gly Val Ala Gly Thr
305                 310                 315                 320

Gly Ala Glu Asn Ala Ala Ile Phe Leu Glu Lys Leu Arg Gln Ala Thr
                325                 330                 335

Ala Thr Ser Cys Thr Val Ala Leu Pro Trp Ala Asn Ala Asp Leu Asn
            340                 345                 350

Ala Val Ser Gln Thr Gly Asn Gln Trp Leu Met Arg Glu Ala Leu Gln
        355                 360                 365

Arg Gly Val Thr Thr Phe Glu Glu Val Leu Gly Val Ile Pro Glu Ser
    370                 375                 380

Asn Val Val Ile Pro Gly Asn Gly Phe Val Glu Pro Ser Thr Val Gly
385                 390                 395                 400

Asp Leu Gly Trp Ala Glu Val Thr Leu Asn Pro Asp Gln Ala Trp Glu
                405                 410                 415

Val Gln Ser Glu Glu Leu Val Ala Ala Pro Asp Ala Thr Glu Gln Ser
            420                 425                 430

Ala Leu Asp Asn Pro Lys Pro Thr Pro Gly Thr Val Thr Pro Pro Thr
        435                 440                 445

Pro Met Ser Thr Val Ser Val Leu Val Ser Asp Asn Thr Val Trp Arg
    450                 455                 460

Thr Thr Ser Ala Asp Arg Phe His Ser Leu Ala Pro Gly Ile Thr Gly
465                 470                 475                 480

Val Ser Tyr Gln Gly Ser Leu Ser Ala Thr Leu Ala Thr Leu Gly Gln
                485                 490                 495

Asn Pro Glu Thr Val Gly Tyr Ser Asn Pro Asp Ser Arg Tyr Asp Tyr
            500                 505                 510

Ala Met Asp Ser Glu Ser Ala Arg Asn Leu Thr Gly Gln Ala Ala Leu
        515                 520                 525

Arg Leu Thr Val Asp Asn Gly Asp Glu Asp Ser Pro Val Leu Ile Met
    530                 535                 540

Pro Ser Ala Val Leu Gly Ala Glu Asp Gly Ala Met Leu Leu Glu Thr
545                 550                 555                 560

Thr Gly Ala Leu Leu Ala Asp Gly Ser Ala Arg Pro Phe Ser Leu Gln
                565                 570                 575

Gln Tyr Val Thr Ala Asn Ala Glu Gln Arg Asn Thr Leu Ala Thr Ala
            580                 585                 590

Thr Thr Pro Pro Asp Asp Thr Ala Phe Gly Ala Pro Tyr Asp Asp Pro
        595                 600                 605

Ala Ser Leu Thr Glu Thr Glu Ile Leu Arg Thr Thr Gln Gln Ala Glu
    610                 615                 620
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Tyr Ile Asp Asp Leu Thr Gly Ile Met Ser Asn Asp Pro Ser Ile Ala
625                 630                 635                 640

Leu Thr Arg Tyr Gly Phe Thr Ala Pro Leu Arg Gln Asp Leu Leu Arg
                645                 650                 655

Ala Leu Ser Ile Ser Glu Arg Arg Ser Leu Ala Arg His Thr Gln Ala
            660                 665                 670

Thr Ser Ala Ala Asp Lys Leu Leu Asn Arg Asn Arg Asp Thr Leu Gln
        675                 680                 685

Lys Leu Arg Ser Ser Val Ala Leu Leu Pro Pro Gly Asn Val Tyr Thr
    690                 695                 700

Arg Thr Ser Glu Ser Ser Pro Leu Leu Ile Val Ala Gln Asn Gly Leu
705                 710                 715                 720

Pro Leu Pro Ala Glu Thr Gln Ile Leu Tyr Ser Gly Asn Gln Asp Ala
                725                 730                 735

His Ile Asn Thr Pro Gly Val Val Arg Ile Pro Ala Gln Gly Ser Ile
            740                 745                 750

Thr Leu Gln Met Thr Ala Asp Leu Pro Asp Asp Asn Leu Arg Thr Asp
        755                 760                 765

Leu Thr Leu Trp Leu Ala Ser Pro Asp Gly Ala Thr Ile Ser Glu Pro
    770                 775                 780

Val Glu Ile Thr Val Gln Pro Arg Pro Asn Leu Gly Thr Thr Leu Phe
785                 790                 795                 800

Phe Val Ala Ala Gly Ile Leu Ala Val Gly Gly Leu Leu Phe Ile Arg
                805                 810                 815

Lys Lys Arg Asn Val Glu Lys Arg Ser Pro Gly Thr Gly Ser Pro Lys
            820                 825                 830

Pro Pro Pro Thr His
        835
```

<210> 2291
<211> 1365
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1342)
<223> RXA01536

<400> 2291

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agcatagatg acttgacact gttgcagcag gcggttttca cctggcctct taggatttgg 60

tcaaatggtt gcaacgacgc cagggaagga ggcgcacccc atg gca ttt gga ttt   115
                                               Met Ala Phe Gly Phe
                                                 1               5
```

```
ttt agt aga cgt aag aaa aag aac aaa gac aaa aac ccg aat gaa aat   163
Phe Ser Arg Arg Lys Lys Lys Asn Lys Asp Lys Asn Pro Asn Glu Asn
                 10                  15                  20

tca gca gtg ccc gca cac tct gaa gat tca cct cag gag gtt ttt gag   211
Ser Ala Val Pro Ala His Ser Glu Asp Ser Pro Gln Glu Val Phe Glu
             25                  30                  35

ggt aat ggt cgt cag gta ggc gac ccc att gaa cag cag gtt gat cga   259
Gly Asn Gly Arg Gln Val Gly Asp Pro Ile Glu Gln Gln Val Asp Arg
         40                  45                  50

gat gct aaa ggt cgt ctc aca gcg gcg gat ttc ttg ccg gac gct gat   307
Asp Ala Lys Gly Arg Leu Thr Ala Ala Asp Phe Leu Pro Asp Ala Asp
     55                  60                  65

ctg cca cag ctg aat cgt tcg cgt gca aat atg ctg cgc cgt gaa ttg   355
Leu Pro Gln Leu Asn Arg Ser Arg Ala Asn Met Leu Arg Arg Glu Leu
 70                  75                  80                  85

gag tac cgt ttt tca ctc cag aat gcc cac att aat atc gat gga aac   403
Glu Tyr Arg Phe Ser Leu Gln Asn Ala His Ile Asn Ile Asp Gly Asn
                 90                  95                 100

acg gcc atg att cag cgt tca gat ggc ggg gca gca cat gtc tcg ttg   451
Thr Ala Met Ile Gln Arg Ser Asp Gly Gly Ala Ala His Val Ser Leu
             105                 110                 115

cgc acc ctc gcg atg aat gca gct ggc ctt gat aac ttt gat caa ctc   499
Arg Thr Leu Ala Met Asn Ala Ala Gly Leu Asp Asn Phe Asp Gln Leu
         120                 125                 130

cct gaa ctg gtg gaa agc ttc gtt cac ggc acg ctg gcc gat gca aca   547
Pro Glu Leu Val Glu Ser Phe Val His Gly Thr Leu Ala Asp Ala Thr
     135                 140                 145

tta aac gat ctt tct act gct gac ctg tat aaa gca ctg cgc ctt cgc   595
Leu Asn Asp Leu Ser Thr Ala Asp Leu Tyr Lys Ala Leu Arg Leu Arg
150                 155                 160                 165

ctg ctg cca aca cct ggc gaa ggc gac gat cta gtt gag cat gga ctc   643
Leu Leu Pro Thr Pro Gly Glu Gly Asp Asp Leu Val Glu His Gly Leu
                 170                 175                 180

gac cgg gaa agc cag atc cgc gac gat tca atc ctg cgc acc ttc acc   691
Asp Arg Glu Ser Gln Ile Arg Asp Asp Ser Ile Leu Arg Thr Phe Thr
             185                 190                 195

tct gac atg tcg atc gcg ctg gtg ctc gat acc gag cat gcc atc cgc   739
Ser Asp Met Ser Ile Ala Leu Val Leu Asp Thr Glu His Ala Ile Arg
         200                 205                 210

atc cag cca ctc aaa gag ctc gag gag ttc gat gac ctc agc gcc cta   787
Ile Gln Pro Leu Lys Glu Leu Glu Glu Phe Asp Asp Leu Ser Ala Leu
     215                 220                 225

gag cgg gct gcg gac cgc aat acc tgg caa gag ctt tac gac gca aac   835
Glu Arg Ala Ala Asp Arg Asn Thr Trp Gln Glu Leu Tyr Asp Ala Asn
230                 235                 240                 245

gtt gac gct tcc ttc gtc gac gct gaa tca gac agc gaa ggg tca tca   883
```

```
Val Asp Ala Ser Phe Val Asp Ala Glu Ser Asp Ser Glu Gly Ser Ser
                250                 255                 260

ttt tgg gct ttc gaa tct aac tcg tac tac ttg ggt agt gca cca ctg   931
Phe Trp Ala Phe Glu Ser Asn Ser Tyr Tyr Leu Gly Ser Ala Pro Leu
            265                 270                 275

ttc ctc aac gat ctg ttg gca aag tgg gca cct gac ctg gac caa agt   979
Phe Leu Asn Asp Leu Leu Ala Lys Trp Ala Pro Asp Leu Asp Gln Ser
        280                 285                 290

gat ggc gtc atc ttt gct gtc cct gat cgt gat ctg ttg att gcg cgt   1027
Asp Gly Val Ile Phe Ala Val Pro Asp Arg Asp Leu Leu Ile Ala Arg
    295                 300                 305

cct gtg acc acc ggc gaa gat ctg atg aac gga atc acc gcg atg gtg   1075
Pro Val Thr Thr Gly Glu Asp Leu Met Asn Gly Ile Thr Ala Met Val
310                 315                 320                 325

agg atc gcg atg cgc ttt ggc ctc ggg aac ccg acg tcg ata agc ccg   1123
Arg Ile Ala Met Arg Phe Gly Leu Gly Asn Pro Thr Ser Ile Ser Pro
                330                 335                 340

cgc ctg cac ctg ctg cgc gac aac cag gtg acc acc ttc acc gac ttc   1171
Arg Leu His Leu Leu Arg Asp Asn Gln Val Thr Thr Phe Thr Asp Phe
            345                 350                 355

cgc gtc gtc tct cct gaa atg gaa gct gaa tgg gaa gac agc gcg ttt   1219
Arg Val Val Ser Pro Glu Met Glu Ala Glu Trp Glu Asp Ser Ala Phe
        360                 365                 370

gac gcg cca ccg gcc ggc gcg atc ggc att gag gtg cgc cca gat ccg   1267
Asp Ala Pro Pro Ala Gly Ala Ile Gly Ile Glu Val Arg Pro Asp Pro
    375                 380                 385

tat ctg atg gag cgc ctc caa cag ggc ggc ttt ggt gat ttc gga gat   1315
Tyr Leu Met Glu Arg Leu Gln Gln Gly Gly Phe Gly Asp Phe Gly Asp
390                 395                 400                 405

ttc ggc aag ccc cgc gat cta gat atg tagcgaaaaa gggaccttca         1362
Phe Gly Lys Pro Arg Asp Leu Asp Met
                410

ctt                                                               1365
```

<210> 2292
<211> 414
<212> PRT
<213> Corynebacterium glutamicum

<400> 2292

```
Met Ala Phe Gly Phe Phe Ser Arg Arg Lys Lys Lys Asn Lys Asp Lys
  1               5                  10                  15

Asn Pro Asn Glu Asn Ser Ala Val Pro Ala His Ser Glu Asp Ser Pro
            20                  25                  30

Gln Glu Val Phe Glu Gly Asn Gly Arg Gln Val Gly Asp Pro Ile Glu
        35                  40                  45
```

```
Gln Gln Val Asp Arg Asp Ala Lys Gly Arg Leu Thr Ala Ala Asp Phe
     50                  55                  60

Leu Pro Asp Ala Asp Leu Pro Gln Leu Asn Arg Ser Arg Ala Asn Met
 65                  70                  75                  80

Leu Arg Arg Glu Leu Glu Tyr Arg Phe Ser Leu Gln Asn Ala His Ile
                 85                  90                  95

Asn Ile Asp Gly Asn Thr Ala Met Ile Gln Arg Ser Asp Gly Gly Ala
            100                 105                 110

Ala His Val Ser Leu Arg Thr Leu Ala Met Asn Ala Ala Gly Leu Asp
        115                 120                 125

Asn Phe Asp Gln Leu Pro Glu Leu Val Glu Ser Phe Val His Gly Thr
    130                 135                 140

Leu Ala Asp Ala Thr Leu Asn Asp Leu Ser Thr Ala Asp Leu Tyr Lys
145                 150                 155                 160

Ala Leu Arg Leu Arg Leu Leu Pro Thr Pro Gly Glu Gly Asp Asp Leu
                165                 170                 175

Val Glu His Gly Leu Asp Arg Glu Ser Gln Ile Arg Asp Asp Ser Ile
            180                 185                 190

Leu Arg Thr Phe Thr Ser Asp Met Ser Ile Ala Leu Val Leu Asp Thr
        195                 200                 205

Glu His Ala Ile Arg Ile Gln Pro Leu Lys Glu Leu Glu Glu Phe Asp
    210                 215                 220

Asp Leu Ser Ala Leu Glu Arg Ala Ala Asp Arg Asn Thr Trp Gln Glu
225                 230                 235                 240

Leu Tyr Asp Ala Asn Val Asp Ala Ser Phe Val Asp Ala Glu Ser Asp
                245                 250                 255

Ser Glu Gly Ser Ser Phe Trp Ala Phe Glu Ser Asn Ser Tyr Tyr Leu
            260                 265                 270

Gly Ser Ala Pro Leu Phe Leu Asn Asp Leu Leu Ala Lys Trp Ala Pro
        275                 280                 285

Asp Leu Asp Gln Ser Asp Gly Val Ile Phe Ala Val Pro Asp Arg Asp
    290                 295                 300

Leu Leu Ile Ala Arg Pro Val Thr Thr Gly Glu Asp Leu Met Asn Gly
305                 310                 315                 320

Ile Thr Ala Met Val Arg Ile Ala Met Arg Phe Gly Leu Gly Asn Pro
                325                 330                 335

Thr Ser Ile Ser Pro Arg Leu His Leu Leu Arg Asp Asn Gln Val Thr
            340                 345                 350

Thr Phe Thr Asp Phe Arg Val Val Ser Pro Glu Met Glu Ala Glu Trp
        355                 360                 365

Glu Asp Ser Ala Phe Asp Ala Pro Pro Ala Gly Ala Ile Gly Ile Glu
```

```
    370                 375                 380

Val Arg Pro Asp Pro Tyr Leu Met Glu Arg Leu Gln Gln Gly Gly Phe
385                 390                 395                 400

Gly Asp Phe Gly Asp Phe Gly Lys Pro Arg Asp Leu Asp Met
                405                 410
```

<210> 2293
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> RXA01540

<400> 2293

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ccatgcagca ctatgggttc cctgatcccg atgcgtactt tgaccatgcc actatcgcag 60

gaaaacacca cacactcatc acaagaaagt aggtctcacc atg act ttt gca gaa   115
                                            Met Thr Phe Ala Glu
                                              1               5

ctt agc tca ccg cgt acc atc atc gct ttt aat ggc cgt gcc gaa tct   163
Leu Ser Ser Pro Arg Thr Ile Ile Ala Phe Asn Gly Arg Ala Glu Ser
                10                  15                  20

ggc aaa gat act gca gca cag tat ctc acc cat atg cac agt ttt cac   211
Gly Lys Asp Thr Ala Ala Gln Tyr Leu Thr His Met His Ser Phe His
            25                  30                  35

cgc atc gcc ttt gcc gat ggt gtc cgt gac gca ctc tat gcg ctt aac   259
Arg Ile Ala Phe Ala Asp Gly Val Arg Asp Ala Leu Tyr Ala Leu Asn
        40                  45                  50

cca ctg gtc tgt gtg gag cag gct atc acc aca cat ggt gcc att tat   307
Pro Leu Val Cys Val Glu Gln Ala Ile Thr Thr His Gly Ala Ile Tyr
    55                  60                  65

gac cgc gtg gcc act gtt gtg gac aca ctt ggt tgg gat acc gca aag   355
Asp Arg Val Ala Thr Val Val Asp Thr Leu Gly Trp Asp Thr Ala Lys
70                  75                  80                  85

caa atc ccc gac atc cgc gca ctt atg cag cgt att ggt acc gaa gct   403
Gln Ile Pro Asp Ile Arg Ala Leu Met Gln Arg Ile Gly Thr Glu Ala
                90                  95                  100

ggt tgg cgc atc cac ggc gag cat ctg tgg gtc aat ctt gct atc aaa   451
Gly Trp Arg Ile His Gly Glu His Leu Trp Val Asn Leu Ala Ile Lys
            105                 110                 115

aag atc aat gaa ctg ccc gct gac cac gcc att gtc atc act gat ttg   499
Lys Ile Asn Glu Leu Pro Ala Asp His Ala Ile Val Ile Thr Asp Leu
        120                 125                 130

cga ttc ccc aat gag att gag tgg ttg aac agc ctc aaa gcc aac ccg   547
Arg Phe Pro Asn Glu Ile Glu Trp Leu Asn Ser Leu Lys Ala Asn Pro
    135                 140                 145
```

```
atg aac acc att cag acc gtc aaa gtc atc cga cca gat cat gaa tcg   595
Met Asn Thr Ile Gln Thr Val Lys Val Ile Arg Pro Asp His Glu Ser
150                 155                 160                 165

acc ttg act gca gga tca ttc ggt act acc tca cat att tcc gaa agc   643
Thr Leu Thr Ala Gly Ser Phe Gly Thr Thr Ser His Ile Ser Glu Ser
                170                 175                 180

ttt aat ctc act acc gac act gtg ctc cgc aac gat ggc acc att gac   691
Phe Asn Leu Thr Thr Asp Thr Val Leu Arg Asn Asp Gly Thr Ile Asp
            185                 190                 195

gat ttg cac tca aag ctg gct gat ttt ttg agc act tcc ccg cag ccc   739
Asp Leu His Ser Lys Leu Ala Asp Phe Leu Ser Thr Ser Pro Gln Pro
        200                 205                 210

gtg ctc tct cgt aac gcc cct gta cca aaa cac aac gca ccg gca cca   787
Val Leu Ser Arg Asn Ala Pro Val Pro Lys His Asn Ala Pro Ala Pro
    215                 220                 225

acc act gat gcc atg taaataaccc ccgtatcaag atc                    825
Thr Thr Asp Ala Met
230
```

<210> 2294
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 2294

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Met Thr Phe Ala Glu Leu Ser Ser Pro Arg Thr Ile Ile Ala Phe Asn
  1               5                  10                  15

Gly Arg Ala Glu Ser Gly Lys Asp Thr Ala Ala Gln Tyr Leu Thr His
             20                  25                  30

Met His Ser Phe His Arg Ile Ala Phe Ala Asp Gly Val Arg Asp Ala
         35                  40                  45

Leu Tyr Ala Leu Asn Pro Leu Val Cys Val Glu Gln Ala Ile Thr Thr
     50                  55                  60

His Gly Ala Ile Tyr Asp Arg Val Ala Thr Val Val Asp Thr Leu Gly
 65                  70                  75                  80

Trp Asp Thr Ala Lys Gln Ile Pro Asp Ile Arg Ala Leu Met Gln Arg
                 85                  90                  95

Ile Gly Thr Glu Ala Gly Trp Arg Ile His Gly Glu His Leu Trp Val
            100                 105                 110

Asn Leu Ala Ile Lys Lys Ile Asn Glu Leu Pro Ala Asp His Ala Ile
        115                 120                 125

Val Ile Thr Asp Leu Arg Phe Pro Asn Glu Ile Glu Trp Leu Asn Ser
    130                 135                 140

Leu Lys Ala Asn Pro Met Asn Thr Ile Gln Thr Val Lys Val Ile Arg
145                 150                 155                 160
```

```
Pro Asp His Glu Ser Thr Leu Thr Ala Gly Ser Phe Gly Thr Thr Ser
                165                 170                 175

His Ile Ser Glu Ser Phe Asn Leu Thr Thr Asp Thr Val Leu Arg Asn
            180                 185                 190

Asp Gly Thr Ile Asp Asp Leu His Ser Lys Leu Ala Asp Phe Leu Ser
        195                 200                 205

Thr Ser Pro Gln Pro Val Leu Ser Arg Asn Ala Pro Val Pro Lys His
    210                 215                 220

Asn Ala Pro Ala Pro Thr Thr Asp Ala Met
225                 230


<210> 2295
<211> 2889
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2866)
<223> RXA01543

<400> 2295
gtgctttagc caaggtgagg catcaagaga agcaacagcg tcgttaccgt ttttttggtg 60

ggggcgctgt tgttgtagtt aaagaaagag cggtgggaaa atg agt ttg aaa caa   115
                                        Met Ser Leu Lys Gln
                                          1               5

gcc att atc gtg cgc aat gaa tat acg att aag cag gca aat ggc aaa   163
Ala Ile Ile Val Arg Asn Glu Tyr Thr Ile Lys Gln Ala Asn Gly Lys
                  10                  15                  20

ggt tca cga gga tca tcg cca ggt aaa tat atc tct ggc tat atg gca   211
Gly Ser Arg Gly Ser Ser Pro Gly Lys Tyr Ile Ser Gly Tyr Met Ala
              25                  30                  35

cgc agc gat gcg gta gaa gca gta gca cct att gtg cgc aat aaa tta   259
Arg Ser Asp Ala Val Glu Ala Val Ala Pro Ile Val Arg Asn Lys Leu
          40                  45                  50

gat gat ttc atc atg cgg tat atg gca cgt gat agt gcc gtg gag cag   307
Asp Asp Phe Ile Met Arg Tyr Met Ala Arg Asp Ser Ala Val Glu Gln
      55                  60                  65

ctc acc acg gac agt aac gca gac tat gac cag caa cct gaa atg aac   355
Leu Thr Thr Asp Ser Asn Ala Asp Tyr Asp Gln Gln Pro Glu Met Asn
  70                  75                  80                  85

tct cgt cgt ggc cgg caa ggt cgc cgc gcg acc ttg aaa caa cgt cgt   403
Ser Arg Arg Gly Arg Gln Gly Arg Arg Ala Thr Leu Lys Gln Arg Arg
                  90                  95                 100

gca gaa cgc agc gcc cgg cga gca gca ttg cga gcg ggc gtg aat aca   451
Ala Glu Arg Ser Ala Arg Arg Ala Ala Leu Arg Ala Gly Val Asn Thr
            105                 110                 115
```

```
gac tcc gac acc acc aac cca tca caa cct gtg cac ccg agg gaa ctc   499
Asp Ser Asp Thr Thr Asn Pro Ser Gln Pro Val His Pro Arg Glu Leu
        120                 125                 130

gcg gaa ttt act acc cag gat ggg cag cgc gtt cat gat ctc atg ctg   547
Ala Glu Phe Thr Thr Gln Asp Gly Gln Arg Val His Asp Leu Met Leu
    135                 140                 145

agg gct cag ggt aat ggg gga gtg gcc ttt ggg tat ggc gat gtc tcg   595
Arg Ala Gln Gly Asn Gly Gly Val Ala Phe Gly Tyr Gly Asp Val Ser
150                 155                 160                 165

ctg tca cat gat gat ctt cat gca gca agt aat aac gtc caa gag ctc   643
Leu Ser His Asp Asp Leu His Ala Ala Ser Asn Asn Val Gln Glu Leu
                170                 175                 180

tat gaa aat agg cat acc gtg atg aaa gtg gtc cta tct ttt acc cag   691
Tyr Glu Asn Arg His Thr Val Met Lys Val Val Leu Ser Phe Thr Gln
            185                 190                 195

gat tac ctg acc gcg cat ggc ctt att cca gag gat ctc gat att aag   739
Asp Tyr Leu Thr Ala His Gly Leu Ile Pro Glu Asp Leu Asp Ile Lys
        200                 205                 210

cgt gct ggt gat tat cgc ggc cag gtt gac caa atg aag cta cgc atg   787
Arg Ala Gly Asp Tyr Arg Gly Gln Val Asp Gln Met Lys Leu Arg Met
    215                 220                 225

gct gtc atg cat ggt gtg gat cgt cta gcc cag cgt cat tat gat gat   835
Ala Val Met His Gly Val Asp Arg Leu Ala Gln Arg His Tyr Asp Asp
230                 235                 240                 245

ttg cgc tat gtc ggc gtg att cag gtt gat acg aag cat gtg cac gcc   883
Leu Arg Tyr Val Gly Val Ile Gln Val Asp Thr Lys His Val His Ala
                250                 255                 260

cac ttg acc atg gtg gat gct ggt tat gga cac cgg gct gct gat ggt   931
His Leu Thr Met Val Asp Ala Gly Tyr Gly His Arg Ala Ala Asp Gly
            265                 270                 275

acg caa aaa ggc aaa atc aat aag cca ggt aag gct att ttg cgg cgt   979
Thr Gln Lys Gly Lys Ile Asn Lys Pro Gly Lys Ala Ile Leu Arg Arg
        280                 285                 290

ggt att gac gcc tgg ctt gat cag cat cag cat atg gcg cac ttg tca  1027
Gly Ile Asp Ala Trp Leu Asp Gln His Gln His Met Ala His Leu Ser
    295                 300                 305

gca gca gtg ggg tat gaa aaa cgc aat gtc acc agc tac gtc aag cgc  1075
Ala Ala Val Gly Tyr Glu Lys Arg Asn Val Thr Ser Tyr Val Lys Arg
310                 315                 320                 325

tgg gcg ttt cat cag ctc acc caa gaa agt gct gcg caa ttt gtg gtc  1123
Trp Ala Phe His Gln Leu Thr Gln Glu Ser Ala Ala Gln Phe Val Val
                330                 335                 340

gct tgt ttg cca gag gat aag cga ctg tgg cgt gca tcg acc aat gcc  1171
Ala Cys Leu Pro Glu Asp Lys Arg Leu Trp Arg Ala Ser Thr Asn Ala
            345                 350                 355
```

```
aag gaa atg gat aag ccg aat aga tta gtg cgc gag ttg gtg gag gcg   1219
Lys Glu Met Asp Lys Pro Asn Arg Leu Val Arg Glu Leu Val Glu Ala
        360                 365                 370

cga ctt ggt gag act gat tca ccg atg ccg gca gca ctg tcg cag gtc   1267
Arg Leu Gly Glu Thr Asp Ser Pro Met Pro Ala Ala Leu Ser Gln Val
    375                 380                 385

tat cag tat gcg caa aaa cgc cgc gtt aaa gaa ggt tta agc aag cag   1315
Tyr Gln Tyr Ala Gln Lys Arg Arg Val Lys Glu Gly Leu Ser Lys Gln
390                 395                 400                 405

gac acc cag cgt ttg att gat aat ggc cgc gaa aag atc att gag cag   1363
Asp Thr Gln Arg Leu Ile Asp Asn Gly Arg Glu Lys Ile Ile Glu Gln
                410                 415                 420

gcc atg aac ggt gtc tac agt gtc cta tcc gcg att tcc gat gag caa   1411
Ala Met Asn Gly Val Tyr Ser Val Leu Ser Ala Ile Ser Asp Glu Gln
            425                 430                 435

cgc gat gtc tct acg gcc atg ttg aca gtc atg cgt caa gac tat gag   1459
Arg Asp Val Ser Thr Ala Met Leu Thr Val Met Arg Gln Asp Tyr Glu
        440                 445                 450

gat ttg ctc gat ggt att gcg cgg aag aag agc aag gat cta gac gag   1507
Asp Leu Leu Asp Gly Ile Ala Arg Lys Lys Ser Lys Asp Leu Asp Glu
    455                 460                 465

cag ggt agt agt gga tca caa gag gtg ggg aaa gaa gag cct gag cca   1555
Gln Gly Ser Ser Gly Ser Gln Glu Val Gly Lys Glu Glu Pro Glu Pro
470                 475                 480                 485

agt att gag gaa ttt ggg ctg cgt ttg cgg tcg tat tca gca cgc ttg   1603
Ser Ile Glu Glu Phe Gly Leu Arg Leu Arg Ser Tyr Ser Ala Arg Leu
                490                 495                 500

aat cat cac cga gaa caa cga gaa gcc ttt gcc gtg aaa aaa cgc tcg   1651
Asn His His Arg Glu Gln Arg Glu Ala Phe Ala Val Lys Lys Arg Ser
            505                 510                 515

tgg gag gac gct aac tct caa ggt ttg gct gat ccc acc tca cag gta   1699
Trp Glu Asp Ala Asn Ser Gln Gly Leu Ala Asp Pro Thr Ser Gln Val
        520                 525                 530

atg tgg agt ttt tat gac act gag gag cag tat cat gcg atg tgc caa   1747
Met Trp Ser Phe Tyr Asp Thr Glu Glu Gln Tyr His Ala Met Cys Gln
    535                 540                 545

tcc aag tac cag cac ttt ttg acc ttt gcc cca cct gtc ggt cag tgg   1795
Ser Lys Tyr Gln His Phe Leu Thr Phe Ala Pro Pro Val Gly Gln Trp
550                 555                 560                 565

gag aag caa tgg gct gag gtt gct gat tac ggt aaa agg gtt gtg ggt   1843
Glu Lys Gln Trp Ala Glu Val Ala Asp Tyr Gly Lys Arg Val Val Gly
                570                 575                 580

ctg cgt gca ctg cgg gca gat cgt tct ttg gca cgc atg agc gat gaa   1891
Leu Arg Ala Leu Arg Ala Asp Arg Ser Leu Ala Arg Met Ser Asp Glu
            585                 590                 595

cgt gca gct gaa gct ttg ggt cgg caa ctt tat gac caa ccc ggt ggt   1939
```

```
Arg Ala Ala Glu Ala Leu Gly Arg Gln Leu Tyr Asp Gln Pro Gly Gly
        600                 605                 610

ggg tta ttg gct cga aca ggc gct gag ggt aaa gct ggg cgt gcg gtc   1987
Gly Leu Leu Ala Arg Thr Gly Ala Glu Gly Lys Ala Gly Arg Ala Val
    615                 620                 625

ctg gat ggc cga att gag cgc atg atg gtg acc tat cag caa aaa att   2035
Leu Asp Gly Arg Ile Glu Arg Met Met Val Thr Tyr Gln Gln Lys Ile
630                 635                 640                 645

gat gat ttg cga cga gaa tgg gca cag ctc ggt gca cgt tta gag gtt   2083
Asp Asp Leu Arg Arg Glu Trp Ala Gln Leu Gly Ala Arg Leu Glu Val
                650                 655                 660

gaa ggt gat gct gta ttg atg gat gca gca gat cta cgt gaa tct ggg   2131
Glu Gly Asp Ala Val Leu Met Asp Ala Ala Asp Leu Arg Glu Ser Gly
            665                 670                 675

gga gag ggt gca gat gaa cgc cag ata cag cag caa aca att gag ttg   2179
Gly Glu Gly Ala Asp Glu Arg Gln Ile Gln Gln Gln Thr Ile Glu Leu
        680                 685                 690

ccg gtc gct gat gta tct gat tct gtg cgc aca tac ctt gac gaa gag   2227
Pro Val Ala Asp Val Ser Asp Ser Val Arg Thr Tyr Leu Asp Glu Glu
    695                 700                 705

tta cgt gat agt cgt gat gtg agc gct cat gat cca gtg cac acc ttg   2275
Leu Arg Asp Ser Arg Asp Val Ser Ala His Asp Pro Val His Thr Leu
710                 715                 720                 725

cgt ggc agg ttt cag gtc gtg ttt cga ccg gag cat gat ttt gag cag   2323
Arg Gly Arg Phe Gln Val Val Phe Arg Pro Glu His Asp Phe Glu Gln
                730                 735                 740

gtg ggt ggc cct gac ctg cgc gat ctt cac tat gcc tgg ttt agc gat   2371
Val Gly Gly Pro Asp Leu Arg Asp Leu His Tyr Ala Trp Phe Ser Asp
            745                 750                 755

cag aag gtc agt cag ccc att gtg tgt agt tac ggt gag tta gtc acc   2419
Gln Lys Val Ser Gln Pro Ile Val Cys Ser Tyr Gly Glu Leu Val Thr
        760                 765                 770

cag cga cgt tat gct ttt gaa cgc gct cgg gag tgg atg atc agt tcg   2467
Gln Arg Arg Tyr Ala Phe Glu Arg Ala Arg Glu Trp Met Ile Ser Ser
    775                 780                 785

cag cag gaa cca gaa gca gtg gca gaa gag ctt gat cat gcc ggc gcg   2515
Gln Gln Glu Pro Glu Ala Val Ala Glu Glu Leu Asp His Ala Gly Ala
790                 795                 800                 805

gac ata act cgc atg gaa gca acc agt agt gag gta tcc cgt aca ggt   2563
Asp Ile Thr Arg Met Glu Ala Thr Ser Ser Glu Val Ser Arg Thr Gly
                810                 815                 820

att ttg cgt agt gcc atg ctt gcc aga att aga gag cag gcg cga caa   2611
Ile Leu Arg Ser Ala Met Leu Ala Arg Ile Arg Glu Gln Ala Arg Gln
            825                 830                 835

cgc gct cag cgt gca gcg gaa gag cag gct cgt cgt gag cgt gag ttg   2659
Arg Ala Gln Arg Ala Ala Glu Glu Gln Ala Arg Arg Glu Arg Glu Leu
```

```
        840                 845                 850

gta gca cag cga caa caa gaa att gat cag gag acc acg caa cca gcg   2707
Val Ala Gln Arg Gln Gln Glu Ile Asp Gln Glu Thr Thr Gln Pro Ala
    855                 860                 865

ttc gag gtg gtg caa cga cat gta caa ccg gag tcg gtg cag att aag   2755
Phe Glu Val Val Gln Arg His Val Gln Pro Glu Ser Val Gln Ile Lys
870                 875                 880                 885

cgg ggt aga aca gtt gcg cta gat aag cga gtg cag cca ctg att cgt   2803
Arg Gly Arg Thr Val Ala Leu Asp Lys Arg Val Gln Pro Leu Ile Arg
                890                 895                 900

gat gct gtg gat cga gct gtg ctg gat tca cag ctg cgg agt acc cgt   2851
Asp Ala Val Asp Arg Ala Val Leu Asp Ser Gln Leu Arg Ser Thr Arg
            905                 910                 915

gat ggt gga ttg ggg taggcggttg attaaaaaaa aag                    2889
Asp Gly Gly Leu Gly
        920
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SEQUENCE LISTING

<210> 2296
<211> 922
<212> PRT
<213> Corynebacterium glutamicum

<400> 2296

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Met Ser Leu Lys Gln Ala Ile Ile Val Arg Asn Glu Tyr Thr Ile Lys
  1               5                  10                  15

Gln Ala Asn Gly Lys Gly Ser Arg Gly Ser Ser Pro Gly Lys Tyr Ile
             20                  25                  30

Ser Gly Tyr Met Ala Arg Ser Asp Ala Val Glu Ala Val Ala Pro Ile
         35                  40                  45

Val Arg Asn Lys Leu Asp Asp Phe Ile Met Arg Tyr Met Ala Arg Asp
     50                  55                  60

Ser Ala Val Glu Gln Leu Thr Thr Asp Ser Asn Ala Asp Tyr Asp Gln
 65                  70                  75                  80

Gln Pro Glu Met Asn Ser Arg Arg Gly Arg Gln Gly Arg Arg Ala Thr
                 85                  90                  95

Leu Lys Gln Arg Arg Ala Glu Arg Ser Ala Arg Arg Ala Ala Leu Arg
            100                 105                 110

Ala Gly Val Asn Thr Asp Ser Asp Thr Thr Asn Pro Ser Gln Pro Val
        115                 120                 125

His Pro Arg Glu Leu Ala Glu Phe Thr Thr Gln Asp Gly Gln Arg Val
    130                 135                 140

His Asp Leu Met Leu Arg Ala Gln Gly Asn Gly Gly Val Ala Phe Gly
145                 150                 155                 160

Tyr Gly Asp Val Ser Leu Ser His Asp Asp Leu His Ala Ala Ser Asn
                165                 170                 175
```

```
Asn Val Gln Glu Leu Tyr Glu Asn Arg His Thr Val Met Lys Val Val
            180                 185                 190

Leu Ser Phe Thr Gln Asp Tyr Leu Thr Ala His Gly Leu Ile Pro Glu
        195                 200                 205

Asp Leu Asp Ile Lys Arg Ala Gly Asp Tyr Arg Gly Gln Val Asp Gln
    210                 215                 220

Met Lys Leu Arg Met Ala Val Met His Gly Val Asp Arg Leu Ala Gln
225                 230                 235                 240

Arg His Tyr Asp Asp Leu Arg Tyr Val Gly Val Ile Gln Val Asp Thr
                245                 250                 255

Lys His Val His Ala His Leu Thr Met Val Asp Ala Gly Tyr Gly His
            260                 265                 270

Arg Ala Ala Asp Gly Thr Gln Lys Gly Lys Ile Asn Lys Pro Gly Lys
        275                 280                 285

Ala Ile Leu Arg Arg Gly Ile Asp Ala Trp Leu Asp Gln His Gln His
    290                 295                 300

Met Ala His Leu Ser Ala Ala Val Gly Tyr Glu Lys Arg Asn Val Thr
305                 310                 315                 320

Ser Tyr Val Lys Arg Trp Ala Phe His Gln Leu Thr Gln Glu Ser Ala
                325                 330                 335

Ala Gln Phe Val Val Ala Cys Leu Pro Glu Asp Lys Arg Leu Trp Arg
            340                 345                 350

Ala Ser Thr Asn Ala Lys Glu Met Asp Lys Pro Asn Arg Leu Val Arg
        355                 360                 365

Glu Leu Val Glu Ala Arg Leu Gly Glu Thr Asp Ser Pro Met Pro Ala
    370                 375                 380

Ala Leu Ser Gln Val Tyr Gln Tyr Ala Gln Lys Arg Arg Val Lys Glu
385                 390                 395                 400

Gly Leu Ser Lys Gln Asp Thr Gln Arg Leu Ile Asp Asn Gly Arg Glu
                405                 410                 415

Lys Ile Ile Glu Gln Ala Met Asn Gly Val Tyr Ser Val Leu Ser Ala
            420                 425                 430

Ile Ser Asp Glu Gln Arg Asp Val Ser Thr Ala Met Leu Thr Val Met
        435                 440                 445

Arg Gln Asp Tyr Glu Asp Leu Leu Asp Gly Ile Ala Arg Lys Lys Ser
    450                 455                 460

Lys Asp Leu Asp Glu Gln Gly Ser Ser Gly Ser Gln Glu Val Gly Lys
465                 470                 475                 480

Glu Glu Pro Glu Pro Ser Ile Glu Glu Phe Gly Leu Arg Leu Arg Ser
                485                 490                 495
```

```
Tyr Ser Ala Arg Leu Asn His His Arg Glu Gln Arg Glu Ala Phe Ala
            500                 505                 510

Val Lys Lys Arg Ser Trp Glu Asp Ala Asn Ser Gln Gly Leu Ala Asp
        515                 520                 525

Pro Thr Ser Gln Val Met Trp Ser Phe Tyr Asp Thr Glu Glu Gln Tyr
    530                 535                 540

His Ala Met Cys Gln Ser Lys Tyr Gln His Phe Leu Thr Phe Ala Pro
545                 550                 555                 560

Pro Val Gly Gln Trp Glu Lys Gln Trp Ala Glu Val Ala Asp Tyr Gly
                565                 570                 575

Lys Arg Val Val Gly Leu Arg Ala Leu Arg Ala Asp Arg Ser Leu Ala
            580                 585                 590

Arg Met Ser Asp Glu Arg Ala Ala Glu Ala Leu Gly Arg Gln Leu Tyr
        595                 600                 605

Asp Gln Pro Gly Gly Gly Leu Leu Ala Arg Thr Gly Ala Glu Gly Lys
    610                 615                 620

Ala Gly Arg Ala Val Leu Asp Gly Arg Ile Glu Arg Met Met Val Thr
625                 630                 635                 640

Tyr Gln Gln Lys Ile Asp Asp Leu Arg Arg Glu Trp Ala Gln Leu Gly
                645                 650                 655

Ala Arg Leu Glu Val Glu Gly Asp Ala Val Leu Met Asp Ala Ala Asp
            660                 665                 670

Leu Arg Glu Ser Gly Gly Glu Gly Ala Asp Glu Arg Gln Ile Gln Gln
        675                 680                 685

Gln Thr Ile Glu Leu Pro Val Ala Asp Val Ser Asp Ser Val Arg Thr
    690                 695                 700

Tyr Leu Asp Glu Glu Leu Arg Asp Ser Arg Asp Val Ser Ala His Asp
705                 710                 715                 720

Pro Val His Thr Leu Arg Gly Arg Phe Gln Val Val Phe Arg Pro Glu
                725                 730                 735

His Asp Phe Glu Gln Val Gly Gly Pro Asp Leu Arg Asp Leu His Tyr
            740                 745                 750

Ala Trp Phe Ser Asp Gln Lys Val Ser Gln Pro Ile Val Cys Ser Tyr
        755                 760                 765

Gly Glu Leu Val Thr Gln Arg Arg Tyr Ala Phe Glu Arg Ala Arg Glu
    770                 775                 780

Trp Met Ile Ser Ser Gln Gln Glu Pro Glu Ala Val Ala Glu Glu Leu
785                 790                 795                 800

Asp His Ala Gly Ala Asp Ile Thr Arg Met Glu Ala Thr Ser Ser Glu
                805                 810                 815

Val Ser Arg Thr Gly Ile Leu Arg Ser Ala Met Leu Ala Arg Ile Arg
```

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            820                 825                 830

Glu Gln Ala Arg Gln Arg Ala Gln Arg Ala Ala Glu Glu Gln Ala Arg
        835                 840                 845

Arg Glu Arg Glu Leu Val Ala Gln Arg Gln Gln Glu Ile Asp Gln Glu
    850                 855                 860

Thr Thr Gln Pro Ala Phe Glu Val Val Gln Arg His Val Gln Pro Glu
865                 870                 875                 880

Ser Val Gln Ile Lys Arg Gly Arg Thr Val Ala Leu Asp Lys Arg Val
                885                 890                 895

Gln Pro Leu Ile Arg Asp Ala Val Asp Arg Ala Val Leu Asp Ser Gln
            900                 905                 910

Leu Arg Ser Thr Arg Asp Gly Gly Leu Gly
        915                 920


<210> 2297
<211> 723
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(700)
<223> RXA01544

<400> 2297
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tttcatagct gtacacacat aaggcaacag gagaaataca gtg aaa ctt gac gac   115
                                            Val Lys Leu Asp Asp
                                              1               5

gct atg gtc atg atc gaa cag cgc ctg gtc aaa ggt cgc ggc gca acc   163
Ala Met Val Met Ile Glu Gln Arg Leu Val Lys Gly Arg Gly Ala Thr
                  10                  15                  20

aag acg caa cta gca ccc tat gag cat atc cag cgc aat att gca gcc   211
Lys Thr Gln Leu Ala Pro Tyr Glu His Ile Gln Arg Asn Ile Ala Ala
              25                  30                  35

cga ggg ttg aga gcc gat gac gga ggc tcg tgc ttc ggt tat ggg gat   259
Arg Gly Leu Arg Ala Asp Asp Gly Gly Ser Cys Phe Gly Tyr Gly Asp
          40                  45                  50

gcg tcg ctg agt aat gac gat gta gca act gct gca gaa gat att cag   307
Ala Ser Leu Ser Asn Asp Asp Val Ala Thr Ala Ala Glu Asp Ile Gln
      55                  60                  65

gat ttg ttt gcg tgc ggg cat acg gtt atc tca gcg att gtc gtt ttt   355
Asp Leu Phe Ala Cys Gly His Thr Val Ile Ser Ala Ile Val Val Phe
  70                  75                  80                  85

gat aag agc tat ctc agt gag cat gga atc atg agc ttt gat ccg aac   403
Asp Lys Ser Tyr Leu Ser Glu His Gly Ile Met Ser Phe Asp Pro Asn
                  90                  95                 100
```

```
tat ttt ggt cag gat att tat gcg gac acc cat cca gag att gat ctc   451
Tyr Phe Gly Gln Asp Ile Tyr Ala Asp Thr His Pro Glu Ile Asp Leu
            105                 110                 115

atg gaa ttg cgt tta gcc gtg atg aat ggg ctc ttg ggg ctt gag gga   499
Met Glu Leu Arg Leu Ala Val Met Asn Gly Leu Leu Gly Leu Glu Gly
        120                 125                 130

acg ttt ttt gag gat atg cgt tat gtc gca tct atc gag gtg agc cgg   547
Thr Phe Phe Glu Asp Met Arg Tyr Val Ala Ser Ile Glu Val Ser Arg
    135                 140                 145

agc tat gtc tat gcg cac ata atg atg gcg gat gca ggc gtt gac gat   595
Ser Tyr Val Tyr Ala His Ile Met Met Ala Asp Ala Gly Val Asp Asp
150                 155                 160                 165

gca cgc ggt aat gca cag gtg aag att acg gac acc gaa cga gtg ctg   643
Ala Arg Gly Asn Ala Gln Val Lys Ile Thr Asp Thr Glu Arg Val Leu
                170                 175                 180

ttt aga cgt ggt gtt gaa tcc cgg ttt gtg gag caa gag gca cgc aac   691
Phe Arg Arg Gly Val Glu Ser Arg Phe Val Glu Gln Glu Ala Arg Asn
            185                 190                 195

gtc gtg ctt tagccaaggt gaggcatcaa gag                            723
Val Val Leu
        200
```

CONFIDENTIAL

<210> 2298
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 2298

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Val Lys Leu Asp Asp Ala Met Val Met Ile Glu Gln Arg Leu Val Lys
  1               5                  10                  15

Gly Arg Gly Ala Thr Lys Thr Gln Leu Ala Pro Tyr Glu His Ile Gln
             20                  25                  30

Arg Asn Ile Ala Ala Arg Gly Leu Arg Ala Asp Asp Gly Gly Ser Cys
         35                  40                  45

Phe Gly Tyr Gly Asp Ala Ser Leu Ser Asn Asp Asp Val Ala Thr Ala
     50                  55                  60

Ala Glu Asp Ile Gln Asp Leu Phe Ala Cys Gly His Thr Val Ile Ser
 65                  70                  75                  80

Ala Ile Val Val Phe Asp Lys Ser Tyr Leu Ser Glu His Gly Ile Met
                 85                  90                  95

Ser Phe Asp Pro Asn Tyr Phe Gly Gln Asp Ile Tyr Ala Asp Thr His
            100                 105                 110

Pro Glu Ile Asp Leu Met Glu Leu Arg Leu Ala Val Met Asn Gly Leu
        115                 120                 125

Leu Gly Leu Glu Gly Thr Phe Phe Glu Asp Met Arg Tyr Val Ala Ser
```

```
    130                 135                 140

Ile Glu Val Ser Arg Ser Tyr Val Tyr Ala His Ile Met Met Ala Asp
145                 150                 155                 160

Ala Gly Val Asp Asp Ala Arg Gly Asn Ala Gln Val Lys Ile Thr Asp
                165                 170                 175

Thr Glu Arg Val Leu Phe Arg Arg Gly Val Glu Ser Arg Phe Val Glu
            180                 185                 190

Gln Glu Ala Arg Asn Val Val Leu
        195                 200


<210> 2299
<211> 1374
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1351)
<223> RXA01545

<400> 2299
ataagaaccg acacgacgcc ctcaacgacg ctgttgcagc agctcgcaac tagctagtta 60

ccacgcctga cacacgatac gtagagaaaa gagaaatgat atg aag ctt gca ggt   115
                                          Met Lys Leu Ala Gly
                                            1               5

ttt aac acc aat tca ccc gca gcg cag cgg gtt gcc gaa cag ggt gaa   163
Phe Asn Thr Asn Ser Pro Ala Ala Gln Arg Val Ala Glu Gln Gly Glu
                10                  15                  20

aag gta cag ctc gat gca ccg gtg tac gcg gtg ttt acc cca gat gtt   211
Lys Val Gln Leu Asp Ala Pro Val Tyr Ala Val Phe Thr Pro Asp Val
            25                  30                  35

gtt gaa gtt gag ttt att ggc acg cag cat gag ccg gta ttg cac gtt   259
Val Glu Val Glu Phe Ile Gly Thr Gln His Glu Pro Val Leu His Val
        40                  45                  50

gag ggt gcc atc gac agc gtg act gca ttg tcg cag cta ccg tac gac   307
Glu Gly Ala Ile Asp Ser Val Thr Ala Leu Ser Gln Leu Pro Tyr Asp
    55                  60                  65

att caa aaa att acg ttt gat tca gaa aac caa cag cgt ttt agt gga   355
Ile Gln Lys Ile Thr Phe Asp Ser Glu Asn Gln Gln Arg Phe Ser Gly
70                  75                  80                  85

ttt tat aaa ttc agt cca cag cag cat aaa gag ctc att gat aaa ggt   403
Phe Tyr Lys Phe Ser Pro Gln Gln His Lys Glu Leu Ile Asp Lys Gly
                90                  95                  100

ctg tat cta gaa ggt ttc cag cca ccg cgc gag atg atg acg agc ctg   451
Leu Tyr Leu Glu Gly Phe Gln Pro Pro Arg Glu Met Met Thr Ser Leu
            105                 110                 115

ccg tgg gaa cta ccc atg aat gcc gat gtc act gtc gtg gca cca gag   499
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```
Pro Trp Glu Leu Pro Met Asn Ala Asp Val Thr Val Val Ala Pro Glu
        120                 125                 130

tcg cag gat gcg cca ccg att gtg ctt gtg ggc tta tct gag att cat   547
Ser Gln Asp Ala Pro Pro Ile Val Leu Val Gly Leu Ser Glu Ile His
    135                 140                 145

ggt gtg gat ttt agt caa gaa tcc tct ggc tat gag ctc acc agc atg   595
Gly Val Asp Phe Ser Gln Glu Ser Ser Gly Tyr Glu Leu Thr Ser Met
150                 155                 160                 165

ttt gag gac tac cgt agc cag cgt gaa gcg ggc gag gcg gac aag gat   643
Phe Glu Asp Tyr Arg Ser Gln Arg Glu Ala Gly Glu Ala Asp Lys Asp
                170                 175                 180

ttc tct gag tca att tct cgt gca gag att gaa ggc aaa gat att ttc   691
Phe Ser Glu Ser Ile Ser Arg Ala Glu Ile Glu Gly Lys Asp Ile Phe
            185                 190                 195

gct gat gct aac cgc acc cgt acc ggt gtc agt gca cat gca cag cgc   739
Ala Asp Ala Asn Arg Thr Arg Thr Gly Val Ser Ala His Ala Gln Arg
        200                 205                 210

ctt gag cag gag cga gcg ctg agc gca gca cag ttg atg gcg aaa ctt   787
Leu Glu Gln Glu Arg Ala Leu Ser Ala Ala Gln Leu Met Ala Lys Leu
    215                 220                 225

gct ggc att tcc ttc cag act gaa ccc gtg ctt gtt ggt gcg gaa gag   835
Ala Gly Ile Ser Phe Gln Thr Glu Pro Val Leu Val Gly Ala Glu Glu
230                 235                 240                 245

agc ttt gat gct gag caa ttc ctc gcc cat gat ctt gat gac acc gct   883
Ser Phe Asp Ala Glu Gln Phe Leu Ala His Asp Leu Asp Asp Thr Ala
                250                 255                 260

ggt atg agt gag tgg gag cgc gag gtt acc gag ttc tac aac gag aag   931
Gly Met Ser Glu Trp Glu Arg Glu Val Thr Glu Phe Tyr Asn Glu Lys
            265                 270                 275

att cgc gcc cag gag cct gtg gtg gag cgg gag gct gag cgg gat agc   979
Ile Arg Ala Gln Glu Pro Val Val Glu Arg Glu Ala Glu Arg Asp Ser
        280                 285                 290

gat att gag act gag gtt gat gca gca cca act gtc agt gct gca gag   1027
Asp Ile Glu Thr Glu Val Asp Ala Ala Pro Thr Val Ser Ala Ala Glu
    295                 300                 305

att aac gat gtt att cat gat ctt gat gag ctt gaa ttc gat gac gtg   1075
Ile Asn Asp Val Ile His Asp Leu Asp Glu Leu Glu Phe Asp Asp Val
310                 315                 320                 325

att gat ctt gat gca gat gat gtt gtc aat acc gcc gag gta gag gcg   1123
Ile Asp Leu Asp Ala Asp Asp Val Val Asn Thr Ala Glu Val Glu Ala
                330                 335                 340

cca gca agt gtc agt gct gca gag att tct gcg aca gag ctt gat ttt   1171
Pro Ala Ser Val Ser Ala Ala Glu Ile Ser Ala Thr Glu Leu Asp Phe
            345                 350                 355

gat cgc gag tca cgg gct aag acc gcg cag cga gaa gcc agc cga cgt   1219
Asp Arg Glu Ser Arg Ala Lys Thr Ala Gln Arg Glu Ala Ser Arg Arg
```

```
        360                 365                 370

gtt gca cag aag att cag act caa gaa tct gtg cgt gag gca tat att   1267
Val Ala Gln Lys Ile Gln Thr Gln Glu Ser Val Arg Glu Ala Tyr Ile
    375                 380                 385

cgc gag caa aag cat ggc tat gac gca tca cct gcg gag ggg cgc aag   1315
Arg Glu Gln Lys His Gly Tyr Asp Ala Ser Pro Ala Glu Gly Arg Lys
390                 395                 400                 405

ttt gat gag aaa att gca gaa cgc ggg cta gat cta taacgaggat        1361
Phe Asp Glu Lys Ile Ala Glu Arg Gly Leu Asp Leu
                410                 415

cggcgctact tta                                                   1374
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<210> 2300
<211> 417
<212> PRT
<213> Corynebacterium glutamicum

<400> 2300

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Met Lys Leu Ala Gly Phe Asn Thr Asn Ser Pro Ala Ala Gln Arg Val
  1               5                  10                  15

Ala Glu Gln Gly Glu Lys Val Gln Leu Asp Ala Pro Val Tyr Ala Val
             20                  25                  30

Phe Thr Pro Asp Val Val Glu Val Glu Phe Ile Gly Thr Gln His Glu
         35                  40                  45

Pro Val Leu His Val Glu Gly Ala Ile Asp Ser Val Thr Ala Leu Ser
     50                  55                  60

Gln Leu Pro Tyr Asp Ile Gln Lys Ile Thr Phe Asp Ser Glu Asn Gln
 65                  70                  75                  80

Gln Arg Phe Ser Gly Phe Tyr Lys Phe Ser Pro Gln Gln His Lys Glu
                 85                  90                  95

Leu Ile Asp Lys Gly Leu Tyr Leu Glu Gly Phe Gln Pro Pro Arg Glu
            100                 105                 110

Met Met Thr Ser Leu Pro Trp Glu Leu Pro Met Asn Ala Asp Val Thr
        115                 120                 125

Val Val Ala Pro Glu Ser Gln Asp Ala Pro Pro Ile Val Leu Val Gly
    130                 135                 140

Leu Ser Glu Ile His Gly Val Asp Phe Ser Gln Glu Ser Ser Gly Tyr
145                 150                 155                 160

Glu Leu Thr Ser Met Phe Glu Asp Tyr Arg Ser Gln Arg Glu Ala Gly
                165                 170                 175

Glu Ala Asp Lys Asp Phe Ser Glu Ser Ile Ser Arg Ala Glu Ile Glu
            180                 185                 190

Gly Lys Asp Ile Phe Ala Asp Ala Asn Arg Thr Arg Thr Gly Val Ser
        195                 200                 205
```

```
Ala His Ala Gln Arg Leu Glu Gln Glu Arg Ala Leu Ser Ala Ala Gln
    210                 215                 220

Leu Met Ala Lys Leu Ala Gly Ile Ser Phe Gln Thr Glu Pro Val Leu
225                 230                 235                 240

Val Gly Ala Glu Glu Ser Phe Asp Ala Glu Gln Phe Leu Ala His Asp
                245                 250                 255

Leu Asp Asp Thr Ala Gly Met Ser Glu Trp Glu Arg Glu Val Thr Glu
            260                 265                 270

Phe Tyr Asn Glu Lys Ile Arg Ala Gln Glu Pro Val Val Glu Arg Glu
        275                 280                 285

Ala Glu Arg Asp Ser Asp Ile Glu Thr Glu Val Asp Ala Ala Pro Thr
    290                 295                 300

Val Ser Ala Ala Glu Ile Asn Asp Val Ile His Asp Leu Asp Glu Leu
305                 310                 315                 320

Glu Phe Asp Asp Val Ile Asp Leu Asp Ala Asp Asp Val Val Asn Thr
                325                 330                 335

Ala Glu Val Glu Ala Pro Ala Ser Val Ser Ala Ala Glu Ile Ser Ala
            340                 345                 350

Thr Glu Leu Asp Phe Asp Arg Glu Ser Arg Ala Lys Thr Ala Gln Arg
        355                 360                 365

Glu Ala Ser Arg Arg Val Ala Gln Lys Ile Gln Thr Gln Glu Ser Val
    370                 375                 380

Arg Glu Ala Tyr Ile Arg Glu Gln Lys His Gly Tyr Asp Ala Ser Pro
385                 390                 395                 400

Ala Glu Gly Arg Lys Phe Asp Glu Lys Ile Ala Glu Arg Gly Leu Asp
                405                 410                 415

Leu
```

<210> 2301
<211> 819
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(796)
<223> RXA01546

<400> 2301
atagttagtt ggtgactagc tattgggggt tttgtctttt aatattataa aaagaaagtg 60

acaaacatac ttgcattaaa aaggaattga gataggcact atg gca cga gcg aaa 115
                                                Met Ala Arg Ala Lys
                                                  1   5

```
aat aag aaa cag cgt caa ttg cag cac gct cat gat gca gca cag gct   163
Asn Lys Lys Gln Arg Gln Leu Gln His Ala His Asp Ala Ala Gln Ala
                 10                  15                  20

gag att gca gaa gcg gta gcg gtt aac acg gtt gaa cca att aat gca   211
Glu Ile Ala Glu Ala Val Ala Val Asn Thr Val Glu Pro Ile Asn Ala
             25                  30                  35

cgc acc ggt gga tgg cct tcg tgg gtc gat aag gtc tgg aag ctc act   259
Arg Thr Gly Gly Trp Pro Ser Trp Val Asp Lys Val Trp Lys Leu Thr
         40                  45                  50

ggt tca ctt ggt ggt tgg ttt gct ttc ctg gtt ttt gcc atc gcc gtg   307
Gly Ser Leu Gly Gly Trp Phe Ala Phe Leu Val Phe Ala Ile Ala Val
     55                  60                  65

tgg ccg gta gcg atc ctt gca gct ggc act gtg gtc acc atc atc ggt   355
Trp Pro Val Ala Ile Leu Ala Ala Gly Thr Val Val Thr Ile Ile Gly
 70                  75                  80                  85

acg tgg gga gta tca gta ctg cca agt ctg gtt att tcc agc atc ggc   403
Thr Trp Gly Val Ser Val Leu Pro Ser Leu Val Ile Ser Ser Ile Gly
                 90                  95                 100

gct tct gct ggt gtg att atc tcc act act gat ggg ttc ctc ttt agc   451
Ala Ser Ala Gly Val Ile Ile Ser Thr Thr Asp Gly Phe Leu Phe Ser
             105                 110                 115

tgg gtc atc ccg gtg ctg ttt ctc atg att gtg ctg gca ctg gtg gtc   499
Trp Val Ile Pro Val Leu Phe Leu Met Ile Val Leu Ala Leu Val Val
         120                 125                 130

atg aaa gtg ctc aat ctt att ttt ggt gca ttg tgg cgc ttc acc atg   547
Met Lys Val Leu Asn Leu Ile Phe Gly Ala Leu Trp Arg Phe Thr Met
     135                 140                 145

act ttg cga cag ggg tta tac gca ggt cgt gaa aag att tct cgc gac   595
Thr Leu Arg Gln Gly Leu Tyr Ala Gly Arg Glu Lys Ile Ser Arg Asp
150                 155                 160                 165

gac gcg aag cgc gca cga gca gaa aag aag ctg act aag cag cag gct   643
Asp Ala Lys Arg Ala Arg Ala Glu Lys Lys Leu Thr Lys Gln Gln Ala
                 170                 175                 180

aaa gaa gcc aaa aag cag cgc aaa ctt gat gcc att tac tcg gct caa   691
Lys Glu Ala Lys Lys Gln Arg Lys Leu Asp Ala Ile Tyr Ser Ala Gln
             185                 190                 195

cag gct gaa gag act ctg gcg caa cag gca cag tct gag cca gaa gag   739
Gln Ala Glu Glu Thr Leu Ala Gln Gln Ala Gln Ser Glu Pro Glu Glu
         200                 205                 210

tca gac gat aag aac cga cac gac gcc ctc aac gac gct gtt gca gca   787
Ser Asp Asp Lys Asn Arg His Asp Ala Leu Asn Asp Ala Val Ala Ala
     215                 220                 225

gct cgc aac tagctagtta ccacgcctga cac                            819
Ala Arg Asn
230
```

<210> 2302
<211> 232
<212> PRT
<213> Corynebacterium glutamicum

<400> 2302
Met Ala Arg Ala Lys Asn Lys Lys Gln Arg Gln Leu Gln His Ala His
1 5 10 15

Asp Ala Ala Gln Ala Glu Ile Ala Glu Ala Val Ala Val Asn Thr Val
20 25 30

Glu Pro Ile Asn Ala Arg Thr Gly Gly Trp Pro Ser Trp Val Asp Lys
35 40 45

Val Trp Lys Leu Thr Gly Ser Leu Gly Gly Trp Phe Ala Phe Leu Val
50 55 60

Phe Ala Ile Ala Val Trp Pro Val Ala Ile Leu Ala Ala Gly Thr Val
65 70 75 80

Val Thr Ile Ile Gly Thr Trp Gly Val Ser Val Leu Pro Ser Leu Val
85 90 95

Ile Ser Ser Ile Gly Ala Ser Ala Gly Val Ile Ile Ser Thr Thr Asp
100 105 110

Gly Phe Leu Phe Ser Trp Val Ile Pro Val Leu Phe Leu Met Ile Val
115 120 125

Leu Ala Leu Val Val Met Lys Val Leu Asn Leu Ile Phe Gly Ala Leu
130 135 140

Trp Arg Phe Thr Met Thr Leu Arg Gln Gly Leu Tyr Ala Gly Arg Glu
145 150 155 160

Lys Ile Ser Arg Asp Asp Ala Lys Arg Ala Arg Ala Glu Lys Lys Leu
165 170 175

Thr Lys Gln Gln Ala Lys Glu Ala Lys Lys Gln Arg Lys Leu Asp Ala
180 185 190

Ile Tyr Ser Ala Gln Gln Ala Glu Glu Thr Leu Ala Gln Gln Ala Gln
195 200 205

Ser Glu Pro Glu Glu Ser Asp Asp Lys Asn Arg His Asp Ala Leu Asn
210 215 220

Asp Ala Val Ala Ala Ala Arg Asn
225 230

<210> 2303
<211> 786
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(763)
<223> RXA01547

<400> 2303
tgcagcgggc actagagatc gctcagctga acaaacagga gaacagataa tgacgacacg 60

aaatgtagat aaccagagtg gtgtaactga ggacgagccg atg ttc gat cag gtc 115
Met Phe Asp Gln Val
1 5

aag cgc ttt ttt gtt cgc aat atc gtc atg atc att gcg ttg atc ttg 163
Lys Arg Phe Phe Val Arg Asn Ile Val Met Ile Ile Ala Leu Ile Leu
10 15 20

gca gtg gtg gtc att att gtt gcc acc agc acc tct gcg gat cga cat 211
Ala Val Val Val Ile Ile Val Ala Thr Ser Thr Ser Ala Asp Arg His
25 30 35

gct gta ctt aag cgt caa act ggt gag att atg gcc ttg caa cag gaa 259
Ala Val Leu Lys Arg Gln Thr Gly Glu Ile Met Ala Leu Gln Gln Glu
40 45 50

cgt gat gca tta aac agt aag ctt gag ggc caa ctt gag cag gtg gtg 307
Arg Asp Ala Leu Asn Ser Lys Leu Glu Gly Gln Leu Glu Gln Val Val
55 60 65

cgt gac gct acc ggt ggt atg gat att gaa cac aag gct gca gat gat 355
Arg Asp Ala Thr Gly Gly Met Asp Ile Glu His Lys Ala Ala Asp Asp
70 75 80 85

gct gtt gtt cga gaa ttt ttg tcc atg gcg ctg acg tgg gac agc gtg 403
Ala Val Val Arg Glu Phe Leu Ser Met Ala Leu Thr Trp Asp Ser Val
90 95 100

cgc gac tac ctt gat gtg cgc gag caa gtg atg cgg gtt tat gac ctg 451
Arg Asp Tyr Leu Asp Val Arg Glu Gln Val Met Arg Val Tyr Asp Leu
105 110 115

gat gaa gaa tca cag ttt atg tcg gtg ttt atg cct ggt gaa atg gcg 499
Asp Glu Glu Ser Gln Phe Met Ser Val Phe Met Pro Gly Glu Met Ala
120 125 130

ggc att gct cgc acc gat cca act ggc gaa gtg cac tat gcc tat gat 547
Gly Ile Ala Arg Thr Asp Pro Thr Gly Glu Val His Tyr Ala Tyr Asp
135 140 145

gca gat ctg tcc aac cgc ttt agc agc tta gaa tcc gtg gtt act cgc 595
Ala Asp Leu Ser Asn Arg Phe Ser Ser Leu Glu Ser Val Val Thr Arg
150 155 160 165

att aat ggt aca gag tac agc tat gta tcc acg gtg acg atg aag tcg 643
Ile Asn Gly Thr Glu Tyr Ser Tyr Val Ser Thr Val Thr Met Lys Ser
170 175 180

aag cgc tct ggt ggt gag gca gaa aca acc tct acc tca cgc ctt gcc 691
Lys Arg Ser Gly Gly Glu Ala Glu Thr Thr Ser Thr Ser Arg Leu Ala
185 190 195

tat gac gtg atc gac ggc aaa att cgt aac ctc gaa gca cgt act gtc 739
Tyr Asp Val Ile Asp Gly Lys Ile Arg Asn Leu Glu Ala Arg Thr Val
200 205 210

ccc ggt ggt gtg aaa tac tcg ggc taaaagtttc tggggcaacc ccc 786

```
Pro Gly Gly Val Lys Tyr Ser Gly
    215                 220


<210> 2304
<211> 221
<212> PRT
<213> Corynebacterium glutamicum

<400> 2304
Met Phe Asp Gln Val Lys Arg Phe Phe Val Arg Asn Ile Val Met Ile
  1               5                  10                  15

Ile Ala Leu Ile Leu Ala Val Val Val Ile Ile Val Ala Thr Ser Thr
             20                  25                  30

Ser Ala Asp Arg His Ala Val Leu Lys Arg Gln Thr Gly Glu Ile Met
         35                  40                  45

Ala Leu Gln Gln Glu Arg Asp Ala Leu Asn Ser Lys Leu Glu Gly Gln
     50                  55                  60

Leu Glu Gln Val Val Arg Asp Ala Thr Gly Gly Met Asp Ile Glu His
 65                  70                  75                  80

Lys Ala Ala Asp Asp Ala Val Val Arg Glu Phe Leu Ser Met Ala Leu
                 85                  90                  95

Thr Trp Asp Ser Val Arg Asp Tyr Leu Asp Val Arg Glu Gln Val Met
            100                 105                 110

Arg Val Tyr Asp Leu Asp Glu Glu Ser Gln Phe Met Ser Val Phe Met
        115                 120                 125

Pro Gly Glu Met Ala Gly Ile Ala Arg Thr Asp Pro Thr Gly Glu Val
    130                 135                 140

His Tyr Ala Tyr Asp Ala Asp Leu Ser Asn Arg Phe Ser Ser Leu Glu
145                 150                 155                 160

Ser Val Val Thr Arg Ile Asn Gly Thr Glu Tyr Ser Tyr Val Ser Thr
                165                 170                 175

Val Thr Met Lys Ser Lys Arg Ser Gly Gly Glu Ala Glu Thr Thr Ser
            180                 185                 190

Thr Ser Arg Leu Ala Tyr Asp Val Ile Asp Gly Lys Ile Arg Asn Leu
        195                 200                 205

Glu Ala Arg Thr Val Pro Gly Gly Val Lys Tyr Ser Gly
    210                 215                 220


<210> 2305
<211> 1131
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1108)
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<223> RXA01548

<400> 2305

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ggcgtgcgag ctgctggttg gcgcttgtgc accccgtttt tgtgtaataa cttatattct 60

agaaacttca ataacttagt aactttaaaa ggggtttaat atg gct gag aat aat   115
                                            Met Ala Glu Asn Asn
                                              1               5

ggc ggg tcg gat gac ctt aag ccc atc tct gtc gat ggg gtc gtc aat   163
Gly Gly Ser Asp Asp Leu Lys Pro Ile Ser Val Asp Gly Val Val Asn
                 10                  15                  20

ggg gaa gtg cgc agc gac aaa gaa aag cag gcg ttc gag aag att acc   211
Gly Glu Val Arg Ser Asp Lys Glu Lys Gln Ala Phe Glu Lys Ile Thr
             25                  30                  35

ggt gat gat ctg cgt cgt cgt gca gaa caa atc cgt aaa cgt cgt tta   259
Gly Asp Asp Leu Arg Arg Arg Ala Glu Gln Ile Arg Lys Arg Arg Leu
         40                  45                  50

gca aaa gcg caa gaa gat gca cgt aag cgt aag cca ttg ttt ggt ttg   307
Ala Lys Ala Gln Glu Asp Ala Arg Lys Arg Lys Pro Leu Phe Gly Leu
     55                  60                  65

ggt cgt atc gct gtc aca gta ctg gct ggc gcc gta ttt att ggt aca   355
Gly Arg Ile Ala Val Thr Val Leu Ala Gly Ala Val Phe Ile Gly Thr
 70                  75                  80                  85

acg ttg tgg atc agt acc acc tcg ggc ggc ttt gac gac aag gtg agt   403
Thr Leu Trp Ile Ser Thr Thr Ser Gly Gly Phe Asp Asp Lys Val Ser
                 90                  95                 100

gca aac aat gag cag att gtc act ctg cgt aat gaa gtc aac gac tta   451
Ala Asn Asn Glu Gln Ile Val Thr Leu Arg Asn Glu Val Asn Asp Leu
            105                 110                 115

aaa aac act gca gag aca atg ccc aaa aaa gag act ctt gct agt caa   499
Lys Asn Thr Ala Glu Thr Met Pro Lys Lys Glu Thr Leu Ala Ser Gln
        120                 125                 130

ttt gac gca gca acc tca cgt gca cag aat gtg gct gac tta cag aat   547
Phe Asp Ala Ala Thr Ser Arg Ala Gln Asn Val Ala Asp Leu Gln Asn
    135                 140                 145

cag tta gcc ggc att att acc agt gtt gat gat gat gcc gcg acc gag   595
Gln Leu Ala Gly Ile Ile Thr Ser Val Asp Asp Asp Ala Ala Thr Glu
150                 155                 160                 165

cag ttc aag aca att gtt gat gag ctg aaa ccg aaa ttc acg gtc tct   643
Gln Phe Lys Thr Ile Val Asp Glu Leu Lys Pro Lys Phe Thr Val Ser
                170                 175                 180

gct ggt acg aca ggt gaa ttt cct gcg gcg ggt cgt tgg tac cag cca   691
Ala Gly Thr Thr Gly Glu Phe Pro Ala Ala Gly Arg Trp Tyr Gln Pro
            185                 190                 195

caa gaa gtt gtt gtc gga gat aac aac cga ccc acc tgg gcg ccg atg   739
Gln Glu Val Val Val Gly Asp Asn Asn Arg Pro Thr Trp Ala Pro Met
        200                 205                 210
```

```
ggg gct gag tcc tgg gga tgg act gtg acc cct aca ctg tcg atg tca   787
Gly Ala Glu Ser Trp Gly Trp Thr Val Thr Pro Thr Leu Ser Met Ser
    215                 220                 225

gat acc gag cac gtt gtg gtg atg tgg gag gcc cgc ttg acc gga ggt   835
Asp Thr Glu His Val Val Val Met Trp Glu Ala Arg Leu Thr Gly Gly
230                 235                 240                 245

gag cgt tac ggt gcg ctg ttg gcg tgg gtg aca gcc gat tac aac atc   883
Glu Arg Tyr Gly Ala Leu Leu Ala Trp Val Thr Ala Asp Tyr Asn Ile
                250                 255                 260

aac acc ggc gtg ttt agc tcg ctg gcg ttg gcg cat acc tat gaa gga   931
Asn Thr Gly Val Phe Ser Ser Leu Ala Leu Ala His Thr Tyr Glu Gly
            265                 270                 275

cac cag cgt att ggt gca acc acc tca cca agt gaa ttt ggt gcc cac   979
His Gln Arg Ile Gly Ala Thr Thr Ser Pro Ser Glu Phe Gly Ala His
        280                 285                 290

ggc aca aat gca gag gcg agc gct gca cgt gct ggc agt gaa ggc ggg   1027
Gly Thr Asn Ala Glu Ala Ser Ala Ala Arg Ala Gly Ser Glu Gly Gly
    295                 300                 305

ggg ctt gag ggc gag gct att ttc gtt gat gag ctg cag cgg gca cta   1075
Gly Leu Glu Gly Glu Ala Ile Phe Val Asp Glu Leu Gln Arg Ala Leu
310                 315                 320                 325

gag atc gct cag ctg aac aaa cag gag aac aga taatgacgac acgaaatgta 1128
Glu Ile Ala Gln Leu Asn Lys Gln Glu Asn Arg
                330                 335

gat                                                               1131
```

<210> 2306
<211> 336
<212> PRT
<213> Corynebacterium glutamicum

<400> 2306

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Met Ala Glu Asn Asn Gly Gly Ser Asp Asp Leu Lys Pro Ile Ser Val
  1               5                  10                  15

Asp Gly Val Val Asn Gly Glu Val Arg Ser Asp Lys Glu Lys Gln Ala
            20                  25                  30

Phe Glu Lys Ile Thr Gly Asp Asp Leu Arg Arg Arg Ala Glu Gln Ile
        35                  40                  45

Arg Lys Arg Arg Leu Ala Lys Ala Gln Glu Asp Ala Arg Lys Arg Lys
    50                  55                  60

Pro Leu Phe Gly Leu Gly Arg Ile Ala Val Thr Val Leu Ala Gly Ala
65                  70                  75                  80

Val Phe Ile Gly Thr Thr Leu Trp Ile Ser Thr Thr Ser Gly Gly Phe
                85                  90                  95

Asp Asp Lys Val Ser Ala Asn Asn Glu Gln Ile Val Thr Leu Arg Asn
            100                 105                 110
```

```
Glu Val Asn Asp Leu Lys Asn Thr Ala Glu Thr Met Pro Lys Lys Glu
        115                 120                 125

Thr Leu Ala Ser Gln Phe Asp Ala Ala Thr Ser Arg Ala Gln Asn Val
    130                 135                 140

Ala Asp Leu Gln Asn Gln Leu Ala Gly Ile Ile Thr Ser Val Asp Asp
145                 150                 155                 160

Asp Ala Ala Thr Glu Gln Phe Lys Thr Ile Val Asp Glu Leu Lys Pro
                165                 170                 175

Lys Phe Thr Val Ser Ala Gly Thr Thr Gly Glu Phe Pro Ala Ala Gly
            180                 185                 190

Arg Trp Tyr Gln Pro Gln Glu Val Val Val Gly Asp Asn Asn Arg Pro
        195                 200                 205

Thr Trp Ala Pro Met Gly Ala Glu Ser Trp Gly Trp Thr Val Thr Pro
    210                 215                 220

Thr Leu Ser Met Ser Asp Thr Glu His Val Val Val Met Trp Glu Ala
225                 230                 235                 240

Arg Leu Thr Gly Gly Glu Arg Tyr Gly Ala Leu Leu Ala Trp Val Thr
                245                 250                 255

Ala Asp Tyr Asn Ile Asn Thr Gly Val Phe Ser Ser Leu Ala Leu Ala
            260                 265                 270

His Thr Tyr Glu Gly His Gln Arg Ile Gly Ala Thr Thr Ser Pro Ser
        275                 280                 285

Glu Phe Gly Ala His Gly Thr Asn Ala Glu Ala Ser Ala Ala Arg Ala
    290                 295                 300

Gly Ser Glu Gly Gly Gly Leu Glu Gly Glu Ala Ile Phe Val Asp Glu
305                 310                 315                 320

Leu Gln Arg Ala Leu Glu Ile Ala Gln Leu Asn Lys Gln Glu Asn Arg
                325                 330                 335
```

<210> 2307
<211> 1101
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1078)
<223> RXA01552

<400> 2307
actttgctct ttttatggcg ctgcacgaga ttcaactcaa agtgaaggtc agctatttga 60

actcagtgca aaagatgatc ggcataccaa actaatgaag atg tat ctg gga atg 115

```
                                                    Met Tyr Leu Gly Met
                                                      1               5

aaa gaa gat tcc cta gcg cca ccc caa aat aga ttc gag tct cat aag   163
Lys Glu Asp Ser Leu Ala Pro Pro Gln Asn Arg Phe Glu Ser His Lys
                 10                  15                  20

act gtc ttt tcc cta aaa cag aaa aac atc cca att aag gat gct gct   211
Thr Val Phe Ser Leu Lys Gln Lys Asn Ile Pro Ile Lys Asp Ala Ala
             25                  30                  35

aaa tct gat cag gtg aat ctc act tgg cat gat tat cca ggt gaa tgg   259
Lys Ser Asp Gln Val Asn Leu Thr Trp His Asp Tyr Pro Gly Glu Trp
         40                  45                  50

ttt gag ggt gga gct gta acg gac tcg gaa aag cag gat aaa gtt gaa   307
Phe Glu Gly Gly Ala Val Thr Asp Ser Glu Lys Gln Asp Lys Val Glu
     55                  60                  65

acg ttt aga aac ctg ctg ggc tca gat gta gcg cta ttt tta gtt gac   355
Thr Phe Arg Asn Leu Leu Gly Ser Asp Val Ala Leu Phe Leu Val Asp
 70                  75                  80                  85

ggt caa aag ctg cat gat tac gcc aat gaa gag gag cgc tat ctt agc   403
Gly Gln Lys Leu His Asp Tyr Ala Asn Glu Glu Glu Arg Tyr Leu Ser
                 90                  95                 100

tat tta ttt gat gga ttc att gaa aac cta aat cag atc aaa gat gca   451
Tyr Leu Phe Asp Gly Phe Ile Glu Asn Leu Asn Gln Ile Lys Asp Ala
             105                 110                 115

atc ctg gag ggt ggg aaa cag ctc caa cag ttc cca cga att tgg gta   499
Ile Leu Glu Gly Gly Lys Gln Leu Gln Gln Phe Pro Arg Ile Trp Val
         120                 125                 130

att gct tta tcc aaa gct gat cta tgg cca gat ctc caa gta aaa gat   547
Ile Ala Leu Ser Lys Ala Asp Leu Trp Pro Asp Leu Gln Val Lys Asp
     135                 140                 145

ttt gag aat cta ctt aat aag aaa gct ggc aat gaa att att gcg ctg   595
Phe Glu Asn Leu Leu Asn Lys Lys Ala Gly Asn Glu Ile Ile Ala Leu
150                 155                 160                 165

cgt tca aag ctt ttg gag ttt atc gat aac gac gaa gct ttc tcc ttc   643
Arg Ser Lys Leu Leu Glu Phe Ile Asp Asn Asp Glu Ala Phe Ser Phe
                 170                 175                 180

ggt aaa gat ttc ctt ttg ctc tct tcg gcg aag ttc act cca ggc cat   691
Gly Lys Asp Phe Leu Leu Leu Ser Ser Ala Lys Phe Thr Pro Gly His
             185                 190                 195

att gat ata agc cag cgc aag ggt gtt gat gtc ctc ctc ccg ttg gct   739
Ile Asp Ile Ser Gln Arg Lys Gly Val Asp Val Leu Leu Pro Leu Ala
         200                 205                 210

tgt gta ttg ccc atg caa cgc cat ttg tgg tgg cag gag ctg aaa gtt   787
Cys Val Leu Pro Met Gln Arg His Leu Trp Trp Gln Glu Leu Lys Val
     215                 220                 225

ttg cca att aac ctg gct gat ata ctt ttg gga aat gaa att gcc caa   835
Leu Pro Ile Asn Leu Ala Asp Ile Leu Leu Gly Asn Glu Ile Ala Gln
```

```
230                 235                 240                 245

atg ggt ttc aag atc gtt tcc aaa gtt ttg aaa aac aaa gta tct gga   883
Met Gly Phe Lys Ile Val Ser Lys Val Leu Lys Asn Lys Val Ser Gly
                250                 255                 260

aca aat aac aag gcg atg gcg gca ttg gtt ttc gct gaa ctt gtg agg   931
Thr Asn Asn Lys Ala Met Ala Ala Leu Val Phe Ala Glu Leu Val Arg
            265                 270                 275

gat atg gtt gat cag cca act gaa ttg ctt cag aag gct cgt gag gaa   979
Asp Met Val Asp Gln Pro Thr Glu Leu Leu Gln Lys Ala Arg Glu Glu
        280                 285                 290

gcc gtc gga agg cgt gaa ttc ctt aaa gcg att act gca gaa ttc acc   1027
Ala Val Gly Arg Arg Glu Phe Leu Lys Ala Ile Thr Ala Glu Phe Thr
    295                 300                 305

agg aag ctg aat caa gcc gaa gct gat cag gtt tta gtt cgg gac ttt   1075
Arg Lys Leu Asn Gln Ala Glu Ala Asp Gln Val Leu Val Arg Asp Phe
310                 315                 320                 325

gca tgacactcat gtgggcaacc cgt                                    1101
Ala
```

Sequence Listing

<210> 2308
<211> 326
<212> PRT
<213> Corynebacterium glutamicum

<400> 2308

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Met Tyr Leu Gly Met Lys Glu Asp Ser Leu Ala Pro Pro Gln Asn Arg
  1               5                  10                  15

Phe Glu Ser His Lys Thr Val Phe Ser Leu Lys Gln Lys Asn Ile Pro
             20                  25                  30

Ile Lys Asp Ala Ala Lys Ser Asp Gln Val Asn Leu Thr Trp His Asp
         35                  40                  45

Tyr Pro Gly Glu Trp Phe Glu Gly Gly Ala Val Thr Asp Ser Glu Lys
     50                  55                  60

Gln Asp Lys Val Glu Thr Phe Arg Asn Leu Leu Gly Ser Asp Val Ala
 65                  70                  75                  80

Leu Phe Leu Val Asp Gly Gln Lys Leu His Asp Tyr Ala Asn Glu Glu
                 85                  90                  95

Glu Arg Tyr Leu Ser Tyr Leu Phe Asp Gly Phe Ile Glu Asn Leu Asn
            100                 105                 110

Gln Ile Lys Asp Ala Ile Leu Glu Gly Gly Lys Gln Leu Gln Gln Phe
        115                 120                 125

Pro Arg Ile Trp Val Ile Ala Leu Ser Lys Ala Asp Leu Trp Pro Asp
    130                 135                 140

Leu Gln Val Lys Asp Phe Glu Asn Leu Leu Asn Lys Lys Ala Gly Asn
```

```
145                 150                 155                 160

Glu Ile Ile Ala Leu Arg Ser Lys Leu Leu Glu Phe Ile Asp Asn Asp
                165                 170                 175

Glu Ala Phe Ser Phe Gly Lys Asp Phe Leu Leu Leu Ser Ser Ala Lys
            180                 185                 190

Phe Thr Pro Gly His Ile Asp Ile Ser Gln Arg Lys Gly Val Asp Val
        195                 200                 205

Leu Leu Pro Leu Ala Cys Val Leu Pro Met Gln Arg His Leu Trp Trp
    210                 215                 220

Gln Glu Leu Lys Val Leu Pro Ile Asn Leu Ala Asp Ile Leu Leu Gly
225                 230                 235                 240

Asn Glu Ile Ala Gln Met Gly Phe Lys Ile Val Ser Lys Val Leu Lys
                245                 250                 255

Asn Lys Val Ser Gly Thr Asn Asn Lys Ala Met Ala Ala Leu Val Phe
            260                 265                 270

Ala Glu Leu Val Arg Asp Met Val Asp Gln Pro Thr Glu Leu Leu Gln
        275                 280                 285

Lys Ala Arg Glu Glu Ala Val Gly Arg Arg Glu Phe Leu Lys Ala Ile
    290                 295                 300

Thr Ala Glu Phe Thr Arg Lys Leu Asn Gln Ala Glu Ala Asp Gln Val
305                 310                 315                 320

Leu Val Arg Asp Phe Ala
                325
```

<210> 2309
<211> 2265
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2242)
<223> RXA01554

<400> 2309

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tggcttaaac cttatttgta gttgtcaata aatatgaaat tccttagcaa cttgtttaaa 60

tagacgtata aacaagtttg aaaaaggaag gttatccatc ttg aaa aag cat gtg   115
                                            Leu Lys Lys His Val
                                              1               5

acc tca gcc gtt acc gcc gtg gtg acg gct ttt tca acg gct gcg ctt   163
Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe Ser Thr Ala Ala Leu
                  10                  15                  20

ggt tta agt att gcc gtt tct cct gct gtt gcc caa gtg gct aat cca   211
Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala Gln Val Ala Asn Pro
              25                  30                  35
```

```
gct cca gat ctt tct gcg ccg tat aca tgg gtg gaa gag ttt gat tcc   259
Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val Glu Glu Phe Asp Ser
         40                  45                  50

gag gat gct ctc aaa ggg tgg aac att ttc cgc cag cca gat tat ggc   307
Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg Gln Pro Asp Tyr Gly
     55                  60                  65

agc gac aaa gtt ctc tat acc gaa gat gct tta agt atc gaa gat ggc   355
Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu Ser Ile Glu Asp Gly
 70                  75                  80                  85

aag ctc acc atc acc act cag cgc cac tgc gtt gac gaa gac ttc gcg   403
Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val Asp Glu Asp Phe Ala
                 90                  95                 100

atc agt gat cct gtc aac cgc gga aag ctc aat gac agc acc gcg caa   451
Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn Asp Ser Thr Ala Gln
            105                 110                 115

gtt gaa cct tgt gct cca ggt cag ttt gaa aag ttc acc agt gcg cgc   499
Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys Phe Thr Ser Ala Arg
        120                 125                 130

atc gtc act ccg aaa att gct cgt gga gag ttc gac ctt tct gtc act   547
Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe Asp Leu Ser Val Thr
    135                 140                 145

gca act ctt aac acc ggt ggc gtc gaa ggt gtc cga agt gcc att tgg   595
Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val Arg Ser Ala Ile Trp
150                 155                 160                 165

atg caa aac ggt gaa cag gcg tgt tcc tca gca acc aac aat ggc ctc   643
Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala Thr Asn Asn Gly Leu
                170                 175                 180

tac gga gaa cta gac ctg gta gag cac ttt tct tac gat ctt cgc tcg   691
Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser Tyr Asp Leu Arg Ser
            185                 190                 195

cca tgg tct cca tca aac acc cac ttg ggt tgt gat cct gaa agt gtc   739
Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys Asp Pro Glu Ser Val
        200                 205                 210

aac ggc acc aac cgt gca cct cgt gaa ctt aaa cta gat gag tca ctc   787
Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys Leu Asp Glu Ser Leu
    215                 220                 225

gat ggc gtg gag cac acc tgg act gtg agc acc acc cgc gac ggc gtt   835
Asp Gly Val Glu His Thr Trp Thr Val Ser Thr Thr Arg Asp Gly Val
230                 235                 240                 245

gag tac ttc att gat gat gag gcg att aac cgc cag tca tgg cgc aac   883
Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg Gln Ser Trp Arg Asn
                250                 255                 260

gat gtc act ttg ggg cat gcc gaa att gat gat ttc ggg atc tcc gcg   931
Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp Phe Gly Ile Ser Ala
            265                 270                 275

cag acg ttt gat gag atc gtc gac cgc gaa tgg act ctc act ctt aat   979
```

```
Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp Thr Leu Thr Leu Asn
        280                 285                 290

caa aag gta gaa agc gcc gac tgg gca aaa cca cgt tcc tct gag gaa   1027
Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro Arg Ser Ser Glu Glu
    295                 300                 305

gat ttc cca gtc cgg tcc atg gtg att gac cgc atc gag gtc acc gga   1075
Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg Ile Glu Val Thr Gly
310                 315                 320                 325

tct ccc gca gta tct gaa gac acc ccc atg cca gat acc acc cag ctt   1123
Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro Asp Thr Thr Gln Leu
                330                 335                 340

ttg acc caa gac act ctg gaa tac ctc ggt cgc atg cca gtg ctg gaa   1171
Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg Met Pro Val Leu Glu
            345                 350                 355

cgc tac gag cca gca agt gct gat ttt gcc gat ggc cgc agg cct tcc   1219
Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp Gly Arg Arg Pro Ser
        360                 365                 370

tgg aac tac ttc aat ttg aag gaa tcg tgg cag aat cca gaa ctc gag   1267
Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln Asn Pro Glu Leu Glu
    375                 380                 385

caa cgc cca gaa gct gtc gaa ttc gtt gat gga cgc atg gat atc gtg   1315
Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly Arg Met Asp Ile Val
390                 395                 400                 405

acc cgt cgc cac tgt ctg gcc acc act gat gac atc gcc act ccg gaa   1363
Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp Ile Ala Thr Pro Glu
                410                 415                 420

aac gca cag gag gaa ccg tgc gcg ccg ggt gag gtg aca cgc tac agc   1411
Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu Val Thr Arg Tyr Ser
            425                 430                 435

tca gcg cgt gtc cac ctt cca gag atc ccc gcc ggc aac ttc cgg ctc   1459
Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala Gly Asn Phe Arg Leu
        440                 445                 450

acc gtg cgc gca cgg gcg cag tcc gaa gag ctt gtc gac ggc gtc cgc   1507
Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu Val Asp Gly Val Arg
    455                 460                 465

ccc gct atc tgg atg cag aac aat acc aac ttc tgt gct gac aac gat   1555
Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe Cys Ala Asp Asn Asp
470                 475                 480                 485

gga cgc cct tat ggt gaa ctg gat att act gag ttc tac agc tct cgt   1603
Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu Phe Tyr Ser Ser Arg
                490                 495                 500

gtg aac acc cag tac tcg gca gta cac ctt gga tgt gct ggc aac cgc   1651
Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly Cys Ala Gly Asn Arg
            505                 510                 515

cca gag atg aag ctt cgc caa atg gaa atg gaa gag tcc atg ttt ggg   1699
Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu Glu Ser Met Phe Gly
```

```
        520                 525                 530

gat tgg cat gac tgg ggc gtc gaa gtc ttc gac ggc cag atc gta ttc   1747
Asp Trp His Asp Trp Gly Val Glu Val Phe Asp Gly Gln Ile Val Phe
    535                 540                 545

acc att gac ggc aag gca gta act tcc tct ggc aaa gat gtc ttt ggc   1795
Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly Lys Asp Val Phe Gly
550                 555                 560                 565

aac tct gtt acc cca gcc gct gca cct ctt cgc ccc gcg cac ttc aag   1843
Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg Pro Ala His Phe Lys
                570                 575                 580

ttg tcg gaa gag gaa tac cgt gaa gtc atc ggg cag cct tgg cac ctt   1891
Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly Gln Pro Trp His Leu
            585                 590                 595

att ttg aac acc atg gtg gag cag tct ggc aaa gac agc tgg att aca   1939
Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys Asp Ser Trp Ile Thr
        600                 605                 610

gcg gtc gac aat aac gag gcg ttc cca gaa cac cgc ttc caa att gac   1987
Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His Arg Phe Gln Ile Asp
    615                 620                 625

cat gtg gca gta gat atc gag tct gac tct gtg gac aat gta tgg cct   2035
His Val Ala Val Asp Ile Glu Ser Asp Ser Val Asp Asn Val Trp Pro
630                 635                 640                 645

gac gct gcg aat gaa atc cca gac aat gtt ggt att gaa gac tct gat   2083
Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly Ile Glu Asp Ser Asp
                650                 655                 660

gat ggc agc gac ctg gag gtt ggt tcg acc gga agc tct aca gct gag   2131
Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly Ser Ser Thr Ala Glu
            665                 670                 675

acc gtg agc tgg atc tcg ttg ttc acc gcg ttg agc tcg ctg gtc ttc   2179
Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu Ser Ser Leu Val Phe
        680                 685                 690

aca ctg gct ctc aat caa gaa gca ttg cag aat ttg att aat cag ttc   2227
Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn Leu Ile Asn Gln Phe
    695                 700                 705

atg aga cag ttc aag taatccttgt gggcgctttg tct                    2265
Met Arg Gln Phe Lys
710
```

<210> 2310
<211> 714
<212> PRT
<213> Corynebacterium glutamicum

<400> 2310

```
Leu Lys Lys His Val Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe
  1               5                  10                  15

Ser Thr Ala Ala Leu Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala
```

```
            20                  25                  30

Gln Val Ala Asn Pro Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val
         35                  40                  45

Glu Glu Phe Asp Ser Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg
     50                  55                  60

Gln Pro Asp Tyr Gly Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu
 65                  70                  75                  80

Ser Ile Glu Asp Gly Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val
                 85                  90                  95

Asp Glu Asp Phe Ala Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn
            100                 105                 110

Asp Ser Thr Ala Gln Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys
        115                 120                 125

Phe Thr Ser Ala Arg Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe
    130                 135                 140

Asp Leu Ser Val Thr Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val
145                 150                 155                 160

Arg Ser Ala Ile Trp Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala
                165                 170                 175

Thr Asn Asn Gly Leu Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser
            180                 185                 190

Tyr Asp Leu Arg Ser Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys
        195                 200                 205

Asp Pro Glu Ser Val Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys
    210                 215                 220

Leu Asp Glu Ser Leu Asp Gly Val Glu His Thr Trp Thr Val Ser Thr
225                 230                 235                 240

Thr Arg Asp Gly Val Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg
                245                 250                 255

Gln Ser Trp Arg Asn Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp
            260                 265                 270

Phe Gly Ile Ser Ala Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp
        275                 280                 285

Thr Leu Thr Leu Asn Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro
    290                 295                 300

Arg Ser Ser Glu Glu Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg
305                 310                 315                 320

Ile Glu Val Thr Gly Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro
                325                 330                 335

Asp Thr Thr Gln Leu Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg
            340                 345                 350
```

```
Met Pro Val Leu Glu Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp
        355                 360                 365

Gly Arg Arg Pro Ser Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln
    370                 375                 380

Asn Pro Glu Leu Glu Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly
385                 390                 395                 400

Arg Met Asp Ile Val Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp
                405                 410                 415

Ile Ala Thr Pro Glu Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu
            420                 425                 430

Val Thr Arg Tyr Ser Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala
        435                 440                 445

Gly Asn Phe Arg Leu Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu
    450                 455                 460

Val Asp Gly Val Arg Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe
465                 470                 475                 480

Cys Ala Asp Asn Asp Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu
                485                 490                 495

Phe Tyr Ser Ser Arg Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly
            500                 505                 510

Cys Ala Gly Asn Arg Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu
        515                 520                 525

Glu Ser Met Phe Gly Asp Trp His Asp Trp Gly Val Glu Val Phe Asp
    530                 535                 540

Gly Gln Ile Val Phe Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly
545                 550                 555                 560

Lys Asp Val Phe Gly Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg
                565                 570                 575

Pro Ala His Phe Lys Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly
            580                 585                 590

Gln Pro Trp His Leu Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys
        595                 600                 605

Asp Ser Trp Ile Thr Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His
    610                 615                 620

Arg Phe Gln Ile Asp His Val Ala Val Asp Ile Glu Ser Asp Ser Val
625                 630                 635                 640

Asp Asn Val Trp Pro Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly
                645                 650                 655

Ile Glu Asp Ser Asp Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly
            660                 665                 670
```

```
Ser Ser Thr Ala Glu Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu
        675                 680                 685

Ser Ser Leu Val Phe Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn
    690                 695                 700

Leu Ile Asn Gln Phe Met Arg Gln Phe Lys
705                 710


<210> 2311
<211> 453
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(430)
<223> RXA01560

<400> 2311
atgggagcaa ggctcattta gctacttcga cgtggaagcg cacatcgttg agttgattcc 60

tgcatcagta agcgatgcgt tttaggcaca tctgcgatcc gtg ggc gtg tcc tac   115
                                        Val Gly Val Ser Tyr
                                          1               5

atc atc gcc ggc gat gag cag ctg gat atg gca gaa gcc gtt cgc aaa   163
Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala Glu Ala Val Arg Lys
                10                  15                  20

att ggg gag acc ttt aaa act gag gaa att atc ctt ggt ggc gga gga   211
Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile Leu Gly Gly Gly Gly
            25                  30                  35

acc ctg aac tgg tcc atg ctc cgc gac ggt ttg tgc gac gag gtt agc   259
Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu Cys Asp Glu Val Ser
        40                  45                  50

atc gtg atg atg cca atc gcc gat ggt gaa aag cac acc cac tct ttg   307
Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys His Thr His Ser Leu
    55                  60                  65

ttc gaa gcc gat gaa aaa tac tca gca ccg ttg ccg atc ggt ttt tca   355
Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu Pro Ile Gly Phe Ser
70                  75                  80                  85

ctc gcc agc gtt gaa cca cta gaa gat gga agc gtt tgg atg cgt tac   403
Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser Val Trp Met Arg Tyr
                90                  95                  100

ggg gtc aat ggc cca gtg gac gcg aac taggtagcaa atactcgctc         450
Gly Val Asn Gly Pro Val Asp Ala Asn
            105                 110

ttt                                                              453


<210> 2312
<211> 110
<212> PRT
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<213> Corynebacterium glutamicum

<400> 2312
Val Gly Val Ser Tyr Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala
1 5 10 15

Glu Ala Val Arg Lys Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile
20 25 30

Leu Gly Gly Gly Gly Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu
35 40 45

Cys Asp Glu Val Ser Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys
50 55 60

His Thr His Ser Leu Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu
65 70 75 80

Pro Ile Gly Phe Ser Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser
85 90 95

Val Trp Met Arg Tyr Gly Val Asn Gly Pro Val Asp Ala Asn
100 105 110

<210> 2313
<211> 1143
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1120)
<223> RXA01575

<400> 2313
gctgtttttt gatgcatcca tgataggaat agagcctagt gcatgatggc tgattttcct 60

gttaggtgcc accgacccca gtgatgataa cttgattgtc atg aaa tcc att gat 115
Met Lys Ser Ile Asp
1 5

ctt gag cag ctg gcg ggc acg caa tcg cgc acg tat caa tcg cga aag 163
Leu Glu Gln Leu Ala Gly Thr Gln Ser Arg Thr Tyr Gln Ser Arg Lys
10 15 20

atc acc gat gag atg gtc gcc cgg ccg gtg cat gtg gcg atc gcg ctg 211
Ile Thr Asp Glu Met Val Ala Arg Pro Val His Val Ala Ile Ala Leu
25 30 35

tgg gaa gtg ccg tgg gag tcg gca aaa tcc ggc aag att gag ggt tgg 259
Trp Glu Val Pro Trp Glu Ser Ala Lys Ser Gly Lys Ile Glu Gly Trp
40 45 50

gtc att gcc gtg gat tcg ccg cgt ggg cgg ttt gtg cgc agc ggg cag 307
Val Ile Ala Val Asp Ser Pro Arg Gly Arg Phe Val Arg Ser Gly Gln
55 60 65

acc aaa aat ggc gac gcc gtc aac cgg act gtg tcg atg ctg aaa tca 355
Thr Lys Asn Gly Asp Ala Val Asn Arg Thr Val Ser Met Leu Lys Ser
70 75 80 85

```
gcg ttg aaa ggg gtc cgc ggg aag gcg tgg att gta act ggg cgt cga   403
Ala Leu Lys Gly Val Arg Gly Lys Ala Trp Ile Val Thr Gly Arg Arg
                 90                  95                 100

caa gca gct tta cgc gca gcc ctg gtg cgc gaa aac tac ctg gtc acc   451
Gln Ala Ala Leu Arg Ala Ala Leu Val Arg Glu Asn Tyr Leu Val Thr
            105                 110                 115

gga agc ttc gcc gag caa aat agg gcc ggc gtg aag gcg tcg gcg atc   499
Gly Ser Phe Ala Glu Gln Asn Arg Ala Gly Val Lys Ala Ser Ala Ile
        120                 125                 130

tcg cgc cgc gcc gaa caa tcc gcg ctc tac aag gcg aaa aaa atc ggc   547
Ser Arg Arg Ala Glu Gln Ser Ala Leu Tyr Lys Ala Lys Lys Ile Gly
    135                 140                 145

gaa ttc gcc gag cgc gcc cca cgc gtc aaa gag cgg caa gag gca cat   595
Glu Phe Ala Glu Arg Ala Pro Arg Val Lys Glu Arg Gln Glu Ala His
150                 155                 160                 165

tgg tgg cca cgg ttg tca cgc acg caa ggc acc gca ggc gtt tta cgc   643
Trp Trp Pro Arg Leu Ser Arg Thr Gln Gly Thr Ala Gly Val Leu Arg
                170                 175                 180

tta gcg acg gac gcc tct acc gat ggg gtc ttc cgc ggc gcc atg tgc   691
Leu Ala Thr Asp Ala Ser Thr Asp Gly Val Phe Arg Gly Ala Met Cys
            185                 190                 195

ttc gta gcc tca aac ggc gac tac ctc ctg gag acc caa gac acc acc   739
Phe Val Ala Ser Asn Gly Asp Tyr Leu Leu Glu Thr Gln Asp Thr Thr
        200                 205                 210

gca agc tcc gac gaa tta gaa ctc gaa agc atc acc cac gcc ctg atc   787
Ala Ser Ser Asp Glu Leu Glu Leu Glu Ser Ile Thr His Ala Leu Ile
    215                 220                 225

tac ctc aaa acc atc ggc gcg acc caa gcc atc atc gaa tcc gac agc   835
Tyr Leu Lys Thr Ile Gly Ala Thr Gln Ala Ile Ile Glu Ser Asp Ser
230                 235                 240                 245

aaa gcc gca ctt gaa gcc atc gac ttc atc ctc aac aac cga ccg cgc   883
Lys Ala Ala Leu Glu Ala Ile Asp Phe Ile Leu Asn Asn Arg Pro Arg
                250                 255                 260

cgg ggc agg tgg cgc ggc atc acc gca tgc gcc cgc aac cgg ttc cgg   931
Arg Gly Arg Trp Arg Gly Ile Thr Ala Cys Ala Arg Asn Arg Phe Arg
            265                 270                 275

gat gcc tgg gaa gcg ctt atc gac gac tgc gtt gtg gaa tta tcc cgc   979
Asp Ala Trp Glu Ala Leu Ile Asp Asp Cys Val Val Glu Leu Ser Arg
        280                 285                 290

gta cta ggg cac gcc ggg gat cca ctg aac caa gca gcc gac caa atc   1027
Val Leu Gly His Ala Gly Asp Pro Leu Asn Gln Ala Ala Asp Gln Ile
    295                 300                 305

gca tac atg ggc atg cgc gcc gta att ttt gaa caa aaa tcc gca cac   1075
Ala Tyr Met Gly Met Arg Ala Val Ile Phe Glu Gln Lys Ser Ala His
310                 315                 320                 325
```

```
ccc aca ttg ctc aaa gga att gac aag gcg ctt cgc aag gcc gag       1120
Pro Thr Leu Leu Lys Gly Ile Asp Lys Ala Leu Arg Lys Ala Glu
                330                 335                 340

taaggtgggc aacgagtcgg tga                                       1143
```

<210> 2314
<211> 340
<212> PRT
<213> Corynebacterium glutamicum

<400> 2314

```
Met Lys Ser Ile Asp Leu Glu Gln Leu Ala Gly Thr Gln Ser Arg Thr
  1               5                  10                  15

Tyr Gln Ser Arg Lys Ile Thr Asp Glu Met Val Ala Arg Pro Val His
             20                  25                  30

Val Ala Ile Ala Leu Trp Glu Val Pro Trp Glu Ser Ala Lys Ser Gly
         35                  40                  45

Lys Ile Glu Gly Trp Val Ile Ala Val Asp Ser Pro Arg Gly Arg Phe
     50                  55                  60

Val Arg Ser Gly Gln Thr Lys Asn Gly Asp Ala Val Asn Arg Thr Val
 65                  70                  75                  80

Ser Met Leu Lys Ser Ala Leu Lys Gly Val Arg Gly Lys Ala Trp Ile
                 85                  90                  95

Val Thr Gly Arg Arg Gln Ala Ala Leu Arg Ala Ala Leu Val Arg Glu
            100                 105                 110

Asn Tyr Leu Val Thr Gly Ser Phe Ala Glu Gln Asn Arg Ala Gly Val
        115                 120                 125

Lys Ala Ser Ala Ile Ser Arg Arg Ala Glu Gln Ser Ala Leu Tyr Lys
    130                 135                 140

Ala Lys Lys Ile Gly Glu Phe Ala Glu Arg Ala Pro Arg Val Lys Glu
145                 150                 155                 160

Arg Gln Glu Ala His Trp Trp Pro Arg Leu Ser Arg Thr Gln Gly Thr
                165                 170                 175

Ala Gly Val Leu Arg Leu Ala Thr Asp Ala Ser Thr Asp Gly Val Phe
            180                 185                 190

Arg Gly Ala Met Cys Phe Val Ala Ser Asn Gly Asp Tyr Leu Leu Glu
        195                 200                 205

Thr Gln Asp Thr Thr Ala Ser Ser Asp Glu Leu Glu Leu Glu Ser Ile
    210                 215                 220

Thr His Ala Leu Ile Tyr Leu Lys Thr Ile Gly Ala Thr Gln Ala Ile
225                 230                 235                 240

Ile Glu Ser Asp Ser Lys Ala Ala Leu Glu Ala Ile Asp Phe Ile Leu
                245                 250                 255
```

```
Asn Asn Arg Pro Arg Arg Gly Arg Trp Arg Gly Ile Thr Ala Cys Ala
            260                 265                 270

Arg Asn Arg Phe Arg Asp Ala Trp Glu Ala Leu Ile Asp Asp Cys Val
        275                 280                 285

Val Glu Leu Ser Arg Val Leu Gly His Ala Gly Asp Pro Leu Asn Gln
    290                 295                 300

Ala Ala Asp Gln Ile Ala Tyr Met Gly Met Arg Ala Val Ile Phe Glu
305                 310                 315                 320

Gln Lys Ser Ala His Pro Thr Leu Leu Lys Gly Ile Asp Lys Ala Leu
                325                 330                 335

Arg Lys Ala Glu
            340
```

<210> 2315
<211> 498
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(475)
<223> RXA01577

<400> 2315

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ccgtagacat cctctacacc gaatactcca tgagcaaggg gcaatccctg ctcaacggcg 60

taaacatcct ggccgacggc ttcctagcga ggagactccc atg acg cag acc acc   115
                                              Met Thr Gln Thr Thr
                                                1               5

acc caa atc atc atc cag ata ctg ctt ctc ctg gca acc gca gca ctg   163
Thr Gln Ile Ile Ile Gln Ile Leu Leu Leu Leu Ala Thr Ala Ala Leu
                10                  15                  20

gca cta tat ttc ctc cga aac cgc cgc aaa gcc cgc gcc aaa gca tgg   211
Ala Leu Tyr Phe Leu Arg Asn Arg Arg Lys Ala Arg Ala Lys Ala Trp
            25                  30                  35

gtg aaa atc ggc ttc gta gta ttc att ttc gcc gca gta tgg gca gtg   259
Val Lys Ile Gly Phe Val Val Phe Ile Phe Ala Ala Val Trp Ala Val
        40                  45                  50

ctc cgc ccc gat gac ctc acc caa cta gcc aac ttt gtg ggc gtg gac   307
Leu Arg Pro Asp Asp Leu Thr Gln Leu Ala Asn Phe Val Gly Val Asp
    55                  60                  65

cgc ggc acc gac cta atg ctt tac gcc ctg gtt gtg gca ttt atg ttc   355
Arg Gly Thr Asp Leu Met Leu Tyr Ala Leu Val Val Ala Phe Met Phe
70                  75                  80                  85

acc acg ctg tcc agt tat gtg cgt ttc cgt gaa caa gag ctg cgt tat   403
Thr Thr Leu Ser Ser Tyr Val Arg Phe Arg Glu Gln Glu Leu Arg Tyr
                90                  95                  100

tcc aag ctg gcc cgc gct gtc gct ttg caa aat gtg gtg ctg ccg gag   451
```

```
Ser Lys Leu Ala Arg Ala Val Ala Leu Gln Asn Val Val Leu Pro Glu
            105                 110                 115

gat tcc cag ggt tct gac ccc gct taggaaagcg cttggcctct gga        498
Asp Ser Gln Gly Ser Asp Pro Ala
        120                 125


<210> 2316
<211> 125
<212> PRT
<213> Corynebacterium glutamicum

<400> 2316
Met Thr Gln Thr Thr Thr Gln Ile Ile Ile Gln Ile Leu Leu Leu Leu
  1               5                  10                  15

Ala Thr Ala Ala Leu Ala Leu Tyr Phe Leu Arg Asn Arg Arg Lys Ala
             20                  25                  30

Arg Ala Lys Ala Trp Val Lys Ile Gly Phe Val Val Phe Ile Phe Ala
         35                  40                  45

Ala Val Trp Ala Val Leu Arg Pro Asp Asp Leu Thr Gln Leu Ala Asn
     50                  55                  60

Phe Val Gly Val Asp Arg Gly Thr Asp Leu Met Leu Tyr Ala Leu Val
 65                  70                  75                  80

Val Ala Phe Met Phe Thr Thr Leu Ser Ser Tyr Val Arg Phe Arg Glu
                 85                  90                  95

Gln Glu Leu Arg Tyr Ser Lys Leu Ala Arg Ala Val Ala Leu Gln Asn
            100                 105                 110

Val Val Leu Pro Glu Asp Ser Gln Gly Ser Asp Pro Ala
        115                 120                 125


<210> 2317
<211> 507
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(484)
<223> RXA01579

<400> 2317
tggcagcatc ctgcgcaagg ttgggcagca gaccattcat tacggcgaat acaccggtca  60

ttgtgagaag ggtgctcagc agcaatgccc aggtgcgtcg ttg acc gag gta ttc    115
                                              Leu Thr Glu Val Phe
                                                1               5

aac act gac cag cgg gtg ctt aac gcg ctt ttc aat gtt gta gaa gaa    163
Asn Thr Asp Gln Arg Val Leu Asn Ala Leu Phe Asn Val Val Glu Glu
                10                  15                  20

gat gac tcc ggc gat acc gat gat gaa cag cac aac cac cag aat cca    211
```

```
Asp Asp Ser Gly Asp Thr Asp Asp Glu Gln His Asn His Gln Asn Pro
             25                  30                  35

gtt cgc ggc acc gag ttt gcc ggc ctc gtt gaa agc cat gag caa aga   259
Val Arg Gly Thr Glu Phe Ala Gly Leu Val Glu Ser His Glu Gln Arg
         40                  45                  50

tcc aat gga cac cgc cag tgg cag cac acc aag cca gtc cat ctt cgg   307
Ser Asn Gly His Arg Gln Trp Gln His Thr Lys Pro Val His Leu Arg
     55                  60                  65

ggt ttc ttc agc ggt gga ttc ctt cac gct gaa agg cag tgc gag ggc   355
Gly Phe Phe Ser Gly Gly Phe Leu His Ala Glu Arg Gln Cys Glu Gly
 70                  75                  80                  85

agc gac agc gca gaa agc agc cat gac cca gaa gat gga acg gaa acc   403
Ser Asp Ser Ala Glu Ser Ser His Asp Pro Glu Asp Gly Thr Glu Thr
                 90                  95                 100

aag tgt ttc agc caa cca gcc acc agc aag cgc gtc cac gcc gcc gat   451
Lys Cys Phe Ser Gln Pro Ala Thr Ser Lys Arg Val His Ala Ala Asp
            105                 110                 115

acc acc gtt gac aga ggt aac aat tcc gag aag tagcgcatat tgcttttcat 504
Thr Thr Val Asp Arg Gly Asn Asn Ser Glu Lys
        120                 125

tgg                                                               507


<210> 2318
<211> 128
<212> PRT
<213> Corynebacterium glutamicum

<400> 2318
Leu Thr Glu Val Phe Asn Thr Asp Gln Arg Val Leu Asn Ala Leu Phe
  1               5                  10                  15

Asn Val Val Glu Glu Asp Asp Ser Gly Asp Thr Asp Asp Glu Gln His
             20                  25                  30

Asn His Gln Asn Pro Val Arg Gly Thr Glu Phe Ala Gly Leu Val Glu
         35                  40                  45

Ser His Glu Gln Arg Ser Asn Gly His Arg Gln Trp Gln His Thr Lys
     50                  55                  60

Pro Val His Leu Arg Gly Phe Phe Ser Gly Gly Phe Leu His Ala Glu
 65                  70                  75                  80

Arg Gln Cys Glu Gly Ser Asp Ser Ala Glu Ser Ser His Asp Pro Glu
                 85                  90                  95

Asp Gly Thr Glu Thr Lys Cys Phe Ser Gln Pro Ala Thr Ser Lys Arg
            100                 105                 110

Val His Ala Ala Asp Thr Thr Val Asp Arg Gly Asn Asn Ser Glu Lys
        115                 120                 125
```

<210> 2319
<211> 750
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(727)
<223> RXA01585

<400> 2319
tgcagactgc tgcgccccgt tccatcagca aggtggagcg caaggtgctg accgctgtcg 60

ctactgatga ggtgcagtcg caggaagctc tagaaaagta gtg gtt gag act ctt 115
Val Val Glu Thr Leu
1 5

tct atc acc tca ggt gcg gct ggc ctg cag gcg ctt gtt gcg cgt gcg 163
Ser Ile Thr Ser Gly Ala Ala Gly Leu Gln Ala Leu Val Ala Arg Ala
10 15 20

gtt ggt ttg aat gag ttg gcg agc gcg cgt ttc cgc cag ctc acg cca 211
Val Gly Leu Asn Glu Leu Ala Ser Ala Arg Phe Arg Gln Leu Thr Pro
25 30 35

gag gtc gtt gat gtt ttt gtc acc act ccg ttc aac gtg acg gcg tcg 259
Glu Val Val Asp Val Phe Val Thr Thr Pro Phe Asn Val Thr Ala Ser
40 45 50

cgc cgg gta ttt ggt gtg gcg ggt cgc gat ggc gct gca gtt ggc gcg 307
Arg Arg Val Phe Gly Val Ala Gly Arg Asp Gly Ala Ala Val Gly Ala
55 60 65

aag gat ttg ctg cag gca ctc agc gag ggc cgg gaa gac gta ggc acc 355
Lys Asp Leu Leu Gln Ala Leu Ser Glu Gly Arg Glu Asp Val Gly Thr
70 75 80 85

tcc cgc gac gcc agc tgg ccg ggc tca ttg ccg cca gcc acg ggc ttt 403
Ser Arg Asp Ala Ser Trp Pro Gly Ser Leu Pro Pro Ala Thr Gly Phe
90 95 100

acg ctt gtc gac gaa ctc ccc acc cac gtg gtg cgc act ttg gct gat 451
Thr Leu Val Asp Glu Leu Pro Thr His Val Val Arg Thr Leu Ala Asp
105 110 115

cag ggt cag gca ttg gct cgc cag ttc tcc ggc ccg ctt ggc cct ccg 499
Gln Gly Gln Ala Leu Ala Arg Gln Phe Ser Gly Pro Leu Gly Pro Pro
120 125 130

gct tcg ttg atg gat cag gaa gtt att tca gca gaa ggc aat ggc aag 547
Ala Ser Leu Met Asp Gln Glu Val Ile Ser Ala Glu Gly Asn Gly Lys
135 140 145

aag gcc gga atc ccg atg cgc acg gta ttt acc tgc act tcg ctt ggt 595
Lys Ala Gly Ile Pro Met Arg Thr Val Phe Thr Cys Thr Ser Leu Gly
150 155 160 165

ttg atc cca ggt ttt gag gca gcc aat gat gtg ccg agg cac ctg cgg 643

```
Leu Ile Pro Gly Phe Glu Ala Ala Asn Asp Val Pro Arg His Leu Arg
                170                 175                 180

gta tcg gtg aat ggt cgt tgg acc cgc gtt gat gct ccc tat ggc agt   691
Val Ser Val Asn Gly Arg Trp Thr Arg Val Asp Ala Pro Tyr Gly Ser
            185                 190                 195

gtt tat cac tcg tca ggt ttg ggt ctg agc gtt ttc taaagcaaga        737
Val Tyr His Ser Ser Gly Leu Gly Leu Ser Val Phe
        200                 205

cccagcctgc aag                                                   750


<210> 2320
<211> 209
<212> PRT
<213> Corynebacterium glutamicum

<400> 2320
Val Val Glu Thr Leu Ser Ile Thr Ser Gly Ala Ala Gly Leu Gln Ala
  1               5                  10                  15

Leu Val Ala Arg Ala Val Gly Leu Asn Glu Leu Ala Ser Ala Arg Phe
             20                  25                  30

Arg Gln Leu Thr Pro Glu Val Val Asp Val Phe Val Thr Thr Pro Phe
         35                  40                  45

Asn Val Thr Ala Ser Arg Arg Val Phe Gly Val Ala Gly Arg Asp Gly
     50                  55                  60

Ala Ala Val Gly Ala Lys Asp Leu Leu Gln Ala Leu Ser Glu Gly Arg
 65                  70                  75                  80

Glu Asp Val Gly Thr Ser Arg Asp Ala Ser Trp Pro Gly Ser Leu Pro
                 85                  90                  95

Pro Ala Thr Gly Phe Thr Leu Val Asp Glu Leu Pro Thr His Val Val
            100                 105                 110

Arg Thr Leu Ala Asp Gln Gly Gln Ala Leu Ala Arg Gln Phe Ser Gly
        115                 120                 125

Pro Leu Gly Pro Pro Ala Ser Leu Met Asp Gln Glu Val Ile Ser Ala
    130                 135                 140

Glu Gly Asn Gly Lys Lys Ala Gly Ile Pro Met Arg Thr Val Phe Thr
145                 150                 155                 160

Cys Thr Ser Leu Gly Leu Ile Pro Gly Phe Glu Ala Ala Asn Asp Val
                165                 170                 175

Pro Arg His Leu Arg Val Ser Val Asn Gly Arg Trp Thr Arg Val Asp
            180                 185                 190

Ala Pro Tyr Gly Ser Val Tyr His Ser Ser Gly Leu Gly Leu Ser Val
        195                 200                 205

Phe
```

<210> 2321
<211> 392
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(369)
<223> RXA01586

<400> 2321
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aac aac gcg gcg ttc att gag atc gcg cag gaa gct cga ttg gcg ttt   48
Asn Asn Ala Ala Phe Ile Glu Ile Ala Gln Glu Ala Arg Leu Ala Phe
  1               5                  10                  15

gcg gag gat cag ttc cgt gag cgt ggc tat gag atc cct gct gtg ttt   96
Ala Glu Asp Gln Phe Arg Glu Arg Gly Tyr Glu Ile Pro Ala Val Phe
             20                  25                  30

gtg cgc cac ttg gaa gtt gat tat ttg cgt gcg atc ttg ccg gat acc   144
Val Arg His Leu Glu Val Asp Tyr Leu Arg Ala Ile Leu Pro Asp Thr
         35                  40                  45

acc cag gct gtc gtg gag aca cag gtg acc aag atc ggt aat act tcc   192
Thr Gln Ala Val Val Glu Thr Gln Val Thr Lys Ile Gly Asn Thr Ser
     50                  55                  60

ttc agc act cgt caa gag gtc aag gat cgt aac ggt cgt gtg tgc tgc   240
Phe Ser Thr Arg Gln Glu Val Lys Asp Arg Asn Gly Arg Val Cys Cys
 65                  70                  75                  80

gtg gtt gag tgc gtg cag gtg gct gtc aat gtg cag act gct gcg ccc   288
Val Val Glu Cys Val Gln Val Ala Val Asn Val Gln Thr Ala Ala Pro
                 85                  90                  95

cgt tcc atc agc aag gtg gag cgc aag gtg ctg acc gct gtc gct act   336
Arg Ser Ile Ser Lys Val Glu Arg Lys Val Leu Thr Ala Val Ala Thr
            100                 105                 110

gat gag gtg cag tcg cag gaa gct cta gaa aag tagtggttga gactctttct 389
Asp Glu Val Gln Ser Gln Glu Ala Leu Glu Lys
        115                 120

atc                                                               392
```

<210> 2322
<211> 123
<212> PRT
<213> Corynebacterium glutamicum

<400> 2322
```
Asn Asn Ala Ala Phe Ile Glu Ile Ala Gln Glu Ala Arg Leu Ala Phe
  1               5                  10                  15

Ala Glu Asp Gln Phe Arg Glu Arg Gly Tyr Glu Ile Pro Ala Val Phe
             20                  25                  30

Val Arg His Leu Glu Val Asp Tyr Leu Arg Ala Ile Leu Pro Asp Thr
```

```
         35                  40                  45

Thr Gln Ala Val Val Glu Thr Gln Val Thr Lys Ile Gly Asn Thr Ser
     50                  55                  60

Phe Ser Thr Arg Gln Glu Val Lys Asp Arg Asn Gly Arg Val Cys Cys
 65                  70                  75                  80

Val Val Glu Cys Val Gln Val Ala Val Asn Val Gln Thr Ala Ala Pro
                 85                  90                  95

Arg Ser Ile Ser Lys Val Glu Arg Lys Val Leu Thr Ala Val Ala Thr
            100                 105                 110

Asp Glu Val Gln Ser Gln Glu Ala Leu Glu Lys
        115                 120


<210> 2323
<211> 1083
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1060)
<223> RXA01595

<400> 2323
aatacttcct gtggctggtt aaagatggtg gcgcttcaat gccggatgac cagcaattgt 60

cggcaatgat tgacacggct gtaaaggaag gtccgcaata atg act gca ccc acg   115
                                              Met Thr Ala Pro Thr
                                                1               5

aac gct ggg gaa ctc agg cga gtt ttg ctg gtt cca cac acc ggg cgt   163
Asn Ala Gly Glu Leu Arg Arg Val Leu Leu Val Pro His Thr Gly Arg
                 10                  15                  20

tct tcc aat att gaa tcc gcc atc ttg gca gcc aag ctg ctc gac gat   211
Ser Ser Asn Ile Glu Ser Ala Ile Leu Ala Ala Lys Leu Leu Asp Asp
            25                  30                  35

gct gga atc gat gtg agg gtg ctg atc aat gat gca gat gat cca att   259
Ala Gly Ile Asp Val Arg Val Leu Ile Asn Asp Ala Asp Asp Pro Ile
        40                  45                  50

gca gag cac tcc gtt tta ggc cgt ttc acc cat gtc agg cac gct gca   307
Ala Glu His Ser Val Leu Gly Arg Phe Thr His Val Arg His Ala Ala
    55                  60                  65

gac gcc gct gac ggc gca gaa cta gtt ctg gtg ctg ggt gga gat ggc   355
Asp Ala Ala Asp Gly Ala Glu Leu Val Leu Val Leu Gly Gly Asp Gly
70                  75                  80                  85

acc ttc ctc cgc gca gca gat atg gcc cac gct gtt gat ttg cct gtt   403
Thr Phe Leu Arg Ala Ala Asp Met Ala His Ala Val Asp Leu Pro Val
                90                  95                 100

ctg ggc atc aac cta ggc cat gtg gga ttc ttg gct gaa tgg gag tct   451
Leu Gly Ile Asn Leu Gly His Val Gly Phe Leu Ala Glu Trp Glu Ser
```

```
            105                 110                 115

gac tca ctt gaa gag gca ctc aaa cgt gtg atc gac cgc gat tac cgt   499
Asp Ser Leu Glu Glu Ala Leu Lys Arg Val Ile Asp Arg Asp Tyr Arg
        120                 125                 130

att gaa gat cgc atg acc tta act gtc gtt gtc cta gac ggc ggt gga   547
Ile Glu Asp Arg Met Thr Leu Thr Val Val Val Leu Asp Gly Gly Gly
    135                 140                 145

gaa gaa atc ggc cga ggc tgg gct ctc aat gag gtc agt att gaa aac   595
Glu Glu Ile Gly Arg Gly Trp Ala Leu Asn Glu Val Ser Ile Glu Asn
150                 155                 160                 165

tta aac cgc agg gga gtg ctc gat gca acc ctc gag gta gat gca cga   643
Leu Asn Arg Arg Gly Val Leu Asp Ala Thr Leu Glu Val Asp Ala Arg
                170                 175                 180

cca gtt gct tcc ttt ggt tgc gat ggc gtg ctg att tcc acc cca acc   691
Pro Val Ala Ser Phe Gly Cys Asp Gly Val Leu Ile Ser Thr Pro Thr
            185                 190                 195

ggc tcc acc gct tat gca ttt tcc gcc ggt ggt cct gta ctg tgg cca   739
Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly Pro Val Leu Trp Pro
        200                 205                 210

gaa ctc gat gcc atc ttg gtg gtt cct aat aac gcc cac gcg ctg ttt   787
Glu Leu Asp Ala Ile Leu Val Val Pro Asn Asn Ala His Ala Leu Phe
    215                 220                 225

acc aaa ccg ctg gtt gtg agc cca aaa tcc acc gta gct gtg gaa tcc   835
Thr Lys Pro Leu Val Val Ser Pro Lys Ser Thr Val Ala Val Glu Ser
230                 235                 240                 245

aat tca gat act tca gca gcg atg gcc gtc atg gat ggt ttc cgt ccc   883
Asn Ser Asp Thr Ser Ala Ala Met Ala Val Met Asp Gly Phe Arg Pro
                250                 255                 260

att cct atg cct cca gga tcc cgt gtt gag gtc acc agg ggt gag cgt   931
Ile Pro Met Pro Pro Gly Ser Arg Val Glu Val Thr Arg Gly Glu Arg
            265                 270                 275

ccc gtg cgt tgg gtg agg ctt gat tct tca ccg ttt acc gac cga ctt   979
Pro Val Arg Trp Val Arg Leu Asp Ser Ser Pro Phe Thr Asp Arg Leu
        280                 285                 290

gtg agc aaa tta agg ctc ccc gtt acc ggt tgg cgg ggt ccg caa aaa   1027
Val Ser Lys Leu Arg Leu Pro Val Thr Gly Trp Arg Gly Pro Gln Lys
    295                 300                 305

cag gcg gaa aat aaa gat ccc agg tca gcg ggg taattcgaaa accattcgaa 1080
Gln Ala Glu Asn Lys Asp Pro Arg Ser Ala Gly
310                 315                 320

caa                                                               1083


<210> 2324
<211> 320
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 2324

```
Met Thr Ala Pro Thr Asn Ala Gly Glu Leu Arg Arg Val Leu Leu Val
  1               5                  10                  15

Pro His Thr Gly Arg Ser Ser Asn Ile Glu Ser Ala Ile Leu Ala Ala
             20                  25                  30

Lys Leu Leu Asp Asp Ala Gly Ile Asp Val Arg Val Leu Ile Asn Asp
         35                  40                  45

Ala Asp Asp Pro Ile Ala Glu His Ser Val Leu Gly Arg Phe Thr His
     50                  55                  60

Val Arg His Ala Ala Asp Ala Ala Asp Gly Ala Glu Leu Val Leu Val
 65                  70                  75                  80

Leu Gly Gly Asp Gly Thr Phe Leu Arg Ala Ala Asp Met Ala His Ala
                 85                  90                  95

Val Asp Leu Pro Val Leu Gly Ile Asn Leu Gly His Val Gly Phe Leu
            100                 105                 110

Ala Glu Trp Glu Ser Asp Ser Leu Glu Glu Ala Leu Lys Arg Val Ile
        115                 120                 125

Asp Arg Asp Tyr Arg Ile Glu Asp Arg Met Thr Leu Thr Val Val Val
    130                 135                 140

Leu Asp Gly Gly Gly Glu Glu Ile Gly Arg Gly Trp Ala Leu Asn Glu
145                 150                 155                 160

Val Ser Ile Glu Asn Leu Asn Arg Arg Gly Val Leu Asp Ala Thr Leu
                165                 170                 175

Glu Val Asp Ala Arg Pro Val Ala Ser Phe Gly Cys Asp Gly Val Leu
            180                 185                 190

Ile Ser Thr Pro Thr Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly
        195                 200                 205

Pro Val Leu Trp Pro Glu Leu Asp Ala Ile Leu Val Val Pro Asn Asn
    210                 215                 220

Ala His Ala Leu Phe Thr Lys Pro Leu Val Val Ser Pro Lys Ser Thr
225                 230                 235                 240

Val Ala Val Glu Ser Asn Ser Asp Thr Ser Ala Ala Met Ala Val Met
                245                 250                 255

Asp Gly Phe Arg Pro Ile Pro Met Pro Pro Gly Ser Arg Val Glu Val
            260                 265                 270

Thr Arg Gly Glu Arg Pro Val Arg Trp Val Arg Leu Asp Ser Ser Pro
        275                 280                 285

Phe Thr Asp Arg Leu Val Ser Lys Leu Arg Leu Pro Val Thr Gly Trp
    290                 295                 300

Arg Gly Pro Gln Lys Gln Ala Glu Asn Lys Asp Pro Arg Ser Ala Gly
305                 310                 315                 320
```

<210> 2325
<211> 792
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(769)
<223> RXA01600

<400> 2325
tgagtacaaa tctcgtccaa cccatgctca tccactgttt tacggcctgg tgaagaccgc 60

tttggagctg cgtgtccacc cttagatcta caatgtgatc atg gtt tcg aag atg 115
Met Val Ser Lys Met
1 5

cac att ccc ggt acc cat gag ttc acg gtg aca gat act gaa ctg ttg 163
His Ile Pro Gly Thr His Glu Phe Thr Val Thr Asp Thr Glu Leu Leu
10 15 20

tta gag tcc cca att ttg ggc gtt cgt cga gat tca ttg atc atg ccg 211
Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp Ser Leu Ile Met Pro
25 30 35

ggt ggt tcc act gcc cgc cgt gaa gtg gtt gaa cac ttt ggg gcg gtc 259
Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu His Phe Gly Ala Val
40 45 50

gca gtg gtt gcc ttt gat ggt gaa aac att gcg atg gtc aag cag tac 307
Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala Met Val Lys Gln Tyr
55 60 65

cgt cgc agc gtg ggg gat tcc ttg tgg gag ctg cct gca ggt ttg ttg 355
Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu Pro Ala Gly Leu Leu
70 75 80 85

gat att gct gat gag gat gaa ctc acg ggc gcg cag cgc gag ctc atg 403
Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala Gln Arg Glu Leu Met
90 95 100

gag gag gct ggt ttg gag gcc agt gag tgg tcc gtg ctc act gat ttg 451
Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser Val Leu Thr Asp Leu
105 110 115

att acc tcg cct ggt ttc tgc gat gaa gcg gtg cgt gtc ttt cta gcc 499
Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val Arg Val Phe Leu Ala
120 125 130

cga ggc ctc aca aag gtt gag cgc ccg aag gtt atg ggc gat gaa gaa 547
Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val Met Gly Asp Glu Glu
135 140 145

gcg gac atg att aac cag tgg gtt ccg cta cat gag gca gtg gga atg 595
Ala Asp Met Ile Asn Gln Trp Val Pro Leu His Glu Ala Val Gly Met
150 155 160 165

```
gtg ttt agt ggc cag ttg gtt aac tcc att gcc att gcg ggt gtc atg   643
Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala Ile Ala Gly Val Met
                170                 175                 180

gct gct gat gct gtg att gcg ggt cgt gcg tct gcg cgt gcc gtc acc   691
Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser Ala Arg Ala Val Thr
            185                 190                 195

gcg ccg ttt acc tat cgc cct acg gcg ttg gcg cag cgt cga aaa gcg   739
Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala Gln Arg Arg Lys Ala
        200                 205                 210

cac ggc att gtt cct gac atg aaa aaa cta tgaaggctcg cgttttagcg     789
His Gly Ile Val Pro Asp Met Lys Lys Leu
    215                 220

aaa                                                               792
```

<210> 2326
<211> 223
<212> PRT
<213> Corynebacterium glutamicum

<400> 2326

```
Met Val Ser Lys Met His Ile Pro Gly Thr His Glu Phe Thr Val Thr
  1               5                  10                  15

Asp Thr Glu Leu Leu Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp
             20                  25                  30

Ser Leu Ile Met Pro Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu
         35                  40                  45

His Phe Gly Ala Val Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala
     50                  55                  60

Met Val Lys Gln Tyr Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu
 65                  70                  75                  80

Pro Ala Gly Leu Leu Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala
                 85                  90                  95

Gln Arg Glu Leu Met Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser
            100                 105                 110

Val Leu Thr Asp Leu Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val
        115                 120                 125

Arg Val Phe Leu Ala Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val
    130                 135                 140

Met Gly Asp Glu Glu Ala Asp Met Ile Asn Gln Trp Val Pro Leu His
145                 150                 155                 160

Glu Ala Val Gly Met Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala
                165                 170                 175

Ile Ala Gly Val Met Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser
            180                 185                 190
```

```
Ala Arg Ala Val Thr Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala
        195                 200                 205

Gln Arg Arg Lys Ala His Gly Ile Val Pro Asp Met Lys Lys Leu
    210                 215                 220


<210> 2327
<211> 1653
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1630)
<223> RXA01602

<400> 2327
tgcaggccac atgcctccca gtgccgtctc tgcacgttga ttttcccctg ccacgactgg 60

tcgcagggcg actttctagc acttttaaag gaatttttta atg gct aaa acc cat   115
                                              Met Ala Lys Thr His
                                                1               5

att cgg tta cag gac ctt tcc ctg tca tac acc tca acc ccg tta att   163
Ile Arg Leu Gln Asp Leu Ser Leu Ser Tyr Thr Ser Thr Pro Leu Ile
                10                  15                  20

acg aag ctc aat atc act gtt tct tct gga cag tgc gca gtg att gtt   211
Thr Lys Leu Asn Ile Thr Val Ser Ser Gly Gln Cys Ala Val Ile Val
            25                  30                  35

ggt gag aat ggt cga ggt aaa acc aca ctt ctg cga gca ctg gct cga   259
Gly Glu Asn Gly Arg Gly Lys Thr Thr Leu Leu Arg Ala Leu Ala Arg
        40                  45                  50

gaa ttc ccg cca tct gca ggt gag att ctc act cat ggc acg gta gca   307
Glu Phe Pro Pro Ser Ala Gly Glu Ile Leu Thr His Gly Thr Val Ala
    55                  60                  65

att gct cat caa cac atg cct gca ggt gat ctg tcc gtc gga gag atc   355
Ile Ala His Gln His Met Pro Ala Gly Asp Leu Ser Val Gly Glu Ile
70                  75                  80                  85

tgt gat gag gca att cgt gat tca aag aat gct ctc gaa gag ctt gag   403
Cys Asp Glu Ala Ile Arg Asp Ser Lys Asn Ala Leu Glu Glu Leu Glu
                90                  95                  100

aga gct gga gct cta ctt gag aca aac act gcg cac gca ctt gat gga   451
Arg Ala Gly Ala Leu Leu Glu Thr Asn Thr Ala His Ala Leu Asp Gly
            105                 110                 115

tat caa caa gcc ctt gat gcc gct gaa gtg ctt gac gca tgg aac gct   499
Tyr Gln Gln Ala Leu Asp Ala Ala Glu Val Leu Asp Ala Trp Asn Ala
        120                 125                 130

gaa cat cga tta gaa aaa gct ctg cgc agc ttt ggc gcg atc acc gat   547
Glu His Arg Leu Glu Lys Ala Leu Arg Ser Phe Gly Ala Ile Thr Asp
    135                 140                 145
```

```
aga tcc cgt gca ctc agt gag cta tcg atc ggg caa agg tat cgg gta   595
Arg Ser Arg Ala Leu Ser Glu Leu Ser Ile Gly Gln Arg Tyr Arg Val
150                 155                 160                 165

cgg ctg gcc tgc ctc atc ggt ggc gat gct gat att ttg ctt ctc gat   643
Arg Leu Ala Cys Leu Ile Gly Gly Asp Ala Asp Ile Leu Leu Leu Asp
                170                 175                 180

gaa ccc acc aat cat ctt gac cgg ggc gcg ctt aac tat ctc acc gaa   691
Glu Pro Thr Asn His Leu Asp Arg Gly Ala Leu Asn Tyr Leu Thr Glu
            185                 190                 195

gcc ata acc tcc cac aaa ggt gtg gta ctt gtt gtt tct cat gat caa   739
Ala Ile Thr Ser His Lys Gly Val Val Leu Val Val Ser His Asp Gln
        200                 205                 210

gca ctg atc aaa gat gtc gcg gat ttc atc atc gat att gat tca acc   787
Ala Leu Ile Lys Asp Val Ala Asp Phe Ile Ile Asp Ile Asp Ser Thr
    215                 220                 225

cca gac ggc cta cca cgg atc tat cat gag ggt ttt gat tct tat cga   835
Pro Asp Gly Leu Pro Arg Ile Tyr His Glu Gly Phe Asp Ser Tyr Arg
230                 235                 240                 245

cgc caa agg agt gcg ctt ctt gaa act tgg agg cag gat tat gcc gct   883
Arg Gln Arg Ser Ala Leu Leu Glu Thr Trp Arg Gln Asp Tyr Ala Ala
                250                 255                 260

gca caa act gtg caa cag caa ttg cag gag gat cta gag cac gca cgc   931
Ala Gln Thr Val Gln Gln Gln Leu Gln Glu Asp Leu Glu His Ala Arg
            265                 270                 275

cag cgg gtg aat tct tcg tgg aaa cct cca aaa gga acg gga aaa cac   979
Gln Arg Val Asn Ser Ser Trp Lys Pro Pro Lys Gly Thr Gly Lys His
        280                 285                 290

act cgc gca tct cgg gct ccc gga gtg gtg cag gcc tta aag cga gca   1027
Thr Arg Ala Ser Arg Ala Pro Gly Val Val Gln Ala Leu Lys Arg Ala
    295                 300                 305

cag gat gcg ttg gat agc aaa gcg ttg gac gtt ccc ccg gct ccg gcc   1075
Gln Asp Ala Leu Asp Ser Lys Ala Leu Asp Val Pro Pro Ala Pro Ala
310                 315                 320                 325

cca ttg ctt ctg cct acc ttg aaa gtg cga cca gat aaa ccc atg gtg   1123
Pro Leu Leu Leu Pro Thr Leu Lys Val Arg Pro Asp Lys Pro Met Val
                330                 335                 340

gac ttt tcg gac ctt ttt gta ccc cac cgc ttg cgt ctg cca ggc tca   1171
Asp Phe Ser Asp Leu Phe Val Pro His Arg Leu Arg Leu Pro Gly Ser
            345                 350                 355

cat tca gtg gta tca ggt gac aaa ata gtg atc act ggt gac aac ggc   1219
His Ser Val Val Ser Gly Asp Lys Ile Val Ile Thr Gly Asp Asn Gly
        360                 365                 370

gct ggc aaa tca acg ctc atc gaa gtc ttg tct ggg gtt ttg act ccg   1267
Ala Gly Lys Ser Thr Leu Ile Glu Val Leu Ser Gly Val Leu Thr Pro
    375                 380                 385

gca agt ggt tcg gtt gca aac cat gcc cga act ggg gtt ctc ggc caa   1315
```

```
Ala Ser Gly Ser Val Ala Asn His Ala Arg Thr Gly Val Leu Gly Gln
390                 395                 400                 405

gaa tca ctt gtc ggc gag gtg cca tca ata gca cga gat cac gca gtt   1363
Glu Ser Leu Val Gly Glu Val Pro Ser Ile Ala Arg Asp His Ala Val
                410                 415                 420

aag tgg gga ctt tta agt gtt gag gag agc cga ttt gcc cta cag gaa   1411
Lys Trp Gly Leu Leu Ser Val Glu Glu Ser Arg Phe Ala Leu Gln Glu
            425                 430                 435

ttc tca att ggt caa cgc aga aga cta gat ttg gcc atg tcg tta gct   1459
Phe Ser Ile Gly Gln Arg Arg Arg Leu Asp Leu Ala Met Ser Leu Ala
        440                 445                 450

ggc aat cct gaa ctg ttg ctt ctc gat gaa cct tcg aac cat ctg tct   1507
Gly Asn Pro Glu Leu Leu Leu Leu Asp Glu Pro Ser Asn His Leu Ser
    455                 460                 465

atg cac ttg gtt tcc gca ctt aca gag tgg ctg gac acg acc gcg gct   1555
Met His Leu Val Ser Ala Leu Thr Glu Trp Leu Asp Thr Thr Ala Ala
470                 475                 480                 485

gca gtg atc atg gta acg cat gat cga cag cta ctc cgc gat acg gct   1603
Ala Val Ile Met Val Thr His Asp Arg Gln Leu Leu Arg Asp Thr Ala
                490                 495                 500

cat tgg agg cac atc gag ttg aaa tct taagaattcg caagggcttt         1650
His Trp Arg His Ile Glu Leu Lys Ser
            505                 510

cac                                                               1653
```

09/09/2004 09:09:09

<210> 2328
<211> 510
<212> PRT
<213> Corynebacterium glutamicum

<400> 2328

```
Met Ala Lys Thr His Ile Arg Leu Gln Asp Leu Ser Leu Ser Tyr Thr
  1               5                  10                  15

Ser Thr Pro Leu Ile Thr Lys Leu Asn Ile Thr Val Ser Ser Gly Gln
             20                  25                  30

Cys Ala Val Ile Val Gly Glu Asn Gly Arg Gly Lys Thr Thr Leu Leu
         35                  40                  45

Arg Ala Leu Ala Arg Glu Phe Pro Pro Ser Ala Gly Glu Ile Leu Thr
     50                  55                  60

His Gly Thr Val Ala Ile Ala His Gln His Met Pro Ala Gly Asp Leu
 65                  70                  75                  80

Ser Val Gly Glu Ile Cys Asp Glu Ala Ile Arg Asp Ser Lys Asn Ala
                 85                  90                  95

Leu Glu Glu Leu Glu Arg Ala Gly Ala Leu Leu Glu Thr Asn Thr Ala
            100                 105                 110
```

```
His Ala Leu Asp Gly Tyr Gln Gln Ala Leu Asp Ala Ala Glu Val Leu
        115                 120                 125

Asp Ala Trp Asn Ala Glu His Arg Leu Glu Lys Ala Leu Arg Ser Phe
    130                 135                 140

Gly Ala Ile Thr Asp Arg Ser Arg Ala Leu Ser Glu Leu Ser Ile Gly
145                 150                 155                 160

Gln Arg Tyr Arg Val Arg Leu Ala Cys Leu Ile Gly Gly Asp Ala Asp
                165                 170                 175

Ile Leu Leu Leu Asp Glu Pro Thr Asn His Leu Asp Arg Gly Ala Leu
            180                 185                 190

Asn Tyr Leu Thr Glu Ala Ile Thr Ser His Lys Gly Val Val Leu Val
        195                 200                 205

Val Ser His Asp Gln Ala Leu Ile Lys Asp Val Ala Asp Phe Ile Ile
    210                 215                 220

Asp Ile Asp Ser Thr Pro Asp Gly Leu Pro Arg Ile Tyr His Glu Gly
225                 230                 235                 240

Phe Asp Ser Tyr Arg Arg Gln Arg Ser Ala Leu Leu Glu Thr Trp Arg
                245                 250                 255

Gln Asp Tyr Ala Ala Ala Gln Thr Val Gln Gln Gln Leu Gln Glu Asp
            260                 265                 270

Leu Glu His Ala Arg Gln Arg Val Asn Ser Ser Trp Lys Pro Pro Lys
        275                 280                 285

Gly Thr Gly Lys His Thr Arg Ala Ser Arg Ala Pro Gly Val Val Gln
    290                 295                 300

Ala Leu Lys Arg Ala Gln Asp Ala Leu Asp Ser Lys Ala Leu Asp Val
305                 310                 315                 320

Pro Pro Ala Pro Ala Pro Leu Leu Leu Pro Thr Leu Lys Val Arg Pro
                325                 330                 335

Asp Lys Pro Met Val Asp Phe Ser Asp Leu Phe Val Pro His Arg Leu
            340                 345                 350

Arg Leu Pro Gly Ser His Ser Val Val Ser Gly Asp Lys Ile Val Ile
        355                 360                 365

Thr Gly Asp Asn Gly Ala Gly Lys Ser Thr Leu Ile Glu Val Leu Ser
    370                 375                 380

Gly Val Leu Thr Pro Ala Ser Gly Ser Val Ala Asn His Ala Arg Thr
385                 390                 395                 400

Gly Val Leu Gly Gln Glu Ser Leu Val Gly Glu Val Pro Ser Ile Ala
                405                 410                 415

Arg Asp His Ala Val Lys Trp Gly Leu Leu Ser Val Glu Glu Ser Arg
            420                 425                 430

Phe Ala Leu Gln Glu Phe Ser Ile Gly Gln Arg Arg Arg Leu Asp Leu
```

```
        435                 440                 445

Ala Met Ser Leu Ala Gly Asn Pro Glu Leu Leu Leu Asp Glu Pro
    450                 455                 460

Ser Asn His Leu Ser Met His Leu Val Ser Ala Leu Thr Glu Trp Leu
465                 470                 475                 480

Asp Thr Thr Ala Ala Ala Val Ile Met Val Thr His Asp Arg Gln Leu
                485                 490                 495

Leu Arg Asp Thr Ala His Trp Arg His Ile Glu Leu Lys Ser
            500                 505                 510


<210> 2329
<211> 1638
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1615)
<223> RXA01605

<400> 2329
agtcaagcgc cgaagaaagg cccgngaagg naatcagacg acgggcacct actacttcgg 60

cattgaaatt ccgaagaact tcagcgattc tattgccagc gtg acc agc gat tca   115
                                            Val Thr Ser Asp Ser
                                              1               5

ccc gcg cca gca acc gtc aac gcg gta ttc aac aac agc aac ggc ttc   163
Pro Ala Pro Ala Thr Val Asn Ala Val Phe Asn Asn Ser Asn Gly Phe
                10                  15                  20

att gcc tcc atg ctg ggc aac cag gtg gtc aac act gtt gtg gag acc   211
Ile Ala Ser Met Leu Gly Asn Gln Val Val Asn Thr Val Val Glu Thr
            25                  30                  35

atg gac acg gaa ttc ggc gtc cgc att gtg gat aac atg ctc gtc ggt   259
Met Asp Thr Glu Phe Gly Val Arg Ile Val Asp Asn Met Leu Val Gly
        40                  45                  50

ttc tcc acc ttg ggc gac ggc atg aac caa gcc gcc gaa ggt gcc act   307
Phe Ser Thr Leu Gly Asp Gly Met Asn Gln Ala Ala Glu Gly Ala Thr
    55                  60                  65

acg ctc agc gat ggc gtc ggt tcc gcc aac gac ggt gca gtt cag ctt   355
Thr Leu Ser Asp Gly Val Gly Ser Ala Asn Asp Gly Ala Val Gln Leu
70                  75                  80                  85

gcc gac ggc gcg gtc acc ctg cgc gac ggc atc gca agt gcc aat gag   403
Ala Asp Gly Ala Val Thr Leu Arg Asp Gly Ile Ala Ser Ala Asn Glu
                90                  95                  100

ggt gcg caa tcg ctt gcc gac ggc gcc agc cag ctc gac acc ggc ctc   451
Gly Ala Gln Ser Leu Ala Asp Gly Ala Ser Gln Leu Asp Thr Gly Leu
            105                 110                 115

ggc tcc gcg gct aca ggc agc caa acg ctc gcc gac ggt cta tcc agc   499
```

```
Gly Ser Ala Ala Thr Gly Ser Gln Thr Leu Ala Asp Gly Leu Ser Ser
        120                 125                 130

ctg tct gcg ggc acc gcc caa cta ggc caa ggc gca acc cag gtt tca   547
Leu Ser Ala Gly Thr Ala Gln Leu Gly Gln Gly Ala Thr Gln Val Ser
    135                 140                 145

gat ggc gtg ggc caa ctt gtc gac caa gta gca cca ctg acc gcc tat   595
Asp Gly Val Gly Gln Leu Val Asp Gln Val Ala Pro Leu Thr Ala Tyr
150                 155                 160                 165

gtt cca gac atc aac tct cag ttg atc acc ctg cgc gac ggc gca gcc   643
Val Pro Asp Ile Asn Ser Gln Leu Ile Thr Leu Arg Asp Gly Ala Ala
                170                 175                 180

acc att gcc tct gaa cta tct gat ccc tcc agc acc tac cgc tcc ggc   691
Thr Ile Ala Ser Glu Leu Ser Asp Pro Ser Ser Thr Tyr Arg Ser Gly
            185                 190                 195

gtg gac tcc gct gtg agc gca tcc cag caa cta gca gcc ggc ctg caa   739
Val Asp Ser Ala Val Ser Ala Ser Gln Gln Leu Ala Ala Gly Leu Gln
        200                 205                 210

acc ctg aaa gac gga tcc agc caa ctc agc atc ggt gca cgc acc ctc   787
Thr Leu Lys Asp Gly Ser Ser Gln Leu Ser Ile Gly Ala Arg Thr Leu
    215                 220                 225

gct gat ggc acc agc caa ttg gcc gca ggt tcc gaa cag cta gtt gtt   835
Ala Asp Gly Thr Ser Gln Leu Ala Ala Gly Ser Glu Gln Leu Val Val
230                 235                 240                 245

ggc gca caa gca ctg cgc gac ggc acc gtc cag ctt gat gaa ggc tcc   883
Gly Ala Gln Ala Leu Arg Asp Gly Thr Val Gln Leu Asp Glu Gly Ser
                250                 255                 260

agc gaa ctc gcc ctc aaa ctc acc gac ggc gca agc caa gta cca acc   931
Ser Glu Leu Ala Leu Lys Leu Thr Asp Gly Ala Ser Gln Val Pro Thr
            265                 270                 275

ttc gct gac ggc gca gac acc acc atc gca acc cca gtt gaa aca gaa   979
Phe Ala Asp Gly Ala Asp Thr Thr Ile Ala Thr Pro Val Glu Thr Glu
        280                 285                 290

caa gca gga gac acc aca ccg ctc ttc ggt att ggt ctc gca cca ttc   1027
Gln Ala Gly Asp Thr Thr Pro Leu Phe Gly Ile Gly Leu Ala Pro Phe
    295                 300                 305

ttc atg gct gtc ggc ctg ttc atg gga gca acc gtt gcc tgg atg atc   1075
Phe Met Ala Val Gly Leu Phe Met Gly Ala Thr Val Ala Trp Met Ile
310                 315                 320                 325

ctg cac cca atc agt cgc cgc gca ctc gac tcc cgc atg gga ggc ttc   1123
Leu His Pro Ile Ser Arg Arg Ala Leu Asp Ser Arg Met Gly Gly Phe
                330                 335                 340

cga ggc acc ctg gca agc tac ctt cca tca aca gtc tta ggc ctt ggc   1171
Arg Gly Thr Leu Ala Ser Tyr Leu Pro Ser Thr Val Leu Gly Leu Gly
            345                 350                 355

caa gca acc atc atg tgg gca gta ctg tac ttc ctg ctc gac ctc aat   1219
Gln Ala Thr Ile Met Trp Ala Val Leu Tyr Phe Leu Leu Asp Leu Asn
```

```
        360                 365                 370

cca gct cac cca gct gga ctg tgg atg gcg atg gtc gcc atc tca tgg   1267
Pro Ala His Pro Ala Gly Leu Trp Met Ala Met Val Ala Ile Ser Trp
    375                 380                 385

gta ttc atc tcc att acc cat atg ttc aac aac gtg gca gga ccc tcc   1315
Val Phe Ile Ser Ile Thr His Met Phe Asn Asn Val Ala Gly Pro Ser
390                 395                 400                 405

gca ggc cgt gtg ctg tcc atc gtg atg atg tcc ttc cag cta gtc tcc   1363
Ala Gly Arg Val Leu Ser Ile Val Met Met Ser Phe Gln Leu Val Ser
                410                 415                 420

tcc ggt ggc cta tac cca cca gaa acc cag cca gca ttc ttc cac tgg   1411
Ser Gly Gly Leu Tyr Pro Pro Glu Thr Gln Pro Ala Phe Phe His Trp
            425                 430                 435

ttc cac acc tac gac ccg atc acc tac gca gtc aac ctc gtg cgc caa   1459
Phe His Thr Tyr Asp Pro Ile Thr Tyr Ala Val Asn Leu Val Arg Gln
        440                 445                 450

atg atc ttc aac gaa acc cca tcc aac gac cca cgc ttc ata caa gca   1507
Met Ile Phe Asn Glu Thr Pro Ser Asn Asp Pro Arg Phe Ile Gln Ala
    455                 460                 465

atc tgg gta ctg ctc ttc atc tgg gca ctg atg ctc gcc atc tcc acc   1555
Ile Trp Val Leu Leu Phe Ile Trp Ala Leu Met Leu Ala Ile Ser Thr
470                 475                 480                 485

ctg gcg aat aga aca aac aag gtt ctt cgc atg aag gac tac cac cca   1603
Leu Ala Asn Arg Thr Asn Lys Val Leu Arg Met Lys Asp Tyr His Pro
                490                 495                 500

gaa ctg aag gtc taaaagcttt tcccgcccgg ttc                        1638
Glu Leu Lys Val
            505
```

<210> 2330
<211> 505
<212> PRT
<213> Corynebacterium glutamicum

<400> 2330

```
Val Thr Ser Asp Ser Pro Ala Pro Ala Thr Val Asn Ala Val Phe Asn
  1               5                  10                  15

Asn Ser Asn Gly Phe Ile Ala Ser Met Leu Gly Asn Gln Val Val Asn
             20                  25                  30

Thr Val Val Glu Thr Met Asp Thr Glu Phe Gly Val Arg Ile Val Asp
         35                  40                  45

Asn Met Leu Val Gly Phe Ser Thr Leu Gly Asp Gly Met Asn Gln Ala
     50                  55                  60

Ala Glu Gly Ala Thr Thr Leu Ser Asp Gly Val Gly Ser Ala Asn Asp
 65                  70                  75                  80

Gly Ala Val Gln Leu Ala Asp Gly Ala Val Thr Leu Arg Asp Gly Ile
```

```
                  85                  90                  95

Ala Ser Ala Asn Glu Gly Ala Gln Ser Leu Ala Asp Gly Ala Ser Gln
            100                 105                 110

Leu Asp Thr Gly Leu Gly Ser Ala Ala Thr Gly Ser Gln Thr Leu Ala
        115                 120                 125

Asp Gly Leu Ser Ser Leu Ser Ala Gly Thr Ala Gln Leu Gly Gln Gly
    130                 135                 140

Ala Thr Gln Val Ser Asp Gly Val Gly Gln Leu Val Asp Gln Val Ala
145                 150                 155                 160

Pro Leu Thr Ala Tyr Val Pro Asp Ile Asn Ser Gln Leu Ile Thr Leu
                165                 170                 175

Arg Asp Gly Ala Ala Thr Ile Ala Ser Glu Leu Ser Asp Pro Ser Ser
            180                 185                 190

Thr Tyr Arg Ser Gly Val Asp Ser Ala Val Ser Ala Ser Gln Gln Leu
        195                 200                 205

Ala Ala Gly Leu Gln Thr Leu Lys Asp Gly Ser Ser Gln Leu Ser Ile
    210                 215                 220

Gly Ala Arg Thr Leu Ala Asp Gly Thr Ser Gln Leu Ala Ala Gly Ser
225                 230                 235                 240

Glu Gln Leu Val Val Gly Ala Gln Ala Leu Arg Asp Gly Thr Val Gln
                245                 250                 255

Leu Asp Glu Gly Ser Ser Glu Leu Ala Leu Lys Leu Thr Asp Gly Ala
            260                 265                 270

Ser Gln Val Pro Thr Phe Ala Asp Gly Ala Asp Thr Thr Ile Ala Thr
        275                 280                 285

Pro Val Glu Thr Glu Gln Ala Gly Asp Thr Thr Pro Leu Phe Gly Ile
    290                 295                 300

Gly Leu Ala Pro Phe Phe Met Ala Val Gly Leu Phe Met Gly Ala Thr
305                 310                 315                 320

Val Ala Trp Met Ile Leu His Pro Ile Ser Arg Arg Ala Leu Asp Ser
                325                 330                 335

Arg Met Gly Gly Phe Arg Gly Thr Leu Ala Ser Tyr Leu Pro Ser Thr
            340                 345                 350

Val Leu Gly Leu Gly Gln Ala Thr Ile Met Trp Ala Val Leu Tyr Phe
        355                 360                 365

Leu Leu Asp Leu Asn Pro Ala His Pro Ala Gly Leu Trp Met Ala Met
    370                 375                 380

Val Ala Ile Ser Trp Val Phe Ile Ser Ile Thr His Met Phe Asn Asn
385                 390                 395                 400

Val Ala Gly Pro Ser Ala Gly Arg Val Leu Ser Ile Val Met Met Ser
                405                 410                 415
```

```
Phe Gln Leu Val Ser Ser Gly Gly Leu Tyr Pro Pro Glu Thr Gln Pro
            420                 425                 430

Ala Phe Phe His Trp Phe His Thr Tyr Asp Pro Ile Thr Tyr Ala Val
        435                 440                 445

Asn Leu Val Arg Gln Met Ile Phe Asn Glu Thr Pro Ser Asn Asp Pro
    450                 455                 460

Arg Phe Ile Gln Ala Ile Trp Val Leu Leu Phe Ile Trp Ala Leu Met
465                 470                 475                 480

Leu Ala Ile Ser Thr Leu Ala Asn Arg Thr Asn Lys Val Leu Arg Met
                485                 490                 495

Lys Asp Tyr His Pro Glu Leu Lys Val
            500                 505


<210> 2331
<211> 852
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(829)
<223> RXA01610

<400> 2331
cattaatcac atgtggttaa tgccttttt gattgcgtag actaggaagg tacgtcaact 60

tccatatctt tagtttgcga aagcgatcaa cttaaaacac gtg tcc ggt ttt ctt   115
                                            Val Ser Gly Phe Leu
                                              1               5

act ccc cca gct aca ccc cat att cgg acg gca act gcc agt att gct   163
Thr Pro Pro Ala Thr Pro His Ile Arg Thr Ala Thr Ala Ser Ile Ala
                  10                  15                  20

acc gca gtt gcc gta gca ctg tca gtg ttc gct gct gca ctc att cca   211
Thr Ala Val Ala Val Ala Leu Ser Val Phe Ala Ala Ala Leu Ile Pro
             25                  30                  35

gga agc gct ctg tat tct gtg ctg acc gct gga ggg gtg gca ctt gga   259
Gly Ser Ala Leu Tyr Ser Val Leu Thr Ala Gly Gly Val Ala Leu Gly
         40                  45                  50

gca gca tca ggc gtt gcc gcg tta cgc cat cgc gga ggg ctt cgc att   307
Ala Ala Ser Gly Val Ala Ala Leu Arg His Arg Gly Gly Leu Arg Ile
     55                  60                  65

ttt caa tgg ctg tct gcg ctt ggt gga atc gtc att ttg ctg atc ggt   355
Phe Gln Trp Leu Ser Ala Leu Gly Gly Ile Val Ile Leu Leu Ile Gly
 70                  75                  80                  85

atc gta gtg gca gtt gca aag ttt ggg gcc tcg gca aaa ctt gcc acg   403
Ile Val Val Ala Val Ala Lys Phe Gly Ala Ser Ala Lys Leu Ala Thr
                 90                  95                 100
```

```
tta ggc ctg gtg acc tcg tat tat ctc atg ccg tct gcg gca ttg gcc   451
Leu Gly Leu Val Thr Ser Tyr Tyr Leu Met Pro Ser Ala Ala Leu Ala
            105                 110                 115

tgt tat atc gga ggg ctt ggc cag cta cca gcc aaa tgg att gcg cca   499
Cys Tyr Ile Gly Gly Leu Gly Gln Leu Pro Ala Lys Trp Ile Ala Pro
        120                 125                 130

gcg ttt atg gct acg gct ggt gca ggt gct gcg gga tgg ttt tca ttg   547
Ala Phe Met Ala Thr Ala Gly Ala Gly Ala Ala Gly Trp Phe Ser Leu
    135                 140                 145

ggg gca ggc acc ggt ttt gaa cgg ttc ctc att gct gtt gca gcg gtg   595
Gly Ala Gly Thr Gly Phe Glu Arg Phe Leu Ile Ala Val Ala Ala Val
150                 155                 160                 165

ttt tca ctg atg gga tgt gta tac cca gtg tgg gga tgc gtc gta aag   643
Phe Ser Leu Met Gly Cys Val Tyr Pro Val Trp Gly Cys Val Val Lys
                170                 175                 180

cgt cca cgt caa gtg gct gca tgg ctg gtc gcg ctg gcg gcc ctg gtg   691
Arg Pro Arg Gln Val Ala Ala Trp Leu Val Ala Leu Ala Ala Leu Val
            185                 190                 195

ctt ggg gcg ctc atg ctt ttt atg gtg agc atg gtg gtg gcg ccg ggt   739
Leu Gly Ala Leu Met Leu Phe Met Val Ser Met Val Val Ala Pro Gly
        200                 205                 210

ttg ctg tgg ctg cag ccc acg acg gtc gca tgg ggt ttt atg att gcc   787
Leu Leu Trp Leu Gln Pro Thr Thr Val Ala Trp Gly Phe Met Ile Ala
    215                 220                 225

ggg gtt ctt gcg acg gtc gca ggc ttg tgg cct agg cgt ttt           829
Gly Val Leu Ala Thr Val Ala Gly Leu Trp Pro Arg Arg Phe
230                 235                 240

tagacggaat cgtctgggag ggt                                        852
```

US20030148461A1

<210> 2332
<211> 243
<212> PRT
<213> Corynebacterium glutamicum

<400> 2332

```
Val Ser Gly Phe Leu Thr Pro Pro Ala Thr Pro His Ile Arg Thr Ala
  1               5                  10                  15

Thr Ala Ser Ile Ala Thr Ala Val Ala Val Ala Leu Ser Val Phe Ala
             20                  25                  30

Ala Ala Leu Ile Pro Gly Ser Ala Leu Tyr Ser Val Leu Thr Ala Gly
         35                  40                  45

Gly Val Ala Leu Gly Ala Ala Ser Gly Val Ala Ala Leu Arg His Arg
     50                  55                  60

Gly Gly Leu Arg Ile Phe Gln Trp Leu Ser Ala Leu Gly Gly Ile Val
 65                  70                  75                  80

Ile Leu Leu Ile Gly Ile Val Val Ala Val Ala Lys Phe Gly Ala Ser
```

```
                 85                  90                  95

Ala Lys Leu Ala Thr Leu Gly Leu Val Thr Ser Tyr Tyr Leu Met Pro
            100                 105                 110

Ser Ala Ala Leu Ala Cys Tyr Ile Gly Gly Leu Gly Gln Leu Pro Ala
        115                 120                 125

Lys Trp Ile Ala Pro Ala Phe Met Ala Thr Ala Gly Ala Gly Ala Ala
    130                 135                 140

Gly Trp Phe Ser Leu Gly Ala Gly Thr Gly Phe Glu Arg Phe Leu Ile
145                 150                 155                 160

Ala Val Ala Ala Val Phe Ser Leu Met Gly Cys Val Tyr Pro Val Trp
                165                 170                 175

Gly Cys Val Val Lys Arg Pro Arg Gln Val Ala Ala Trp Leu Val Ala
            180                 185                 190

Leu Ala Ala Leu Val Leu Gly Ala Leu Met Leu Phe Met Val Ser Met
        195                 200                 205

Val Val Ala Pro Gly Leu Leu Trp Leu Gln Pro Thr Thr Val Ala Trp
    210                 215                 220

Gly Phe Met Ile Ala Gly Val Leu Ala Thr Val Ala Gly Leu Trp Pro
225                 230                 235                 240

Arg Arg Phe
```

<210> 2333
<211> 480
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(457)
<223> RXA01611

<400> 2333

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cccgcttaca actacttggt ttacaccggt gttatcaagg gctaaatcgc ctaacctcta 60

tcttcatcta tagcttagct ttactgaaag gcttttcatc atg cgt aaa ttc cgc   115
                                            Met Arg Lys Phe Arg
                                              1               5

aac act gca att gca cta gtt tct gca gct gca atc acc ttg ggt ggc   163
Asn Thr Ala Ile Ala Leu Val Ser Ala Ala Ala Ile Thr Leu Gly Gly
                 10                  15                  20

gtt acc gct gct acc gct cag gaa gac gaa act cct cct gca gca gag   211
Val Thr Ala Ala Thr Ala Gln Glu Asp Glu Thr Pro Pro Ala Ala Glu
             25                  30                  35

acc gag acc act tct cct tcc ggt tcc tca ggc tct tcc tgg aac gac   259
Thr Glu Thr Thr Ser Pro Ser Gly Ser Ser Gly Ser Ser Trp Asn Asp
         40                  45                  50
```

```
tac aac gaa gag tac gaa ggc gac caa gag ggc tac gga atc gac ggc   307
Tyr Asn Glu Glu Tyr Glu Gly Asp Gln Glu Gly Tyr Gly Ile Asp Gly
     55                  60                  65

ttt ggt tct tcc cgc gat gac tcc gga gaa gaa gtt cca cgt tgg ttg   355
Phe Gly Ser Ser Arg Asp Asp Ser Gly Glu Glu Val Pro Arg Trp Leu
 70                  75                  80                  85

gag acc tgg ggc aag gta ttt gac gct ttg acc att acc tcc gtt ctt   403
Glu Thr Trp Gly Lys Val Phe Asp Ala Leu Thr Ile Thr Ser Val Leu
                 90                  95                 100

ggt ctt gtt gtc ttc cct gtt gtt aac ttc ctg aag tac aac ggc ctc   451
Gly Leu Val Val Phe Pro Val Val Asn Phe Leu Lys Tyr Asn Gly Leu
            105                 110                 115

att aag taatctgcaa tttcctgtca aat                                480
Ile Lys
```

<210> 2334
<211> 119
<212> PRT
<213> Corynebacterium glutamicum

<400> 2334

```
Met Arg Lys Phe Arg Asn Thr Ala Ile Ala Leu Val Ser Ala Ala Ala
  1               5                  10                  15

Ile Thr Leu Gly Gly Val Thr Ala Ala Thr Ala Gln Glu Asp Glu Thr
             20                  25                  30

Pro Pro Ala Ala Glu Thr Glu Thr Thr Ser Pro Ser Gly Ser Ser Gly
         35                  40                  45

Ser Ser Trp Asn Asp Tyr Asn Glu Glu Tyr Glu Gly Asp Gln Glu Gly
     50                  55                  60

Tyr Gly Ile Asp Gly Phe Gly Ser Ser Arg Asp Asp Ser Gly Glu Glu
 65                  70                  75                  80

Val Pro Arg Trp Leu Glu Thr Trp Gly Lys Val Phe Asp Ala Leu Thr
                 85                  90                  95

Ile Thr Ser Val Leu Gly Leu Val Val Phe Pro Val Val Asn Phe Leu
            100                 105                 110

Lys Tyr Asn Gly Leu Ile Lys
        115
```

<210> 2335
<211> 468
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(445)

<223> RXA01612

<400> 2335
gaaaaaacga cgttggttcg tagtcgctgg aaatttaata attcctccgt ccccttcaac 60

```
tagggggtgg aaacccgact atttccgaag gactattctc atg cgt tct ttc cgt   115
                                            Met Arg Ser Phe Arg
                                              1               5

acc gcg gca gtt gca ggc ctt act gca gtt gca ctt tcc gta ggt tcc   163
Thr Ala Ala Val Ala Gly Leu Thr Ala Val Ala Leu Ser Val Gly Ser
                  10                  15                  20

gcc acc gtg gca act gcg gaa gaa tct gat caa aac ctc tca tcc ggc   211
Ala Thr Val Ala Thr Ala Glu Glu Ser Asp Gln Asn Leu Ser Ser Gly
              25                  30                  35

ttc tca gca ctt tct tcc ggt ggc gca gcg gcc gta ggt gag gac tgg   259
Phe Ser Ala Leu Ser Ser Gly Gly Ala Ala Ala Val Gly Glu Asp Trp
          40                  45                  50

gat gca gac cag ccc gtc aca ggt gaa gac atc ttt ggt gaa gag cac   307
Asp Ala Asp Gln Pro Val Thr Gly Glu Asp Ile Phe Gly Glu Glu His
      55                  60                  65

gag cgc gat aac gaa aac acc cca gcg tgg gct aag aac atg tac gat   355
Glu Arg Asp Asn Glu Asn Thr Pro Ala Trp Ala Lys Asn Met Tyr Asp
  70                  75                  80                  85

cta acc gtc ttg ggt ggc att gct tcc ctt ctc ggt gtc atc gta ttc   403
Leu Thr Val Leu Gly Gly Ile Ala Ser Leu Leu Gly Val Ile Val Phe
                  90                  95                 100

ccc gct tac aac tac ttg gtt tac acc ggt gtt atc aag ggc           445
Pro Ala Tyr Asn Tyr Leu Val Tyr Thr Gly Val Ile Lys Gly
              105                 110                 115

taaatcgcct aacctctatc ttc                                        468
```

<210> 2336
<211> 115
<212> PRT
<213> Corynebacterium glutamicum

<400> 2336

```
Met Arg Ser Phe Arg Thr Ala Ala Val Ala Gly Leu Thr Ala Val Ala
  1               5                  10                  15

Leu Ser Val Gly Ser Ala Thr Val Ala Thr Ala Glu Glu Ser Asp Gln
              20                  25                  30

Asn Leu Ser Ser Gly Phe Ser Ala Leu Ser Ser Gly Gly Ala Ala Ala
          35                  40                  45

Val Gly Glu Asp Trp Asp Ala Asp Gln Pro Val Thr Gly Glu Asp Ile
      50                  55                  60

Phe Gly Glu Glu His Glu Arg Asp Asn Glu Asn Thr Pro Ala Trp Ala
  65                  70                  75                  80
```

```
Lys Asn Met Tyr Asp Leu Thr Val Leu Gly Gly Ile Ala Ser Leu Leu
                 85                  90                  95

Gly Val Ile Val Phe Pro Ala Tyr Asn Tyr Leu Val Tyr Thr Gly Val
            100                 105                 110

Ile Lys Gly
        115
```

<210> 2337
<211> 1098
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1075)
<223> RXA01619

<400> 2337

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cctgcaagtt tactgctcgg ccgtcacggg ggaatggaaa aagtacgctt ggtgttcata 60

tagcgaaccc attttctatt gcgatgagag gaacaccacc atg cgc gca atc act   115
                                            Met Arg Ala Ile Thr
                                              1               5

cac aac act ttc ggc gac ccc gcc gac gtc cta cag att acc gag aag   163
His Asn Thr Phe Gly Asp Pro Ala Asp Val Leu Gln Ile Thr Glu Lys
                 10                  15                  20

gaa att ccc act ccc ggc cca ggt cag gtt cgt att caa gtg acg ctg   211
Glu Ile Pro Thr Pro Gly Pro Gly Gln Val Arg Ile Gln Val Thr Leu
            25                  30                  35

gca acc atc cac aac cat gat ttg tgg acc gtg aag ggc tct tac ggc   259
Ala Thr Ile His Asn His Asp Leu Trp Thr Val Lys Gly Ser Tyr Gly
        40                  45                  50

ttc gtc cca gat ctg ccg gcc gcc gca ggc acc gag gca gtc ggc atc   307
Phe Val Pro Asp Leu Pro Ala Ala Ala Gly Thr Glu Ala Val Gly Ile
    55                  60                  65

gtc gac gcc ctg ggc gag ggc gtc gaa ggt ttg cag gtc ggt cag cgt   355
Val Asp Ala Leu Gly Glu Gly Val Glu Gly Leu Gln Val Gly Gln Arg
70                  75                  80                  85

gtt gcg tcc ggc acc agc ttt ggc atc tgg gcg gag tac gcg ctt gtc   403
Val Ala Ser Gly Thr Ser Phe Gly Ile Trp Ala Glu Tyr Ala Leu Val
                90                  95                 100

gac gcc tcc ggc ctc att ccc gta cca gaa cag ctc tcc gac gaa agc   451
Asp Ala Ser Gly Leu Ile Pro Val Pro Glu Gln Leu Ser Asp Glu Ser
            105                 110                 115

gca gct cag ctc gtc gca atg cct ttc agc gcc atc agc ctt ctt gat   499
Ala Ala Gln Leu Val Ala Met Pro Phe Ser Ala Ile Ser Leu Leu Asp
        120                 125                 130

ttc ctg gat atg aaa cca ggg gag tgg ctg atc caa aac tcc gca aac   547
Phe Leu Asp Met Lys Pro Gly Glu Trp Leu Ile Gln Asn Ser Ala Asn
```

```
    135                 140                 145

ggt gcc gtc ggc cgc atg ctc gca cag ctg gca gaa tcc cgc ggc atc   595
Gly Ala Val Gly Arg Met Leu Ala Gln Leu Ala Glu Ser Arg Gly Ile
150                 155                 160                 165

cat gtc gtt ggt ctc gtc cgc cgt gac gcc ggt gtc caa gaa ctc gct   643
His Val Val Gly Leu Val Arg Arg Asp Ala Gly Val Gln Glu Leu Ala
                170                 175                 180

gct caa aac atc agc ggc gtc gtt tcc act gag acc cca ggc tgg gaa   691
Ala Gln Asn Ile Ser Gly Val Val Ser Thr Glu Thr Pro Gly Trp Glu
            185                 190                 195

aag cag gtc gaa gac atc acc ggt ggc gca agc atc gcc gtc gca ctt   739
Lys Gln Val Glu Asp Ile Thr Gly Gly Ala Ser Ile Ala Val Ala Leu
        200                 205                 210

gat tcc gtc ggt gga tcc tcc gca gct gac ctg gtg aaa ctg ctt ggc   787
Asp Ser Val Gly Gly Ser Ser Ala Ala Asp Leu Val Lys Leu Leu Gly
    215                 220                 225

gaa ggc ggc acc ctc gtc tcc ttc ggc gcc atg ggc aac cca atc atg   835
Glu Gly Gly Thr Leu Val Ser Phe Gly Ala Met Gly Asn Pro Ile Met
230                 235                 240                 245

gaa atc cca tcc ggc ccc gtc atc ttc aag cac atc acc gtc aag ggc   883
Glu Ile Pro Ser Gly Pro Val Ile Phe Lys His Ile Thr Val Lys Gly
                250                 255                 260

ttc tgg gga agc aaa gtc agc cgc gaa atg cca gca gag aag aaa acc   931
Phe Trp Gly Ser Lys Val Ser Arg Glu Met Pro Ala Glu Lys Lys Thr
            265                 270                 275

cag ttg ttc ggc gag ctc att gcg cgc ata ctt gat gga aca ttg acc   979
Gln Leu Phe Gly Glu Leu Ile Ala Arg Ile Leu Asp Gly Thr Leu Thr
        280                 285                 290

ctt cca gtt gat tcc acc ttt gat gcc gct gac atc gtc tcg gcc gtg   1027
Leu Pro Val Asp Ser Thr Phe Asp Ala Ala Asp Ile Val Ser Ala Val
    295                 300                 305

cgc gcc tcc agc gag cct ggc cgt gcc gga aaa gtg ctc att cgt ttc   1075
Arg Ala Ser Ser Glu Pro Gly Arg Ala Gly Lys Val Leu Ile Arg Phe
310                 315                 320                 325

taaacgttta aggcccatta gac                                        1098


<210> 2338
<211> 325
<212> PRT
<213> Corynebacterium glutamicum

<400> 2338
Met Arg Ala Ile Thr His Asn Thr Phe Gly Asp Pro Ala Asp Val Leu
  1               5                  10                  15

Gln Ile Thr Glu Lys Glu Ile Pro Thr Pro Gly Pro Gly Gln Val Arg
             20                  25                  30
```

```
Ile Gln Val Thr Leu Ala Thr Ile His Asn His Asp Leu Trp Thr Val
         35                  40                  45

Lys Gly Ser Tyr Gly Phe Val Pro Asp Leu Pro Ala Ala Ala Gly Thr
     50                  55                  60

Glu Ala Val Gly Ile Val Asp Ala Leu Gly Glu Gly Val Glu Gly Leu
 65                  70                  75                  80

Gln Val Gly Gln Arg Val Ala Ser Gly Thr Ser Phe Gly Ile Trp Ala
                 85                  90                  95

Glu Tyr Ala Leu Val Asp Ala Ser Gly Leu Ile Pro Val Pro Glu Gln
            100                 105                 110

Leu Ser Asp Glu Ser Ala Ala Gln Leu Val Ala Met Pro Phe Ser Ala
        115                 120                 125

Ile Ser Leu Leu Asp Phe Leu Asp Met Lys Pro Gly Glu Trp Leu Ile
    130                 135                 140

Gln Asn Ser Ala Asn Gly Ala Val Gly Arg Met Leu Ala Gln Leu Ala
145                 150                 155                 160

Glu Ser Arg Gly Ile His Val Val Gly Leu Val Arg Arg Asp Ala Gly
                165                 170                 175

Val Gln Glu Leu Ala Ala Gln Asn Ile Ser Gly Val Val Ser Thr Glu
            180                 185                 190

Thr Pro Gly Trp Glu Lys Gln Val Glu Asp Ile Thr Gly Gly Ala Ser
        195                 200                 205

Ile Ala Val Ala Leu Asp Ser Val Gly Gly Ser Ser Ala Ala Asp Leu
    210                 215                 220

Val Lys Leu Leu Gly Glu Gly Gly Thr Leu Val Ser Phe Gly Ala Met
225                 230                 235                 240

Gly Asn Pro Ile Met Glu Ile Pro Ser Gly Pro Val Ile Phe Lys His
                245                 250                 255

Ile Thr Val Lys Gly Phe Trp Gly Ser Lys Val Ser Arg Glu Met Pro
            260                 265                 270

Ala Glu Lys Lys Thr Gln Leu Phe Gly Glu Leu Ile Ala Arg Ile Leu
        275                 280                 285

Asp Gly Thr Leu Thr Leu Pro Val Asp Ser Thr Phe Asp Ala Ala Asp
    290                 295                 300

Ile Val Ser Ala Val Arg Ala Ser Ser Glu Pro Gly Arg Ala Gly Lys
305                 310                 315                 320

Val Leu Ile Arg Phe
                325
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<210> 2339
<211> 726
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> RXA01622

<400> 2339
aaggcgtggg cgtttttgaa ggagcttcgt ttggagcgcg gtcctttgga tcgtgaagtt 60

gccatcgcag agctgaagag ctggtgggaa ggagaaaaca atg agt gat ttt tat 115
Met Ser Asp Phe Tyr
1 5

gcc gac agg ttg ttt aac gcg atg gag cgc aat gag gta gct cca ggc 163
Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn Glu Val Ala Pro Gly
10 15 20

atg ttg ttg gtg gct gcg ccc gat atg gcg tcg gag gat ttt gag cgc 211
Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser Glu Asp Phe Glu Arg
25 30 35

agc atc gtg ttg atc atc gag cat tct cct gcc acc act ttt ggt gtg 259
Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala Thr Thr Phe Gly Val
40 45 50

aac att tct tca cgt tcc gat gtt gct gtg gcc aat gtg ttg ccc gag 307
Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala Asn Val Leu Pro Glu
55 60 65

tgg gtg gac ctc acc tcg aag cca cag gca ctg tac atc ggt ggg ccg 355
Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu Tyr Ile Gly Gly Pro
70 75 80 85

ttg agc cag cag gct gtg gtt ggt ttg ggc gtg acc aag ccg ggc gtg 403
Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val Thr Lys Pro Gly Val
90 95 100

gat att gaa aat tcc acc agc ttc aac aag ctc gcc aac cgc ctg gtg 451
Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu Ala Asn Arg Leu Val
105 110 115

cac gtg gat ctg cgt tct gca cct gaa gat gtg gct gat gat ctt gag 499
His Val Asp Leu Arg Ser Ala Pro Glu Asp Val Ala Asp Asp Leu Glu
120 125 130

ggc atg cgc ttt ttt gcg ggc tac gcg gag tgg gct ccg ggc cag ctc 547
Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp Ala Pro Gly Gln Leu
135 140 145

aac gag gaa att gag cag ggt gat tgg ttc gtc aca cct gcg ttg ccg 595
Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val Thr Pro Ala Leu Pro
150 155 160 165

tcg gac att atc gcg ccg ggc cgc gtc gat att tgg ggc gac gtg atg 643
Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile Trp Gly Asp Val Met
170 175 180

cgt cga caa gca atg cct ttg ccg ttg tat tcc acg ttt ccg tcg gac 691
Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser Thr Phe Pro Ser Asp
185 190 195

cct tca gat aat tagatgagtt ccgaaaattt aaa 726
Pro Ser Asp Asn
200

<210> 2340
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 2340
Met Ser Asp Phe Tyr Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn
1 5 10 15

Glu Val Ala Pro Gly Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser
20 25 30

Glu Asp Phe Glu Arg Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala
35 40 45

Thr Thr Phe Gly Val Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala
50 55 60

Asn Val Leu Pro Glu Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu
65 70 75 80

Tyr Ile Gly Gly Pro Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val
85 90 95

Thr Lys Pro Gly Val Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu
100 105 110

Ala Asn Arg Leu Val His Val Asp Leu Arg Ser Ala Pro Glu Asp Val
115 120 125

Ala Asp Asp Leu Glu Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp
130 135 140

Ala Pro Gly Gln Leu Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val
145 150 155 160

Thr Pro Ala Leu Pro Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile
165 170 175

Trp Gly Asp Val Met Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser
180 185 190

Thr Phe Pro Ser Asp Pro Ser Asp Asn
195 200

<210> 2341
<211> 834
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(811)
<223> RXA01623

<400> 2341
cgcgccgggc cgcgtcgata tttggggcga cgtgatgcgt cgacaagcaa tgcctttgcc 60

gttgtattcc acgtttccgt cggacccttc agataattag atg agt tcc gaa aat 115
Met Ser Ser Glu Asn
1 5

tta aaa gaa att cgc ggc gga atc ggt gag act tta acg gtc ggt ttg 163
Leu Lys Glu Ile Arg Gly Gly Ile Gly Glu Thr Leu Thr Val Gly Leu
10 15 20

ggg ctg att ccg ctg ggt ttg gcc ttt ggg ctg ttg atg gtc cag aca 211
Gly Leu Ile Pro Leu Gly Leu Ala Phe Gly Leu Leu Met Val Gln Thr
25 30 35

ggt ttc gcc tgg tgg tgg acg ccg att ttc tcc ttc gtg atc tat gcc 259
Gly Phe Ala Trp Trp Trp Thr Pro Ile Phe Ser Phe Val Ile Tyr Ala
40 45 50

ggt tcg atg gaa ttt ctg gca atc ggc atg gtc acc gca ggt atc ggc 307
Gly Ser Met Glu Phe Leu Ala Ile Gly Met Val Thr Ala Gly Ile Gly
55 60 65

ccg ttt tcg gcg gcg gtc gct ggt ttc atg gtg aat ttc cgc cac att 355
Pro Phe Ser Ala Ala Val Ala Gly Phe Met Val Asn Phe Arg His Ile
70 75 80 85

ttc tac ggt ctc acc ttc cca cgc cac cgc atc aag tcc ggc gcc ggc 403
Phe Tyr Gly Leu Thr Phe Pro Arg His Arg Ile Lys Ser Gly Ala Gly
90 95 100

cgc gcc tat tcc acc tac gcg ctt acc gac gag tcc tac gcc atc gtg 451
Arg Ala Tyr Ser Thr Tyr Ala Leu Thr Asp Glu Ser Tyr Ala Ile Val
105 110 115

tca gcc cgc cca cct ggc gat atc agt ggc acg cgg gtg ctt acc gtt 499
Ser Ala Arg Pro Pro Gly Asp Ile Ser Gly Thr Arg Val Leu Thr Val
120 125 130

caa att ttg tgc caa gct ctg tgg gtt atc cca gga att att ggc gcc 547
Gln Ile Leu Cys Gln Ala Leu Trp Val Ile Pro Gly Ile Ile Gly Ala
135 140 145

ttg gtt ggt caa gtg ctg ccc gat gat cta aaa ggc atg gat ttt gcc 595
Leu Val Gly Gln Val Leu Pro Asp Asp Leu Lys Gly Met Asp Phe Ala
150 155 160 165

ctg acc gcg ctg ttt gtg gtg ctg gcg tgg gag gca ttc aaa aat aac 643
Leu Thr Ala Leu Phe Val Val Leu Ala Trp Glu Ala Phe Lys Asn Asn
170 175 180

aag gat tat tcg ctg cca tta ttc gcg gtg gta ttg gct ctg gtt tcc 691
Lys Asp Tyr Ser Leu Pro Leu Phe Ala Val Val Leu Ala Leu Val Ser
185 190 195

ggt ttt gtg gcg ccc gag cag atg ctg gtt atc gct ttg acc acg tac 739
Gly Phe Val Ala Pro Glu Gln Met Leu Val Ile Ala Leu Thr Thr Tyr
200 205 210

ttt ttg atc ctt ctt ctc cgc gtc cgc ttc ccc aac ctg gac aag aaa 787

```
Phe Leu Ile Leu Leu Leu Arg Val Arg Phe Pro Asn Leu Asp Lys Lys
    215                 220                 225

ctg gag atc agg act tcc cat gag tgagtttggc ctgccagaag gcg        834
Leu Glu Ile Arg Thr Ser His Glu
230                 235


<210> 2342
<211> 237
<212> PRT
<213> Corynebacterium glutamicum

<400> 2342
Met Ser Ser Glu Asn Leu Lys Glu Ile Arg Gly Gly Ile Gly Glu Thr
  1               5                  10                  15

Leu Thr Val Gly Leu Gly Leu Ile Pro Leu Gly Leu Ala Phe Gly Leu
             20                  25                  30

Leu Met Val Gln Thr Gly Phe Ala Trp Trp Trp Thr Pro Ile Phe Ser
         35                  40                  45

Phe Val Ile Tyr Ala Gly Ser Met Glu Phe Leu Ala Ile Gly Met Val
     50                  55                  60

Thr Ala Gly Ile Gly Pro Phe Ser Ala Ala Val Ala Gly Phe Met Val
 65                  70                  75                  80

Asn Phe Arg His Ile Phe Tyr Gly Leu Thr Phe Pro Arg His Arg Ile
                 85                  90                  95

Lys Ser Gly Ala Gly Arg Ala Tyr Ser Thr Tyr Ala Leu Thr Asp Glu
            100                 105                 110

Ser Tyr Ala Ile Val Ser Ala Arg Pro Pro Gly Asp Ile Ser Gly Thr
        115                 120                 125

Arg Val Leu Thr Val Gln Ile Leu Cys Gln Ala Leu Trp Val Ile Pro
    130                 135                 140

Gly Ile Ile Gly Ala Leu Val Gly Gln Val Leu Pro Asp Asp Leu Lys
145                 150                 155                 160

Gly Met Asp Phe Ala Leu Thr Ala Leu Phe Val Val Leu Ala Trp Glu
                165                 170                 175

Ala Phe Lys Asn Asn Lys Asp Tyr Ser Leu Pro Leu Phe Ala Val Val
            180                 185                 190

Leu Ala Leu Val Ser Gly Phe Val Ala Pro Glu Gln Met Leu Val Ile
        195                 200                 205

Ala Leu Thr Thr Tyr Phe Leu Ile Leu Leu Leu Arg Val Arg Phe Pro
    210                 215                 220

Asn Leu Asp Lys Lys Leu Glu Ile Arg Thr Ser His Glu
225                 230                 235


<210> 2343
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<211> 468
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(445)
<223> RXA01624

<400> 2343
gagcagatgc tggttatcgc tttgaccacg tacttttga tccttcttct ccgcgtccgc 60

ttccccaacc tggacaagaa actggagatc aggacttccc atg agt gag ttt ggc 115
Met Ser Glu Phe Gly
1 5

ctg cca gaa ggc gtc acg ctg ctc aac gtc gcc gcc gtg ttg atc ccc 163
Leu Pro Glu Gly Val Thr Leu Leu Asn Val Ala Ala Val Leu Ile Pro
10 15 20

atc gcg atc atc acc ttg ctg ctg cgc atc ttc ccc ttc gcc gcg atg 211
Ile Ala Ile Ile Thr Leu Leu Leu Arg Ile Phe Pro Phe Ala Ala Met
25 30 35

aaa cgc gtc aac agc aac caa ctc atg gga gtt ttg ggg cgc aca atg 259
Lys Arg Val Asn Ser Asn Gln Leu Met Gly Val Leu Gly Arg Thr Met
40 45 50

cca gtc gga gtg atg gtc gta ttg gtc att tac acg ctc ttt ggc cag 307
Pro Val Gly Val Met Val Val Leu Val Ile Tyr Thr Leu Phe Gly Gln
55 60 65

gtc agt gcg cca ggt ggt gtg ggt gct tca ctg atc gcg gtg gca ttc 355
Val Ser Ala Pro Gly Gly Val Gly Ala Ser Leu Ile Ala Val Ala Phe
70 75 80 85

acc gcg ctg ctg cac tgg ttg aaa ggc tcc gcc ggg ctg tcc atc gtc 403
Thr Ala Leu Leu His Trp Leu Lys Gly Ser Ala Gly Leu Ser Ile Val
90 95 100

ggt ggc acc ttg gcc tac atg ttt ctg gtc aac gtc gtt ttt 445
Gly Gly Thr Leu Ala Tyr Met Phe Leu Val Asn Val Val Phe
105 110 115

taaaagatgc ttctcgacgc aaa 468

<210> 2344
<211> 115
<212> PRT
<213> Corynebacterium glutamicum

<400> 2344
Met Ser Glu Phe Gly Leu Pro Glu Gly Val Thr Leu Leu Asn Val Ala
1 5 10 15

Ala Val Leu Ile Pro Ile Ala Ile Ile Thr Leu Leu Leu Arg Ile Phe
20 25 30

Pro Phe Ala Ala Met Lys Arg Val Asn Ser Asn Gln Leu Met Gly Val
35 40 45

```
Leu Gly Arg Thr Met Pro Val Gly Val Met Val Val Leu Val Ile Tyr
     50                  55                  60

Thr Leu Phe Gly Gln Val Ser Ala Pro Gly Gly Val Gly Ala Ser Leu
 65                  70                  75                  80

Ile Ala Val Ala Phe Thr Ala Leu Leu His Trp Leu Lys Gly Ser Ala
                 85                  90                  95

Gly Leu Ser Ile Val Gly Gly Thr Leu Ala Tyr Met Phe Leu Val Asn
            100                 105                 110

Val Val Phe
        115


<210> 2345
<211> 1137
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1114)
<223> RXA01628

<400> 2345
cttccccttt cagcccgttg aagaaccaat gagccctgcc cgcacccagc cccgagcggc 60

tttcctaagg aagctccgac ccatcacatg tagcctttcc ttg gtt ctc gta ggg   115
                                          Leu Val Leu Val Gly
                                            1               5

tgc agc aac acg gca gag tcc acg acc acc gat acg gca ggc tcc act   163
Cys Ser Asn Thr Ala Glu Ser Thr Thr Thr Asp Thr Ala Gly Ser Thr
                 10                  15                  20

gaa act tca tca cag att tca ccc acc act cca gtc agc acc acc gaa   211
Glu Thr Ser Ser Gln Ile Ser Pro Thr Thr Pro Val Ser Thr Thr Glu
             25                  30                  35

gca gcg ccg cct gaa gat cca agc gca aac gct ttg gaa gag tat gct   259
Ala Ala Pro Pro Glu Asp Pro Ser Ala Asn Ala Leu Glu Glu Tyr Ala
         40                  45                  50

cag atc ctt gcc aat cca agc atc tac ccc tta acc gaa att tca caa   307
Gln Ile Leu Ala Asn Pro Ser Ile Tyr Pro Leu Thr Glu Ile Ser Gln
     55                  60                  65

ttc gtc ccc aca ggc aca tat gcc tac aca ctt gtt gaa gca act tcc   355
Phe Val Pro Thr Gly Thr Tyr Ala Tyr Thr Leu Val Glu Ala Thr Ser
 70                  75                  80                  85

gat tcc atc cca gaa cta cta ctc cgc gcc gat agt cac gaa ttc gcg   403
Asp Ser Ile Pro Glu Leu Leu Leu Arg Ala Asp Ser His Glu Phe Ala
                 90                  95                 100

cca att ttg gtt ttc acc tat gac gaa aac aca caa tcc gca acc caa   451
Pro Ile Leu Val Phe Thr Tyr Asp Glu Asn Thr Gln Ser Ala Thr Gln
            105                 110                 115
```

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gct gga gga gtc cta att gac ggt gtc gcc agc gcc ggc ggt tca cga   499
Ala Gly Gly Val Leu Ile Asp Gly Val Ala Ser Ala Gly Gly Ser Arg
        120                 125                 130

gtc aag gtc aga gct tca aat tca gga gca gga atc tac caa ttg aat   547
Val Lys Val Arg Ala Ser Asn Ser Gly Ala Gly Ile Tyr Gln Leu Asn
    135                 140                 145

tgg tac tcg ata caa cca gtt ggc gaa agc tct ttg tac gga atc caa   595
Trp Tyr Ser Ile Gln Pro Val Gly Glu Ser Ser Leu Tyr Gly Ile Gln
150                 155                 160                 165

gga aac tcc ctg aca caa atc gca gac ccc gag gat ttc atg gtc cgt   643
Gly Asn Ser Leu Thr Gln Ile Ala Asp Pro Glu Asp Phe Met Val Arg
                170                 175                 180

gaa cta tta cct gac cac cac gaa att acc tgg gtt gat tcc aac gac   691
Glu Leu Leu Pro Asp His His Glu Ile Thr Trp Val Asp Ser Asn Asp
            185                 190                 195

ccc tcc ggc cta tca acc gtt cag act ggt gga gcc aac att caa caa   739
Pro Ser Gly Leu Ser Thr Val Gln Thr Gly Gly Ala Asn Ile Gln Gln
        200                 205                 210

gca gcc cca act ccc gtt caa cag cct gcg tca aac ctg cac tac ttc   787
Ala Ala Pro Thr Pro Val Gln Gln Pro Ala Ser Asn Leu His Tyr Phe
    215                 220                 225

tct ggt gta gta acg atg cag acc gcc ggc gaa ctc atg cga ggt gaa   835
Ser Gly Val Val Thr Met Gln Thr Ala Gly Glu Leu Met Arg Gly Glu
230                 235                 240                 245

cga act ccc aat ggt gag cct gcc act gat ctc tat ctc gta ctg gtc   883
Arg Thr Pro Asn Gly Glu Pro Ala Thr Asp Leu Tyr Leu Val Leu Val
                250                 255                 260

ctt gat tcc cca att gaa atc aca gca cga aac gca gct aca gac cct   931
Leu Asp Ser Pro Ile Glu Ile Thr Ala Arg Asn Ala Ala Thr Asp Pro
            265                 270                 275

cag act cgt acc att tcc gaa gtc agc ctc ggc cga tac atc ccc gct   979
Gln Thr Arg Thr Ile Ser Glu Val Ser Leu Gly Arg Tyr Ile Pro Ala
        280                 285                 290

gat ggt gac aat gat tgg ata ggc tac ctc gac acc cac gtg gaa atc   1027
Asp Gly Asp Asn Asp Trp Ile Gly Tyr Leu Asp Thr His Val Glu Ile
    295                 300                 305

act gca aca acg gat cag gtc tgg ttc cca acc gac acc ggt cta cct   1075
Thr Ala Thr Thr Asp Gln Val Trp Phe Pro Thr Asp Thr Gly Leu Pro
310                 315                 320                 325

ctt gga atg ctt cgt cta gcg gac tac aaa agc atc tca taaaccgacg    1124
Leu Gly Met Leu Arg Leu Ala Asp Tyr Lys Ser Ile Ser
                330                 335

cagcactcgt cga                                                   1137
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<210> 2346

<211> 338
<212> PRT
<213> Corynebacterium glutamicum

<400> 2346

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Leu Val Leu Val Gly Cys Ser Asn Thr Ala Glu Ser Thr Thr Thr Asp
  1               5                  10                  15

Thr Ala Gly Ser Thr Glu Thr Ser Ser Gln Ile Ser Pro Thr Thr Pro
             20                  25                  30

Val Ser Thr Thr Glu Ala Ala Pro Pro Glu Asp Pro Ser Ala Asn Ala
         35                  40                  45

Leu Glu Glu Tyr Ala Gln Ile Leu Ala Asn Pro Ser Ile Tyr Pro Leu
     50                  55                  60

Thr Glu Ile Ser Gln Phe Val Pro Thr Gly Thr Tyr Ala Tyr Thr Leu
 65                  70                  75                  80

Val Glu Ala Thr Ser Asp Ser Ile Pro Glu Leu Leu Leu Arg Ala Asp
                 85                  90                  95

Ser His Glu Phe Ala Pro Ile Leu Val Phe Thr Tyr Asp Glu Asn Thr
            100                 105                 110

Gln Ser Ala Thr Gln Ala Gly Gly Val Leu Ile Asp Gly Val Ala Ser
        115                 120                 125

Ala Gly Gly Ser Arg Val Lys Val Arg Ala Ser Asn Ser Gly Ala Gly
    130                 135                 140

Ile Tyr Gln Leu Asn Trp Tyr Ser Ile Gln Pro Val Gly Glu Ser Ser
145                 150                 155                 160

Leu Tyr Gly Ile Gln Gly Asn Ser Leu Thr Gln Ile Ala Asp Pro Glu
                165                 170                 175

Asp Phe Met Val Arg Glu Leu Leu Pro Asp His His Glu Ile Thr Trp
            180                 185                 190

Val Asp Ser Asn Asp Pro Ser Gly Leu Ser Thr Val Gln Thr Gly Gly
        195                 200                 205

Ala Asn Ile Gln Gln Ala Ala Pro Thr Pro Val Gln Gln Pro Ala Ser
    210                 215                 220

Asn Leu His Tyr Phe Ser Gly Val Val Thr Met Gln Thr Ala Gly Glu
225                 230                 235                 240

Leu Met Arg Gly Glu Arg Thr Pro Asn Gly Glu Pro Ala Thr Asp Leu
                245                 250                 255

Tyr Leu Val Leu Val Leu Asp Ser Pro Ile Glu Ile Thr Ala Arg Asn
            260                 265                 270

Ala Ala Thr Asp Pro Gln Thr Arg Thr Ile Ser Glu Val Ser Leu Gly
        275                 280                 285

Arg Tyr Ile Pro Ala Asp Gly Asp Asn Asp Trp Ile Gly Tyr Leu Asp
    290                 295                 300
```

```
Thr His Val Glu Ile Thr Ala Thr Thr Asp Gln Val Trp Phe Pro Thr
305                 310                 315                 320

Asp Thr Gly Leu Pro Leu Gly Met Leu Arg Leu Ala Asp Tyr Lys Ser
                325                 330                 335

Ile Ser
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<210> 2347
<211> 1200
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1177)
<223> RXA01630

<400> 2347

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gtaggtgagt cttcgtgaga tacccccggc cagtcataca gttcaaccaa gctccaccac 60

ccagataaaa acctgcgggt tgcgttttag gagaattccc atg agt gat caa aaa   115
                                            Met Ser Asp Gln Lys
                                              1               5

att gtt gtt ggc ctg cta ggc atc acc cac ccg cat gcg tcg gcg cgg   163
Ile Val Val Gly Leu Leu Gly Ile Thr His Pro His Ala Ser Ala Arg
                10                  15                  20

gtg cgt gcc ctc cgt gaa att gat ggg gta gag gtc gtc gcc gcc gcg   211
Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu Val Val Ala Ala Ala
            25                  30                  35

gat act gat tcc cgc ctc cag tac ttc acc gac aaa tat gat gtt gaa   259
Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp Lys Tyr Asp Val Glu
        40                  45                  50

ccc cgc gag atc gat gac gtc ttg aac gac gat cgc atc aac gcc atc   307
Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp Arg Ile Asn Ala Ile
    55                  60                  65

atg gtt cac tcc aag agc aag gac atg gtc cct cac gcc aag cgc gcg   355
Met Val His Ser Lys Ser Lys Asp Met Val Pro His Ala Lys Arg Ala
70                  75                  80                  85

ctc gcg gcc gga aaa tcc gtc gtc gtg gag aag ccc ggc ggg gga aca   403
Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys Pro Gly Gly Gly Thr
                90                  95                  100

gtg gcg gat ctt gag gag ctc ctg gcc ctc aaa gaa gct gcc gat cct   451
Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys Glu Ala Ala Asp Pro
            105                 110                 115

cag cga atc gtg cag gtc ggg tac aac gtc cgc ctg tct gaa tcg gtt   499
Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg Leu Ser Glu Ser Val
        120                 125                 130

cag aga tta aaa gag ctt ctc gac gcc ggc ctc atc ggc gaa gtc gtc   547
```

```
Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu Ile Gly Glu Val Val
    135                 140                 145

agc gtg caa gca cgc ggc gcc gca aaa gta ggt gag cat atc acc gag   595
Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly Glu His Ile Thr Glu
150                 155                 160                 165

cac ctc aac caa ccc gca gac atg ggc ggt gtg ttg tgg att ctt ggc   643
His Leu Asn Gln Pro Ala Asp Met Gly Gly Val Leu Trp Ile Leu Gly
                170                 175                 180

tgc cac atg ctc gat gca ttg gtg gaa gtc ttc gga gct cca gaa tcc   691
Cys His Met Leu Asp Ala Leu Val Glu Val Phe Gly Ala Pro Glu Ser
            185                 190                 195

gtg aac gcc cga gtg cat aag acc gca aaa ctc tct gac gac acc agc   739
Val Asn Ala Arg Val His Lys Thr Ala Lys Leu Ser Asp Asp Thr Ser
        200                 205                 210

cgc gaa gac tca gcc tcc gca ctg ctg tac tac cca gat ttc tcc gtc   787
Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr Pro Asp Phe Ser Val
    215                 220                 225

agc ttc agc ttc gac ggc cac gat gat ctg gaa tgg ttc gaa agc tcc   835
Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu Trp Phe Glu Ser Ser
230                 235                 240                 245

cga ctc acg gtc tat gga acc aag ggc atg atc gaa gcc gga atc ctc   883
Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile Glu Ala Gly Ile Leu
                250                 255                 260

cct cag aca ctg cgc gta tac ctc aat gag tca cgc cag ggc tgg cca   931
Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser Arg Gln Gly Trp Pro
            265                 270                 275

cag ggt tgg acc gag tgg acc cag agc tac ttc acc cca ccg ttt gct   979
Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe Thr Pro Pro Phe Ala
        280                 285                 290

cgc aca gaa tcc aac aaa ttc tca gag ctt cca gag cta gaa aac atc   1027
Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro Glu Leu Glu Asn Ile
    295                 300                 305

agc aac ttc cgc aca gaa atg cag ggg tgg gtg aat tcc att cgc act   1075
Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val Asn Ser Ile Arg Thr
310                 315                 320                 325

gga tcc cgc aat gtg gcg cca gtt gag gat gct ctc aca gtc gct cgc   1123
Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala Leu Thr Val Ala Arg
                330                 335                 340

att gtc agt gca tgc tac gaa tcc gac aac aac cag ggc att tcc gta   1171
Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn Gln Gly Ile Ser Val
            345                 350                 355

aac atc taagaggagc actccatgaa acc                                1200
Asn Ile
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<210> 2348

<211> 359
<212> PRT
<213> Corynebacterium glutamicum

<400> 2348

```
Met Ser Asp Gln Lys Ile Val Val Gly Leu Leu Gly Ile Thr His Pro
  1               5                  10                  15

His Ala Ser Ala Arg Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu
             20                  25                  30

Val Val Ala Ala Ala Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp
         35                  40                  45

Lys Tyr Asp Val Glu Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp
     50                  55                  60

Arg Ile Asn Ala Ile Met Val His Ser Lys Ser Lys Asp Met Val Pro
 65                  70                  75                  80

His Ala Lys Arg Ala Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys
                 85                  90                  95

Pro Gly Gly Gly Thr Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys
            100                 105                 110

Glu Ala Ala Asp Pro Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg
        115                 120                 125

Leu Ser Glu Ser Val Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu
    130                 135                 140

Ile Gly Glu Val Val Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly
145                 150                 155                 160

Glu His Ile Thr Glu His Leu Asn Gln Pro Ala Asp Met Gly Gly Val
                165                 170                 175

Leu Trp Ile Leu Gly Cys His Met Leu Asp Ala Leu Val Glu Val Phe
            180                 185                 190

Gly Ala Pro Glu Ser Val Asn Ala Arg Val His Lys Thr Ala Lys Leu
        195                 200                 205

Ser Asp Asp Thr Ser Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr
    210                 215                 220

Pro Asp Phe Ser Val Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu
225                 230                 235                 240

Trp Phe Glu Ser Ser Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile
                245                 250                 255

Glu Ala Gly Ile Leu Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser
            260                 265                 270

Arg Gln Gly Trp Pro Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe
        275                 280                 285

Thr Pro Pro Phe Ala Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro
    290                 295                 300
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Glu Leu Glu Asn Ile Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val
305                 310                 315                 320

Asn Ser Ile Arg Thr Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala
                325                 330                 335

Leu Thr Val Ala Arg Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn
            340                 345                 350

Gln Gly Ile Ser Val Asn Ile
        355


<210> 2349
<211> 1494
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1471)
<223> RXA01641

<400> 2349
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agacacattt gttgggggac aattttgggg gttggttatt ttg gca atc gat aat   115
                                              Leu Ala Ile Asp Asn
                                                1               5

gcg ctg cgc gtg agc atc cgc ata gat ctc acc gtt ggc gat gcg ccc   163
Ala Leu Arg Val Ser Ile Arg Ile Asp Leu Thr Val Gly Asp Ala Pro
                10                  15                  20

gct gct gtg gct gat gtg gcg cta cct gca ggt tcg agt ctg gcg gac   211
Ala Ala Val Ala Asp Val Ala Leu Pro Ala Gly Ser Ser Leu Ala Asp
            25                  30                  35

att ttg gat gaa att tta gaa ctc acc gat gca ccc cgg att tcc agg   259
Ile Leu Asp Glu Ile Leu Glu Leu Thr Asp Ala Pro Arg Ile Ser Arg
        40                  45                  50

ccg tgg gtg gct cac act gct gcg gga agt ccc att gat tgc ggg att   307
Pro Trp Val Ala His Thr Ala Ala Gly Ser Pro Ile Asp Cys Gly Ile
    55                  60                  65

ccg ctt gca gaa aca caa gtg gaa caa ggc agc gtg gtg gtc ctt tca   355
Pro Leu Ala Glu Thr Gln Val Glu Gln Gly Ser Val Val Val Leu Ser
70                  75                  80                  85

ccc gaa agg gac ttg gaa gcc ccc gtg ttg cgt gat gtc gcc gaa gcg   403
Pro Glu Arg Asp Leu Glu Ala Pro Val Leu Arg Asp Val Ala Glu Ala
                90                  95                  100

ttg gtg gag ttt tct tcc acg aac cgc gcc ggg cac ctc gtg gaa ttg   451
Leu Val Glu Phe Ser Ser Thr Asn Arg Ala Gly His Leu Val Glu Leu
            105                 110                 115

atg act ttc gcg ggg ctc atc ggg gct gcc gtg tta atg aca agt cct   499
Met Thr Phe Ala Gly Leu Ile Gly Ala Ala Val Leu Met Thr Ser Pro
```

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        120                 125                 130

gct gcc tcc gga att att gtg ccc ggc cgc atg gga atc ttc gtc gca   547
Ala Ala Ser Gly Ile Ile Val Pro Gly Arg Met Gly Ile Phe Val Ala
    135                 140                 145

atc tgc gct cta ctg ctt ctg tgg ctc cca ccc gcg cac acc ccg atc   595
Ile Cys Ala Leu Leu Leu Leu Trp Leu Pro Pro Ala His Thr Pro Ile
150                 155                 160                 165

ctt cga aac gtc ctg ccg att acc ctg atc ttg ggc gca ggc gga gcg   643
Leu Arg Asn Val Leu Pro Ile Thr Leu Ile Leu Gly Ala Gly Gly Ala
                170                 175                 180

gta tca gtg ctg gtt gca ggc act tct ggg act tct ccc ggc gcg ctt   691
Val Ser Val Leu Val Ala Gly Thr Ser Gly Thr Ser Pro Gly Ala Leu
            185                 190                 195

acc tgg acg att ttc gct ggc gcg tgc act att ctt gcc agt tcg ctg   739
Thr Trp Thr Ile Phe Ala Gly Ala Cys Thr Ile Leu Ala Ser Ser Leu
        200                 205                 210

ctg gtt cat gtg gtg tat cgt cca gca att ctt ctg gtg gca aca ctg   787
Leu Val His Val Val Tyr Arg Pro Ala Ile Leu Leu Val Ala Thr Leu
    215                 220                 225

tcc aca ttg ggg ctc ggt ctc tta gtc ctt gca gca acc acc act ctg   835
Ser Thr Leu Gly Leu Gly Leu Leu Val Leu Ala Ala Thr Thr Thr Leu
230                 235                 240                 245

tgg aag ctc aaa gct acc gaa gat ttc agc ggt cca gca gcg atc acg   883
Trp Lys Leu Lys Ala Thr Glu Asp Phe Ser Gly Pro Ala Ala Ile Thr
                250                 255                 260

gtc acc gct tcc acc atc acc atg tgc ttc gcc ccg aaa atc gca gca   931
Val Thr Ala Ser Thr Ile Thr Met Cys Phe Ala Pro Lys Ile Ala Ala
            265                 270                 275

tcg cta gca ggc ctg cgc gtc cca tcg ctt ccc acc gcc ggc gaa gat   979
Ser Leu Ala Gly Leu Arg Val Pro Ser Leu Pro Thr Ala Gly Glu Asp
        280                 285                 290

ctc tcc gtc agc gac ctc acc atg act gat ccc gag aaa aga ata aaa  1027
Leu Ser Val Ser Asp Leu Thr Met Thr Asp Pro Glu Lys Arg Ile Lys
    295                 300                 305

aca aca aag acg ctt ttc gac gcc cag atc ctt ggc ctt ggc gtt ttg  1075
Thr Thr Lys Thr Leu Phe Asp Ala Gln Ile Leu Gly Leu Gly Val Leu
310                 315                 320                 325

agc ggg cct ttg gcg ttg ttg tcg gtt acc ccg ggc acc tgg aca acc  1123
Ser Gly Pro Leu Ala Leu Leu Ser Val Thr Pro Gly Thr Trp Thr Thr
                330                 335                 340

acc gtt ttt agt tta tgc atc gcg gtg gct tcg ctg ctt cac gct aat  1171
Thr Val Phe Ser Leu Cys Ile Ala Val Ala Ser Leu Leu His Ala Asn
            345                 350                 355

cgt cat caa gca cca att ccc acg tgg aca ttg atg ggg tta tct gcc  1219
Arg His Gln Ala Pro Ile Pro Thr Trp Thr Leu Met Gly Leu Ser Ala
        360                 365                 370
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ctt ggt ttc att tcc atg gcg tta tcc gca agc cga tca ggt tca cta   1267
Leu Gly Phe Ile Ser Met Ala Leu Ser Ala Ser Arg Ser Gly Ser Leu
    375                 380                 385

att gca ctg atc ggt tct gtg gtt atc atc gct gtg ctg gtc agc gtg   1315
Ile Ala Leu Ile Gly Ser Val Val Ile Ile Ala Val Leu Val Ser Val
390                 395                 400                 405

gca ttg tgg atc agt aca gtc ccc acg ctg gaa ccc acc acc att gtg   1363
Ala Leu Trp Ile Ser Thr Val Pro Thr Leu Glu Pro Thr Thr Ile Val
                410                 415                 420

tgg ctt gaa agg ttg gaa tca ctg tgt ctt gca gct agt ctg cca ctc   1411
Trp Leu Glu Arg Leu Glu Ser Leu Cys Leu Ala Ala Ser Leu Pro Leu
            425                 430                 435

gca ctg cat ttg ctg gat gta ttt gga atg ctg cgc ggt ctt gat att   1459
Ala Leu His Leu Leu Asp Val Phe Gly Met Leu Arg Gly Leu Asp Ile
        440                 445                 450

gga ttc ggt gga taagatgcgc agactcatcg cgg                        1494
Gly Phe Gly Gly
    455
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US20050009150A1

<210> 2350
<211> 457
<212> PRT
<213> Corynebacterium glutamicum

<400> 2350

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Leu Ala Ile Asp Asn Ala Leu Arg Val Ser Ile Arg Ile Asp Leu Thr
  1               5                  10                  15

Val Gly Asp Ala Pro Ala Ala Val Ala Asp Val Ala Leu Pro Ala Gly
             20                  25                  30

Ser Ser Leu Ala Asp Ile Leu Asp Glu Ile Leu Glu Leu Thr Asp Ala
         35                  40                  45

Pro Arg Ile Ser Arg Pro Trp Val Ala His Thr Ala Ala Gly Ser Pro
     50                  55                  60

Ile Asp Cys Gly Ile Pro Leu Ala Glu Thr Gln Val Glu Gln Gly Ser
 65                  70                  75                  80

Val Val Val Leu Ser Pro Glu Arg Asp Leu Glu Ala Pro Val Leu Arg
                 85                  90                  95

Asp Val Ala Glu Ala Leu Val Glu Phe Ser Ser Thr Asn Arg Ala Gly
            100                 105                 110

His Leu Val Glu Leu Met Thr Phe Ala Gly Leu Ile Gly Ala Ala Val
        115                 120                 125

Leu Met Thr Ser Pro Ala Ala Ser Gly Ile Ile Val Pro Gly Arg Met
    130                 135                 140

Gly Ile Phe Val Ala Ile Cys Ala Leu Leu Leu Leu Trp Leu Pro Pro
145                 150                 155                 160
```

```
Ala His Thr Pro Ile Leu Arg Asn Val Leu Pro Ile Thr Leu Ile Leu
                165                 170                 175

Gly Ala Gly Gly Ala Val Ser Val Leu Val Ala Gly Thr Ser Gly Thr
            180                 185                 190

Ser Pro Gly Ala Leu Thr Trp Thr Ile Phe Ala Gly Ala Cys Thr Ile
        195                 200                 205

Leu Ala Ser Ser Leu Leu Val His Val Val Tyr Arg Pro Ala Ile Leu
    210                 215                 220

Leu Val Ala Thr Leu Ser Thr Leu Gly Leu Gly Leu Leu Val Leu Ala
225                 230                 235                 240

Ala Thr Thr Thr Leu Trp Lys Leu Lys Ala Thr Glu Asp Phe Ser Gly
                245                 250                 255

Pro Ala Ala Ile Thr Val Thr Ala Ser Thr Ile Thr Met Cys Phe Ala
            260                 265                 270

Pro Lys Ile Ala Ala Ser Leu Ala Gly Leu Arg Val Pro Ser Leu Pro
        275                 280                 285

Thr Ala Gly Glu Asp Leu Ser Val Ser Asp Leu Thr Met Thr Asp Pro
    290                 295                 300

Glu Lys Arg Ile Lys Thr Thr Lys Thr Leu Phe Asp Ala Gln Ile Leu
305                 310                 315                 320

Gly Leu Gly Val Leu Ser Gly Pro Leu Ala Leu Leu Ser Val Thr Pro
                325                 330                 335

Gly Thr Trp Thr Thr Thr Val Phe Ser Leu Cys Ile Ala Val Ala Ser
            340                 345                 350

Leu Leu His Ala Asn Arg His Gln Ala Pro Ile Pro Thr Trp Thr Leu
        355                 360                 365

Met Gly Leu Ser Ala Leu Gly Phe Ile Ser Met Ala Leu Ser Ala Ser
    370                 375                 380

Arg Ser Gly Ser Leu Ile Ala Leu Ile Gly Ser Val Val Ile Ile Ala
385                 390                 395                 400

Val Leu Val Ser Val Ala Leu Trp Ile Ser Thr Val Pro Thr Leu Glu
                405                 410                 415

Pro Thr Thr Ile Val Trp Leu Glu Arg Leu Glu Ser Leu Cys Leu Ala
            420                 425                 430

Ala Ser Leu Pro Leu Ala Leu His Leu Leu Asp Val Phe Gly Met Leu
        435                 440                 445

Arg Gly Leu Asp Ile Gly Phe Gly Gly
    450                 455
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<210> 2351
<211> 1365

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1342)
<223> RXA01642

<400> 2351
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ggaatgctgc gcggtcttga tattggattc ggtggataag atg cgc aga ctc atc 115
Met Arg Arg Leu Ile
1 5

gcg gtt agc ttg gcc gct ctg ttt atg ttg gct tcc act cca gcg acg 163
Ala Val Ser Leu Ala Ala Leu Phe Met Leu Ala Ser Thr Pro Ala Thr
10 15 20

agg gca cag gaa gta gaa gct ctc gct tgc ccc gag gta gcg atc gcc 211
Arg Ala Gln Glu Val Glu Ala Leu Ala Cys Pro Glu Val Ala Ile Ala
25 30 35

gat cct tcc tcc gca gtt tta gat gaa cac ctt tcg cag tca tta tcc 259
Asp Pro Ser Ser Ala Val Leu Asp Glu His Leu Ser Gln Ser Leu Ser
40 45 50

caa gct cac caa cta gca act ggc gcc ggt gtg atg gtg gca gtc atc 307
Gln Ala His Gln Leu Ala Thr Gly Ala Gly Val Met Val Ala Val Ile
55 60 65

gac acc gga gta tcc ctg cat cca cgt ctg ccc cac tta att ccc ggc 355
Asp Thr Gly Val Ser Leu His Pro Arg Leu Pro His Leu Ile Pro Gly
70 75 80 85

ggt gat ttc gtg ggc gcc cac caa agc ccc gat gtg cca ggt gaa ctt 403
Gly Asp Phe Val Gly Ala His Gln Ser Pro Asp Val Pro Gly Glu Leu
90 95 100

atc gat tgc gac ggc cac ggc acc atc gtc gcc gga atc atc gcc tcc 451
Ile Asp Cys Asp Gly His Gly Thr Ile Val Ala Gly Ile Ile Ala Ser
105 110 115

caa gga aac ccc ggc acc ggc tgg cca tat gac ggc agc tcc gat cct 499
Gln Gly Asn Pro Gly Thr Gly Trp Pro Tyr Asp Gly Ser Ser Asp Pro
120 125 130

tat atc ggt gtc gcc cca gat tcc gga atc atc tcc att aaa caa acc 547
Tyr Ile Gly Val Ala Pro Asp Ser Gly Ile Ile Ser Ile Lys Gln Thr
135 140 145

agc tca tat gtg cgt act cgt gaa gat tcc aac gtc gga acg ctg agc 595
Ser Ser Tyr Val Arg Thr Arg Glu Asp Ser Asn Val Gly Thr Leu Ser
150 155 160 165

acc ctg gcg gaa tcc atc cac cga gct ctc gat tcc ggt gcc cac gtg 643
Thr Leu Ala Glu Ser Ile His Arg Ala Leu Asp Ser Gly Ala His Val
170 175 180

atc aat att tcc gtg gtg tcc tgt ttg ccc caa tca ccc gac gag gcc 691
Ile Asn Ile Ser Val Val Ser Cys Leu Pro Gln Ser Pro Asp Glu Ala

```
                185                 190                 195

gca tcg ttc cag cct ctg acg gat gct ctt aac aga gca gaa ctt caa   739
Ala Ser Phe Gln Pro Leu Thr Asp Ala Leu Asn Arg Ala Glu Leu Gln
        200                 205                 210

ggg gtg ata gtg gtg gca gca gca gga aac ctc ggg cag gat tgt cca   787
Gly Val Ile Val Val Ala Ala Ala Gly Asn Leu Gly Gln Asp Cys Pro
    215                 220                 225

gtt gga tct acc gtt tat cct gca cat tca gac act gtg ctc tct gtg   835
Val Gly Ser Thr Val Tyr Pro Ala His Ser Asp Thr Val Leu Ser Val
230                 235                 240                 245

tcg gca cgt ttt gat tct cac acg ctt gca gaa tat tcc atg cct ggc   883
Ser Ala Arg Phe Asp Ser His Thr Leu Ala Glu Tyr Ser Met Pro Gly
                250                 255                 260

aac caa caa atc ctc tct gca cca agc cac att cag gct ggt cta tca   931
Asn Gln Gln Ile Leu Ser Ala Pro Ser His Ile Gln Ala Gly Leu Ser
            265                 270                 275

ccg cgt ggc gac ggc ttc gcc agc cac atg atc acc acc gct ggc gaa   979
Pro Arg Gly Asp Gly Phe Ala Ser His Met Ile Thr Thr Ala Gly Glu
        280                 285                 290

agc ccc ttc gag ggc acc agt ttt gcc gct cca gtt gtc agc gcc aca  1027
Ser Pro Phe Glu Gly Thr Ser Phe Ala Ala Pro Val Val Ser Ala Thr
    295                 300                 305

gct gca ctg ctt cgc cag cat ttt ccc ttt gcc aca ccc tat gaa att  1075
Ala Ala Leu Leu Arg Gln His Phe Pro Phe Ala Thr Pro Tyr Glu Ile
310                 315                 320                 325

cgt gca cga atc ttc aac agc atc gac cct gca aga ggc gct att gat  1123
Arg Ala Arg Ile Phe Asn Ser Ile Asp Pro Ala Arg Gly Ala Ile Asp
                330                 335                 340

ccc tac ctg gca ctt act caa gaa atc tat ccc acc act ccc ctg gtt  1171
Pro Tyr Leu Ala Leu Thr Gln Glu Ile Tyr Pro Thr Thr Pro Leu Val
            345                 350                 355

cat gag atc gca cta agt gtt ccc acg ccg ccg gat gat tct cca cgg  1219
His Glu Ile Ala Leu Ser Val Pro Thr Pro Pro Asp Asp Ser Pro Arg
        360                 365                 370

gag cgg ggc atc cta gtt acc gca atc att gtt ggg ttg ctc gca gtg  1267
Glu Arg Gly Ile Leu Val Thr Ala Ile Ile Val Gly Leu Leu Ala Val
    375                 380                 385

tta gct gtg ctg atg gga cta cgc cga att cat cat cac tcg gcc ttt  1315
Leu Ala Val Leu Met Gly Leu Arg Arg Ile His His His Ser Ala Phe
390                 395                 400                 405

caa aaa gct agc tca agt gtt atc act taatctatga ggcaccgttc        1362
Gln Lys Ala Ser Ser Ser Val Ile Thr
                410

aga                                                             1365
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<210> 2352
<211> 414
<212> PRT
<213> Corynebacterium glutamicum

<400> 2352
Met Arg Arg Leu Ile Ala Val Ser Leu Ala Ala Leu Phe Met Leu Ala
1 5 10 15

Ser Thr Pro Ala Thr Arg Ala Gln Glu Val Glu Ala Leu Ala Cys Pro
20 25 30

Glu Val Ala Ile Ala Asp Pro Ser Ser Ala Val Leu Asp Glu His Leu
35 40 45

Ser Gln Ser Leu Ser Gln Ala His Gln Leu Ala Thr Gly Ala Gly Val
50 55 60

Met Val Ala Val Ile Asp Thr Gly Val Ser Leu His Pro Arg Leu Pro
65 70 75 80

His Leu Ile Pro Gly Gly Asp Phe Val Gly Ala His Gln Ser Pro Asp
85 90 95

Val Pro Gly Glu Leu Ile Asp Cys Asp Gly His Gly Thr Ile Val Ala
100 105 110

Gly Ile Ile Ala Ser Gln Gly Asn Pro Gly Thr Gly Trp Pro Tyr Asp
115 120 125

Gly Ser Ser Asp Pro Tyr Ile Gly Val Ala Pro Asp Ser Gly Ile Ile
130 135 140

Ser Ile Lys Gln Thr Ser Ser Tyr Val Arg Thr Arg Glu Asp Ser Asn
145 150 155 160

Val Gly Thr Leu Ser Thr Leu Ala Glu Ser Ile His Arg Ala Leu Asp
165 170 175

Ser Gly Ala His Val Ile Asn Ile Ser Val Val Ser Cys Leu Pro Gln
180 185 190

Ser Pro Asp Glu Ala Ala Ser Phe Gln Pro Leu Thr Asp Ala Leu Asn
195 200 205

Arg Ala Glu Leu Gln Gly Val Ile Val Val Ala Ala Ala Gly Asn Leu
210 215 220

Gly Gln Asp Cys Pro Val Gly Ser Thr Val Tyr Pro Ala His Ser Asp
225 230 235 240

Thr Val Leu Ser Val Ser Ala Arg Phe Asp Ser His Thr Leu Ala Glu
245 250 255

Tyr Ser Met Pro Gly Asn Gln Gln Ile Leu Ser Ala Pro Ser His Ile
260 265 270

Gln Ala Gly Leu Ser Pro Arg Gly Asp Gly Phe Ala Ser His Met Ile
275 280 285

Thr Thr Ala Gly Glu Ser Pro Phe Glu Gly Thr Ser Phe Ala Ala Pro

```
    290                 295                 300

Val Val Ser Ala Thr Ala Ala Leu Leu Arg Gln His Phe Pro Phe Ala
305                 310                 315                 320

Thr Pro Tyr Glu Ile Arg Ala Arg Ile Phe Asn Ser Ile Asp Pro Ala
                325                 330                 335

Arg Gly Ala Ile Asp Pro Tyr Leu Ala Leu Thr Gln Glu Ile Tyr Pro
            340                 345                 350

Thr Thr Pro Leu Val His Glu Ile Ala Leu Ser Val Pro Thr Pro Pro
        355                 360                 365

Asp Asp Ser Pro Arg Glu Arg Gly Ile Leu Val Thr Ala Ile Ile Val
    370                 375                 380

Gly Leu Leu Ala Val Leu Ala Val Leu Met Gly Leu Arg Arg Ile His
385                 390                 395                 400

His His Ser Ala Phe Gln Lys Ala Ser Ser Ser Val Ile Thr
                405                 410
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US20090305363A1

<210> 2353
<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(526)
<223> RXA01643

<400> 2353

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cggatttcaa cactttcagg atgcatctgt aactatgccc atgccacacc ccatgtttat 60

cgatgtctcc ttcccacccg cggagacctg tagttaaccc atg ggc acg atg cga   115
                                            Met Gly Thr Met Arg
                                              1               5

gaa atg gtc agt gac cgc att gac cga cta caa gaa gca cac gcg cga   163
Glu Met Val Ser Asp Arg Ile Asp Arg Leu Gln Glu Ala His Ala Arg
                 10                  15                  20

tca aag cag aag aag ttc ggc ttc tta gtt cgg cca ggc acc ctg atc   211
Ser Lys Gln Lys Lys Phe Gly Phe Leu Val Arg Pro Gly Thr Leu Ile
             25                  30                  35

ctt gga tgg ttg gtc acg atc atc ggt ctg atc acc att cca ctt ccc   259
Leu Gly Trp Leu Val Thr Ile Ile Gly Leu Ile Thr Ile Pro Leu Pro
         40                  45                  50

ggc caa ggc tgg ctg acc acc ttc att ggt gtg ggc att ttg tct ctg   307
Gly Gln Gly Trp Leu Thr Thr Phe Ile Gly Val Gly Ile Leu Ser Leu
     55                  60                  65

gag ctt aaa tgg gcg aag aac ctc ctg gcc tgg gga gtg cat cag tat   355
Glu Leu Lys Trp Ala Lys Asn Leu Leu Ala Trp Gly Val His Gln Tyr
 70                  75                  80                  85
```

```
gat cgc ttc ttc acc tgg tac ggc aag aaa tca ttc cgc ttc cgc atg   403
Asp Arg Phe Phe Thr Trp Tyr Gly Lys Lys Ser Phe Arg Phe Arg Met
                 90                  95                 100

gcg atg ttg gca ctg atg att ctg ctg att tgg gtg gtg ttc atc gtg   451
Ala Met Leu Ala Leu Met Ile Leu Leu Ile Trp Val Val Phe Ile Val
            105                 110                 115

aca ttt tgg ttg atg tgg cac gcc gga act atc ccg tgg gca gat gag   499
Thr Phe Trp Leu Met Trp His Ala Gly Thr Ile Pro Trp Ala Asp Glu
        120                 125                 130

ttc ttc acc tgg ctt ggg ttg agc cgc tagcaactat tcgctttgaa        546
Phe Phe Thr Trp Leu Gly Leu Ser Arg
    135                 140

ggc                                                              549
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<210> 2354
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 2354

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Met Gly Thr Met Arg Glu Met Val Ser Asp Arg Ile Asp Arg Leu Gln
  1               5                  10                  15

Glu Ala His Ala Arg Ser Lys Gln Lys Lys Phe Gly Phe Leu Val Arg
             20                  25                  30

Pro Gly Thr Leu Ile Leu Gly Trp Leu Val Thr Ile Ile Gly Leu Ile
         35                  40                  45

Thr Ile Pro Leu Pro Gly Gln Gly Trp Leu Thr Thr Phe Ile Gly Val
     50                  55                  60

Gly Ile Leu Ser Leu Glu Leu Lys Trp Ala Lys Asn Leu Leu Ala Trp
 65                  70                  75                  80

Gly Val His Gln Tyr Asp Arg Phe Phe Thr Trp Tyr Gly Lys Lys Ser
                 85                  90                  95

Phe Arg Phe Arg Met Ala Met Leu Ala Leu Met Ile Leu Leu Ile Trp
            100                 105                 110

Val Val Phe Ile Val Thr Phe Trp Leu Met Trp His Ala Gly Thr Ile
        115                 120                 125

Pro Trp Ala Asp Glu Phe Phe Thr Trp Leu Gly Leu Ser Arg
    130                 135                 140
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<210> 2355
<211> 729
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(706)

<223> RXA01645

<400> 2355

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agagggcatc acctatgacc gcctgacaat ccgcgattac atctggcgct gggacaccga 60

ctggttctgg tgttcacgcg cattcggcac ccaaaacccc gtg gtg cgc aaa ctc   115
                                             Val Val Arg Lys Leu
                                               1               5

tgg ccc agg gat ctg ctg cgc tcg agt ttc tat tgg aag atc atc ggc   163
Trp Pro Arg Asp Leu Leu Arg Ser Ser Phe Tyr Trp Lys Ile Ile Gly
                 10                  15                  20

tgg gat cga aaa tac tcc atc gct gat cgc ctg gaa gag cgc aaa ggc   211
Trp Asp Arg Lys Tyr Ser Ile Ala Asp Arg Leu Glu Glu Arg Lys Gly
             25                  30                  35

cgc ccg gct agg gaa cgg gtg gtc caa gac gtg gaa gtt acg att gat   259
Arg Pro Ala Arg Glu Arg Val Val Gln Asp Val Glu Val Thr Ile Asp
         40                  45                  50

aaa ctg cca gaa ttt ttg aaa tgg ttc ttt gaa agc agc gac atc gag   307
Lys Leu Pro Glu Phe Leu Lys Trp Phe Phe Glu Ser Ser Asp Ile Glu
     55                  60                  65

ccg ctg tgg ctg tgc ccg atc aag ctt cgg gag gta cca ggt agt tcg   355
Pro Leu Trp Leu Cys Pro Ile Lys Leu Arg Glu Val Pro Gly Ser Ser
 70                  75                  80                  85

gtt ggt gct gga gaa att ttg agc tcc gct gaa gca atc gac tcc ggt   403
Val Gly Ala Gly Glu Ile Leu Ser Ser Ala Glu Ala Ile Asp Ser Gly
                 90                  95                 100

gct gct gaa cac cct tgg ccg ctg tat ccc ttg aag aag gac gtg ctg   451
Ala Ala Glu His Pro Trp Pro Leu Tyr Pro Leu Lys Lys Asp Val Leu
            105                 110                 115

tgg gtc aac atc gga ttc tgg tcc tca gtg ccg gtt gat ctg atg ggc   499
Trp Val Asn Ile Gly Phe Trp Ser Ser Val Pro Val Asp Leu Met Gly
        120                 125                 130

tcc gat gca cca gag gga gca ttt aac aga gaa atc gaa cgc gtc atg   547
Ser Asp Ala Pro Glu Gly Ala Phe Asn Arg Glu Ile Glu Arg Val Met
    135                 140                 145

gca gag cta ggc gga cat aaa tcg ctg tac tcc gaa gcg ttc tac acc   595
Ala Glu Leu Gly Gly His Lys Ser Leu Tyr Ser Glu Ala Phe Tyr Thr
150                 155                 160                 165

agg gaa gac ttt gaa aaa ctt tat ggc gga acc atc ccg gcg ctg cta   643
Arg Glu Asp Phe Glu Lys Leu Tyr Gly Gly Thr Ile Pro Ala Leu Leu
                170                 175                 180

aaa aag cag tgg gat ccc cac agc cga ttc ccc ggt ttg tat gaa aag   691
Lys Lys Gln Trp Asp Pro His Ser Arg Phe Pro Gly Leu Tyr Glu Lys
            185                 190                 195

aca gta aaa ggc gcc taggatcgct cactgtaggt aga                    729
Thr Val Lys Gly Ala
        200
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<210> 2356
<211> 202
<212> PRT
<213> Corynebacterium glutamicum

<400> 2356
Val Val Arg Lys Leu Trp Pro Arg Asp Leu Leu Arg Ser Ser Phe Tyr
1 5 10 15

Trp Lys Ile Ile Gly Trp Asp Arg Lys Tyr Ser Ile Ala Asp Arg Leu
20 25 30

Glu Glu Arg Lys Gly Arg Pro Ala Arg Glu Arg Val Val Gln Asp Val
35 40 45

Glu Val Thr Ile Asp Lys Leu Pro Glu Phe Leu Lys Trp Phe Phe Glu
50 55 60

Ser Ser Asp Ile Glu Pro Leu Trp Leu Cys Pro Ile Lys Leu Arg Glu
65 70 75 80

Val Pro Gly Ser Ser Val Gly Ala Gly Glu Ile Leu Ser Ser Ala Glu
85 90 95

Ala Ile Asp Ser Gly Ala Ala Glu His Pro Trp Pro Leu Tyr Pro Leu
100 105 110

Lys Lys Asp Val Leu Trp Val Asn Ile Gly Phe Trp Ser Ser Val Pro
115 120 125

Val Asp Leu Met Gly Ser Asp Ala Pro Glu Gly Ala Phe Asn Arg Glu
130 135 140

Ile Glu Arg Val Met Ala Glu Leu Gly Gly His Lys Ser Leu Tyr Ser
145 150 155 160

Glu Ala Phe Tyr Thr Arg Glu Asp Phe Glu Lys Leu Tyr Gly Gly Thr
165 170 175

Ile Pro Ala Leu Leu Lys Lys Gln Trp Asp Pro His Ser Arg Phe Pro
180 185 190

Gly Leu Tyr Glu Lys Thr Val Lys Gly Ala
195 200

<210> 2357
<211> 942
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(919)
<223> RXA01646

<400> 2357
ggtcgtgccg tggagcgtgc tgcgattgtt gccgcaggga agtgaattag caaaagagac 60

agcgctcgcg cccacctatt aaggagtatg gtggccttac atg agc gga tta gtt 115

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                                                    Met Ser Gly Leu Val
                                                      1               5

gac ccg gat agt act ttt tta aag acc atc gga aaa ctg agc aac agc   163
Asp Pro Asp Ser Thr Phe Leu Lys Thr Ile Gly Lys Leu Ser Asn Ser
                 10                  15                  20

ttg tcc att ggt cgt gga gta gat caa aaa gag gta atc ccc aaa ggc   211
Leu Ser Ile Gly Arg Gly Val Asp Gln Lys Glu Val Ile Pro Lys Gly
             25                  30                  35

tgg aac gcc cat tgg gag gca att aca aag ctt aag aga agc ttt gac   259
Trp Asn Ala His Trp Glu Ala Ile Thr Lys Leu Lys Arg Ser Phe Asp
         40                  45                  50

gcg att cct gct ggg gag cgg gtg cgt tta gct aag aaa acc tcc aac   307
Ala Ile Pro Ala Gly Glu Arg Val Arg Leu Ala Lys Lys Thr Ser Asn
     55                  60                  65

ctg ttc cgt gga cgc tcc gat gca ggt cac ggc cta gat gtg gca gcg   355
Leu Phe Arg Gly Arg Ser Asp Ala Gly His Gly Leu Asp Val Ala Ala
 70                  75                  80                  85

ctt ggg gga gtg att gcc att gat ccg gtc aat gcc acc gcc gat gta   403
Leu Gly Gly Val Ile Ala Ile Asp Pro Val Asn Ala Thr Ala Asp Val
                 90                  95                 100

cag ggc atg tgc acg tat gaa gac ctg gta gat gcc act tta agt tat   451
Gln Gly Met Cys Thr Tyr Glu Asp Leu Val Asp Ala Thr Leu Ser Tyr
             105                 110                 115

ggt ctg atg ccg ttg gtt gtg cct caa ctg aaa acc atc acg ctt ggt   499
Gly Leu Met Pro Leu Val Val Pro Gln Leu Lys Thr Ile Thr Leu Gly
         120                 125                 130

ggc gca gtg acc gga atg ggc gtg gaa tcc aca tcc ttc cgc aac ggt   547
Gly Ala Val Thr Gly Met Gly Val Glu Ser Thr Ser Phe Arg Asn Gly
     135                 140                 145

ttg cca cac gaa tca gtg ctg gag atg gat att ttt acc ggc act ggt   595
Leu Pro His Glu Ser Val Leu Glu Met Asp Ile Phe Thr Gly Thr Gly
150                 155                 160                 165

gag atc gtg act tgc tcg ccc aca gaa aat gtc gac ctt tac aga ggt   643
Glu Ile Val Thr Cys Ser Pro Thr Glu Asn Val Asp Leu Tyr Arg Gly
                 170                 175                 180

ttt ccc aac tct tat ggt tcg ctg gga tac gcg gtg cgg cta aaa att   691
Phe Pro Asn Ser Tyr Gly Ser Leu Gly Tyr Ala Val Arg Leu Lys Ile
             185                 190                 195

gag ctg gaa cca gtg caa gat tac gtc cag ctg cgc cac gtg cgc ttc   739
Glu Leu Glu Pro Val Gln Asp Tyr Val Gln Leu Arg His Val Arg Phe
         200                 205                 210

aac gat tta gag tct ttg acc aaa gcg att gag gaa gtc gcg tct tct   787
Asn Asp Leu Glu Ser Leu Thr Lys Ala Ile Glu Glu Val Ala Ser Ser
     215                 220                 225

ctg gag ttt gat aac caa ccc gtc gat tac ctt gac ggc gtg gtg ttt   835
Leu Glu Phe Asp Asn Gln Pro Val Asp Tyr Leu Asp Gly Val Val Phe
```

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230                 235                 240                 245

tca ccc acg gaa gcc tac tta gtt ctt ggc acg caa acc tca caa cct   883
Ser Pro Thr Glu Ala Tyr Leu Val Leu Gly Thr Gln Thr Ser Gln Pro
                250                 255                 260

ggc ccc acc agc gat tac acc agg gat tta agc tac taacgctccc       929
Gly Pro Thr Ser Asp Tyr Thr Arg Asp Leu Ser Tyr
            265                 270

tgcaacaccc aga                                                   942


<210> 2358
<211> 273
<212> PRT
<213> Corynebacterium glutamicum

<400> 2358
Met Ser Gly Leu Val Asp Pro Asp Ser Thr Phe Leu Lys Thr Ile Gly
  1               5                  10                  15

Lys Leu Ser Asn Ser Leu Ser Ile Gly Arg Gly Val Asp Gln Lys Glu
             20                  25                  30

Val Ile Pro Lys Gly Trp Asn Ala His Trp Glu Ala Ile Thr Lys Leu
         35                  40                  45

Lys Arg Ser Phe Asp Ala Ile Pro Ala Gly Glu Arg Val Arg Leu Ala
     50                  55                  60

Lys Lys Thr Ser Asn Leu Phe Arg Gly Arg Ser Asp Ala Gly His Gly
 65                  70                  75                  80

Leu Asp Val Ala Ala Leu Gly Gly Val Ile Ala Ile Asp Pro Val Asn
                 85                  90                  95

Ala Thr Ala Asp Val Gln Gly Met Cys Thr Tyr Glu Asp Leu Val Asp
            100                 105                 110

Ala Thr Leu Ser Tyr Gly Leu Met Pro Leu Val Val Pro Gln Leu Lys
        115                 120                 125

Thr Ile Thr Leu Gly Gly Ala Val Thr Gly Met Gly Val Glu Ser Thr
    130                 135                 140

Ser Phe Arg Asn Gly Leu Pro His Glu Ser Val Leu Glu Met Asp Ile
145                 150                 155                 160

Phe Thr Gly Thr Gly Glu Ile Val Thr Cys Ser Pro Thr Glu Asn Val
                165                 170                 175

Asp Leu Tyr Arg Gly Phe Pro Asn Ser Tyr Gly Ser Leu Gly Tyr Ala
            180                 185                 190

Val Arg Leu Lys Ile Glu Leu Glu Pro Val Gln Asp Tyr Val Gln Leu
        195                 200                 205

Arg His Val Arg Phe Asn Asp Leu Glu Ser Leu Thr Lys Ala Ile Glu
    210                 215                 220
```

```
Glu Val Ala Ser Ser Leu Glu Phe Asp Asn Gln Pro Val Asp Tyr Leu
225                 230                 235                 240

Asp Gly Val Val Phe Ser Pro Thr Glu Ala Tyr Leu Val Leu Gly Thr
                245                 250                 255

Gln Thr Ser Gln Pro Gly Pro Thr Ser Asp Tyr Thr Arg Asp Leu Ser
            260                 265                 270

Tyr
```

<210> 2359
<211> 1020
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(997)
<223> RXA01656

<400> 2359

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tcggcaagca tggcttcatc gtcctcaaaa aagtggtcta atgcaagtga ctgaaagtgg 60

atctaccgct agtccacttt gtggcgttgg atcatctgtc atg acc gaa act caa   115
                                            Met Thr Glu Thr Gln
                                              1               5

gaa act tac caa gca acc act cgt gtg aag cgc ggc ctt gcc gac atg   163
Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg Gly Leu Ala Asp Met
                 10                  15                  20

ctc aag ggt ggt gtg atc atg gat gtg gtc acc cct gaa caa gcg cgc   211
Leu Lys Gly Gly Val Ile Met Asp Val Val Thr Pro Glu Gln Ala Arg
             25                  30                  35

atc gcc gaa gat gca ggt gcc agc gca gtt atg gca ctc gag cgc gtt   259
Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met Ala Leu Glu Arg Val
         40                  45                  50

ccc gcc gat atc cgt tct cag ggc ggc gtt gct cgc atg agt gat cct   307
Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala Arg Met Ser Asp Pro
     55                  60                  65

gac ctg atc gaa gga atc gtc aat gcg gtc tcc atc ccg gtc atg gcg   355
Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser Ile Pro Val Met Ala
 70                  75                  80                  85

aaa gct cgc atc ggt cac ttc gtg gaa gct cag gtt ctg gaa gct ctc   403
Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Val Leu Glu Ala Leu
                 90                  95                 100

ggt gtt gat ttc atc gac gag tcc gaa gtt ctc agc cct gcc gac tac   451
Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu Ser Pro Ala Asp Tyr
            105                 110                 115

acg cac cac atc aac aag tgg aag ttc gac gtt cct ttc gtc tgt ggc   499
Thr His His Ile Asn Lys Trp Lys Phe Asp Val Pro Phe Val Cys Gly
        120                 125                 130
```

```
gcg acc aac ctc ggc gaa gct ttg cga cgc atc acc gaa ggc gct gca   547
Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile Thr Glu Gly Ala Ala
    135                 140                 145

atg atc cgt tcc aag ggc gaa gcc ggc acc ggc gat gtc tct gaa gct   595
Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly Asp Val Ser Glu Ala
150                 155                 160                 165

gtc cgt cac ctg cgc acc atc cgc ggc gac atc aat cgc ctg cgc tcc   643
Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile Asn Arg Leu Arg Ser
                170                 175                 180

ctg gat gag gat gaa ctc ttc gtc gcc gcc aag gaa ttc cag gca cca   691
Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys Glu Phe Gln Ala Pro
            185                 190                 195

tac gac ctg gtc cgc gaa gtc gcc tcc acc ggc aag ctc cct gtg gtc   739
Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly Lys Leu Pro Val Val
        200                 205                 210

acc ttc gtt gca ggt ggc gtc gca acc cca gcc gac gct gca ctc gtg   787
Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Val
    215                 220                 225

cgc caa atg ggc gcc gaa ggc gtc ttt gtc ggc tcc ggc atc ttc aaa   835
Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly Ser Gly Ile Phe Lys
230                 235                 240                 245

tcc ggc aat cca gcc gcc cgc gcc gca gcg atc gtc aag gct gca acg   883
Ser Gly Asn Pro Ala Ala Arg Ala Ala Ala Ile Val Lys Ala Ala Thr
                250                 255                 260

ctt ttc gac gac ccc tcc gtc att gcc gac gta tcc cgc ggc ctg ggt   931
Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val Ser Arg Gly Leu Gly
            265                 270                 275

gaa gcc atg gtg ggc atc aac gta tcc gac gtt cca gca cca cac cga   979
Glu Ala Met Val Gly Ile Asn Val Ser Asp Val Pro Ala Pro His Arg
        280                 285                 290

ctc gcc gag cgc ggc tgg tgatcgttgg agttttagct ctc                1020
Leu Ala Glu Arg Gly Trp
    295
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Filing Date: 05/05/2010
Application No.: 10/577,890

<210> 2360
<211> 299
<212> PRT
<213> Corynebacterium glutamicum

<400> 2360

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Met Thr Glu Thr Gln Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg
  1               5                  10                  15

Gly Leu Ala Asp Met Leu Lys Gly Gly Val Ile Met Asp Val Val Thr
             20                  25                  30

Pro Glu Gln Ala Arg Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met
         35                  40                  45
```

```
Ala Leu Glu Arg Val Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala
     50                  55                  60

Arg Met Ser Asp Pro Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser
 65                  70                  75                  80

Ile Pro Val Met Ala Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln
                 85                  90                  95

Val Leu Glu Ala Leu Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu
            100                 105                 110

Ser Pro Ala Asp Tyr Thr His His Ile Asn Lys Trp Lys Phe Asp Val
        115                 120                 125

Pro Phe Val Cys Gly Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile
    130                 135                 140

Thr Glu Gly Ala Ala Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly
145                 150                 155                 160

Asp Val Ser Glu Ala Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile
                165                 170                 175

Asn Arg Leu Arg Ser Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys
            180                 185                 190

Glu Phe Gln Ala Pro Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly
        195                 200                 205

Lys Leu Pro Val Val Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala
    210                 215                 220

Asp Ala Ala Leu Val Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly
225                 230                 235                 240

Ser Gly Ile Phe Lys Ser Gly Asn Pro Ala Ala Arg Ala Ala Ala Ile
                245                 250                 255

Val Lys Ala Ala Thr Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val
            260                 265                 270

Ser Arg Gly Leu Gly Glu Ala Met Val Gly Ile Asn Val Ser Asp Val
        275                 280                 285

Pro Ala Pro His Arg Leu Ala Glu Arg Gly Trp
    290                 295
```

<210> 2361
<211> 843
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(820)
<223> RXA01665

<400> 2361
aggattggcg cccgtgacgc tactgaaaag gtggaggggc gcgtcgaaaa gcgttggccg 60

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gtgcttgagc gaaaacccgt gatgattagc atggtttgtt gtg aag atc gat gaa   115
                                              Val Lys Ile Asp Glu
                                                1               5

ttg att gct ctc gcc gcg gag caa ccc act cgc atc tcc agg cgt tcc   163
Leu Ile Ala Leu Ala Ala Glu Gln Pro Thr Arg Ile Ser Arg Arg Ser
               10                  15                  20

ggt gtc tcg cgc tcg acc ctg aag cgg gtc ggc gat ggc acc agc gag   211
Gly Val Ser Arg Ser Thr Leu Lys Arg Val Gly Asp Gly Thr Ser Glu
           25                  30                  35

ccc acc ctg tcg acg ctg cgt gag gtc gcg ttg gcg ctc ggg ctt gat   259
Pro Thr Leu Ser Thr Leu Arg Glu Val Ala Leu Ala Leu Gly Leu Asp
       40                  45                  50

att aag gtc gcc gcg cac cac gcc tgc gat ccc ttt gcg gcc gct gca   307
Ile Lys Val Ala Ala His His Ala Cys Asp Pro Phe Ala Ala Ala Ala
   55                  60                  65

gcg cgc acg ctt atc gac gcc tcc gtc ccc gaa aat ccc cac aac cag   355
Ala Arg Thr Leu Ile Asp Ala Ser Val Pro Glu Asn Pro His Asn Gln
70                  75                  80                  85

gaa att ctc gct tgg ttg cac cgt ttt gag cgg tgg aat atc aac gat   403
Glu Ile Leu Ala Trp Leu His Arg Phe Glu Arg Trp Asn Ile Asn Asp
               90                  95                 100

ccg ctc acc ctt gtc tct gaa gcc gga acg ctt cag ggc atc aca cat   451
Pro Leu Thr Leu Val Ser Glu Ala Gly Thr Leu Gln Gly Ile Thr His
           105                 110                 115

cgc cag gat gcg cag ttt gtg aaa ctc aat cca cgc ggc atc gct gag   499
Arg Gln Asp Ala Gln Phe Val Lys Leu Asn Pro Arg Gly Ile Ala Glu
       120                 125                 130

cta ccg gag ctt ttc caa cag cac aaa acc aaa tgg gcg ctg tcg ggc   547
Leu Pro Glu Leu Phe Gln Gln His Lys Thr Lys Trp Ala Leu Ser Gly
   135                 140                 145

gct gcg gct gcc acg gtg atc atg gga caa att gtg ctg ggg aat tcg   595
Ala Ala Ala Ala Thr Val Ile Met Gly Gln Ile Val Leu Gly Asn Ser
150                 155                 160                 165

att gtg tgg cac gaa cct gcc cac gat ctc gat gtc tca gcg ctg ggc   643
Ile Val Trp His Glu Pro Ala His Asp Leu Asp Val Ser Ala Leu Gly
               170                 175                 180

acc att gtt gat gtg gca gaa gac gcc gat cta att ctc ctg ccc gca   691
Thr Ile Val Asp Val Ala Glu Asp Ala Asp Leu Ile Leu Leu Pro Ala
           185                 190                 195

acg gtc acg gaa ctg gtg gga agt tac acc cag gac agg cta aat ttt   739
Thr Val Thr Glu Leu Val Gly Ser Tyr Thr Gln Asp Arg Leu Asn Phe
       200                 205                 210

gtg gca cct gtg caa tta gtt att gat cta cac agc ctc cac atg ttc   787
Val Ala Pro Val Gln Leu Val Ile Asp Leu His Ser Leu His Met Phe
   215                 220                 225
```

```
gag gaa gcc gat tac ctc acg agc ggt tgg cgc taaaatactt agcgtacgca 840
Glu Glu Ala Asp Tyr Leu Thr Ser Gly Trp Arg
230                 235                 240

ccc                                                               843


<210> 2362
<211> 240
<212> PRT
<213> Corynebacterium glutamicum

<400> 2362
Val Lys Ile Asp Glu Leu Ile Ala Leu Ala Ala Glu Gln Pro Thr Arg
  1               5                  10                  15

Ile Ser Arg Arg Ser Gly Val Ser Arg Ser Thr Leu Lys Arg Val Gly
             20                  25                  30

Asp Gly Thr Ser Glu Pro Thr Leu Ser Thr Leu Arg Glu Val Ala Leu
         35                  40                  45

Ala Leu Gly Leu Asp Ile Lys Val Ala Ala His His Ala Cys Asp Pro
     50                  55                  60

Phe Ala Ala Ala Ala Ala Arg Thr Leu Ile Asp Ala Ser Val Pro Glu
 65                  70                  75                  80

Asn Pro His Asn Gln Glu Ile Leu Ala Trp Leu His Arg Phe Glu Arg
                 85                  90                  95

Trp Asn Ile Asn Asp Pro Leu Thr Leu Val Ser Glu Ala Gly Thr Leu
            100                 105                 110

Gln Gly Ile Thr His Arg Gln Asp Ala Gln Phe Val Lys Leu Asn Pro
        115                 120                 125

Arg Gly Ile Ala Glu Leu Pro Glu Leu Phe Gln Gln His Lys Thr Lys
    130                 135                 140

Trp Ala Leu Ser Gly Ala Ala Ala Ala Thr Val Ile Met Gly Gln Ile
145                 150                 155                 160

Val Leu Gly Asn Ser Ile Val Trp His Glu Pro Ala His Asp Leu Asp
                165                 170                 175

Val Ser Ala Leu Gly Thr Ile Val Asp Val Ala Glu Asp Ala Asp Leu
            180                 185                 190

Ile Leu Leu Pro Ala Thr Val Thr Glu Leu Val Gly Ser Tyr Thr Gln
        195                 200                 205

Asp Arg Leu Asn Phe Val Ala Pro Val Gln Leu Val Ile Asp Leu His
    210                 215                 220

Ser Leu His Met Phe Glu Glu Ala Asp Tyr Leu Thr Ser Gly Trp Arg
225                 230                 235                 240
```

<210> 2363
<211> 738
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(715)
<223> RXA01671

<400> 2363
tctaaaaaca catttttaag ccctcccggc gcagctgaaa actcagtcgc cgggagggct 60

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ttttttgtacc cgaatttgta cccgaattta aggaatcgct atg aat cat gtt gtt   115
                                            Met Asn His Val Val
                                              1               5

aat ttt gct tca cat ttg gaa gac gca gcc ctg aag caa gcc gaa gct   163
Asn Phe Ala Ser His Leu Glu Asp Ala Ala Leu Lys Gln Ala Glu Ala
                  10                  15                  20

act gcc acc atg ccg ttt att tac ccg cat gtg gcg ttg atg cct gat   211
Thr Ala Thr Met Pro Phe Ile Tyr Pro His Val Ala Leu Met Pro Asp
             25                  30                  35

gct cac ttt ggg ctg ggt tcg tcg gtg gga acg gtg ttc ggc acc aag   259
Ala His Phe Gly Leu Gly Ser Ser Val Gly Thr Val Phe Gly Thr Lys
         40                  45                  50

ggt gcg atc att ccg gcg gct gtg ggt gtg gat ata ggt tgc gga atg   307
Gly Ala Ile Ile Pro Ala Ala Val Gly Val Asp Ile Gly Cys Gly Met
     55                  60                  65

ata gga gtg tgt acc aat tac acg gcc tct gac ctg gag gga cgt gat   355
Ile Gly Val Cys Thr Asn Tyr Thr Ala Ser Asp Leu Glu Gly Arg Asp
 70                  75                  80                  85

ttg gtg acg ctt cgg gat tac atc gag cgg gtg att ccg ttg tct cct   403
Leu Val Thr Leu Arg Asp Tyr Ile Glu Arg Val Ile Pro Leu Ser Pro
                 90                  95                 100

gga aat tac aat tcc acc acc ttg aag gaa acc gcg aag gtg aag gtc   451
Gly Asn Tyr Asn Ser Thr Thr Leu Lys Glu Thr Ala Lys Val Lys Val
            105                 110                 115

gcg gag ttg gag gaa ctc gcg gag cgc gat ggt gta gat ttg tcg cac   499
Ala Glu Leu Glu Glu Leu Ala Glu Arg Asp Gly Val Asp Leu Ser His
        120                 125                 130

tct ccg acg tgg aag cgc cag ttg ggt tcg ctt ggt gga ggt aat cac   547
Ser Pro Thr Trp Lys Arg Gln Leu Gly Ser Leu Gly Gly Gly Asn His
    135                 140                 145

ttc att gag ttg tgt ctt gat gag ttg gat cgg gtg tgg atg ttt ttg   595
Phe Ile Glu Leu Cys Leu Asp Glu Leu Asp Arg Val Trp Met Phe Leu
150                 155                 160                 165

cac tct ggt tcc cgc ggt gtg ggt aac aag att gcc cat aag cac atc   643
His Ser Gly Ser Arg Gly Val Gly Asn Lys Ile Ala His Lys His Ile
                170                 175                 180
```

```
aag aac gcg cag gcc cag tgt aag aat gag gag ctt ccc gat aag gat   691
Lys Asn Ala Gln Ala Gln Cys Lys Asn Glu Glu Leu Pro Asp Lys Asp
            185                 190                 195

ctt gcg tac ctt gac cga ggg gac tgaggagttt gagtcttaca tca        738
Leu Ala Tyr Leu Asp Arg Gly Asp
        200                 205
```

<210> 2364
<211> 205
<212> PRT
<213> Corynebacterium glutamicum

<400> 2364

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Met Asn His Val Val Asn Phe Ala Ser His Leu Glu Asp Ala Ala Leu
  1               5                  10                  15

Lys Gln Ala Glu Ala Thr Ala Thr Met Pro Phe Ile Tyr Pro His Val
             20                  25                  30

Ala Leu Met Pro Asp Ala His Phe Gly Leu Gly Ser Ser Val Gly Thr
         35                  40                  45

Val Phe Gly Thr Lys Gly Ala Ile Ile Pro Ala Ala Val Gly Val Asp
     50                  55                  60

Ile Gly Cys Gly Met Ile Gly Val Cys Thr Asn Tyr Thr Ala Ser Asp
 65                  70                  75                  80

Leu Glu Gly Arg Asp Leu Val Thr Leu Arg Asp Tyr Ile Glu Arg Val
                 85                  90                  95

Ile Pro Leu Ser Pro Gly Asn Tyr Asn Ser Thr Thr Leu Lys Glu Thr
            100                 105                 110

Ala Lys Val Lys Val Ala Glu Leu Glu Glu Leu Ala Glu Arg Asp Gly
        115                 120                 125

Val Asp Leu Ser His Ser Pro Thr Trp Lys Arg Gln Leu Gly Ser Leu
    130                 135                 140

Gly Gly Gly Asn His Phe Ile Glu Leu Cys Leu Asp Glu Leu Asp Arg
145                 150                 155                 160

Val Trp Met Phe Leu His Ser Gly Ser Arg Gly Val Gly Asn Lys Ile
                165                 170                 175

Ala His Lys His Ile Lys Asn Ala Gln Ala Gln Cys Lys Asn Glu Glu
            180                 185                 190

Leu Pro Asp Lys Asp Leu Ala Tyr Leu Asp Arg Gly Asp
        195                 200                 205
```

<210> 2365
<211> 1158
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1135)
<223> RXA01673

<400> 2365
agtttgcagg ttcggccacc cattatccat atcaacatta tatgggtgga tatgaaagta 60

ccgtctaccg cgttcttttc aattagcgca accttgaagc atg tct aca aac ctt 115
Met Ser Thr Asn Leu
1 5

ctg gaa tcg acg ccg ccc ttt acc caa ctt cgc acc gga gtc ctc cag 163
Leu Glu Ser Thr Pro Pro Phe Thr Gln Leu Arg Thr Gly Val Leu Gln
10 15 20

aag tac acc ccg ggc ctg ctc tta tgc tcc att gcg gta ctc atc gct 211
Lys Tyr Thr Pro Gly Leu Leu Leu Cys Ser Ile Ala Val Leu Ile Ala
25 30 35

atg atc gtg aat cac ttt ttc tct ggt gtg agt ccg ctt atc gtc gcg 259
Met Ile Val Asn His Phe Phe Ser Gly Val Ser Pro Leu Ile Val Ala
40 45 50

atc att ctt ggc atc atc ctg acc aac ctg att cag ctc cca gca tcg 307
Ile Ile Leu Gly Ile Ile Leu Thr Asn Leu Ile Gln Leu Pro Ala Ser
55 60 65

acc tca ccc ggc atc acg ttg gcg tcg aaa aag ctt ttg cgg ctg gga 355
Thr Ser Pro Gly Ile Thr Leu Ala Ser Lys Lys Leu Leu Arg Leu Gly
70 75 80 85

atc gtc ttc ctt ggt ctg cag tta gtt ttc tca gat att ttg tca ctt 403
Ile Val Phe Leu Gly Leu Gln Leu Val Phe Ser Asp Ile Leu Ser Leu
90 95 100

ggt ttc ccc atg ctg gcg gtg att gtg tgc atc gtt gcc ggt ggt att 451
Gly Phe Pro Met Leu Ala Val Ile Val Cys Ile Val Ala Gly Gly Ile
105 110 115

ttt ggg acc atc ctc atg gga cac ctg ctc aga atg aaa cca acc caa 499
Phe Gly Thr Ile Leu Met Gly His Leu Leu Arg Met Lys Pro Thr Gln
120 125 130

gtt ctg ttg att gct tgt ggc ttt tct att tgt ggc gct gcg gcc gtg 547
Val Leu Leu Ile Ala Cys Gly Phe Ser Ile Cys Gly Ala Ala Ala Val
135 140 145

gca ggt gtt gaa gga gta act gat tcc gaa gaa gaa gag gtc gtt act 595
Ala Gly Val Glu Gly Val Thr Asp Ser Glu Glu Glu Glu Val Val Thr
150 155 160 165

gcg gtt gca ctt gtt gtt att ttc gga acg ctg atg att cct ttt atc 643
Ala Val Ala Leu Val Val Ile Phe Gly Thr Leu Met Ile Pro Phe Ile
170 175 180

cca ttc gca acc aaa gtc ttg ggg tta tcc cct gaa atc ggt ggg atg 691
Pro Phe Ala Thr Lys Val Leu Gly Leu Ser Pro Glu Ile Gly Gly Met
185 190 195

tgg gca ggc gga tcc atc cat gaa atc gcc caa gta gta gca gct gga 739

```
Trp Ala Gly Gly Ser Ile His Glu Ile Ala Gln Val Val Ala Ala Gly
       200                 205                 210

gga gtc att ggt ggt gga gca tta ggt gtt gca gtt gtg gtg aaa ctc   787
Gly Val Ile Gly Gly Gly Ala Leu Gly Val Ala Val Val Val Lys Leu
    215                 220                 225

gcc cga gta ctc cta ctt gca ccc att gct gcc att tta agt ttt cgc   835
Ala Arg Val Leu Leu Leu Ala Pro Ile Ala Ala Ile Leu Ser Phe Arg
230                 235                 240                 245

cag cgc cgc cag ggt tac acg tcc ccc gat gga aag aga cca ccg gtc   883
Gln Arg Arg Gln Gly Tyr Thr Ser Pro Asp Gly Lys Arg Pro Pro Val
                250                 255                 260

gtt ccc cta ttt atc ctt gga ttc ttg gcg atg gta gtt ttg cgc tcc   931
Val Pro Leu Phe Ile Leu Gly Phe Leu Ala Met Val Val Leu Arg Ser
            265                 270                 275

act gtt gcg ctc cca gac gag gta att gcg gct gga ggt ttc cta cag   979
Thr Val Ala Leu Pro Asp Glu Val Ile Ala Ala Gly Gly Phe Leu Gln
        280                 285                 290

aca gcc ttg ctc tct gca gca atg ttt ggt ctc ggg tgt ggc gta aaa   1027
Thr Ala Leu Leu Ser Ala Ala Met Phe Gly Leu Gly Cys Gly Val Lys
    295                 300                 305

atc cag aac ctg atc cat gtt ggg gtc aag cct ttc att ctg gct ttc   1075
Ile Gln Asn Leu Ile His Val Gly Val Lys Pro Phe Ile Leu Ala Phe
310                 315                 320                 325

gga tcc acg aca ctt gtc acc agt atc gca ctt gca ggc acc cta ctc   1123
Gly Ser Thr Thr Leu Val Thr Ser Ile Ala Leu Ala Gly Thr Leu Leu
                330                 335                 340

acc cac ctc gga tagaaccgaa gacccagttg tac                        1158
Thr His Leu Gly
            345
```

<210> 2366
<211> 345
<212> PRT
<213> Corynebacterium glutamicum

<400> 2366

```
Met Ser Thr Asn Leu Leu Glu Ser Thr Pro Pro Phe Thr Gln Leu Arg
  1               5                  10                  15

Thr Gly Val Leu Gln Lys Tyr Thr Pro Gly Leu Leu Leu Cys Ser Ile
             20                  25                  30

Ala Val Leu Ile Ala Met Ile Val Asn His Phe Phe Ser Gly Val Ser
         35                  40                  45

Pro Leu Ile Val Ala Ile Ile Leu Gly Ile Ile Leu Thr Asn Leu Ile
     50                  55                  60

Gln Leu Pro Ala Ser Thr Ser Pro Gly Ile Thr Leu Ala Ser Lys Lys
 65                  70                  75                  80
```

```
Leu Leu Arg Leu Gly Ile Val Phe Leu Gly Leu Gln Leu Val Phe Ser
                 85                  90                  95

Asp Ile Leu Ser Leu Gly Phe Pro Met Leu Ala Val Ile Val Cys Ile
            100                 105                 110

Val Ala Gly Gly Ile Phe Gly Thr Ile Leu Met Gly His Leu Leu Arg
        115                 120                 125

Met Lys Pro Thr Gln Val Leu Leu Ile Ala Cys Gly Phe Ser Ile Cys
    130                 135                 140

Gly Ala Ala Ala Val Ala Gly Val Glu Gly Val Thr Asp Ser Glu Glu
145                 150                 155                 160

Glu Glu Val Val Thr Ala Val Ala Leu Val Val Ile Phe Gly Thr Leu
                165                 170                 175

Met Ile Pro Phe Ile Pro Phe Ala Thr Lys Val Leu Gly Leu Ser Pro
            180                 185                 190

Glu Ile Gly Gly Met Trp Ala Gly Gly Ser Ile His Glu Ile Ala Gln
        195                 200                 205

Val Val Ala Ala Gly Gly Val Ile Gly Gly Gly Ala Leu Gly Val Ala
    210                 215                 220

Val Val Val Lys Leu Ala Arg Val Leu Leu Leu Ala Pro Ile Ala Ala
225                 230                 235                 240

Ile Leu Ser Phe Arg Gln Arg Arg Gln Gly Tyr Thr Ser Pro Asp Gly
                245                 250                 255

Lys Arg Pro Pro Val Val Pro Leu Phe Ile Leu Gly Phe Leu Ala Met
            260                 265                 270

Val Val Leu Arg Ser Thr Val Ala Leu Pro Asp Glu Val Ile Ala Ala
        275                 280                 285

Gly Gly Phe Leu Gln Thr Ala Leu Leu Ser Ala Ala Met Phe Gly Leu
    290                 295                 300

Gly Cys Gly Val Lys Ile Gln Asn Leu Ile His Val Gly Val Lys Pro
305                 310                 315                 320

Phe Ile Leu Ala Phe Gly Ser Thr Thr Leu Val Thr Ser Ile Ala Leu
                325                 330                 335

Ala Gly Thr Leu Leu Thr His Leu Gly
            340                 345
```

<210> 2367
<211> 534
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> RXA01675

<400> 2367
ttgccgattc tagcgggaga attagtgtcc atcgcatcga accacatctg attttgagcc 60

ctggctaacg gattgttttt gacagattgg aatgacaata atg aac gag att cca 115
Met Asn Glu Ile Pro
1 5

gaa tgg ttg act ctt gta tct gtt gaa gca gga aag aga ctt ggg cgg 163
Glu Trp Leu Thr Leu Val Ser Val Glu Ala Gly Lys Arg Leu Gly Arg
10 15 20

cct ggg cca ttg gtg ttt ccg ccg gag ttg gtc act ttg gca gtt gaa 211
Pro Gly Pro Leu Val Phe Pro Pro Glu Leu Val Thr Leu Ala Val Glu
25 30 35

ggg att gag ctt att gaa ctt gag cct tca tgg act tct gat ttg cct 259
Gly Ile Glu Leu Ile Glu Leu Glu Pro Ser Trp Thr Ser Asp Leu Pro
40 45 50

ctg ccg gaa ttc ggg ttc cta gct gcg gat atg gtt gat ttc tat gat 307
Leu Pro Glu Phe Gly Phe Leu Ala Ala Asp Met Val Asp Phe Tyr Asp
55 60 65

gat tat gag ttt agt gaa tgg att ccg ggt gcg tgg cct ctt gct tta 355
Asp Tyr Glu Phe Ser Glu Trp Ile Pro Gly Ala Trp Pro Leu Ala Leu
70 75 80 85

gat ggt gga gga ggt ttc ttt tgc ctt gat ctc cgt gct gcc aac gct 403
Asp Gly Gly Gly Gly Phe Phe Cys Leu Asp Leu Arg Ala Ala Asn Ala
90 95 100

gat gga gag att cct gtt gtg tgg gtg cat gcc agc aac ttg ggt tgg 451
Asp Gly Glu Ile Pro Val Val Trp Val His Ala Ser Asn Leu Gly Trp
105 110 115

ggt gat gat gag gca gta cgc gta gct gcc tcg ttg gca gat ttg ttg 499
Gly Asp Asp Glu Ala Val Arg Val Ala Ala Ser Leu Ala Asp Leu Leu
120 125 130

agt ccg tcg aaa tagaagaatt agcatttacc gga 534
Ser Pro Ser Lys
135

<210> 2368
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 2368
Met Asn Glu Ile Pro Glu Trp Leu Thr Leu Val Ser Val Glu Ala Gly
1 5 10 15

Lys Arg Leu Gly Arg Pro Gly Pro Leu Val Phe Pro Pro Glu Leu Val
20 25 30

Thr Leu Ala Val Glu Gly Ile Glu Leu Ile Glu Leu Glu Pro Ser Trp
35 40 45

Thr Ser Asp Leu Pro Leu Pro Glu Phe Gly Phe Leu Ala Ala Asp Met

```
     50                  55                  60

Val Asp Phe Tyr Asp Asp Tyr Glu Phe Ser Glu Trp Ile Pro Gly Ala
 65                  70                  75                  80

Trp Pro Leu Ala Leu Asp Gly Gly Gly Gly Phe Phe Cys Leu Asp Leu
                 85                  90                  95

Arg Ala Ala Asn Ala Asp Gly Glu Ile Pro Val Val Trp Val His Ala
            100                 105                 110

Ser Asn Leu Gly Trp Gly Asp Asp Glu Ala Val Arg Val Ala Ala Ser
        115                 120                 125

Leu Ala Asp Leu Leu Ser Pro Ser Lys
    130                 135


<210> 2369
<211> 879
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(856)
<223> RXA01676

<400> 2369
agttacagct tttctcggtg gcacactcgc gctacttagc ccttgtgccg cactcctttt 60

accagcattt tttgcatcct cagtgggtgc tggcccgcgc atg atc ctt cac ggt   115
                                            Met Ile Leu His Gly
                                              1               5

gtt gtg ttc tac gca gga ctt cta gta ctt ctc gtg cca ctt ggc ctt   163
Val Val Phe Tyr Ala Gly Leu Leu Val Leu Leu Val Pro Leu Gly Leu
                 10                  15                  20

ggt gcg gga atc ctc ggc gag ctg ttt atc acc caa cgc cag acc atc   211
Gly Ala Gly Ile Leu Gly Glu Leu Phe Ile Thr Gln Arg Gln Thr Ile
             25                  30                  35

atc gtg gtt tca tcg atc gtg ctg att atc cta ggt ttt gtc cag atc   259
Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu Gly Phe Val Gln Ile
         40                  45                  50

ttc ggc ggc gga ttc gac ttc gga aaa gca ctc cca gga tta gat cgt   307
Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu Pro Gly Leu Asp Arg
     55                  60                  65

ctg caa tct aag gcc act gtg acc tca ggt cta gga aag agc ttt tta   355
Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu Gly Lys Ser Phe Leu
 70                  75                  80                  85

cta gga atg acc agt agt att gcc ggt ttt tgt tcc gga cca atc ctc   403
Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys Ser Gly Pro Ile Leu
                 90                  95                 100

ggc gcc gtt ctt act ttg gct gcc acc agt gga aac tcc atc acc tca   451
Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly Asn Ser Ile Thr Ser
```

```
            105                 110                 115

gca ctc att ttg agt gct tat ggt gcg gga atg gtg ctg ccc ctg atg   499
Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met Val Leu Pro Leu Met
        120                 125                 130

gct att gca gcg ctc tgg gcc aaa ctc gga cag cgt gga cag cag atg   547
Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln Arg Gly Gln Gln Met
    135                 140                 145

ctc cgc ggc cgg gaa ttc acc ttc ttg ggc agg cag tgg cac att gtt   595
Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg Gln Trp His Ile Val
150                 155                 160                 165

tct gtc att agc ggt gcc ctg atc atc gct gtc gga atc ctc ttt tgg   643
Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val Gly Ile Leu Phe Trp
                170                 175                 180

tcc acg aac ggc ctt gtc agc atg ccg gag ctc gtt cca atg gac acc   691
Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu Val Pro Met Asp Thr
            185                 190                 195

cag atc tgg cta cag gaa gcc aca ttc tca ctc ggg tca cca ctc ttt   739
Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu Gly Ser Pro Leu Phe
        200                 205                 210

gac atc gca ttg atc att gtc gcc gct ggc ttg ttc ttg tac ttc tgg   787
Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu Phe Leu Tyr Phe Trp
    215                 220                 225

aac aaa cga caa aag cga aaa gaa gaa gct cag cga ccc aaa gaa agt   835
Asn Lys Arg Gln Lys Arg Lys Glu Glu Ala Gln Arg Pro Lys Glu Ser
230                 235                 240                 245

gga tgg gtt att aac cct cgc taattattag ttttggagcg agg            879
Gly Trp Val Ile Asn Pro Arg
                250
```

US20050170452A1

<210> 2370
<211> 252
<212> PRT
<213> Corynebacterium glutamicum

<400> 2370

```
Met Ile Leu His Gly Val Val Phe Tyr Ala Gly Leu Leu Val Leu Leu
  1               5                  10                  15

Val Pro Leu Gly Leu Gly Ala Gly Ile Leu Gly Glu Leu Phe Ile Thr
             20                  25                  30

Gln Arg Gln Thr Ile Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu
         35                  40                  45

Gly Phe Val Gln Ile Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu
     50                  55                  60

Pro Gly Leu Asp Arg Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu
 65                  70                  75                  80

Gly Lys Ser Phe Leu Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys
```

```
                85                  90                  95

Ser Gly Pro Ile Leu Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly
            100                 105                 110

Asn Ser Ile Thr Ser Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met
        115                 120                 125

Val Leu Pro Leu Met Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln
    130                 135                 140

Arg Gly Gln Gln Met Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg
145                 150                 155                 160

Gln Trp His Ile Val Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val
                165                 170                 175

Gly Ile Leu Phe Trp Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu
            180                 185                 190

Val Pro Met Asp Thr Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu
        195                 200                 205

Gly Ser Pro Leu Phe Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu
    210                 215                 220

Phe Leu Tyr Phe Trp Asn Lys Arg Gln Lys Arg Lys Glu Glu Ala Gln
225                 230                 235                 240

Arg Pro Lys Glu Ser Gly Trp Val Ile Asn Pro Arg
                245                 250
```

<210> 2371
<211> 867
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(844)
<223> RXA01677

<400> 2371

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gtcgccatag ttgagtttta ttcatggctt ttagctaggc gactttagtt gagggctttt 60

agttgagggc ttcccagcag ggatggttaa ggagaattca gtg aac caa cag agt   115
                                            Val Asn Gln Gln Ser
                                              1               5

aaa aag tgg ctc gta ccg aca ctg gtc gtc atc att gca gtg ctc ctc   163
Lys Lys Trp Leu Val Pro Thr Leu Val Val Ile Ile Ala Val Leu Leu
                  10                  15                  20

atc gca gtt gtt ctg ttg atg tac cga gga aat gcg agt gat acg gcc   211
Ile Ala Val Val Leu Leu Met Tyr Arg Gly Asn Ala Ser Asp Thr Ala
              25                  30                  35

gag ggc gtt tca gcc gct gcg act tcg gac tcg gct gct gct tcg act   259
Glu Gly Val Ser Ala Ala Ala Thr Ser Asp Ser Ala Ala Ala Ser Thr
          40                  45                  50
```

```
gct gct tcg ggt tcc gct tct ggt gct gcg gac tcc gat ctg acc agc   307
Ala Ala Ser Gly Ser Ala Ser Gly Ala Ala Asp Ser Asp Leu Thr Ser
     55                  60                  65

gtg gaa gca cgc gac cct tcc gac cct gtt gcg gtg gga gac gtt gat   355
Val Glu Ala Arg Asp Pro Ser Asp Pro Val Ala Val Gly Asp Val Asp
 70                  75                  80                  85

gca cct gtt ggg tta gtg gtg ttt tcc gac tac caa tgc ccg ttc tgt   403
Ala Pro Val Gly Leu Val Val Phe Ser Asp Tyr Gln Cys Pro Phe Cys
                 90                  95                 100

gca aag tgg agc gat gaa acc ctg cca cag atg atg aag cat gtg gaa   451
Ala Lys Trp Ser Asp Glu Thr Leu Pro Gln Met Met Lys His Val Glu
            105                 110                 115

gat gga aac ctc cgc att gaa tgg cgt gaa gtg aac atc ttt gga gaa   499
Asp Gly Asn Leu Arg Ile Glu Trp Arg Glu Val Asn Ile Phe Gly Glu
        120                 125                 130

cca tct gag cgt gga gct cgc gcg gca tac gct gcg ggt ttg cag gac   547
Pro Ser Glu Arg Gly Ala Arg Ala Ala Tyr Ala Ala Gly Leu Gln Asp
    135                 140                 145

gca tac ttg gaa tac cac aac gca ctc ttt gcc aac ggt gaa aaa ccc   595
Ala Tyr Leu Glu Tyr His Asn Ala Leu Phe Ala Asn Gly Glu Lys Pro
150                 155                 160                 165

agc gaa gac ctg ctc agc gaa gag gga ctt att aag ctt gct ggt gac   643
Ser Glu Asp Leu Leu Ser Glu Glu Gly Leu Ile Lys Leu Ala Gly Asp
                170                 175                 180

ctt gga cta gac gaa tcg aaa ttc act gcc gat ttc caa tcc cct gaa   691
Leu Gly Leu Asp Glu Ser Lys Phe Thr Ala Asp Phe Gln Ser Pro Glu
            185                 190                 195

act gca gtc gca att gcg caa cat caa cag ctg gga atc gat ctt ggc   739
Thr Ala Val Ala Ile Ala Gln His Gln Gln Leu Gly Ile Asp Leu Gly
        200                 205                 210

gcc tac tcc acc cca gct ttc ctc cta ggt ggc cag cca atc atg ggc   787
Ala Tyr Ser Thr Pro Ala Phe Leu Leu Gly Gly Gln Pro Ile Met Gly
    215                 220                 225

gct cag cct gct tct gta ttt gaa gcc gcc ttc gag caa gca ctg gca   835
Ala Gln Pro Ala Ser Val Phe Glu Ala Ala Phe Glu Gln Ala Leu Ala
230                 235                 240                 245

gcg aaa gaa taaaccgtgg atgtcggcct agt                             867
Ala Lys Glu
```

<210> 2372
<211> 248
<212> PRT
<213> Corynebacterium glutamicum

<400> 2372
Val Asn Gln Gln Ser Lys Lys Trp Leu Val Pro Thr Leu Val Val Ile

```
  1               5                  10                  15
Ile Ala Val Leu Leu Ile Ala Val Val Leu Leu Met Tyr Arg Gly Asn
             20                  25                  30
Ala Ser Asp Thr Ala Glu Gly Val Ser Ala Ala Ala Thr Ser Asp Ser
         35                  40                  45
Ala Ala Ala Ser Thr Ala Ala Ser Gly Ser Ala Ser Gly Ala Ala Asp
     50                  55                  60
Ser Asp Leu Thr Ser Val Glu Ala Arg Asp Pro Ser Asp Pro Val Ala
 65                  70                  75                  80
Val Gly Asp Val Asp Ala Pro Val Gly Leu Val Val Phe Ser Asp Tyr
                 85                  90                  95
Gln Cys Pro Phe Cys Ala Lys Trp Ser Asp Glu Thr Leu Pro Gln Met
            100                 105                 110
Met Lys His Val Glu Asp Gly Asn Leu Arg Ile Glu Trp Arg Glu Val
        115                 120                 125
Asn Ile Phe Gly Glu Pro Ser Glu Arg Gly Ala Arg Ala Ala Tyr Ala
    130                 135                 140
Ala Gly Leu Gln Asp Ala Tyr Leu Glu Tyr His Asn Ala Leu Phe Ala
145                 150                 155                 160
Asn Gly Glu Lys Pro Ser Glu Asp Leu Leu Ser Glu Glu Gly Leu Ile
                165                 170                 175
Lys Leu Ala Gly Asp Leu Gly Leu Asp Glu Ser Lys Phe Thr Ala Asp
            180                 185                 190
Phe Gln Ser Pro Glu Thr Ala Val Ala Ile Ala Gln His Gln Gln Leu
        195                 200                 205
Gly Ile Asp Leu Gly Ala Tyr Ser Thr Pro Ala Phe Leu Leu Gly Gly
    210                 215                 220
Gln Pro Ile Met Gly Ala Gln Pro Ala Ser Val Phe Glu Ala Ala Phe
225                 230                 235                 240
Glu Gln Ala Leu Ala Ala Lys Glu
                245
```

<210> 2373
<211> 756
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)
<223> RXA01681

<400> 2373
ctttaacgaa agacttgtcg ttactttagt aattagacca acatggtggt gagtggttga 60

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aatcttgcca tcaaaattat cgagtgagtt gaagcattcc gtg gaa gta cta cta   115
                                            Val Glu Val Leu Leu
                                              1               5

ctt atc gca atc gtc gtt ggt ggt ggc gtt ttt gtc gcc tca aag atg   163
Leu Ile Ala Ile Val Val Gly Gly Gly Val Phe Val Ala Ser Lys Met
                 10                  15                  20

gga tcc aat aac aat aag aag caa gaa gaa gcc aag ttt gct gac gca   211
Gly Ser Asn Asn Asn Lys Lys Gln Glu Glu Ala Lys Phe Ala Asp Ala
             25                  30                  35

cag gca gat gcg cgt cgg tgg att gag cgt ctt ggt tcc cag gtt ttg   259
Gln Ala Asp Ala Arg Arg Trp Ile Glu Arg Leu Gly Ser Gln Val Leu
         40                  45                  50

acc atc gca ggt aca gat gct gcg tcg acc cag gct att gct gac gcc   307
Thr Ile Ala Gly Thr Asp Ala Ala Ser Thr Gln Ala Ile Ala Asp Ala
     55                  60                  65

tca gag cgc tat acc gct gcg tct tct cag att tct tct gcc act act   355
Ser Glu Arg Tyr Thr Ala Ala Ser Ser Gln Ile Ser Ser Ala Thr Thr
 70                  75                  80                  85

cct cgt cag gca gag ttg gct cga gaa tct gca cta gag ggt ctg cat   403
Pro Arg Gln Ala Glu Leu Ala Arg Glu Ser Ala Leu Glu Gly Leu His
                 90                  95                 100

tat atg aac gcg gct cgt gag atc atg ggt atg act gct ggc cct gag   451
Tyr Met Asn Ala Ala Arg Glu Ile Met Gly Met Thr Ala Gly Pro Glu
             105                 110                 115

ctg cct cct ctg gaa ggt cag cgc aat gct ggt cgc gtt aca gaa aag   499
Leu Pro Pro Leu Glu Gly Gln Arg Asn Ala Gly Arg Val Thr Glu Lys
         120                 125                 130

cgc acc att gag cag gag ggt cgc cag atc act gct tcc ccc gtc gca   547
Arg Thr Ile Glu Gln Glu Gly Arg Gln Ile Thr Ala Ser Pro Val Ala
     135                 140                 145

aca gat gaa act ccg aac tac tac cct ggc ggt aac gtt gcg ggt cgc   595
Thr Asp Glu Thr Pro Asn Tyr Tyr Pro Gly Gly Asn Val Ala Gly Arg
150                 155                 160                 165

cca gtc cct gct ggt tgg tac tcc gag cct tgg tgg gca agc gca ttg   643
Pro Val Pro Ala Gly Trp Tyr Ser Glu Pro Trp Trp Ala Ser Ala Leu
                 170                 175                 180

cgt tcc ggt ctg tgg act gca ggt tcg gtc atg atg ttc tca gca atg   691
Arg Ser Gly Leu Trp Thr Ala Gly Ser Val Met Met Phe Ser Ala Met
             185                 190                 195

ttt aac ggc atg gct ggt gtc ggc tac tcc gct gca gac ctt           733
Phe Asn Gly Met Ala Gly Val Gly Tyr Ser Ala Ala Asp Leu
         200                 205                 210

tgaaaaatgg ctatggcgag ggc                                        756
```

<210> 2374
<211> 211

<212> PRT
<213> Corynebacterium glutamicum

<400> 2374

```
Val Glu Val Leu Leu Leu Ile Ala Ile Val Val Gly Gly Gly Val Phe
  1               5                  10                  15

Val Ala Ser Lys Met Gly Ser Asn Asn Asn Lys Lys Gln Glu Glu Ala
             20                  25                  30

Lys Phe Ala Asp Ala Gln Ala Asp Ala Arg Arg Trp Ile Glu Arg Leu
         35                  40                  45

Gly Ser Gln Val Leu Thr Ile Ala Gly Thr Asp Ala Ala Ser Thr Gln
     50                  55                  60

Ala Ile Ala Asp Ala Ser Glu Arg Tyr Thr Ala Ala Ser Ser Gln Ile
 65                  70                  75                  80

Ser Ser Ala Thr Thr Pro Arg Gln Ala Glu Leu Ala Arg Glu Ser Ala
                 85                  90                  95

Leu Glu Gly Leu His Tyr Met Asn Ala Ala Arg Glu Ile Met Gly Met
            100                 105                 110

Thr Ala Gly Pro Glu Leu Pro Pro Leu Glu Gly Gln Arg Asn Ala Gly
        115                 120                 125

Arg Val Thr Glu Lys Arg Thr Ile Glu Gln Glu Gly Arg Gln Ile Thr
    130                 135                 140

Ala Ser Pro Val Ala Thr Asp Glu Thr Pro Asn Tyr Tyr Pro Gly Gly
145                 150                 155                 160

Asn Val Ala Gly Arg Pro Val Pro Ala Gly Trp Tyr Ser Glu Pro Trp
                165                 170                 175

Trp Ala Ser Ala Leu Arg Ser Gly Leu Trp Thr Ala Gly Ser Val Met
            180                 185                 190

Met Phe Ser Ala Met Phe Asn Gly Met Ala Gly Val Gly Tyr Ser Ala
        195                 200                 205

Ala Asp Leu
    210
```

<210> 2375
<211> 702
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(679)
<223> RXA01685

<400> 2375

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caataattag gtgagcaacc ctaataagaa acctttagat cccgcacaaa gattctccct 60

ccccaccaga tgggcgatgt tctttgtcgg gatctttatt atg tcc ttc gcc atc   115
```

```
                                                    Met Ser Phe Ala Ile
                                                      1               5

ggc atc acc gtc cac gca gga cta gga acc acc aca att tca tca ctt   163
Gly Ile Thr Val His Ala Gly Leu Gly Thr Thr Thr Ile Ser Ser Leu
                 10                  15                  20

ccc gtg gtg tgg act gct gcc agc gga tta tcc ctg ggc tgg acc aca   211
Pro Val Val Trp Thr Ala Ala Ser Gly Leu Ser Leu Gly Trp Thr Thr
             25                  30                  35

att tac ttc aat ggc ttc atg att ctg tgc caa ata att gtg ctg cgt   259
Ile Tyr Phe Asn Gly Phe Met Ile Leu Cys Gln Ile Ile Val Leu Arg
         40                  45                  50

tcc cag ttc aaa cca caa atg tta gtc caa atc ctg tgg gca ttc ctc   307
Ser Gln Phe Lys Pro Gln Met Leu Val Gln Ile Leu Trp Ala Phe Leu
     55                  60                  65

ttt ggg ttt ctt tgt gat tta agc ctg caa cta acc acc tgg gcg caa   355
Phe Gly Phe Leu Cys Asp Leu Ser Leu Gln Leu Thr Thr Trp Ala Gln
 70                  75                  80                  85

act gac aat tat ttt gtg gcc tgg atc tgg gtt att gtg tcc acc att   403
Thr Asp Asn Tyr Phe Val Ala Trp Ile Trp Val Ile Val Ser Thr Ile
                 90                  95                 100

ttg atg tcg atc gga gtt ttt att caa gta ctc ccc aac atc act ttc   451
Leu Met Ser Ile Gly Val Phe Ile Gln Val Leu Pro Asn Ile Thr Phe
             105                 110                 115

atc gct ggt gaa ggc att gtc tct gcg ctg gtg aag aaa ttt ccc aac   499
Ile Ala Gly Glu Gly Ile Val Ser Ala Leu Val Lys Lys Phe Pro Asn
         120                 125                 130

gtg gaa ttt ggc acc atg aaa caa atc gtc gac tgg act ttc gtc tcc   547
Val Glu Phe Gly Thr Met Lys Gln Ile Val Asp Trp Thr Phe Val Ser
     135                 140                 145

gtc gct gcc att ttg tcc tgg atc acc atg ggt gga ctt att ggc gtg   595
Val Ala Ala Ile Leu Ser Trp Ile Thr Met Gly Gly Leu Ile Gly Val
150                 155                 160                 165

cgc gaa gga aca gtg ttc gcg gcg ttt ttc atc gga ttc ttc gtc cgc   643
Arg Glu Gly Thr Val Phe Ala Ala Phe Phe Ile Gly Phe Phe Val Arg
                 170                 175                 180

cag tgg cgc aaa ctc tac ctc cgc tcc atc ggt cac taaagagctt       689
Gln Trp Arg Lys Leu Tyr Leu Arg Ser Ile Gly His
             185                 190

gttccaggaa gag                                                   702
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<210> 2376
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 2376
Met Ser Phe Ala Ile Gly Ile Thr Val His Ala Gly Leu Gly Thr Thr

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  1               5                  10                  15

Thr Ile Ser Ser Leu Pro Val Val Trp Thr Ala Ala Ser Gly Leu Ser
            20                  25                  30

Leu Gly Trp Thr Thr Ile Tyr Phe Asn Gly Phe Met Ile Leu Cys Gln
        35                  40                  45

Ile Ile Val Leu Arg Ser Gln Phe Lys Pro Gln Met Leu Val Gln Ile
    50                  55                  60

Leu Trp Ala Phe Leu Phe Gly Phe Leu Cys Asp Leu Ser Leu Gln Leu
65                  70                  75                  80

Thr Thr Trp Ala Gln Thr Asp Asn Tyr Phe Val Ala Trp Ile Trp Val
                85                  90                  95

Ile Val Ser Thr Ile Leu Met Ser Ile Gly Val Phe Ile Gln Val Leu
            100                 105                 110

Pro Asn Ile Thr Phe Ile Ala Gly Glu Gly Ile Val Ser Ala Leu Val
        115                 120                 125

Lys Lys Phe Pro Asn Val Glu Phe Gly Thr Met Lys Gln Ile Val Asp
    130                 135                 140

Trp Thr Phe Val Ser Val Ala Ala Ile Leu Ser Trp Ile Thr Met Gly
145                 150                 155                 160

Gly Leu Ile Gly Val Arg Glu Gly Thr Val Phe Ala Ala Phe Phe Ile
                165                 170                 175

Gly Phe Phe Val Arg Gln Trp Arg Lys Leu Tyr Leu Arg Ser Ile Gly
            180                 185                 190

His
```

<210> 2377
<211> 564
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(541)
<223> RXA01686

<400> 2377
ggaggaaggg ttgcaacgct ttttcaagag aatgaccgtg cgtccgctta aacgaagcgt 60

cgaacgccgg tcttttctca tttcacttaa gatgtagaac atg act tca ctc agg 115
                                        Met Thr Ser Leu Arg
                                          1   5

gac tta ctt gtt tcc acc aat gcc gac gca gca att gca gat atg tca 163
Asp Leu Leu Val Ser Thr Asn Ala Asp Ala Ala Ile Ala Asp Met Ser
                10   15   20

gca ttt atc gaa gaa acc gtg ggc aag caa tcc ggc atc agc ggc atc 211

```
Ala Phe Ile Glu Glu Thr Val Gly Lys Gln Ser Gly Ile Ser Gly Ile
             25                  30                  35

gca ctc aaa ggc gca atg ggt gct gca acc aag atc gac tcc gac atc   259
Ala Leu Lys Gly Ala Met Gly Ala Ala Thr Lys Ile Asp Ser Asp Ile
         40                  45                  50

gta gcc aaa ggc tcc agg cgc ctc ctc ccg gaa atc gct gac tcc ctc   307
Val Ala Lys Gly Ser Arg Arg Leu Leu Pro Glu Ile Ala Asp Ser Leu
     55                  60                  65

gac gga ctc tgg cag gaa tac caa aat ggt ggc acc gcc gca gat ttc   355
Asp Gly Leu Trp Gln Glu Tyr Gln Asn Gly Gly Thr Ala Ala Asp Phe
 70                  75                  80                  85

ggc gcc cac ctc gag gcc aac agc tcc acc gca ctc gac gcg att ctc   403
Gly Ala His Leu Glu Ala Asn Ser Ser Thr Ala Leu Asp Ala Ile Leu
                 90                  95                 100

agc gtt gct gac aaa aac gca gag agc atc aac gtt cca gga ctt ggc   451
Ser Val Ala Asp Lys Asn Ala Glu Ser Ile Asn Val Pro Gly Leu Gly
            105                 110                 115

aag gtc tac aag ggc gtg cgc ggc aag gct gcc aaa gta atc gag cag   499
Lys Val Tyr Lys Gly Val Arg Gly Lys Ala Ala Lys Val Ile Glu Gln
        120                 125                 130

gaa ctt cct gca att ggc cag ttg atc gaa aag aac gca caa           541
Glu Leu Pro Ala Ile Gly Gln Leu Ile Glu Lys Asn Ala Gln
    135                 140                 145

taattaggtg agcaacccta ata                                        564


<210> 2378
<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 2378
Met Thr Ser Leu Arg Asp Leu Leu Val Ser Thr Asn Ala Asp Ala Ala
  1               5                  10                  15

Ile Ala Asp Met Ser Ala Phe Ile Glu Glu Thr Val Gly Lys Gln Ser
             20                  25                  30

Gly Ile Ser Gly Ile Ala Leu Lys Gly Ala Met Gly Ala Ala Thr Lys
         35                  40                  45

Ile Asp Ser Asp Ile Val Ala Lys Gly Ser Arg Arg Leu Leu Pro Glu
     50                  55                  60

Ile Ala Asp Ser Leu Asp Gly Leu Trp Gln Glu Tyr Gln Asn Gly Gly
 65                  70                  75                  80

Thr Ala Ala Asp Phe Gly Ala His Leu Glu Ala Asn Ser Ser Thr Ala
                 85                  90                  95

Leu Asp Ala Ile Leu Ser Val Ala Asp Lys Asn Ala Glu Ser Ile Asn
            100                 105                 110
```

```
Val Pro Gly Leu Gly Lys Val Tyr Lys Gly Val Arg Gly Lys Ala Ala
        115                 120                 125

Lys Val Ile Glu Gln Glu Leu Pro Ala Ile Gly Gln Leu Ile Glu Lys
    130                 135                 140

Asn Ala Gln
145
```

<210> 2379
<211> 1545
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1522)
<223> RXA01693

<400> 2379

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aggagactgg ctggattatt ggctggtttt cttgggaaat cgtcatgggc attaatccta 60

gtcccaacaa ttgccagaac ccgaacacta ggcttgaacc atg aat act gca cct   115
                                            Met Asn Thr Ala Pro
                                              1               5

ttc aaa ctc gaa gct gac ttc gca tca gcc ctg ccc acc atg gca gcc   163
Phe Lys Leu Glu Ala Asp Phe Ala Ser Ala Leu Pro Thr Met Ala Ala
                10                  15                  20

ccc tgg caa ggt gag gaa gcc ccc aac cct gag ctc gtg att tta aat   211
Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu Leu Val Ile Leu Asn
            25                  30                  35

gac gac ctc gcc tac agc ctc ggg ctt gat ccg aca tgg ctt cgc aca   259
Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro Thr Trp Leu Arg Thr
        40                  45                  50

cct gag ggc gtt caa ttt ctt ctc gga ctc aac ccc gag ccc tta aca   307
Pro Glu Gly Val Gln Phe Leu Leu Gly Leu Asn Pro Glu Pro Leu Thr
    55                  60                  65

aaa gca gtt gcg cag gcc tat tcc ggc cac caa ttc gga cag ttt gtg   355
Lys Ala Val Ala Gln Ala Tyr Ser Gly His Gln Phe Gly Gln Phe Val
70                  75                  80                  85

gca agc ctt ggt gat ggc cga gcg ctt ctt ctc ggc gaa gcc cgc tca   403
Ala Ser Leu Gly Asp Gly Arg Ala Leu Leu Leu Gly Glu Ala Arg Ser
                90                  95                  100

gct gac ggc gta ctg cat gat atc cac ctc aaa gga tct gga cga acc   451
Ala Asp Gly Val Leu His Asp Ile His Leu Lys Gly Ser Gly Arg Thr
            105                 110                 115

caa ttc tcc cga gga gcc gat gga cgc gcc gtc ctt ggc ccc gtc tta   499
Gln Phe Ser Arg Gly Ala Asp Gly Arg Ala Val Leu Gly Pro Val Leu
        120                 125                 130

cgc gaa tac atc atc tcc gaa gcg atg cat gca ctt ggt gtt ccc acc   547
Arg Glu Tyr Ile Ile Ser Glu Ala Met His Ala Leu Gly Val Pro Thr
```

```
    135                 140                 145

acc agg tca ctt gca gta att agc acc ggt agg aaa atc caa cga gga   595
Thr Arg Ser Leu Ala Val Ile Ser Thr Gly Arg Lys Ile Gln Arg Gly
150                 155                 160                 165

agc gta gcc cca ggc gca gtc ctt gtt cga gta gca acc agc ctc att   643
Ser Val Ala Pro Gly Ala Val Leu Val Arg Val Ala Thr Ser Leu Ile
                170                 175                 180

cga gtc gga tcc ttc caa tac tcc aac atc tct ggt ggc atc gaa cta   691
Arg Val Gly Ser Phe Gln Tyr Ser Asn Ile Ser Gly Gly Ile Glu Leu
            185                 190                 195

tct caa cac ctg gcg aac tat acg atc acc agg cat ttc cct tcg ttg   739
Ser Gln His Leu Ala Asn Tyr Thr Ile Thr Arg His Phe Pro Ser Leu
        200                 205                 210

gta gct gaa cta tcc gca cca acc ccc gca act tat gta tca ctg ttt   787
Val Ala Glu Leu Ser Ala Pro Thr Pro Ala Thr Tyr Val Ser Leu Phe
    215                 220                 225

aaa gcg att ctt cag cgc caa gca gac acc gtt gga aaa tgg acc agg   835
Lys Ala Ile Leu Gln Arg Gln Ala Asp Thr Val Gly Lys Trp Thr Arg
230                 235                 240                 245

ctg ggt ttc gtt cac gga gcc ctc aac aca gac aac acg ttg ata tcc   883
Leu Gly Phe Val His Gly Ala Leu Asn Thr Asp Asn Thr Leu Ile Ser
                250                 255                 260

gga gaa act gtt gac tac ggc cca tgc gct ttc atg gag cgc tac cgt   931
Gly Glu Thr Val Asp Tyr Gly Pro Cys Ala Phe Met Glu Arg Tyr Arg
            265                 270                 275

ggc gac gcg aaa ttt agc tcc atc gac act tat ggt cgc tac aaa ttt   979
Gly Asp Ala Lys Phe Ser Ser Ile Asp Thr Tyr Gly Arg Tyr Lys Phe
        280                 285                 290

gaa aac caa cct atg atc ctc gga tgg aac atg gcc cgc ctc gta gaa   1027
Glu Asn Gln Pro Met Ile Leu Gly Trp Asn Met Ala Arg Leu Val Glu
    295                 300                 305

acc ctc ctc cca ctc ctg ggc gcc aca cca gac gaa ggc atg aca gca   1075
Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp Glu Gly Met Thr Ala
310                 315                 320                 325

gcc caa gaa gct ctc gta gaa ttc gat gac ctc tgc gaa caa gca atc   1123
Ala Gln Glu Ala Leu Val Glu Phe Asp Asp Leu Cys Glu Gln Ala Ile
                330                 335                 340

cga aaa gaa ttc gcc act gca ctg ggc ctt gac gag tca gac acc ggc   1171
Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp Glu Ser Asp Thr Gly
            345                 350                 355

acg gta gag cag ttc cgt gaa ctg ctc tac ctc cat aac ccc gac atc   1219
Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu His Asn Pro Asp Ile
        360                 365                 370

acc acg ctg ctg cgc gca ctc acc gac aac acc gca cca ccg agt ggc   1267
Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr Ala Pro Pro Ser Gly
    375                 380                 385
```

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ttt gaa gca ttc gtt cac gac tgg aaa acc caa gac cca gat atc gaa   1315
Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln Asp Pro Asp Ile Glu
390                 395                 400                 405

gca atg cga gca gta aat cca ctt ttc att cca cgc aat cac ctc gtg   1363
Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro Arg Asn His Leu Val
                410                 415                 420

gaa gct gct ctc gca gac gca gtt gaa ggg aat cta gaa aag ttc cac   1411
Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn Leu Glu Lys Phe His
            425                 430                 435

gaa ctc ctc gct gct gtc acc aat cct ttt gat cca act gcg ggc ccc   1459
Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp Pro Thr Ala Gly Pro
        440                 445                 450

gat gaa cta cgc ctg cca agc gaa gaa gga ttt gaa gaa gac tac atg   1507
Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe Glu Glu Asp Tyr Met
    455                 460                 465

acc ttc tgc ggt acc taggacagat ggtggggcag acg                    1545
Thr Phe Cys Gly Thr
470
```

US 6,955,901 B2

<210> 2380
<211> 474
<212> PRT
<213> Corynebacterium glutamicum

<400> 2380

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Met Asn Thr Ala Pro Phe Lys Leu Glu Ala Asp Phe Ala Ser Ala Leu
  1               5                  10                  15

Pro Thr Met Ala Ala Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu
             20                  25                  30

Leu Val Ile Leu Asn Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro
         35                  40                  45

Thr Trp Leu Arg Thr Pro Glu Gly Val Gln Phe Leu Leu Gly Leu Asn
     50                  55                  60

Pro Glu Pro Leu Thr Lys Ala Val Ala Gln Ala Tyr Ser Gly His Gln
 65                  70                  75                  80

Phe Gly Gln Phe Val Ala Ser Leu Gly Asp Gly Arg Ala Leu Leu Leu
                 85                  90                  95

Gly Glu Ala Arg Ser Ala Asp Gly Val Leu His Asp Ile His Leu Lys
            100                 105                 110

Gly Ser Gly Arg Thr Gln Phe Ser Arg Gly Ala Asp Gly Arg Ala Val
        115                 120                 125

Leu Gly Pro Val Leu Arg Glu Tyr Ile Ile Ser Glu Ala Met His Ala
    130                 135                 140

Leu Gly Val Pro Thr Thr Arg Ser Leu Ala Val Ile Ser Thr Gly Arg
145                 150                 155                 160
```

```
Lys Ile Gln Arg Gly Ser Val Ala Pro Gly Ala Val Leu Val Arg Val
                165                 170                 175

Ala Thr Ser Leu Ile Arg Val Gly Ser Phe Gln Tyr Ser Asn Ile Ser
            180                 185                 190

Gly Gly Ile Glu Leu Ser Gln His Leu Ala Asn Tyr Thr Ile Thr Arg
        195                 200                 205

His Phe Pro Ser Leu Val Ala Glu Leu Ser Ala Pro Thr Pro Ala Thr
    210                 215                 220

Tyr Val Ser Leu Phe Lys Ala Ile Leu Gln Arg Gln Ala Asp Thr Val
225                 230                 235                 240

Gly Lys Trp Thr Arg Leu Gly Phe Val His Gly Ala Leu Asn Thr Asp
                245                 250                 255

Asn Thr Leu Ile Ser Gly Glu Thr Val Asp Tyr Gly Pro Cys Ala Phe
            260                 265                 270

Met Glu Arg Tyr Arg Gly Asp Ala Lys Phe Ser Ser Ile Asp Thr Tyr
        275                 280                 285

Gly Arg Tyr Lys Phe Glu Asn Gln Pro Met Ile Leu Gly Trp Asn Met
    290                 295                 300

Ala Arg Leu Val Glu Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp
305                 310                 315                 320

Glu Gly Met Thr Ala Ala Gln Glu Ala Leu Val Glu Phe Asp Asp Leu
                325                 330                 335

Cys Glu Gln Ala Ile Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp
            340                 345                 350

Glu Ser Asp Thr Gly Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu
        355                 360                 365

His Asn Pro Asp Ile Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr
    370                 375                 380

Ala Pro Pro Ser Gly Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln
385                 390                 395                 400

Asp Pro Asp Ile Glu Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro
                405                 410                 415

Arg Asn His Leu Val Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn
            420                 425                 430

Leu Glu Lys Phe His Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp
        435                 440                 445

Pro Thr Ala Gly Pro Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe
    450                 455                 460

Glu Glu Asp Tyr Met Thr Phe Cys Gly Thr
465                 470
```

<210> 2381
<211> 738
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(715)
<223> RXA01714

<400> 2381
cattggataa ttagcaggag tgaagttgca tcaaaggaca aacataaaat aaacggcgcg 60

cctccccaga gttaccccaa taattagtaa attgcagatt gtg atc gat tcc gaa 115
Val Ile Asp Ser Glu
1 5

gcg acc tct cag cac aag acc tca gct acc ccg gca gag agc act ccc 163
Ala Thr Ser Gln His Lys Thr Ser Ala Thr Pro Ala Glu Ser Thr Pro
10 15 20

gcg gag ttt tcc gaa gcg gtt gag tct atg cac aga gcg cgc ctg cgc 211
Ala Glu Phe Ser Glu Ala Val Glu Ser Met His Arg Ala Arg Leu Arg
25 30 35

cca gaa ctt act ttg ggc acg att agg ccg cct cag cgc ctg gcg ccg 259
Pro Glu Leu Thr Leu Gly Thr Ile Arg Pro Pro Gln Arg Leu Ala Pro
40 45 50

ttt tcg cac gcc att gga ctc gaa gtc gga aat caa gaa gag tca gac 307
Phe Ser His Ala Ile Gly Leu Glu Val Gly Asn Gln Glu Glu Ser Asp
55 60 65

gat gtc tcc acc aac agc gaa ggt gat tcc ttt ggt cgt ttg att ctg 355
Asp Val Ser Thr Asn Ser Glu Gly Asp Ser Phe Gly Arg Leu Ile Leu
70 75 80 85

ctc cac gat ccg ggt gcc gaa gaa acc tgg gaa gga gca atg cgc ctt 403
Leu His Asp Pro Gly Ala Glu Glu Thr Trp Glu Gly Ala Met Arg Leu
90 95 100

gtc gcc tat att caa gct gac atg gat cac gct gtt gct tcc gac ccg 451
Val Ala Tyr Ile Gln Ala Asp Met Asp His Ala Val Ala Ser Asp Pro
105 110 115

cta ttg ccg gaa gta gcg tgg caa tgg ctt aac gaa ggt ttg gaa caa 499
Leu Leu Pro Glu Val Ala Trp Gln Trp Leu Asn Glu Gly Leu Glu Gln
120 125 130

gcc ggc gca gga ttt acc aac cta ggc gga acc gta acc tcc aca acc 547
Ala Gly Ala Gly Phe Thr Asn Leu Gly Gly Thr Val Thr Ser Thr Thr
135 140 145

tcg gtg cgc ttt ggt gaa atc ggt gga ccg cca agt gcc tac caa gtg 595
Ser Val Arg Phe Gly Glu Ile Gly Gly Pro Pro Ser Ala Tyr Gln Val
150 155 160 165

gaa atg cgt gcg tcc tgg acc gcg act ggc acc gac ctc acc gcg cat 643
Glu Met Arg Ala Ser Trp Thr Ala Thr Gly Thr Asp Leu Thr Ala His
170 175 180

```
gtt gaa gcg ttc gca gca gtg ctt gcc tct gtt gct gga ctt ccc cca   691
Val Glu Ala Phe Ala Ala Val Leu Ala Ser Val Ala Gly Leu Pro Pro
            185                 190                 195

gag ggc gtc acc gaa cta cga agg tagattggac accatggttt ccg        738
Glu Gly Val Thr Glu Leu Arg Arg
        200                 205


<210> 2382
<211> 205
<212> PRT
<213> Corynebacterium glutamicum

<400> 2382
Val Ile Asp Ser Glu Ala Thr Ser Gln His Lys Thr Ser Ala Thr Pro
  1               5                  10                  15

Ala Glu Ser Thr Pro Ala Glu Phe Ser Glu Ala Val Glu Ser Met His
             20                  25                  30

Arg Ala Arg Leu Arg Pro Glu Leu Thr Leu Gly Thr Ile Arg Pro Pro
         35                  40                  45

Gln Arg Leu Ala Pro Phe Ser His Ala Ile Gly Leu Glu Val Gly Asn
     50                  55                  60

Gln Glu Glu Ser Asp Asp Val Ser Thr Asn Ser Glu Gly Asp Ser Phe
 65                  70                  75                  80

Gly Arg Leu Ile Leu Leu His Asp Pro Gly Ala Glu Glu Thr Trp Glu
                 85                  90                  95

Gly Ala Met Arg Leu Val Ala Tyr Ile Gln Ala Asp Met Asp His Ala
            100                 105                 110

Val Ala Ser Asp Pro Leu Leu Pro Glu Val Ala Trp Gln Trp Leu Asn
        115                 120                 125

Glu Gly Leu Glu Gln Ala Gly Ala Gly Phe Thr Asn Leu Gly Gly Thr
    130                 135                 140

Val Thr Ser Thr Thr Ser Val Arg Phe Gly Glu Ile Gly Gly Pro Pro
145                 150                 155                 160

Ser Ala Tyr Gln Val Glu Met Arg Ala Ser Trp Thr Ala Thr Gly Thr
                165                 170                 175

Asp Leu Thr Ala His Val Glu Ala Phe Ala Ala Val Leu Ala Ser Val
            180                 185                 190

Ala Gly Leu Pro Pro Glu Gly Val Thr Glu Leu Arg Arg
        195                 200                 205


<210> 2383
<211> 819
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(796)
<223> RXA01715

<400> 2383
acatgttgtt ggaacatgcc ggcagagccg acactacgat tcattcgcta aagggtctgg 60

ccactgacac tggcaaagat ccacgaaagg aagttaccct gtg agc gag ctc gat 115
Val Ser Glu Leu Asp
1 5

att aaa cag ctc aac aaa ctg cag cgc tac tct cag tgg gcg gtg ttc 163
Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser Gln Trp Ala Val Phe
10 15 20

cgt gct att cct gga gcg ctc gat gat gat cgc aca gaa gtc act gac 211
Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg Thr Glu Val Thr Asp
25 30 35

caa gca gcc aag ttc ttt gcc gac ctt gaa gca gaa ggc aaa gtc act 259
Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala Glu Gly Lys Val Thr
40 45 50

gtc cgt ggc att tac aac gcc tcc ggc ctg cgc gca gac gct gac tac 307
Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg Ala Asp Ala Asp Tyr
55 60 65

atg atc tgg tgg cac gca gaa gaa ttc gaa gac att cag aag gcc ttc 355
Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp Ile Gln Lys Ala Phe
70 75 80 85

gct gat ttc cgc cgc acc acc att ttg ggt cag gtt tct gag gtc ttc 403
Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln Val Ser Glu Val Phe
90 95 100

tgg atc gga aac gct ctc cac cgt cca tct gag ttc aac aag gct cac 451
Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu Phe Asn Lys Ala His
105 110 115

ttg cct tca ttc atc atg ggt gaa gaa gca aag gac tgg atc act gtt 499
Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys Asp Trp Ile Thr Val
120 125 130

tac ccg ttc gtg cgc agc tac gac tgg tac atc atg gag ccc ttg aag 547
Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile Met Glu Pro Leu Lys
135 140 145

cgt tcc cgc att ctc cgc gag cac gga caa gct gct gtg gaa ttc cca 595
Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala Ala Val Glu Phe Pro
150 155 160 165

gat gtt cgt gcc aac act gtg ccg gct ttc gca ctg ggt gac tac gaa 643
Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala Leu Gly Asp Tyr Glu
170 175 180

tgg gtg ctg gct ttc gag gct gat gag ttg cac cgc att gtc gat ttg 691
Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His Arg Ile Val Asp Leu
185 190 195

atg cac aag atg cgt tac acc gag gct cgc ctc cac gtc cgt gag gag 739

```
Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu His Val Arg Glu Glu
        200                 205                 210

ctg cca ttt att tct gga cag cgc gtc gac att gca gat ctg att aag   787
Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile Ala Asp Leu Ile Lys
    215                 220                 225

gtt ctt cct taaaagctgc ttttctaaac gat                             819
Val Leu Pro
230
```

<210> 2384
<211> 232
<212> PRT
<213> Corynebacterium glutamicum

<400> 2384

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Val Ser Glu Leu Asp Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser
  1               5                  10                  15

Gln Trp Ala Val Phe Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg
             20                  25                  30

Thr Glu Val Thr Asp Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala
         35                  40                  45

Glu Gly Lys Val Thr Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg
     50                  55                  60

Ala Asp Ala Asp Tyr Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp
 65                  70                  75                  80

Ile Gln Lys Ala Phe Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln
                 85                  90                  95

Val Ser Glu Val Phe Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu
            100                 105                 110

Phe Asn Lys Ala His Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys
        115                 120                 125

Asp Trp Ile Thr Val Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile
    130                 135                 140

Met Glu Pro Leu Lys Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala
145                 150                 155                 160

Ala Val Glu Phe Pro Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala
                165                 170                 175

Leu Gly Asp Tyr Glu Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His
            180                 185                 190

Arg Ile Val Asp Leu Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu
        195                 200                 205

His Val Arg Glu Glu Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile
    210                 215                 220

Ala Asp Leu Ile Lys Val Leu Pro
```

225 230

<210> 2385
<211> 642
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(619)
<223> RXA01729

<400> 2385
tcaaggtccg gcgattcttc aattcttcga gttcaggaaa tcgcatactc tctaggctag 60

taaacttttc tacgaaccta ttactaagaa ggagcccgaa gtg aag ttg agg aca 115
Val Lys Leu Arg Thr
1 5

atc cca gcc ctg tta gcc gtc gca ctt ctt gca ggc tgt tcg ggt gaa 163
Ile Pro Ala Leu Leu Ala Val Ala Leu Leu Ala Gly Cys Ser Gly Glu
10 15 20

agt gct gat agc caa gcc gtt tcc gct gag gaa acc atg gaa gta acc 211
Ser Ala Asp Ser Gln Ala Val Ser Ala Glu Glu Thr Met Glu Val Thr
25 30 35

act acc tca acc ccg gtg ttc gaa gcc aaa gag gta agc cca atc aca 259
Thr Thr Ser Thr Pro Val Phe Glu Ala Lys Glu Val Ser Pro Ile Thr
40 45 50

gtc cca agc ggc gat atc agg gtt gaa gac cca ggt ctc aat gtt gaa 307
Val Pro Ser Gly Asp Ile Arg Val Glu Asp Pro Gly Leu Asn Val Glu
55 60 65

ttt atc ttc cga ggc acc cgc tac ggc acc aac ggt ggc tca att att 355
Phe Ile Phe Arg Gly Thr Arg Tyr Gly Thr Asn Gly Gly Ser Ile Ile
70 75 80 85

cac atc gcg gtg aaa aac cta aac gac gta gcc ctg cca gcc gac gcc 403
His Ile Ala Val Lys Asn Leu Asn Asp Val Ala Leu Pro Ala Asp Ala
90 95 100

atc gat cca ccc acc ctg gac atc gaa gac tac aac ggc aac aaa acc 451
Ile Asp Pro Pro Thr Leu Asp Ile Glu Asp Tyr Asn Gly Asn Lys Thr
105 110 115

aac atc gaa acc ctc tcc ggc gac gac aac atc cca ctc gac cta cca 499
Asn Ile Glu Thr Leu Ser Gly Asp Asp Asn Ile Pro Leu Asp Leu Pro
120 125 130

ctg ggt gcc ggc gcg aca acg aac ctg caa tac gcg ttc aac acc tca 547
Leu Gly Ala Gly Ala Thr Thr Asn Leu Gln Tyr Ala Phe Asn Thr Ser
135 140 145

aac ggc tca ttg tcg aat gct aaa ttc cag atc gga aac gtc atc tac 595
Asn Gly Ser Leu Ser Asn Ala Lys Phe Gln Ile Gly Asn Val Ile Tyr
150 155 160 165

tca ggc aat ttg aac agc ttg gcg taagttcaaa aaataatttg aat 642

Ser Gly Asn Leu Asn Ser Leu Ala
170

<210> 2386
<211> 173
<212> PRT
<213> Corynebacterium glutamicum

<400> 2386
Val Lys Leu Arg Thr Ile Pro Ala Leu Leu Ala Val Ala Leu Leu Ala
1 5 10 15

Gly Cys Ser Gly Glu Ser Ala Asp Ser Gln Ala Val Ser Ala Glu Glu
20 25 30

Thr Met Glu Val Thr Thr Thr Ser Thr Pro Val Phe Glu Ala Lys Glu
35 40 45

Val Ser Pro Ile Thr Val Pro Ser Gly Asp Ile Arg Val Glu Asp Pro
50 55 60

Gly Leu Asn Val Glu Phe Ile Phe Arg Gly Thr Arg Tyr Gly Thr Asn
65 70 75 80

Gly Gly Ser Ile Ile His Ile Ala Val Lys Asn Leu Asn Asp Val Ala
85 90 95

Leu Pro Ala Asp Ala Ile Asp Pro Pro Thr Leu Asp Ile Glu Asp Tyr
100 105 110

Asn Gly Asn Lys Thr Asn Ile Glu Thr Leu Ser Gly Asp Asp Asn Ile
115 120 125

Pro Leu Asp Leu Pro Leu Gly Ala Gly Ala Thr Thr Asn Leu Gln Tyr
130 135 140

Ala Phe Asn Thr Ser Asn Gly Ser Leu Ser Asn Ala Lys Phe Gln Ile
145 150 155 160

Gly Asn Val Ile Tyr Ser Gly Asn Leu Asn Ser Leu Ala
165 170

<210> 2387
<211> 822
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(799)
<223> RXA01731

<400> 2387
gcttttgcag ctgtggggtt gggctggggg caagtgttca tgtaggtgtc attgatcgtt 60

cactcaaggt tggacgttgt gttcatgaat aacttttatg atg aac gca tcg tcc 115
Met Asn Ala Ser Ser
1 5

```
att tct tcc cga ttc aag gat ctt ttt gtg aca ccc agt att gtt ttt   163
Ile Ser Ser Arg Phe Lys Asp Leu Phe Val Thr Pro Ser Ile Val Phe
                 10                  15                  20

gat ttc gat ggc acg ctt gcc att ggc cat ggc cct gtc ctt gcg tat   211
Asp Phe Asp Gly Thr Leu Ala Ile Gly His Gly Pro Val Leu Ala Tyr
             25                  30                  35

gca ttg tgt gtt gca ccg gag ggt tcc aag gac ttt ctg gag cgt gtg   259
Ala Leu Cys Val Ala Pro Glu Gly Ser Lys Asp Phe Leu Glu Arg Val
         40                  45                  50

cgc agg gag ctt cgg cgc tat gac gat ggt cag agt att tac cgt gat   307
Arg Arg Glu Leu Arg Arg Tyr Asp Asp Gly Gln Ser Ile Tyr Arg Asp
     55                  60                  65

ggg tat gac att gtg gct aag ttg gcg tcg gaa ttg ggg att gat gat   355
Gly Tyr Asp Ile Val Ala Lys Leu Ala Ser Glu Leu Gly Ile Asp Asp
 70                  75                  80                  85

ggc acg atg tct gtc gct tat ggc gag agc cgg aag ttg ctt ggt tcg   403
Gly Thr Met Ser Val Ala Tyr Gly Glu Ser Arg Lys Leu Leu Gly Ser
                 90                  95                 100

gat tta gcg cct gtt gag cat gtg cgg ggt att aag gat att ttg tcc   451
Asp Leu Ala Pro Val Glu His Val Arg Gly Ile Lys Asp Ile Leu Ser
             105                 110                 115

tcg ttg aaa ggt cat gct cgg ttg gtt tta gct acc aat gcc ccg gaa   499
Ser Leu Lys Gly His Ala Arg Leu Val Leu Ala Thr Asn Ala Pro Glu
         120                 125                 130

aat ggc gtg cat gat ttg ctg cgt cag tgg ggt gtt gct gat ttg ttt   547
Asn Gly Val His Asp Leu Leu Arg Gln Trp Gly Val Ala Asp Leu Phe
     135                 140                 145

gat cag ttg cat ttt gtg gtg ggt aag cct gca ggg ttg att tcg atc   595
Asp Gln Leu His Phe Val Val Gly Lys Pro Ala Gly Leu Ile Ser Ile
150                 155                 160                 165

att tct gat ttg cag ctt gat ggt ccg gtg ctt gcg gtg ggc gat att   643
Ile Ser Asp Leu Gln Leu Asp Gly Pro Val Leu Ala Val Gly Asp Ile
                 170                 175                 180

tat gaa ttc gat ctg agt cct gca gcg cag tta ggt gca gat acg gct   691
Tyr Glu Phe Asp Leu Ser Pro Ala Ala Gln Leu Gly Ala Asp Thr Ala
             185                 190                 195

ctg gtt gga gct aca gca acc att tct gaa gcg aag gtc tcc atg cgt   739
Leu Val Gly Ala Thr Ala Thr Ile Ser Glu Ala Lys Val Ser Met Arg
         200                 205                 210

gga gat tct atc gct gat ctc cct ctc ctt gcc tgg gtt tgt tcc cgg   787
Gly Asp Ser Ile Ala Asp Leu Pro Leu Leu Ala Trp Val Cys Ser Arg
     215                 220                 225

gtc tcc tct tct taactttctt gtctcatgtc gct                        822
Val Ser Ser Ser
230
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<210> 2388
<211> 233
<212> PRT
<213> Corynebacterium glutamicum

<400> 2388
Met Asn Ala Ser Ser Ile Ser Ser Arg Phe Lys Asp Leu Phe Val Thr
1 5 10 15

Pro Ser Ile Val Phe Asp Phe Asp Gly Thr Leu Ala Ile Gly His Gly
20 25 30

Pro Val Leu Ala Tyr Ala Leu Cys Val Ala Pro Glu Gly Ser Lys Asp
35 40 45

Phe Leu Glu Arg Val Arg Arg Glu Leu Arg Arg Tyr Asp Asp Gly Gln
50 55 60

Ser Ile Tyr Arg Asp Gly Tyr Asp Ile Val Ala Lys Leu Ala Ser Glu
65 70 75 80

Leu Gly Ile Asp Asp Gly Thr Met Ser Val Ala Tyr Gly Glu Ser Arg
85 90 95

Lys Leu Leu Gly Ser Asp Leu Ala Pro Val Glu His Val Arg Gly Ile
100 105 110

Lys Asp Ile Leu Ser Ser Leu Lys Gly His Ala Arg Leu Val Leu Ala
115 120 125

Thr Asn Ala Pro Glu Asn Gly Val His Asp Leu Leu Arg Gln Trp Gly
130 135 140

Val Ala Asp Leu Phe Asp Gln Leu His Phe Val Val Gly Lys Pro Ala
145 150 155 160

Gly Leu Ile Ser Ile Ile Ser Asp Leu Gln Leu Asp Gly Pro Val Leu
165 170 175

Ala Val Gly Asp Ile Tyr Glu Phe Asp Leu Ser Pro Ala Ala Gln Leu
180 185 190

Gly Ala Asp Thr Ala Leu Val Gly Ala Thr Ala Thr Ile Ser Glu Ala
195 200 205

Lys Val Ser Met Arg Gly Asp Ser Ile Ala Asp Leu Pro Leu Leu Ala
210 215 220

Trp Val Cys Ser Arg Val Ser Ser Ser
225 230

<210> 2389
<211> 837
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(814)
<223> RXA01738

<400> 2389
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tttacgttcg ccgagtattt agcgaggagg taaatgacaa atg aga att ctt ccc 115
Met Arg Ile Leu Pro
1 5

atc ggc ccc cac gat gaa atc gcc gtc aac gga tca ata gtc ctt cta 163
Ile Gly Pro His Asp Glu Ile Ala Val Asn Gly Ser Ile Val Leu Leu
10 15 20

tcc gag cac gac gga gac atc gta tcg gtc ggc ccc gac ctc ggc acg 211
Ser Glu His Asp Gly Asp Ile Val Ser Val Gly Pro Asp Leu Gly Thr
25 30 35

gtg cga gtt acc ctt gaa gag atc gaa agt tta ggt aca ccg acg gca 259
Val Arg Val Thr Leu Glu Glu Ile Glu Ser Leu Gly Thr Pro Thr Ala
40 45 50

ccc cgc gat ctg ggt tct cgg gaa gtc gac gca tgc gta tcg ttg ctc 307
Pro Arg Asp Leu Gly Ser Arg Glu Val Asp Ala Cys Val Ser Leu Leu
55 60 65

cgc aac cgc gag tta gtg cga ttc gat ccc cac gat ggc agt gaa tta 355
Arg Asn Arg Glu Leu Val Arg Phe Asp Pro His Asp Gly Ser Glu Leu
70 75 80 85

acc tat cgg gaa cat agc gtt gct tac ggt gcg agt ggc aag cca ttg 403
Thr Tyr Arg Glu His Ser Val Ala Tyr Gly Ala Ser Gly Lys Pro Leu
90 95 100

ttt ccc cga ttg gat cca gcg gtg atc ggc att gtg gag ctg cga ggt 451
Phe Pro Arg Leu Asp Pro Ala Val Ile Gly Ile Val Glu Leu Arg Gly
105 110 115

gag gat cgt ttg ctt ctg ggc atg aat gcg cag aaa cgc caa cgc tat 499
Glu Asp Arg Leu Leu Leu Gly Met Asn Ala Gln Lys Arg Gln Arg Tyr
120 125 130

tca tta atc gca ggt tat gtt tcg cat ggt gag tcg ctg gaa gac gca 547
Ser Leu Ile Ala Gly Tyr Val Ser His Gly Glu Ser Leu Glu Asp Ala
135 140 145

ttc acc aga gaa gtg ttc gag gaa gcg gcg cgc cgg gta tct gag att 595
Phe Thr Arg Glu Val Phe Glu Glu Ala Ala Arg Arg Val Ser Glu Ile
150 155 160 165

tcc tat gtg tcg tct caa cca tgg ccg atc tct ggt tcg ctg atg ctg 643
Ser Tyr Val Ser Ser Gln Pro Trp Pro Ile Ser Gly Ser Leu Met Leu
170 175 180

ggt atg aag ggc ttc acg gaa gat gag ttg cct caa ggc gaa act gat 691
Gly Met Lys Gly Phe Thr Glu Asp Glu Leu Pro Gln Gly Glu Thr Asp
185 190 195

ggt gaa tta gcg gag aca atc tgg gct tcg cca cta gac att atc gat 739
Gly Glu Leu Ala Glu Thr Ile Trp Ala Ser Pro Leu Asp Ile Ile Asp
200 205 210

cgt aag att ccg atc gcc cca ccc gga tcg att gcc tac gac atg atc 787

```
Arg Lys Ile Pro Ile Ala Pro Pro Gly Ser Ile Ala Tyr Asp Met Ile
    215                 220                 225

aac gcc tgg gcg cga gat aaa caa aac taagggagct ttttacagtg        834
Asn Ala Trp Ala Arg Asp Lys Gln Asn
230                 235

atc                                                              837


<210> 2390
<211> 238
<212> PRT
<213> Corynebacterium glutamicum

<400> 2390
Met Arg Ile Leu Pro Ile Gly Pro His Asp Glu Ile Ala Val Asn Gly
  1               5                  10                  15

Ser Ile Val Leu Leu Ser Glu His Asp Gly Asp Ile Val Ser Val Gly
             20                  25                  30

Pro Asp Leu Gly Thr Val Arg Val Thr Leu Glu Glu Ile Glu Ser Leu
         35                  40                  45

Gly Thr Pro Thr Ala Pro Arg Asp Leu Gly Ser Arg Glu Val Asp Ala
     50                  55                  60

Cys Val Ser Leu Leu Arg Asn Arg Glu Leu Val Arg Phe Asp Pro His
 65                  70                  75                  80

Asp Gly Ser Glu Leu Thr Tyr Arg Glu His Ser Val Ala Tyr Gly Ala
                 85                  90                  95

Ser Gly Lys Pro Leu Phe Pro Arg Leu Asp Pro Ala Val Ile Gly Ile
            100                 105                 110

Val Glu Leu Arg Gly Glu Asp Arg Leu Leu Leu Gly Met Asn Ala Gln
        115                 120                 125

Lys Arg Gln Arg Tyr Ser Leu Ile Ala Gly Tyr Val Ser His Gly Glu
    130                 135                 140

Ser Leu Glu Asp Ala Phe Thr Arg Glu Val Phe Glu Glu Ala Ala Arg
145                 150                 155                 160

Arg Val Ser Glu Ile Ser Tyr Val Ser Ser Gln Pro Trp Pro Ile Ser
                165                 170                 175

Gly Ser Leu Met Leu Gly Met Lys Gly Phe Thr Glu Asp Glu Leu Pro
            180                 185                 190

Gln Gly Glu Thr Asp Gly Glu Leu Ala Glu Thr Ile Trp Ala Ser Pro
        195                 200                 205

Leu Asp Ile Ile Asp Arg Lys Ile Pro Ile Ala Pro Pro Gly Ser Ile
    210                 215                 220

Ala Tyr Asp Met Ile Asn Ala Trp Ala Arg Asp Lys Gln Asn
225                 230                 235
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<210> 2391
<211> 921
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(898)
<223> RXA01741

<400> 2391
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aagtaactgt gtcgattaag ttttgggggа aatttttcag atg aca cac atc gct 115
Met Thr His Ile Ala
1 5

tta gcc aac tct gcc caa gtt ctg atc cgc ccg gat tct gcg att caa 163
Leu Ala Asn Ser Ala Gln Val Leu Ile Arg Pro Asp Ser Ala Ile Gln
10 15 20

ttc ggc atc gac gcc acc cgc gct ggc gtc tta aat atc gat cca tcg 211
Phe Gly Ile Asp Ala Thr Arg Ala Gly Val Leu Asn Ile Asp Pro Ser
25 30 35

ctg tcg tcg cga gtc gtc ccg gtg ctg cgg aat ctg cgg acc gcc cga 259
Leu Ser Ser Arg Val Val Pro Val Leu Arg Asn Leu Arg Thr Ala Arg
40 45 50

ccg atc gtt gat gtc atc gcc gac ctc acg act gca ggc ctc gca ccc 307
Pro Ile Val Asp Val Ile Ala Asp Leu Thr Thr Ala Gly Leu Ala Pro
55 60 65

acc gct gcg agc agt ttg ctc gag gac ctt tta gaa ttc ggt gtg gtc 355
Thr Ala Ala Ser Ser Leu Leu Glu Asp Leu Leu Glu Phe Gly Val Val
70 75 80 85

cgc gaa tcg gcg gcg gcg cag gtg ttg ctg ttc ggg gac ggt tcg ctt 403
Arg Glu Ser Ala Ala Ala Gln Val Leu Leu Phe Gly Asp Gly Ser Leu
90 95 100

gtc gac gtc acc tcc ttc ctt ttg gaa acc tcc ggc ttt gtt ccc aga 451
Val Asp Val Thr Ser Phe Leu Leu Glu Thr Ser Gly Phe Val Pro Arg
105 110 115

ccc cag atc atc gat gag tcg cct cga gag ttt ttc gag ctt ccc tcc 499
Pro Gln Ile Ile Asp Glu Ser Pro Arg Glu Phe Phe Glu Leu Pro Ser
120 125 130

agc cac att ttg gtt ctc aac aag ctc gca cat tcc caa cgt cta tcc 547
Ser His Ile Leu Val Leu Asn Lys Leu Ala His Ser Gln Arg Leu Ser
135 140 145

ccg ctg ctt cac aaa tat gcg ccg acg tat ctg tgc gcc gcg atc gtc 595
Pro Leu Leu His Lys Tyr Ala Pro Thr Tyr Leu Cys Ala Ala Ile Val
150 155 160 165

gat aat cgt ggc atc atc ggc ccg ggc cgg aga tca cga tcg ggg ccg 643
Asp Asn Arg Gly Ile Ile Gly Pro Gly Arg Arg Ser Arg Ser Gly Pro
170 175 180

```
tgt ttg atg tgt gtg gat ctg cat cgc tgc gat atc gat ccg cat tgg   691
Cys Leu Met Cys Val Asp Leu His Arg Cys Asp Ile Asp Pro His Trp
            185                 190                 195

ctc tct att atc aat cag caa ccc aac ggt ccc acc ttt cct gat ccc   739
Leu Ser Ile Ile Asn Gln Gln Pro Asn Gly Pro Thr Phe Pro Asp Pro
        200                 205                 210

gtc acg gag atg gcg acg gct gcc cga ctc gtc gcc tgg gtc act gcc   787
Val Thr Glu Met Ala Thr Ala Ala Arg Leu Val Ala Trp Val Thr Ala
    215                 220                 225

gat aca tgg ttg ccc ggc gtt gtg gag gaa gta aac ccc cac gat cga   835
Asp Thr Trp Leu Pro Gly Val Val Glu Glu Val Asn Pro His Asp Arg
230                 235                 240                 245

aca aac tcg gta cgc acc ctc cct gtg cat cca aaa tgt ccg atg tgt   883
Thr Asn Ser Val Arg Thr Leu Pro Val His Pro Lys Cys Pro Met Cys
                250                 255                 260

tgg agt tta ggt tcc taaagtgctc ccaaaatcgc gag                    921
Trp Ser Leu Gly Ser
            265
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<210> 2392
<211> 266
<212> PRT
<213> Corynebacterium glutamicum

<400> 2392

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Met Thr His Ile Ala Leu Ala Asn Ser Ala Gln Val Leu Ile Arg Pro
  1               5                  10                  15

Asp Ser Ala Ile Gln Phe Gly Ile Asp Ala Thr Arg Ala Gly Val Leu
             20                  25                  30

Asn Ile Asp Pro Ser Leu Ser Ser Arg Val Val Pro Val Leu Arg Asn
         35                  40                  45

Leu Arg Thr Ala Arg Pro Ile Val Asp Val Ile Ala Asp Leu Thr Thr
     50                  55                  60

Ala Gly Leu Ala Pro Thr Ala Ala Ser Ser Leu Leu Glu Asp Leu Leu
 65                  70                  75                  80

Glu Phe Gly Val Val Arg Glu Ser Ala Ala Ala Gln Val Leu Leu Phe
                 85                  90                  95

Gly Asp Gly Ser Leu Val Asp Val Thr Ser Phe Leu Leu Glu Thr Ser
            100                 105                 110

Gly Phe Val Pro Arg Pro Gln Ile Ile Asp Glu Ser Pro Arg Glu Phe
        115                 120                 125

Phe Glu Leu Pro Ser Ser His Ile Leu Val Leu Asn Lys Leu Ala His
    130                 135                 140

Ser Gln Arg Leu Ser Pro Leu Leu His Lys Tyr Ala Pro Thr Tyr Leu
145                 150                 155                 160
```

```
Cys Ala Ala Ile Val Asp Asn Arg Gly Ile Ile Gly Pro Gly Arg Arg
                165                 170                 175

Ser Arg Ser Gly Pro Cys Leu Met Cys Val Asp Leu His Arg Cys Asp
            180                 185                 190

Ile Asp Pro His Trp Leu Ser Ile Ile Asn Gln Gln Pro Asn Gly Pro
        195                 200                 205

Thr Phe Pro Asp Pro Val Thr Glu Met Ala Thr Ala Ala Arg Leu Val
    210                 215                 220

Ala Trp Val Thr Ala Asp Thr Trp Leu Pro Gly Val Val Glu Glu Val
225                 230                 235                 240

Asn Pro His Asp Arg Thr Asn Ser Val Arg Thr Leu Pro Val His Pro
                245                 250                 255

Lys Cys Pro Met Cys Trp Ser Leu Gly Ser
            260                 265
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<210> 2393
<211> 903
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(880)
<223> RXA01748

<400> 2393

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atcaccaaat gtggcggttt tgcgtcgaaa agcgtgctct ttctacacct ctttgaggtt 60

cattttcgcg gtttcctcac aatcgcctat tgttaagtac atg gca gac gcg aaa   115
                                            Met Ala Asp Ala Lys
                                              1               5

aag cag gcg gat aaa gcc gcc aag aag cag gta aga gca gcc aag aag   163
Lys Gln Ala Asp Lys Ala Ala Lys Lys Gln Val Arg Ala Ala Lys Lys
                  10                  15                  20

gca cag cgc aag gag act cgc tca caa atg tgg cag gtc ttc aac atg   211
Ala Gln Arg Lys Glu Thr Arg Ser Gln Met Trp Gln Val Phe Asn Met
              25                  30                  35

caa cgc aag cag gat aag gct ctt att ccg ctt ctg ttg ctc gct att   259
Gln Arg Lys Gln Asp Lys Ala Leu Ile Pro Leu Leu Leu Leu Ala Ile
          40                  45                  50

ctt ggt atc ccg ctg gtc ctt ttc ctc atc ggt ttg att tgg ggt ggt   307
Leu Gly Ile Pro Leu Val Leu Phe Leu Ile Gly Leu Ile Trp Gly Gly
      55                  60                  65

cag tgg tgg atg ctt ccg atc ggc att gct gca ggt gtt gta gct gca   355
Gln Trp Trp Met Leu Pro Ile Gly Ile Ala Ala Gly Val Val Ala Ala
  70                  75                  80                  85

atg ttt att ttc acc cgt cgc gtt gag cgt gac gtg tac aag cgc gcc   403
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Met Phe Ile Phe Thr Arg Arg Val Glu Arg Asp Val Tyr Lys Arg Ala
                 90                  95                 100

gaa ggt cag cag ggt gct gct ggt tgg gct gtg gag aac ctc cgc tct   451
Glu Gly Gln Gln Gly Ala Ala Gly Trp Ala Val Glu Asn Leu Arg Ser
            105                 110                 115

ggc gtg ggc atg acc tgg cgc acc aag acc gct gtt gca gtg acc act   499
Gly Val Gly Met Thr Trp Arg Thr Lys Thr Ala Val Ala Val Thr Thr
        120                 125                 130

cag atg gat gca gtg cac cgc gtc att ggt ctg tgt ggt gtt gtg ctg   547
Gln Met Asp Ala Val His Arg Val Ile Gly Leu Cys Gly Val Val Leu
    135                 140                 145

gtc ggc gag ggc tcc cct cac cgc ctg aag cca atg ctt gcg cag caa   595
Val Gly Glu Gly Ser Pro His Arg Leu Lys Pro Met Leu Ala Gln Gln
150                 155                 160                 165

aag aag cgc ctg aac cgc gtg gca cct ggt gtt cca gtg tat gaa atc   643
Lys Lys Arg Leu Asn Arg Val Ala Pro Gly Val Pro Val Tyr Glu Ile
                170                 175                 180

atc acg ggc aac ggc gaa ggc cag acc cct atc gcg aag ctg cag cgt   691
Ile Thr Gly Asn Gly Glu Gly Gln Thr Pro Ile Ala Lys Leu Gln Arg
            185                 190                 195

gaa ctg gtc aag ctg cct cgc aac tac aag aag aac gac gtc gct gcc   739
Glu Leu Val Lys Leu Pro Arg Asn Tyr Lys Lys Asn Asp Val Ala Ala
        200                 205                 210

ctg gcc gct cgc att gag gct atg gac aat gtc gga aac gct cct ggc   787
Leu Ala Ala Arg Ile Glu Ala Met Asp Asn Val Gly Asn Ala Pro Gly
    215                 220                 225

gga tct ttg cct aag ggt cca ttg cca aag ggc gca agc atg tcc ggt   835
Gly Ser Leu Pro Lys Gly Pro Leu Pro Lys Gly Ala Ser Met Ser Gly
230                 235                 240                 245

atg aac cgc cgc gct cgc cga cag gct gaa cgc aag ggc gag gct       880
Met Asn Arg Arg Ala Arg Arg Gln Ala Glu Arg Lys Gly Glu Ala
                250                 255                 260

taaagccttt tcgctttcgc gtc                                        903


<210> 2394
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

<400> 2394
Met Ala Asp Ala Lys Lys Gln Ala Asp Lys Ala Ala Lys Lys Gln Val
  1               5                  10                  15

Arg Ala Ala Lys Lys Ala Gln Arg Lys Glu Thr Arg Ser Gln Met Trp
             20                  25                  30

Gln Val Phe Asn Met Gln Arg Lys Gln Asp Lys Ala Leu Ile Pro Leu
         35                  40                  45
```

```
Leu Leu Leu Ala Ile Leu Gly Ile Pro Leu Val Leu Phe Leu Ile Gly
     50                  55                  60

Leu Ile Trp Gly Gly Gln Trp Trp Met Leu Pro Ile Gly Ile Ala Ala
 65                  70                  75                  80

Gly Val Val Ala Ala Met Phe Ile Phe Thr Arg Arg Val Glu Arg Asp
                 85                  90                  95

Val Tyr Lys Arg Ala Glu Gly Gln Gln Gly Ala Ala Gly Trp Ala Val
            100                 105                 110

Glu Asn Leu Arg Ser Gly Val Gly Met Thr Trp Arg Thr Lys Thr Ala
        115                 120                 125

Val Ala Val Thr Thr Gln Met Asp Ala Val His Arg Val Ile Gly Leu
    130                 135                 140

Cys Gly Val Val Leu Val Gly Glu Gly Ser Pro His Arg Leu Lys Pro
145                 150                 155                 160

Met Leu Ala Gln Gln Lys Lys Arg Leu Asn Arg Val Ala Pro Gly Val
                165                 170                 175

Pro Val Tyr Glu Ile Ile Thr Gly Asn Gly Glu Gly Gln Thr Pro Ile
            180                 185                 190

Ala Lys Leu Gln Arg Glu Leu Val Lys Leu Pro Arg Asn Tyr Lys Lys
        195                 200                 205

Asn Asp Val Ala Ala Leu Ala Ala Arg Ile Glu Ala Met Asp Asn Val
    210                 215                 220

Gly Asn Ala Pro Gly Gly Ser Leu Pro Lys Gly Pro Leu Pro Lys Gly
225                 230                 235                 240

Ala Ser Met Ser Gly Met Asn Arg Arg Ala Arg Arg Gln Ala Glu Arg
                245                 250                 255

Lys Gly Glu Ala
            260
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<210> 2395
<211> 1740
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1717)
<223> RXA01749

<400> 2395
ggtttttgcg tgctctggtt tagggactgg ttttgggaac gtgcccagtt ccacatcaaa 60

taacgctgag gtcgtactta atccatgaga tcatgaatgg gtg agc ttc ctt gta 115
                                              Val Ser Phe Leu Val
                                                1   5

gaa aat caa tta ctc gcg ttg gtt gtc atc atg acg gtc gga cta ttg 163

```
Glu Asn Gln Leu Leu Ala Leu Val Val Ile Met Thr Val Gly Leu Leu
                 10                  15                  20

ctc ggc cgc atc aaa att ttc ggg ttc cgt ctc ggc gtc gcc gct gta   211
Leu Gly Arg Ile Lys Ile Phe Gly Phe Arg Leu Gly Val Ala Ala Val
             25                  30                  35

ctg ttt gta ggt cta gcg cta tcc acc att gag ccg gat att tcc gtc   259
Leu Phe Val Gly Leu Ala Leu Ser Thr Ile Glu Pro Asp Ile Ser Val
         40                  45                  50

cca tcc ctc att tac gtg gtt gga ctg tcg ctt ttt gtc tac acg atc   307
Pro Ser Leu Ile Tyr Val Val Gly Leu Ser Leu Phe Val Tyr Thr Ile
     55                  60                  65

ggt ctg gaa gcc ggc cct gga ttc ttc acc tcc atg aaa acc act ggt   355
Gly Leu Glu Ala Gly Pro Gly Phe Phe Thr Ser Met Lys Thr Thr Gly
 70                  75                  80                  85

ctg cgc aac aac gca ctg acc ttg ggc gcc atc atc gcc acc acg gca   403
Leu Arg Asn Asn Ala Leu Thr Leu Gly Ala Ile Ile Ala Thr Thr Ala
                 90                  95                 100

ctc gca tgg gca ctc atc aca gtt ttg aac atc gat gcc gcc tcc ggc   451
Leu Ala Trp Ala Leu Ile Thr Val Leu Asn Ile Asp Ala Ala Ser Gly
            105                 110                 115

gcc ggc atg ctc acc ggc gcg ctc acc aac acc cca gcc atg gcc gca   499
Ala Gly Met Leu Thr Gly Ala Leu Thr Asn Thr Pro Ala Met Ala Ala
        120                 125                 130

gtt gtt gac gca ctt cct tcg ctt atc gac gac acc ggc cag ctt cac   547
Val Val Asp Ala Leu Pro Ser Leu Ile Asp Asp Thr Gly Gln Leu His
    135                 140                 145

ctc atc gcc gag ctg ccc gtc gtc gca tat tcc ttg gca tac ccc ctc   595
Leu Ile Ala Glu Leu Pro Val Val Ala Tyr Ser Leu Ala Tyr Pro Leu
150                 155                 160                 165

ggt gtg ctc atc gtt att ctc tcc atc gcc atc ttc agc tct gtg ttc   643
Gly Val Leu Ile Val Ile Leu Ser Ile Ala Ile Phe Ser Ser Val Phe
                170                 175                 180

aaa gtc gac cac aac aaa gaa gcc gaa gaa gcg ggc gtt gcg gtc cag   691
Lys Val Asp His Asn Lys Glu Ala Glu Glu Ala Gly Val Ala Val Gln
            185                 190                 195

gaa ctc aaa ggc cgt cgc atc cgc gtc acc gtc gct gat ctt cca gcc   739
Glu Leu Lys Gly Arg Arg Ile Arg Val Thr Val Ala Asp Leu Pro Ala
        200                 205                 210

ctg gag aac atc cca gag ctg ctc aac ctc cac gtc att gtg tcc cga   787
Leu Glu Asn Ile Pro Glu Leu Leu Asn Leu His Val Ile Val Ser Arg
    215                 220                 225

gtg gaa cga gac ggt gag caa ttc atc ccg ctt tat ggc gaa cac gca   835
Val Glu Arg Asp Gly Glu Gln Phe Ile Pro Leu Tyr Gly Glu His Ala
230                 235                 240                 245

cgc atc ggc gat gtc tta aca gtg gtg ggt gcc gat gaa gaa ctc aac   883
Arg Ile Gly Asp Val Leu Thr Val Val Gly Ala Asp Glu Glu Leu Asn
```

```
                    250                 255                 260

cgc gcg gaa aaa gcc atc ggt gaa ctc att gac ggc gac ccc tac agc   931
Arg Ala Glu Lys Ala Ile Gly Glu Leu Ile Asp Gly Asp Pro Tyr Ser
            265                 270                 275

aat gtg gaa ctt gat tac cga cgc atc ttc gtc tca aac aca gca gtc   979
Asn Val Glu Leu Asp Tyr Arg Arg Ile Phe Val Ser Asn Thr Ala Val
        280                 285                 290

gtg ggc act ccc cta tcc aag ctc cag cca ctg ttt aaa gac atg ctg   1027
Val Gly Thr Pro Leu Ser Lys Leu Gln Pro Leu Phe Lys Asp Met Leu
    295                 300                 305

atc acc cgc atc agg cgc ggc gac aca gat ttg gtg gcc tcc tcc gac   1075
Ile Thr Arg Ile Arg Arg Gly Asp Thr Asp Leu Val Ala Ser Ser Asp
310                 315                 320                 325

atg act ttg cag ctc ggt gac cgt gtc cgc gtt gtc gca cca gca gaa   1123
Met Thr Leu Gln Leu Gly Asp Arg Val Arg Val Val Ala Pro Ala Glu
                330                 335                 340

aaa ctc cgc gaa gca acc caa ttg ctc ggc gat tcc tac aag aaa ctc   1171
Lys Leu Arg Glu Ala Thr Gln Leu Leu Gly Asp Ser Tyr Lys Lys Leu
            345                 350                 355

tcc gat ttc aac ctg ctc cca ctc gct gcc ggc ctc atg atc ggt gtg   1219
Ser Asp Phe Asn Leu Leu Pro Leu Ala Ala Gly Leu Met Ile Gly Val
        360                 365                 370

ctt gtc ggc atg gtg gag ttc cca cta cca ggt gga agc tcc ctg aaa   1267
Leu Val Gly Met Val Glu Phe Pro Leu Pro Gly Gly Ser Ser Leu Lys
    375                 380                 385

ctg ggt aac gca ggt gga ccg cta gtt gtt gcg ctg ctg ctc ggc atg   1315
Leu Gly Asn Ala Gly Gly Pro Leu Val Val Ala Leu Leu Leu Gly Met
390                 395                 400                 405

atc aat cgc aca ggc aag ttc gtc tgg caa atc ccc tac gga gca aac   1363
Ile Asn Arg Thr Gly Lys Phe Val Trp Gln Ile Pro Tyr Gly Ala Asn
                410                 415                 420

ctt gcc ctt cgc caa ctg ggc atc aca cta ttt ttg gct gcc atc ggt   1411
Leu Ala Leu Arg Gln Leu Gly Ile Thr Leu Phe Leu Ala Ala Ile Gly
            425                 430                 435

acc tca gcg ggc gca gga ttt cga tca gcg atc agc gac ccc caa tca   1459
Thr Ser Ala Gly Ala Gly Phe Arg Ser Ala Ile Ser Asp Pro Gln Ser
        440                 445                 450

ctc acc atc atc ggc ttc ggt gcg ctg ctc act ttg ttc atc tcc atc   1507
Leu Thr Ile Ile Gly Phe Gly Ala Leu Leu Thr Leu Phe Ile Ser Ile
    455                 460                 465

acg gtg ctg ttc gtt ggc cac aaa ctg atg aaa atc ccc ttc ggt gaa   1555
Thr Val Leu Phe Val Gly His Lys Leu Met Lys Ile Pro Phe Gly Glu
470                 475                 480                 485

acc gct ggc atc ctc gcc ggt acg caa acc cac cct gct gtg ctg agt   1603
Thr Ala Gly Ile Leu Ala Gly Thr Gln Thr His Pro Ala Val Leu Ser
                490                 495                 500
```

```
tat gtg tca gat gcc tcc cgc aac gag ctc cct gcc atg ggt tat acc   1651
Tyr Val Ser Asp Ala Ser Arg Asn Glu Leu Pro Ala Met Gly Tyr Thr
            505                 510                 515

tct gtg tat ccg ctg gcg atg atc gca aag atc ctg gcc gcc caa acg   1699
Ser Val Tyr Pro Leu Ala Met Ile Ala Lys Ile Leu Ala Ala Gln Thr
        520                 525                 530

ttg ttg ttc cta ctt atc tagcattgac cccttaagcg cag                 1740
Leu Leu Phe Leu Leu Ile
    535
```

<210> 2396
<211> 539
<212> PRT
<213> Corynebacterium glutamicum

<400> 2396

```
Val Ser Phe Leu Val Glu Asn Gln Leu Leu Ala Leu Val Val Ile Met
  1               5                  10                  15

Thr Val Gly Leu Leu Leu Gly Arg Ile Lys Ile Phe Gly Phe Arg Leu
             20                  25                  30

Gly Val Ala Ala Val Leu Phe Val Gly Leu Ala Leu Ser Thr Ile Glu
         35                  40                  45

Pro Asp Ile Ser Val Pro Ser Leu Ile Tyr Val Val Gly Leu Ser Leu
     50                  55                  60

Phe Val Tyr Thr Ile Gly Leu Glu Ala Gly Pro Gly Phe Phe Thr Ser
 65                  70                  75                  80

Met Lys Thr Thr Gly Leu Arg Asn Asn Ala Leu Thr Leu Gly Ala Ile
                 85                  90                  95

Ile Ala Thr Thr Ala Leu Ala Trp Ala Leu Ile Thr Val Leu Asn Ile
            100                 105                 110

Asp Ala Ala Ser Gly Ala Gly Met Leu Thr Gly Ala Leu Thr Asn Thr
        115                 120                 125

Pro Ala Met Ala Ala Val Val Asp Ala Leu Pro Ser Leu Ile Asp Asp
    130                 135                 140

Thr Gly Gln Leu His Leu Ile Ala Glu Leu Pro Val Val Ala Tyr Ser
145                 150                 155                 160

Leu Ala Tyr Pro Leu Gly Val Leu Ile Val Ile Leu Ser Ile Ala Ile
                165                 170                 175

Phe Ser Ser Val Phe Lys Val Asp His Asn Lys Glu Ala Glu Glu Ala
            180                 185                 190

Gly Val Ala Val Gln Glu Leu Lys Gly Arg Arg Ile Arg Val Thr Val
        195                 200                 205

Ala Asp Leu Pro Ala Leu Glu Asn Ile Pro Glu Leu Leu Asn Leu His
    210                 215                 220
```

```
Val Ile Val Ser Arg Val Glu Arg Asp Gly Glu Gln Phe Ile Pro Leu
225                 230                 235                 240

Tyr Gly Glu His Ala Arg Ile Gly Asp Val Leu Thr Val Val Gly Ala
                245                 250                 255

Asp Glu Glu Leu Asn Arg Ala Glu Lys Ala Ile Gly Glu Leu Ile Asp
            260                 265                 270

Gly Asp Pro Tyr Ser Asn Val Glu Leu Asp Tyr Arg Arg Ile Phe Val
        275                 280                 285

Ser Asn Thr Ala Val Val Gly Thr Pro Leu Ser Lys Leu Gln Pro Leu
    290                 295                 300

Phe Lys Asp Met Leu Ile Thr Arg Ile Arg Arg Gly Asp Thr Asp Leu
305                 310                 315                 320

Val Ala Ser Ser Asp Met Thr Leu Gln Leu Gly Asp Arg Val Arg Val
                325                 330                 335

Val Ala Pro Ala Glu Lys Leu Arg Glu Ala Thr Gln Leu Leu Gly Asp
            340                 345                 350

Ser Tyr Lys Lys Leu Ser Asp Phe Asn Leu Leu Pro Leu Ala Ala Gly
        355                 360                 365

Leu Met Ile Gly Val Leu Val Gly Met Val Glu Phe Pro Leu Pro Gly
    370                 375                 380

Gly Ser Ser Leu Lys Leu Gly Asn Ala Gly Gly Pro Leu Val Val Ala
385                 390                 395                 400

Leu Leu Leu Gly Met Ile Asn Arg Thr Gly Lys Phe Val Trp Gln Ile
                405                 410                 415

Pro Tyr Gly Ala Asn Leu Ala Leu Arg Gln Leu Gly Ile Thr Leu Phe
            420                 425                 430

Leu Ala Ala Ile Gly Thr Ser Ala Gly Ala Gly Phe Arg Ser Ala Ile
        435                 440                 445

Ser Asp Pro Gln Ser Leu Thr Ile Ile Gly Phe Gly Ala Leu Leu Thr
    450                 455                 460

Leu Phe Ile Ser Ile Thr Val Leu Phe Val Gly His Lys Leu Met Lys
465                 470                 475                 480

Ile Pro Phe Gly Glu Thr Ala Gly Ile Leu Ala Gly Thr Gln Thr His
                485                 490                 495

Pro Ala Val Leu Ser Tyr Val Ser Asp Ala Ser Arg Asn Glu Leu Pro
            500                 505                 510

Ala Met Gly Tyr Thr Ser Val Tyr Pro Leu Ala Met Ile Ala Lys Ile
        515                 520                 525

Leu Ala Ala Gln Thr Leu Leu Phe Leu Leu Ile
    530                 535
```

<210> 2397
<211> 1764
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1741)
<223> RXA01750

<400> 2397
tcgcccccga ggattgtgtt gcgaacagtc ctgaagatca tgtcagacct acattgagcc 60

aatgatcgac atgtggacga gggaaactcg accgaacaat atg tgt atc aac gac 115
Met Cys Ile Asn Asp
1 5

cct aaa ggc gag ttg ctg aag aaa aat tat gtt cgg atg tct aag cgc 163
Pro Lys Gly Glu Leu Leu Lys Lys Asn Tyr Val Arg Met Ser Lys Arg
10 15 20

ggt ttt cag gtt gtt cag ttt aac ctg att aac aac ctg aaa act gat 211
Gly Phe Gln Val Val Gln Phe Asn Leu Ile Asn Asn Leu Lys Thr Asp
25 30 35

att tat aac ccg ttg gga tta gca gcc gaa gca gct cgc gaa ggt aac 259
Ile Tyr Asn Pro Leu Gly Leu Ala Ala Glu Ala Ala Arg Glu Gly Asn
40 45 50

ggg atg aag tgc gca acc tat gtg gaa aat atc gca gag gtg ttc ttt 307
Gly Met Lys Cys Ala Thr Tyr Val Glu Asn Ile Ala Glu Val Phe Phe
55 60 65

ccg gtg gac ggt gcc gat gat ccg gta tgg ccg aat gcg gcc aac aat 355
Pro Val Asp Gly Ala Asp Asp Pro Val Trp Pro Asn Ala Ala Asn Asn
70 75 80 85

gcc ttc aag cgt gca gcc tat ggt ctt atc gac ttc tat ttg gaa gag 403
Ala Phe Lys Arg Ala Ala Tyr Gly Leu Ile Asp Phe Tyr Leu Glu Glu
90 95 100

gag cgc gag atg cgc aag cag gct gca gct gag aat tgg gat gcc aag 451
Glu Arg Glu Met Arg Lys Gln Ala Ala Ala Glu Asn Trp Asp Ala Lys
105 110 115

gtg ctt gat aca cgt att gat cag atg tgg ggt aag gtc acg ctc tac 499
Val Leu Asp Thr Arg Ile Asp Gln Met Trp Gly Lys Val Thr Leu Tyr
120 125 130

aac tgc tac cag ctc ttt gtg cag ctt tcg gca aag aag ctg aag aat 547
Asn Cys Tyr Gln Leu Phe Val Gln Leu Ser Ala Lys Lys Leu Lys Asn
135 140 145

ccc gtt gag cga ctc aat gaa cgt gca cgt gcc ggt gaa ttc ggt aac 595
Pro Val Glu Arg Leu Asn Glu Arg Ala Arg Ala Gly Glu Phe Gly Asn
150 155 160 165

tta gag act gat gaa aat gca gcc atg atg ttc cag gat gct gtg aca 643
Leu Glu Thr Asp Glu Asn Ala Ala Met Met Phe Gln Asp Ala Val Thr
170 175 180

```
gag gcc gaa gag aac gaa atg ttt ctg tgg gag ggt gag aaa gaa aaa   691
Glu Ala Glu Glu Asn Glu Met Phe Leu Trp Glu Gly Glu Lys Glu Lys
            185                 190                 195

gac atg ctc acc ttg ttc ttt agt gcc aca gac ggt ctg cca aag tcc   739
Asp Met Leu Thr Leu Phe Phe Ser Ala Thr Asp Gly Leu Pro Lys Ser
        200                 205                 210

agt gtt cgt act ctg gtg ggc aac gca gat aag gcc ctg aaa gca atg   787
Ser Val Arg Thr Leu Val Gly Asn Ala Asp Lys Ala Leu Lys Ala Met
    215                 220                 225

ggt ggc gct gaa aaa atg atg gcg tcg gtc tac ggt atc gcg att aca   835
Gly Gly Ala Glu Lys Met Met Ala Ser Val Tyr Gly Ile Ala Ile Thr
230                 235                 240                 245

gcg atg tcc ttc ttt aca gac ccc aca att tca acg tta acc tca ggc   883
Ala Met Ser Phe Phe Thr Asp Pro Thr Ile Ser Thr Leu Thr Ser Gly
                250                 255                 260

aca cta agt cag aac gtt gac ttg gcc gga ttg tcg ttt cca cgg cgc   931
Thr Leu Ser Gln Asn Val Asp Leu Ala Gly Leu Ser Phe Pro Arg Arg
            265                 270                 275

atg ggt gtt cgt ttt gcg gcc ccc tat gtg aag cgc tac aac ctg gtt   979
Met Gly Val Arg Phe Ala Ala Pro Tyr Val Lys Arg Tyr Asn Leu Val
        280                 285                 290

gga tca cag gtg aaa tgg gat gcg tat agt gac gcc aag ttc acc aag   1027
Gly Ser Gln Val Lys Trp Asp Ala Tyr Ser Asp Ala Lys Phe Thr Lys
    295                 300                 305

ccg ttg ggt aag aat ttt gtt cat gat gac acg ctg tcg gtt gag ggt   1075
Pro Leu Gly Lys Asn Phe Val His Asp Asp Thr Leu Ser Val Glu Gly
310                 315                 320                 325

tgg gcg cgg ttc tat att aaa gac tcg ttc ccg agt aat act gcg tac   1123
Trp Ala Arg Phe Tyr Ile Lys Asp Ser Phe Pro Ser Asn Thr Ala Tyr
                330                 335                 340

ctg cgt ttg cgg att ctc aat ggt act tct ggc acg ttg atc aag act   1171
Leu Arg Leu Arg Ile Leu Asn Gly Thr Ser Gly Thr Leu Ile Lys Thr
            345                 350                 355

ctg tac ttc aag ttc acc aag ggc tac caa acg aac ctt aaa ggc cgt   1219
Leu Tyr Phe Lys Phe Thr Lys Gly Tyr Gln Thr Asn Leu Lys Gly Arg
        360                 365                 370

gcg ttt att act gat ccg gtg acc gat gag aag atc att aag aat ggt   1267
Ala Phe Ile Thr Asp Pro Val Thr Asp Glu Lys Ile Ile Lys Asn Gly
    375                 380                 385

ctg ctg atc gag ctg gtg aaa aac gat gct ggt gac ttt gtt cca ggt   1315
Leu Leu Ile Glu Leu Val Lys Asn Asp Ala Gly Asp Phe Val Pro Gly
390                 395                 400                 405

cat gtg cag ttt aag acg aag aaa ctg aat ctt gac caa ctc acg cag   1363
His Val Gln Phe Lys Thr Lys Lys Leu Asn Leu Asp Gln Leu Thr Gln
                410                 415                 420
```

```
gaa cag atc aat atg ccg ggt cat gac atg atc aag cag gtt gat gcg   1411
Glu Gln Ile Asn Met Pro Gly His Asp Met Ile Lys Gln Val Asp Ala
            425                 430                 435

atg gtt gat gcg gtg tcg gct ctg aat gtg cgg tat tcg gag aag cct   1459
Met Val Asp Ala Val Ser Ala Leu Asn Val Arg Tyr Ser Glu Lys Pro
        440                 445                 450

aag gca gtg ttc ttc gta acg cct ccg cat ctt atg aaa tat gcg aag   1507
Lys Ala Val Phe Phe Val Thr Pro Pro His Leu Met Lys Tyr Ala Lys
    455                 460                 465

ttg att ttg att ctc atc aaa cag ctt gtg gat ctg aac ttc gat tcc   1555
Leu Ile Leu Ile Leu Ile Lys Gln Leu Val Asp Leu Asn Phe Asp Ser
470                 475                 480                 485

tcg tat atg acg cgt gag aat cag aag ccg gat tat aag act cgt ttc   1603
Ser Tyr Met Thr Arg Glu Asn Gln Lys Pro Asp Tyr Lys Thr Arg Phe
                490                 495                 500

atg ttg gac gag ttg gga aac ctt cag agt gag ggt cat ggt att gcg   1651
Met Leu Asp Glu Leu Gly Asn Leu Gln Ser Glu Gly His Gly Ile Ala
            505                 510                 515

gga ttt gaa acc atg ctc tcg atc ggt ctg gga caa gaa caa caa ttt   1699
Gly Phe Glu Thr Met Leu Ser Ile Gly Leu Gly Gln Glu Gln Gln Phe
        520                 525                 530

agt gcg acc agt tgc gta gcg aaa aac tac gct ctt gca gct           1741
Ser Ala Thr Ser Cys Val Ala Lys Asn Tyr Ala Leu Ala Ala
    535                 540                 545

taaagttgca agaaactgtt tca                                        1764
```

<210> 2398
<211> 547
<212> PRT
<213> Corynebacterium glutamicum

<400> 2398

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Met Cys Ile Asn Asp Pro Lys Gly Glu Leu Leu Lys Lys Asn Tyr Val
  1               5                  10                  15

Arg Met Ser Lys Arg Gly Phe Gln Val Val Gln Phe Asn Leu Ile Asn
             20                  25                  30

Asn Leu Lys Thr Asp Ile Tyr Asn Pro Leu Gly Leu Ala Ala Glu Ala
         35                  40                  45

Ala Arg Glu Gly Asn Gly Met Lys Cys Ala Thr Tyr Val Glu Asn Ile
     50                  55                  60

Ala Glu Val Phe Phe Pro Val Asp Gly Ala Asp Asp Pro Val Trp Pro
 65                  70                  75                  80

Asn Ala Ala Asn Asn Ala Phe Lys Arg Ala Ala Tyr Gly Leu Ile Asp
                 85                  90                  95

Phe Tyr Leu Glu Glu Glu Arg Glu Met Arg Lys Gln Ala Ala Ala Glu
            100                 105                 110
```

```
Asn Trp Asp Ala Lys Val Leu Asp Thr Arg Ile Asp Gln Met Trp Gly
        115                 120                 125

Lys Val Thr Leu Tyr Asn Cys Tyr Gln Leu Phe Val Gln Leu Ser Ala
    130                 135                 140

Lys Lys Leu Lys Asn Pro Val Glu Arg Leu Asn Glu Arg Ala Arg Ala
145                 150                 155                 160

Gly Glu Phe Gly Asn Leu Glu Thr Asp Glu Asn Ala Ala Met Met Phe
                165                 170                 175

Gln Asp Ala Val Thr Glu Ala Glu Glu Asn Glu Met Phe Leu Trp Glu
            180                 185                 190

Gly Glu Lys Glu Lys Asp Met Leu Thr Leu Phe Phe Ser Ala Thr Asp
        195                 200                 205

Gly Leu Pro Lys Ser Ser Val Arg Thr Leu Val Gly Asn Ala Asp Lys
    210                 215                 220

Ala Leu Lys Ala Met Gly Gly Ala Glu Lys Met Met Ala Ser Val Tyr
225                 230                 235                 240

Gly Ile Ala Ile Thr Ala Met Ser Phe Phe Thr Asp Pro Thr Ile Ser
                245                 250                 255

Thr Leu Thr Ser Gly Thr Leu Ser Gln Asn Val Asp Leu Ala Gly Leu
            260                 265                 270

Ser Phe Pro Arg Arg Met Gly Val Arg Phe Ala Ala Pro Tyr Val Lys
        275                 280                 285

Arg Tyr Asn Leu Val Gly Ser Gln Val Lys Trp Asp Ala Tyr Ser Asp
    290                 295                 300

Ala Lys Phe Thr Lys Pro Leu Gly Lys Asn Phe Val His Asp Asp Thr
305                 310                 315                 320

Leu Ser Val Glu Gly Trp Ala Arg Phe Tyr Ile Lys Asp Ser Phe Pro
                325                 330                 335

Ser Asn Thr Ala Tyr Leu Arg Leu Arg Ile Leu Asn Gly Thr Ser Gly
            340                 345                 350

Thr Leu Ile Lys Thr Leu Tyr Phe Lys Phe Thr Lys Gly Tyr Gln Thr
        355                 360                 365

Asn Leu Lys Gly Arg Ala Phe Ile Thr Asp Pro Val Thr Asp Glu Lys
    370                 375                 380

Ile Ile Lys Asn Gly Leu Leu Ile Glu Leu Val Lys Asn Asp Ala Gly
385                 390                 395                 400

Asp Phe Val Pro Gly His Val Gln Phe Lys Thr Lys Lys Leu Asn Leu
                405                 410                 415

Asp Gln Leu Thr Gln Glu Gln Ile Asn Met Pro Gly His Asp Met Ile
            420                 425                 430
```

```
Lys Gln Val Asp Ala Met Val Asp Ala Val Ser Ala Leu Asn Val Arg
        435                 440                 445

Tyr Ser Glu Lys Pro Lys Ala Val Phe Phe Val Thr Pro Pro His Leu
    450                 455                 460

Met Lys Tyr Ala Lys Leu Ile Leu Ile Leu Ile Lys Gln Leu Val Asp
465                 470                 475                 480

Leu Asn Phe Asp Ser Ser Tyr Met Thr Arg Glu Asn Gln Lys Pro Asp
                485                 490                 495

Tyr Lys Thr Arg Phe Met Leu Asp Glu Leu Gly Asn Leu Gln Ser Glu
            500                 505                 510

Gly His Gly Ile Ala Gly Phe Glu Thr Met Leu Ser Ile Gly Leu Gly
        515                 520                 525

Gln Glu Gln Gln Phe Ser Ala Thr Ser Cys Val Ala Lys Asn Tyr Ala
    530                 535                 540

Leu Ala Ala
545
```

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<210> 2399
<211> 652
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(652)
<223> RXA01752

<400> 2399
gaaatgacgt gaccatcgat accaataccc aattgaaaga tcttgacctg gtcagccaag 60

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ttggccgtca gatcgtggca gaacaacagg tggggaggtc atg atg gaa caa gat   115
                                              Met Met Glu Gln Asp
                                                1               5

ctc agc tac cgt gaa att ctt ccc ctc aac gcg agt gag gag aag aaa   163
Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala Ser Glu Glu Lys Lys
                10                  15                  20

aag gct gca ctg att gat gcc att gaa ggg tta agg gtg cgc gat ccg   211
Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu Arg Val Arg Asp Pro
            25                  30                  35

cta ctc tct gcc tcg att gca ttt act aga ggg cag aaa gtc gcc ttc   259
Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly Gln Lys Val Ala Phe
        40                  45                  50

att gct gtg gtg gtg ggc ttt atc ttg atg ctc att ttt gct cgg caa   307
Ile Ala Val Val Val Gly Phe Ile Leu Met Leu Ile Phe Ala Arg Gln
    55                  60                  65

gca gca ctt att gga ctg tca gca acg tgt acg ttc atg tac ctc att   355
Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr Phe Met Tyr Leu Ile
70                  75                  80                  85
```

```
aca ttg ttg gac aga ttt atc atg ttt tcc aga ggt atc cgc gcg gaa   403
Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg Gly Ile Arg Ala Glu
                 90                  95                 100

tcc atc atc cag gta tcg gat gaa gat gcg ctg gct ttc cct gag gac   451
Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu Ala Phe Pro Glu Asp
            105                 110                 115

aag ctg aaa acc tac acg gtg ttg gtg ccc gcc tat ggc gaa cct gag   499
Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala Tyr Gly Glu Pro Glu
        120                 125                 130

gtg att gcg cag ctg ctg gca tcc atg cac gct ttt gat tac ccc aag   547
Val Ile Ala Gln Leu Leu Ala Ser Met His Ala Phe Asp Tyr Pro Lys
    135                 140                 145

cat ctt ctg cag gta ttg ctc atg ttg gag gaa gat gat ctg ccc acg   595
His Leu Leu Gln Val Leu Leu Met Leu Glu Glu Asp Asp Leu Pro Thr
150                 155                 160                 165

atc gcc gcg gca gag gca gcg gga gtg gat cag gtg gca acg atc att   643
Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln Val Ala Thr Ile Ile
                170                 175                 180

aag gtg ccg                                                      652
Lys Val Pro
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<210> 2400
<211> 184
<212> PRT
<213> Corynebacterium glutamicum

<400> 2400

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Met Met Glu Gln Asp Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala
  1               5                  10                  15

Ser Glu Glu Lys Lys Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu
             20                  25                  30

Arg Val Arg Asp Pro Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly
         35                  40                  45

Gln Lys Val Ala Phe Ile Ala Val Val Val Gly Phe Ile Leu Met Leu
     50                  55                  60

Ile Phe Ala Arg Gln Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr
 65                  70                  75                  80

Phe Met Tyr Leu Ile Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg
                 85                  90                  95

Gly Ile Arg Ala Glu Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu
            100                 105                 110

Ala Phe Pro Glu Asp Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala
        115                 120                 125

Tyr Gly Glu Pro Glu Val Ile Ala Gln Leu Leu Ala Ser Met His Ala
```

```
    130                 135                 140

Phe Asp Tyr Pro Lys His Leu Leu Gln Val Leu Leu Met Leu Glu Glu
145                 150                 155                 160

Asp Asp Leu Pro Thr Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln
                165                 170                 175

Val Ala Thr Ile Ile Lys Val Pro
            180
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<210> 2401
<211> 1662
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1639)
<223> RXA01753

<400> 2401

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ctgattgtcg cagccgtggt gtcagtgtcc aggcgttcgc aaaaaggata caaatgattt 60

cttctttacc cagtagaacg caggggagga ggttgggtcc atg agt aac ccg tcg   115
                                            Met Ser Asn Pro Ser
                                              1               5

cta gaa cct cta gaa ccg atc gag ctt tct gac ggt act gaa att gaa   163
Leu Glu Pro Leu Glu Pro Ile Glu Leu Ser Asp Gly Thr Glu Ile Glu
                10                  15                  20

gtt tca gac gtt gat cca gaa ccg caa gct ggc aat gcg cag atg gaa   211
Val Ser Asp Val Asp Pro Glu Pro Gln Ala Gly Asn Ala Gln Met Glu
            25                  30                  35

gta ccc agc tta cgg aca tat gtt ttt cgc gga atc att gcc att gcc   259
Val Pro Ser Leu Arg Thr Tyr Val Phe Arg Gly Ile Ile Ala Ile Ala
        40                  45                  50

tgt ttg atc att ggt ttt tat gag agc ttt gtg ctg atg tgg caa aac   307
Cys Leu Ile Ile Gly Phe Tyr Glu Ser Phe Val Leu Met Trp Gln Asn
    55                  60                  65

ctc cga atc ggc gtg gcc aac tac tca cta ctt gtg gtg ctc atg gcg   355
Leu Arg Ile Gly Val Ala Asn Tyr Ser Leu Leu Val Val Leu Met Ala
70                  75                  80                  85

atc gtg ttg ttt atc gga ctg gac cgc aag cgt gct cgt gca ttg aac   403
Ile Val Leu Phe Ile Gly Leu Asp Arg Lys Arg Ala Arg Ala Leu Asn
                90                  95                  100

att cac gac cgc gaa gtc gac tac atc att ggt ggc att gtc gta ctg   451
Ile His Asp Arg Glu Val Asp Tyr Ile Ile Gly Gly Ile Val Val Leu
            105                 110                 115

ata gcc atc acg att aag agc cag ctt ctg cca cgt ttt gtg gac tgg   499
Ile Ala Ile Thr Ile Lys Ser Gln Leu Leu Pro Arg Phe Val Asp Trp
        120                 125                 130
```

```
gaa act ctg ctg cgc ttg gat atg ttc gca ctg tta ttc ttt gcg ttt   547
Glu Thr Leu Leu Arg Leu Asp Met Phe Ala Leu Leu Phe Phe Ala Phe
    135                 140                 145

ggt att tcc ggc ctg gtg ttt ggc atg cgc tct acc ttt tct ttt gca   595
Gly Ile Ser Gly Leu Val Phe Gly Met Arg Ser Thr Phe Ser Phe Ala
150                 155                 160                 165

ccc ggc tgg att ttg ctg ttt ggc tac aac gcg gtg gca cac ctg atc   643
Pro Gly Trp Ile Leu Leu Phe Gly Tyr Asn Ala Val Ala His Leu Ile
                170                 175                 180

atc tcg gtg att ttc ggt ggt ggc ttt tgg ggc ccg gtg atg gca aac   691
Ile Ser Val Ile Phe Gly Gly Gly Phe Trp Gly Pro Val Met Ala Asn
            185                 190                 195

atc att gga ctg tct ctt gcg gtg ttg gtg tcc tcc aac agg gac ctg   739
Ile Ile Gly Leu Ser Leu Ala Val Leu Val Ser Ser Asn Arg Asp Leu
        200                 205                 210

gtt cag gcc acc tat ttg gca ctg atg acg gtg ttg ttt ggc gtc att   787
Val Gln Ala Thr Tyr Leu Ala Leu Met Thr Val Leu Phe Gly Val Ile
    215                 220                 225

att gcc atc atc gtg tgg gcg ctg acc gat ggc agt aag ttc ctc acc   835
Ile Ala Ile Ile Val Trp Ala Leu Thr Asp Gly Ser Lys Phe Leu Thr
230                 235                 240                 245

ttg gtc cca gca gtg ctg gca acc atc act gtg gtg ttg gtg tct tcg   883
Leu Val Pro Ala Val Leu Ala Thr Ile Thr Val Val Leu Val Ser Ser
                250                 255                 260

cgt tgg agg ctt ggt cag tgg aaa att cgt cgt aga caa ccc acg gtg   931
Arg Trp Arg Leu Gly Gln Trp Lys Ile Arg Arg Arg Gln Pro Thr Val
            265                 270                 275

gaa aaa gcc gga ccc gcg ctt atc gcg gtc gtg gtt gcg aca gca ctc   979
Glu Lys Ala Gly Pro Ala Leu Ile Ala Val Val Val Ala Thr Ala Leu
        280                 285                 290

ttg gcg tgg att cct act cct tat gtg gag cgc gtc aac aac ctc ccc   1027
Leu Ala Trp Ile Pro Thr Pro Tyr Val Glu Arg Val Asn Asn Leu Pro
    295                 300                 305

ggg ctt caa atg ctg gca aag cct gcc cca ggt gtt atc gca cct att   1075
Gly Leu Gln Met Leu Ala Lys Pro Ala Pro Gly Val Ile Ala Pro Ile
310                 315                 320                 325

ggt tgg cac atc gac gat gtg cag tat tac aac tgg gct tcg cgc tac   1123
Gly Trp His Ile Asp Asp Val Gln Tyr Tyr Asn Trp Ala Ser Arg Tyr
                330                 335                 340

ttc ggc ccc ggt tcc tct ctg ctt agg cag acg atg acg gca gat cat   1171
Phe Gly Pro Gly Ser Ser Leu Leu Arg Gln Thr Met Thr Ala Asp His
            345                 350                 355

tac aac gag gcg tgg gat cca gat gga ctc gac cga act gtt gtg gtg   1219
Tyr Asn Glu Ala Trp Asp Pro Asp Gly Leu Asp Arg Thr Val Val Val
        360                 365                 370

gat acc ctc caa tcg gcg gaa cgg ttc cag cag cgt gcc ttt ggt gac   1267
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Asp Thr Leu Gln Ser Ala Glu Arg Phe Gln Gln Arg Ala Phe Gly Asp
    375                 380                 385

gag acg ctg tat tcc act ctg aga ggt cga aag tca gat acc gtc cag   1315
Glu Thr Leu Tyr Ser Thr Leu Arg Gly Arg Lys Ser Asp Thr Val Gln
390                 395                 400                 405

gtg gat ctg gga tac ggc gtg gac gga cgc gcc tac acg gtg ctc gat   1363
Val Asp Leu Gly Tyr Gly Val Asp Gly Arg Ala Tyr Thr Val Leu Asp
                410                 415                 420

gaa act gac ttc ttg acg tac acc aag ctg gtt ttt gaa tgg cag acc   1411
Glu Thr Asp Phe Leu Thr Tyr Thr Lys Leu Val Phe Glu Trp Gln Thr
            425                 430                 435

acc aac aac acc gtg gag aag atc tcc gtc atc gcg gtg gat gat cac   1459
Thr Asn Asn Thr Val Glu Lys Ile Ser Val Ile Ala Val Asp Asp His
        440                 445                 450

cgc gca gaa gcg aag ttc ccg gag ctt gca cca tcg gtt acc aga atg   1507
Arg Ala Glu Ala Lys Phe Pro Glu Leu Ala Pro Ser Val Thr Arg Met
    455                 460                 465

ttt atc cag gtg gct acc att ttg ttc cgt gga aat gac gtg acc atc   1555
Phe Ile Gln Val Ala Thr Ile Leu Phe Arg Gly Asn Asp Val Thr Ile
470                 475                 480                 485

gat acc aat acc caa ttg aaa gat ctt gac ctg gtc agc caa gtt ggc   1603
Asp Thr Asn Thr Gln Leu Lys Asp Leu Asp Leu Val Ser Gln Val Gly
                490                 495                 500

cgt cag atc gtg gca gaa caa cag gtg ggg agg tca tgatggaaca        1649
Arg Gln Ile Val Ala Glu Gln Gln Val Gly Arg Ser
            505                 510

agatctcagc tac                                                   1662


<210> 2402
<211> 513
<212> PRT
<213> Corynebacterium glutamicum

<400> 2402
Met Ser Asn Pro Ser Leu Glu Pro Leu Glu Pro Ile Glu Leu Ser Asp
  1               5                  10                  15

Gly Thr Glu Ile Glu Val Ser Asp Val Asp Pro Glu Pro Gln Ala Gly
             20                  25                  30

Asn Ala Gln Met Glu Val Pro Ser Leu Arg Thr Tyr Val Phe Arg Gly
         35                  40                  45

Ile Ile Ala Ile Ala Cys Leu Ile Ile Gly Phe Tyr Glu Ser Phe Val
     50                  55                  60

Leu Met Trp Gln Asn Leu Arg Ile Gly Val Ala Asn Tyr Ser Leu Leu
 65                  70                  75                  80

Val Val Leu Met Ala Ile Val Leu Phe Ile Gly Leu Asp Arg Lys Arg
                 85                  90                  95
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Ala Arg Ala Leu Asn Ile His Asp Arg Glu Val Asp Tyr Ile Ile Gly
            100                 105                 110

Gly Ile Val Val Leu Ile Ala Ile Thr Ile Lys Ser Gln Leu Leu Pro
        115                 120                 125

Arg Phe Val Asp Trp Glu Thr Leu Leu Arg Leu Asp Met Phe Ala Leu
    130                 135                 140

Leu Phe Phe Ala Phe Gly Ile Ser Gly Leu Val Phe Gly Met Arg Ser
145                 150                 155                 160

Thr Phe Ser Phe Ala Pro Gly Trp Ile Leu Leu Phe Gly Tyr Asn Ala
                165                 170                 175

Val Ala His Leu Ile Ile Ser Val Ile Phe Gly Gly Gly Phe Trp Gly
            180                 185                 190

Pro Val Met Ala Asn Ile Ile Gly Leu Ser Leu Ala Val Leu Val Ser
        195                 200                 205

Ser Asn Arg Asp Leu Val Gln Ala Thr Tyr Leu Ala Leu Met Thr Val
    210                 215                 220

Leu Phe Gly Val Ile Ile Ala Ile Ile Val Trp Ala Leu Thr Asp Gly
225                 230                 235                 240

Ser Lys Phe Leu Thr Leu Val Pro Ala Val Leu Ala Thr Ile Thr Val
                245                 250                 255

Val Leu Val Ser Ser Arg Trp Arg Leu Gly Gln Trp Lys Ile Arg Arg
            260                 265                 270

Arg Gln Pro Thr Val Glu Lys Ala Gly Pro Ala Leu Ile Ala Val Val
        275                 280                 285

Val Ala Thr Ala Leu Leu Ala Trp Ile Pro Thr Pro Tyr Val Glu Arg
    290                 295                 300

Val Asn Asn Leu Pro Gly Leu Gln Met Leu Ala Lys Pro Ala Pro Gly
305                 310                 315                 320

Val Ile Ala Pro Ile Gly Trp His Ile Asp Asp Val Gln Tyr Tyr Asn
                325                 330                 335

Trp Ala Ser Arg Tyr Phe Gly Pro Gly Ser Ser Leu Leu Arg Gln Thr
            340                 345                 350

Met Thr Ala Asp His Tyr Asn Glu Ala Trp Asp Pro Asp Gly Leu Asp
        355                 360                 365

Arg Thr Val Val Val Asp Thr Leu Gln Ser Ala Glu Arg Phe Gln Gln
    370                 375                 380

Arg Ala Phe Gly Asp Glu Thr Leu Tyr Ser Thr Leu Arg Gly Arg Lys
385                 390                 395                 400

Ser Asp Thr Val Gln Val Asp Leu Gly Tyr Gly Val Asp Gly Arg Ala
                405                 410                 415
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Tyr Thr Val Leu Asp Glu Thr Asp Phe Leu Thr Tyr Thr Lys Leu Val
            420                 425                 430

Phe Glu Trp Gln Thr Thr Asn Asn Thr Val Glu Lys Ile Ser Val Ile
        435                 440                 445

Ala Val Asp Asp His Arg Ala Glu Ala Lys Phe Pro Glu Leu Ala Pro
    450                 455                 460

Ser Val Thr Arg Met Phe Ile Gln Val Ala Thr Ile Leu Phe Arg Gly
465                 470                 475                 480

Asn Asp Val Thr Ile Asp Thr Asn Thr Gln Leu Lys Asp Leu Asp Leu
                485                 490                 495

Val Ser Gln Val Gly Arg Gln Ile Val Ala Glu Gln Gln Val Gly Arg
            500                 505                 510

Ser
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09/25/2003 09:50:50

<210> 2403
<211> 405
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(382)
<223> RXA01760

<400> 2403

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acctactcaa actttcctct gcgccataac gtgaagtgag tgccggggca gtcccggcag 60

cacccaaaag cgcatttttg atacgaaagt gagtcatacg atg gca gca ttt cta   115
                                            Met Ala Ala Phe Leu
                                              1               5

gag atc acc ttg aaa atc aat gac gaa ggc cgc cca tca gca gct ggc   163
Glu Ile Thr Leu Lys Ile Asn Asp Glu Gly Arg Pro Ser Ala Ala Gly
                 10                  15                  20

gtc tac cag gaa tac aag caa cca ttc ctc agc tca att gct ggc gct   211
Val Tyr Gln Glu Tyr Lys Gln Pro Phe Leu Ser Ser Ile Ala Gly Ala
             25                  30                  35

aca agc aaa gaa ctc ctc atc cga gaa gaa gac gtg cag gtg ctc cac   259
Thr Ser Lys Glu Leu Leu Ile Arg Glu Glu Asp Val Gln Val Leu His
         40                  45                  50

ggc tgt gac acc gta gct aat gct gaa gat tat ctt gtc agc gaa ctg   307
Gly Cys Asp Thr Val Ala Asn Ala Glu Asp Tyr Leu Val Ser Glu Leu
     55                  60                  65

ttc acg gcc gat gtt gtc ggt ggt cta gct cca cta ttg cag gct gat   355
Phe Thr Ala Asp Val Val Gly Gly Leu Ala Pro Leu Leu Gln Ala Asp
 70                  75                  80                  85

cca gag att cgt att tac cag gtc gcg taactgctgt ggcaggctca         402
Pro Glu Ile Arg Ile Tyr Gln Val Ala
```

90

tcg 405

<210> 2404
<211> 94
<212> PRT
<213> Corynebacterium glutamicum

<400> 2404
Met Ala Ala Phe Leu Glu Ile Thr Leu Lys Ile Asn Asp Glu Gly Arg
1 5 10 15

Pro Ser Ala Ala Gly Val Tyr Gln Glu Tyr Lys Gln Pro Phe Leu Ser
20 25 30

Ser Ile Ala Gly Ala Thr Ser Lys Glu Leu Leu Ile Arg Glu Glu Asp
35 40 45

Val Gln Val Leu His Gly Cys Asp Thr Val Ala Asn Ala Glu Asp Tyr
50 55 60

Leu Val Ser Glu Leu Phe Thr Ala Asp Val Val Gly Gly Leu Ala Pro
65 70 75 80

Leu Leu Gln Ala Asp Pro Glu Ile Arg Ile Tyr Gln Val Ala
85 90

<210> 2405
<211> 501
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(478)
<223> RXA01768

<400> 2405
gacaacgaac acaacaccca gatcctgcac tggtccggcg ttaatcgcta cctcatgcag 60

gcactctccc gtactcattt ctagaaaggt ttttcccgtc atg tct gaa tct act 115
Met Ser Glu Ser Thr
1 5

tct tct gct aac tcc acc acc atc ctc aac gac acc ttc aac ccg aag 163
Ser Ser Ala Asn Ser Thr Thr Ile Leu Asn Asp Thr Phe Asn Pro Lys
10 15 20

cct ggc gta cct tat gca cgc gtc gat aat ctc gaa ttt gcc aca cgt 211
Pro Gly Val Pro Tyr Ala Arg Val Asp Asn Leu Glu Phe Ala Thr Arg
25 30 35

gac gaa ttc cgc gct tgg gct acc gca gag atg gag gcc ggt aac gtt 259
Asp Glu Phe Arg Ala Trp Ala Thr Ala Glu Met Glu Ala Gly Asn Val
40 45 50

atc tct gca acc atc gcc aat gcc cca cgc gaa gac cgc atc aag tct 307
Ile Ser Ala Thr Ile Ala Asn Ala Pro Arg Glu Asp Arg Ile Lys Ser

```
     55                  60                  65

ttt gtc atg gat ctt gtt cga gac ggt att gac gac gct gct gag gaa   355
Phe Val Met Asp Leu Val Arg Asp Gly Ile Asp Asp Ala Ala Glu Glu
 70                  75                  80                  85

atc gtc tca cgc att gat agc ggt gac ttc act atg aag gaa gct ctc   403
Ile Val Ser Arg Ile Asp Ser Gly Asp Phe Thr Met Lys Glu Ala Leu
                 90                  95                 100

acc gcg atc gcg gca tca atc aac gac ctc gat gct gac gat gta gtc   451
Thr Ala Ile Ala Ala Ser Ile Asn Asp Leu Asp Ala Asp Asp Val Val
            105                 110                 115

agc gac atc gtt gaa aac cac ttc aac tagtcaacac accagccctc         498
Ser Asp Ile Val Glu Asn His Phe Asn
        120                 125

cac                                                               501


<210> 2406
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 2406
Met Ser Glu Ser Thr Ser Ser Ala Asn Ser Thr Thr Ile Leu Asn Asp
  1               5                  10                  15

Thr Phe Asn Pro Lys Pro Gly Val Pro Tyr Ala Arg Val Asp Asn Leu
             20                  25                  30

Glu Phe Ala Thr Arg Asp Glu Phe Arg Ala Trp Ala Thr Ala Glu Met
         35                  40                  45

Glu Ala Gly Asn Val Ile Ser Ala Thr Ile Ala Asn Ala Pro Arg Glu
     50                  55                  60

Asp Arg Ile Lys Ser Phe Val Met Asp Leu Val Arg Asp Gly Ile Asp
 65                  70                  75                  80

Asp Ala Ala Glu Glu Ile Val Ser Arg Ile Asp Ser Gly Asp Phe Thr
                 85                  90                  95

Met Lys Glu Ala Leu Thr Ala Ile Ala Ala Ser Ile Asn Asp Leu Asp
            100                 105                 110

Ala Asp Asp Val Val Ser Asp Ile Val Glu Asn His Phe Asn
        115                 120                 125


<210> 2407
<211> 3888
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(3865)
<223> RXA01770
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acacctccac tttttctact tttaagaaag ccacattctc atg cca att atc att 115
Met Pro Ile Ile Ile
1 5

gat aac ctc aat tct gac gac gac tcc acc atc ggc act gcc acc gaa 163
Asp Asn Leu Asn Ser Asp Asp Asp Ser Thr Ile Gly Thr Ala Thr Glu
10 15 20

tac aac cct gac act gac gcc gat tta ctt gat gct att aac gct gat 211
Tyr Asn Pro Asp Thr Asp Ala Asp Leu Leu Asp Ala Ile Asn Ala Asp
25 30 35

gct gac ctt gat ggc gac gcc acc atc agc act aac gcg aca gaa gaa 259
Ala Asp Leu Asp Gly Asp Ala Thr Ile Ser Thr Asn Ala Thr Glu Glu
40 45 50

ggt gta gac gca gca gct gaa aaa cct aag aaa aag cgt aaa gcc cct 307
Gly Val Asp Ala Ala Ala Glu Lys Pro Lys Lys Lys Arg Lys Ala Pro
55 60 65

gct ctg aag cct aaa gga ctc acg gca aag ttc ttc cac cgt gat ctt 355
Ala Leu Lys Pro Lys Gly Leu Thr Ala Lys Phe Phe His Arg Asp Leu
70 75 80 85

act ggc gta ggt ggt agg acc ggt cgc ctc aac aag aac gta cac ccg 403
Thr Gly Val Gly Gly Arg Thr Gly Arg Leu Asn Lys Asn Val His Pro
90 95 100

acc aac cca gat ctg tcc tac cag cca gtc tct gat gtc tac acc cca 451
Thr Asn Pro Asp Leu Ser Tyr Gln Pro Val Ser Asp Val Tyr Thr Pro
105 110 115

caa tca gca gat cac aag ggt att aag acc cgc tac atc ctt acc cat 499
Gln Ser Ala Asp His Lys Gly Ile Lys Thr Arg Tyr Ile Leu Thr His
120 125 130

cca acc ccc gct gtt gtt ctc agt gag tcc atc agc aac gcg ttt cat 547
Pro Thr Pro Ala Val Val Leu Ser Glu Ser Ile Ser Asn Ala Phe His
135 140 145

gtc tct acc ctg cgt cgc aac aat aat gtc aac aac tct gat tcg gaa 595
Val Ser Thr Leu Arg Arg Asn Asn Asn Val Asn Asn Ser Asp Ser Glu
150 155 160 165

ttg gct gcc tgg ccg tac ctc tac caa ctc gat att ccg cag ctg gac 643
Leu Ala Ala Trp Pro Tyr Leu Tyr Gln Leu Asp Ile Pro Gln Leu Asp
170 175 180

cag atg att aat gtc gct gac atc tgt gat tac cat ttc cac gga tat 691
Gln Met Ile Asn Val Ala Asp Ile Cys Asp Tyr His Phe His Gly Tyr
185 190 195

aac ctg tgg gtg gat ttt acc ccg cag act atc gct cta cga tcc ggt 739
Asn Leu Trp Val Asp Phe Thr Pro Gln Thr Ile Ala Leu Arg Ser Gly
200 205 210

aag acg gta ctc gat gac ggt acc acc gcc tct gat aac acc act cat 787

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Lys Thr Val Leu Asp Asp Gly Thr Thr Ala Ser Asp Asn Thr Thr His
    215                 220                 225

gtc tat tac cgc gtc acc gtt cac gtt att gcc ggt caa gat cat gga   835
Val Tyr Tyr Arg Val Thr Val His Val Ile Ala Gly Gln Asp His Gly
230                 235                 240                 245

tct act ctg ctt gat gac cag ggc aac cag gtg ctt gat agg gat gat   883
Ser Thr Leu Leu Asp Asp Gln Gly Asn Gln Val Leu Asp Arg Asp Asp
                250                 255                 260

aat cct att tct acc cca agt atc aag cgt att ggc gct gtc act gat   931
Asn Pro Ile Ser Thr Pro Ser Ile Lys Arg Ile Gly Ala Val Thr Asp
            265                 270                 275

ctt ttc gat cac aat cct ttt ggc ttc gct agt gta aac tct ttc gca   979
Leu Phe Asp His Asn Pro Phe Gly Phe Ala Ser Val Asn Ser Phe Ala
        280                 285                 290

ttt gtc gat ttc tca tgg gac cca gcc acc acc ttg gtc gat atg ctc   1027
Phe Val Asp Phe Ser Trp Asp Pro Ala Thr Thr Leu Val Asp Met Leu
    295                 300                 305

aac aac ctt gat tca tat ctc tct aat cac atc aat att gcc agc tcc   1075
Asn Asn Leu Asp Ser Tyr Leu Ser Asn His Ile Asn Ile Ala Ser Ser
310                 315                 320                 325

cca acc ccc att gcc ctc gat atg gtt gtg ctc aat gaa tgg tct gaa   1123
Pro Thr Pro Ile Ala Leu Asp Met Val Val Leu Asn Glu Trp Ser Glu
                330                 335                 340

aag tcc tat cag ctg tgc gaa cgc gtt gtt gca cag gca aag ctc atc   1171
Lys Ser Tyr Gln Leu Cys Glu Arg Val Val Ala Gln Ala Lys Leu Ile
            345                 350                 355

aac agc aac aag atc acc gca cat gtg agt gat gtc atc aag caa aat   1219
Asn Ser Asn Lys Ile Thr Ala His Val Ser Asp Val Ile Lys Gln Asn
        360                 365                 370

gcc cac aat atc ttg tgg ttt acc gaa cag atg aac cct ggc acc acc   1267
Ala His Asn Ile Leu Trp Phe Thr Glu Gln Met Asn Pro Gly Thr Thr
    375                 380                 385

aac ctc agc gag gta cct atc tcc aag aag tct atg ctg ccg atg tct   1315
Asn Leu Ser Glu Val Pro Ile Ser Lys Lys Ser Met Leu Pro Met Ser
390                 395                 400                 405

cgc cag cta cgt att ttg gag cac tac gat gta cca ctg acc gcg tac   1363
Arg Gln Leu Arg Ile Leu Glu His Tyr Asp Val Pro Leu Thr Ala Tyr
                410                 415                 420

tct gct ctt ttc tgg act gtc agc gcc att aag aat gaa tct atg gtg   1411
Ser Ala Leu Phe Trp Thr Val Ser Ala Ile Lys Asn Glu Ser Met Val
            425                 430                 435

cag tac ctt gtg cga cag aat atg cag ctc acc ttg agc tca aat ctg   1459
Gln Tyr Leu Val Arg Gln Asn Met Gln Leu Thr Leu Ser Ser Asn Leu
        440                 445                 450

gat gca ctc aac tcc att gtc tcc cag ctc cct gta cca gat aag gac   1507
Asp Ala Leu Asn Ser Ile Val Ser Gln Leu Pro Val Pro Asp Lys Asp
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    455                 460                 465

gtt gtg gct gct tct ggc tac cag att cag cca cac ttc tcc acg cag   1555
Val Val Ala Ala Ser Gly Tyr Gln Ile Gln Pro His Phe Ser Thr Gln
470                 475                 480                 485

cag cgt gaa gca atc acc act gat aat cct ctc gcg att att cag gcc   1603
Gln Arg Glu Ala Ile Thr Thr Asp Asn Pro Leu Ala Ile Ile Gln Ala
                490                 495                 500

ggt gct ggt acc ggt aaa tcc acc gtg att ctg gaa cgc att gag tac   1651
Gly Ala Gly Thr Gly Lys Ser Thr Val Ile Leu Glu Arg Ile Glu Tyr
            505                 510                 515

ttg tgc gct gca ggc acc aac cct gaa gag att gct gtg ctg tct ttt   1699
Leu Cys Ala Ala Gly Thr Asn Pro Glu Glu Ile Ala Val Leu Ser Phe
        520                 525                 530

act aat gct gcc gcc gat aac atc aca gca aaa aat gac aag gtg acc   1747
Thr Asn Ala Ala Ala Asp Asn Ile Thr Ala Lys Asn Asp Lys Val Thr
    535                 540                 545

tct atg acc atc tcc aag atg gtt cat gag att tac gca cac aat ttc   1795
Ser Met Thr Ile Ser Lys Met Val His Glu Ile Tyr Ala His Asn Phe
550                 555                 560                 565

cct gat cat gag atc tcc acc atc gac acc att atc aat acg ctt gat   1843
Pro Asp His Glu Ile Ser Thr Ile Asp Thr Ile Ile Asn Thr Leu Asp
                570                 575                 580

att gaa tac ggc gat caa atg gtg acc tcc gat tac atg att cag ctc   1891
Ile Glu Tyr Gly Asp Gln Met Val Thr Ser Asp Tyr Met Ile Gln Leu
            585                 590                 595

cgt gac ctg ctc tat aag gtc atg acg cag ggt ggc aac gcc aac ctg   1939
Arg Asp Leu Leu Tyr Lys Val Met Thr Gln Gly Gly Asn Ala Asn Leu
        600                 605                 610

aca gcg ttg agc atc ttc atg gaa tcc cat atc gag gcg ttc atc tcg   1987
Thr Ala Leu Ser Ile Phe Met Glu Ser His Ile Glu Ala Phe Ile Ser
    615                 620                 625

gtg ttg gat cag atc aag cag act tct ctt gag ctg gaa atc atc atc   2035
Val Leu Asp Gln Ile Lys Gln Thr Ser Leu Glu Leu Glu Ile Ile Ile
630                 635                 640                 645

tgc tac ctg ctc ttg gat aag ctg atc gag cct cat gca tcg ccg aag   2083
Cys Tyr Leu Leu Leu Asp Lys Leu Ile Glu Pro His Ala Ser Pro Lys
                650                 655                 660

tac ctc att att gat gag gtg cag gac aac tcg gtc ttc gag ttc gtc   2131
Tyr Leu Ile Ile Asp Glu Val Gln Asp Asn Ser Val Phe Glu Phe Val
            665                 670                 675

ttt gca ctt cgt ttt gcg gca aag cac aat acg agt ctg tac ttg gtg   2179
Phe Ala Leu Arg Phe Ala Ala Lys His Asn Thr Ser Leu Tyr Leu Val
        680                 685                 690

ggt gac tcg tca cag acc ttg tat gag ttc cgt tct gct aac cct aag   2227
Gly Asp Ser Ser Gln Thr Leu Tyr Glu Phe Arg Ser Ala Asn Pro Lys
    695                 700                 705
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gct ctg aac tcc ctg gaa gca tct ggt gtt ttc ggt acc tac cgt ttg   2275
Ala Leu Asn Ser Leu Glu Ala Ser Gly Val Phe Gly Thr Tyr Arg Leu
710                 715                 720                 725

acc acc aat tac cgt tcc aac cag gaa att ctt gac ttc gct aat atc   2323
Thr Thr Asn Tyr Arg Ser Asn Gln Glu Ile Leu Asp Phe Ala Asn Ile
                730                 735                 740

cac ctc tcg gat att gaa gct aac cag ttc gca ggt att cag ctc tac   2371
His Leu Ser Asp Ile Glu Ala Asn Gln Phe Ala Gly Ile Gln Leu Tyr
            745                 750                 755

gcc aac tct ttt gat gca cct act gcg gac agc ttc aaa gaa aag gtt   2419
Ala Asn Ser Phe Asp Ala Pro Thr Ala Asp Ser Phe Lys Glu Lys Val
        760                 765                 770

gaa ctg gac atg cac cat gtg tct aag cag tct gag ttt acc gac agc   2467
Glu Leu Asp Met His His Val Ser Lys Gln Ser Glu Phe Thr Asp Ser
    775                 780                 785

att cct tat ttc atg gag tcc aat aaa gct cgc ttt gat gct gcg atc   2515
Ile Pro Tyr Phe Met Glu Ser Asn Lys Ala Arg Phe Asp Ala Ala Ile
790                 795                 800                 805

ttg aac aat gag caa acc att gtg ctt gct cat tct ggt cgt gaa att   2563
Leu Asn Asn Glu Gln Thr Ile Val Leu Ala His Ser Gly Arg Glu Ile
                810                 815                 820

cgt gca gcg cag caa gcg cta gcc gag atg tac ccc agc atc acg gtg   2611
Arg Ala Ala Gln Gln Ala Leu Ala Glu Met Tyr Pro Ser Ile Thr Val
            825                 830                 835

cgt aac ttg cag tcc gat aag ggt ttc aac aac acg gta ttt tcg acc   2659
Arg Asn Leu Gln Ser Asp Lys Gly Phe Asn Asn Thr Val Phe Ser Thr
        840                 845                 850

ttt att aag gat ttc tgg ttt gag gtc acc gct gta gac cca gct cat   2707
Phe Ile Lys Asp Phe Trp Phe Glu Val Thr Ala Val Asp Pro Ala His
    855                 860                 865

gcc gca ttt acc ttt acc agc caa gtc acc gct cat cta gat aag ttg   2755
Ala Ala Phe Thr Phe Thr Ser Gln Val Thr Ala His Leu Asp Lys Leu
870                 875                 880                 885

gta cgc gga aag cgt gag cag atg gag gat cgc gtt atc cgg tct atg   2803
Val Arg Gly Lys Arg Glu Gln Met Glu Asp Arg Val Ile Arg Ser Met
                890                 895                 900

gct gca tgg tgg cgt gaa aat gag cgt gac atc cag ggt tgg gtg cag   2851
Ala Ala Trp Trp Arg Glu Asn Glu Arg Asp Ile Gln Gly Trp Val Gln
            905                 910                 915

caa act cag tcc ggt gcg atc acc aac gaa gag ttc ttc tac cgt ctt   2899
Gln Thr Gln Ser Gly Ala Ile Thr Asn Glu Glu Phe Phe Tyr Arg Leu
        920                 925                 930

cgt cag tgc att ctt gac tat gaa atc agg aat aac cga gca cgt cag   2947
Arg Gln Cys Ile Leu Asp Tyr Glu Ile Arg Asn Asn Arg Ala Arg Gln
    935                 940                 945
```

```
tcc atg ctc aat gcg cgc aac aac gct aac aag gag gct gtc gca cag   2995
Ser Met Leu Asn Ala Arg Asn Asn Ala Asn Lys Glu Ala Val Ala Gln
950                 955                 960                 965

gag aaa cca ctg ctc atg gtc tcc acc att cac agt gca aag ggt ctg   3043
Glu Lys Pro Leu Leu Met Val Ser Thr Ile His Ser Ala Lys Gly Leu
                970                 975                 980

gaa ttc gat aat gtc atc gtg ctt caa aaa cca agc tcc gat gca gag   3091
Glu Phe Asp Asn Val Ile Val Leu Gln Lys Pro Ser Ser Asp Ala Glu
            985                 990                 995

atg acc gaa gaa ggt aag cgc gca acc tat gtg gcg ctg acc cgt gca   3139
Met Thr Glu Glu Gly Lys Arg Ala Thr Tyr Val Ala Leu Thr Arg Ala
        1000                1005                1010

aaa aag cgt gaa ctc att att gct ggt tct act cgc gca tac cca cgc   3187
Lys Lys Arg Glu Leu Ile Ile Ala Gly Ser Thr Arg Ala Tyr Pro Arg
    1015                1020                1025

atc gtc acc gat tat gag caa atc gtt gat ctt ctt gaa aag cgc gat   3235
Ile Val Thr Asp Tyr Glu Gln Ile Val Asp Leu Leu Glu Lys Arg Asp
1030                1035                1040                1045

gag gag cgc aaa att aag gag gaa gag gct gca gca ctc gcc acc ctt   3283
Glu Glu Arg Lys Ile Lys Glu Glu Glu Ala Ala Ala Leu Ala Thr Leu
                1050                1055                1060

gaa gct gaa cag gag acg cgc gcc ctt gct gct gct gag gcg cag gct   3331
Glu Ala Glu Gln Glu Thr Arg Ala Leu Ala Ala Ala Glu Ala Gln Ala
            1065                1070                1075

cag gcg ttg ttg ctt gag cac aac ccg tgg ttg cgt gat ctc agc gat   3379
Gln Ala Leu Leu Leu Glu His Asn Pro Trp Leu Arg Asp Leu Ser Asp
        1080                1085                1090

gaa gaa gtc act gct cta act gag caa gag atc atc aac aat gtt gag   3427
Glu Glu Val Thr Ala Leu Thr Glu Gln Glu Ile Ile Asn Asn Val Glu
    1095                1100                1105

cca gcc cta cag att gaa gaa gag gag gaa gag gct cgt gca ctc gct   3475
Pro Ala Leu Gln Ile Glu Glu Glu Glu Glu Glu Ala Arg Ala Leu Ala
1110                1115                1120                1125

gca gca gag cca gca att cag cag tac ttg tct cag ttt gct ttc gat   3523
Ala Ala Glu Pro Ala Ile Gln Gln Tyr Leu Ser Gln Phe Ala Phe Asp
                1130                1135                1140

gag ttc ccg gac gac gac aat gta gcc aac act gtc gta cat gta gca   3571
Glu Phe Pro Asp Asp Asp Asn Val Ala Asn Thr Val Val His Val Ala
            1145                1150                1155

cca cag cct att ctc cac cag gca gtg cct gca gat gtg act gta caa   3619
Pro Gln Pro Ile Leu His Gln Ala Val Pro Ala Asp Val Thr Val Gln
        1160                1165                1170

tca agc acc gcc ccc gta aca cct gtt gtt gcg gat ctt gag gta acc   3667
Ser Ser Thr Ala Pro Val Thr Pro Val Val Ala Asp Leu Glu Val Thr
    1175                1180                1185

act gtt gca gct gat cca gtc gaa ccg act atc gtt gct gca cag cct   3715
```

```
Thr Val Ala Ala Asp Pro Val Glu Pro Thr Ile Val Ala Ala Gln Pro
1190                1195                1200                1205

gag gtg gac gac aac ctt gtc tac agc acg tcc acc cct aat agt cac   3763
Glu Val Asp Asp Asn Leu Val Tyr Ser Thr Ser Thr Pro Asn Ser His
               1210                1215                1220

agt gac gtt att gca gtg aac tct gat acc tca gaa aac gct gct gtt   3811
Ser Asp Val Ile Ala Val Asn Ser Asp Thr Ser Glu Asn Ala Ala Val
           1225                1230                1235

aat cca gtt ctg tcc gat att gag gca ctc cga gca att ttc aac aac   3859
Asn Pro Val Leu Ser Asp Ile Glu Ala Leu Arg Ala Ile Phe Asn Asn
       1240                1245                1250

cag gac taaaacacct gctgctgttg agc                                3888
Gln Asp
    1255
```

<210> 2408
<211> 1255
<212> PRT
<213> Corynebacterium glutamicum

<400> 2408

```
Met Pro Ile Ile Ile Asp Asn Leu Asn Ser Asp Asp Asp Ser Thr Ile
  1               5                  10                  15

Gly Thr Ala Thr Glu Tyr Asn Pro Asp Thr Asp Ala Asp Leu Leu Asp
             20                  25                  30

Ala Ile Asn Ala Asp Ala Asp Leu Asp Gly Asp Ala Thr Ile Ser Thr
         35                  40                  45

Asn Ala Thr Glu Glu Gly Val Asp Ala Ala Ala Glu Lys Pro Lys Lys
     50                  55                  60

Lys Arg Lys Ala Pro Ala Leu Lys Pro Lys Gly Leu Thr Ala Lys Phe
 65                  70                  75                  80

Phe His Arg Asp Leu Thr Gly Val Gly Gly Arg Thr Gly Arg Leu Asn
                 85                  90                  95

Lys Asn Val His Pro Thr Asn Pro Asp Leu Ser Tyr Gln Pro Val Ser
            100                 105                 110

Asp Val Tyr Thr Pro Gln Ser Ala Asp His Lys Gly Ile Lys Thr Arg
        115                 120                 125

Tyr Ile Leu Thr His Pro Thr Pro Ala Val Val Leu Ser Glu Ser Ile
    130                 135                 140

Ser Asn Ala Phe His Val Ser Thr Leu Arg Arg Asn Asn Asn Val Asn
145                 150                 155                 160

Asn Ser Asp Ser Glu Leu Ala Ala Trp Pro Tyr Leu Tyr Gln Leu Asp
                165                 170                 175

Ile Pro Gln Leu Asp Gln Met Ile Asn Val Ala Asp Ile Cys Asp Tyr
            180                 185                 190
```

```
His Phe His Gly Tyr Asn Leu Trp Val Asp Phe Thr Pro Gln Thr Ile
        195                 200                 205

Ala Leu Arg Ser Gly Lys Thr Val Leu Asp Asp Gly Thr Thr Ala Ser
    210                 215                 220

Asp Asn Thr Thr His Val Tyr Tyr Arg Val Thr Val His Val Ile Ala
225                 230                 235                 240

Gly Gln Asp His Gly Ser Thr Leu Leu Asp Asp Gln Gly Asn Gln Val
                245                 250                 255

Leu Asp Arg Asp Asp Asn Pro Ile Ser Thr Pro Ser Ile Lys Arg Ile
            260                 265                 270

Gly Ala Val Thr Asp Leu Phe Asp His Asn Pro Phe Gly Phe Ala Ser
        275                 280                 285

Val Asn Ser Phe Ala Phe Val Asp Phe Ser Trp Asp Pro Ala Thr Thr
    290                 295                 300

Leu Val Asp Met Leu Asn Asn Leu Asp Ser Tyr Leu Ser Asn His Ile
305                 310                 315                 320

Asn Ile Ala Ser Ser Pro Thr Pro Ile Ala Leu Asp Met Val Val Leu
                325                 330                 335

Asn Glu Trp Ser Glu Lys Ser Tyr Gln Leu Cys Glu Arg Val Val Ala
            340                 345                 350

Gln Ala Lys Leu Ile Asn Ser Asn Lys Ile Thr Ala His Val Ser Asp
        355                 360                 365

Val Ile Lys Gln Asn Ala His Asn Ile Leu Trp Phe Thr Glu Gln Met
    370                 375                 380

Asn Pro Gly Thr Thr Asn Leu Ser Glu Val Pro Ile Ser Lys Lys Ser
385                 390                 395                 400

Met Leu Pro Met Ser Arg Gln Leu Arg Ile Leu Glu His Tyr Asp Val
                405                 410                 415

Pro Leu Thr Ala Tyr Ser Ala Leu Phe Trp Thr Val Ser Ala Ile Lys
            420                 425                 430

Asn Glu Ser Met Val Gln Tyr Leu Val Arg Gln Asn Met Gln Leu Thr
        435                 440                 445

Leu Ser Ser Asn Leu Asp Ala Leu Asn Ser Ile Val Ser Gln Leu Pro
    450                 455                 460

Val Pro Asp Lys Asp Val Val Ala Ala Ser Gly Tyr Gln Ile Gln Pro
465                 470                 475                 480

His Phe Ser Thr Gln Gln Arg Glu Ala Ile Thr Thr Asp Asn Pro Leu
                485                 490                 495

Ala Ile Ile Gln Ala Gly Ala Gly Thr Gly Lys Ser Thr Val Ile Leu
            500                 505                 510
```

```
Glu Arg Ile Glu Tyr Leu Cys Ala Ala Gly Thr Asn Pro Glu Glu Ile
        515                 520                 525

Ala Val Leu Ser Phe Thr Asn Ala Ala Ala Asp Asn Ile Thr Ala Lys
    530                 535                 540

Asn Asp Lys Val Thr Ser Met Thr Ile Ser Lys Met Val His Glu Ile
545                 550                 555                 560

Tyr Ala His Asn Phe Pro Asp His Glu Ile Ser Thr Ile Asp Thr Ile
                565                 570                 575

Ile Asn Thr Leu Asp Ile Glu Tyr Gly Asp Gln Met Val Thr Ser Asp
            580                 585                 590

Tyr Met Ile Gln Leu Arg Asp Leu Leu Tyr Lys Val Met Thr Gln Gly
        595                 600                 605

Gly Asn Ala Asn Leu Thr Ala Leu Ser Ile Phe Met Glu Ser His Ile
    610                 615                 620

Glu Ala Phe Ile Ser Val Leu Asp Gln Ile Lys Gln Thr Ser Leu Glu
625                 630                 635                 640

Leu Glu Ile Ile Ile Cys Tyr Leu Leu Leu Asp Lys Leu Ile Glu Pro
                645                 650                 655

His Ala Ser Pro Lys Tyr Leu Ile Ile Asp Glu Val Gln Asp Asn Ser
            660                 665                 670

Val Phe Glu Phe Val Phe Ala Leu Arg Phe Ala Ala Lys His Asn Thr
        675                 680                 685

Ser Leu Tyr Leu Val Gly Asp Ser Ser Gln Thr Leu Tyr Glu Phe Arg
    690                 695                 700

Ser Ala Asn Pro Lys Ala Leu Asn Ser Leu Glu Ala Ser Gly Val Phe
705                 710                 715                 720

Gly Thr Tyr Arg Leu Thr Thr Asn Tyr Arg Ser Asn Gln Glu Ile Leu
                725                 730                 735

Asp Phe Ala Asn Ile His Leu Ser Asp Ile Glu Ala Asn Gln Phe Ala
            740                 745                 750

Gly Ile Gln Leu Tyr Ala Asn Ser Phe Asp Ala Pro Thr Ala Asp Ser
        755                 760                 765

Phe Lys Glu Lys Val Glu Leu Asp Met His His Val Ser Lys Gln Ser
    770                 775                 780

Glu Phe Thr Asp Ser Ile Pro Tyr Phe Met Glu Ser Asn Lys Ala Arg
785                 790                 795                 800

Phe Asp Ala Ala Ile Leu Asn Asn Glu Gln Thr Ile Val Leu Ala His
                805                 810                 815

Ser Gly Arg Glu Ile Arg Ala Ala Gln Gln Ala Leu Ala Glu Met Tyr
            820                 825                 830

Pro Ser Ile Thr Val Arg Asn Leu Gln Ser Asp Lys Gly Phe Asn Asn
```

```
        835                 840                 845

Thr Val Phe Ser Thr Phe Ile Lys Asp Phe Trp Phe Glu Val Thr Ala
    850                 855                 860

Val Asp Pro Ala His Ala Ala Phe Thr Phe Thr Ser Gln Val Thr Ala
865                 870                 875                 880

His Leu Asp Lys Leu Val Arg Gly Lys Arg Glu Gln Met Glu Asp Arg
                885                 890                 895

Val Ile Arg Ser Met Ala Ala Trp Trp Arg Glu Asn Glu Arg Asp Ile
            900                 905                 910

Gln Gly Trp Val Gln Gln Thr Gln Ser Gly Ala Ile Thr Asn Glu Glu
        915                 920                 925

Phe Phe Tyr Arg Leu Arg Gln Cys Ile Leu Asp Tyr Glu Ile Arg Asn
    930                 935                 940

Asn Arg Ala Arg Gln Ser Met Leu Asn Ala Arg Asn Asn Ala Asn Lys
945                 950                 955                 960

Glu Ala Val Ala Gln Glu Lys Pro Leu Leu Met Val Ser Thr Ile His
                965                 970                 975

Ser Ala Lys Gly Leu Glu Phe Asp Asn Val Ile Val Leu Gln Lys Pro
            980                 985                 990

Ser Ser Asp Ala Glu Met Thr Glu Glu Gly Lys Arg Ala Thr Tyr Val
        995                 1000                1005

Ala Leu Thr Arg Ala Lys Lys Arg Glu Leu Ile Ile Ala Gly Ser Thr
    1010                1015                1020

Arg Ala Tyr Pro Arg Ile Val Thr Asp Tyr Glu Gln Ile Val Asp Leu
1025                1030                1035                1040

Leu Glu Lys Arg Asp Glu Glu Arg Lys Ile Lys Glu Glu Glu Ala Ala
                1045                1050                1055

Ala Leu Ala Thr Leu Glu Ala Glu Gln Glu Thr Arg Ala Leu Ala Ala
            1060                1065                1070

Ala Glu Ala Gln Ala Gln Ala Leu Leu Leu Glu His Asn Pro Trp Leu
        1075                1080                1085

Arg Asp Leu Ser Asp Glu Glu Val Thr Ala Leu Thr Glu Gln Glu Ile
    1090                1095                1100

Ile Asn Asn Val Glu Pro Ala Leu Gln Ile Glu Glu Glu Glu Glu Glu
1105                1110                1115                1120

Ala Arg Ala Leu Ala Ala Ala Glu Pro Ala Ile Gln Gln Tyr Leu Ser
                1125                1130                1135

Gln Phe Ala Phe Asp Glu Phe Pro Asp Asp Asp Asn Val Ala Asn Thr
            1140                1145                1150

Val Val His Val Ala Pro Gln Pro Ile Leu His Gln Ala Val Pro Ala
        1155                1160                1165
```

```
Asp Val Thr Val Gln Ser Ser Thr Ala Pro Val Thr Pro Val Val Ala
    1170                1175                1180

Asp Leu Glu Val Thr Thr Val Ala Ala Asp Pro Val Glu Pro Thr Ile
1185                1190                1195                1200

Val Ala Ala Gln Pro Glu Val Asp Asp Asn Leu Val Tyr Ser Thr Ser
                1205                1210                1215

Thr Pro Asn Ser His Ser Asp Val Ile Ala Val Asn Ser Asp Thr Ser
            1220                1225                1230

Glu Asn Ala Ala Val Asn Pro Val Leu Ser Asp Ile Glu Ala Leu Arg
        1235                1240                1245

Ala Ile Phe Asn Asn Gln Asp
    1250                1255


<210> 2409
<211> 467
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (34)..(444)
<223> RXA01773

<400> 2409
tttcagcgag atggcgtgcg ctttgatcat acgatg atc acc cac att caa gcc   54
                                    Met Ile Thr His Ile Gln Ala
                                      1               5

ggc ctg cat ctt ggt ggc tgc cgc gca gca ggt tta ctg cct ata cca   102
Gly Leu His Leu Gly Gly Cys Arg Ala Ala Gly Leu Leu Pro Ile Pro
         10                  15                  20

gca cat att gat cat att gtg cgc ctg aca gcc gca gat ttc tat gac   150
Ala His Ile Asp His Ile Val Arg Leu Thr Ala Ala Asp Phe Tyr Asp
     25                  30                  35

acc cag tca gca ccg cag ctg ctc agc aac act gtg ctt gat gta ttg   198
Thr Gln Ser Ala Pro Gln Leu Leu Ser Asn Thr Val Leu Asp Val Leu
 40                  45                  50                  55

gac acc acc act caa gac ttg aag gca ttg tgg cct gtt gca gaa cat   246
Asp Thr Thr Thr Gln Asp Leu Lys Ala Leu Trp Pro Val Ala Glu His
                 60                  65                  70

att gct aca acc att cct gaa tct gag aac gtg ctt atc cac tgc cag   294
Ile Ala Thr Thr Ile Pro Glu Ser Glu Asn Val Leu Ile His Cys Gln
             75                  80                  85

atg ggt atc aac cgc tca gct gca ctc atg aca cgg gtg ttg atg ttg   342
Met Gly Ile Asn Arg Ser Ala Ala Leu Met Thr Arg Val Leu Met Leu
         90                  95                  100

cgc aac gat tgc acc gcc gat gaa gca att gca ctg ctg cgt gat cga   390
Arg Asn Asp Cys Thr Ala Asp Glu Ala Ile Ala Leu Leu Arg Asp Arg
```

```
    105                 110                 115

cgc tca ccg ttt gta ctg ttc aat gag cat ttt gtg gaa caa ctt cga   438
Arg Ser Pro Phe Val Leu Phe Asn Glu His Phe Val Glu Gln Leu Arg
120                 125                 130                 135

gca ctg taagcgctca aagacccatt acc                                 467
Ala Leu
```

<210> 2410
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 2410

```
Met Ile Thr His Ile Gln Ala Gly Leu His Leu Gly Gly Cys Arg Ala
  1               5                  10                  15

Ala Gly Leu Leu Pro Ile Pro Ala His Ile Asp His Ile Val Arg Leu
             20                  25                  30

Thr Ala Ala Asp Phe Tyr Asp Thr Gln Ser Ala Pro Gln Leu Leu Ser
         35                  40                  45

Asn Thr Val Leu Asp Val Leu Asp Thr Thr Thr Gln Asp Leu Lys Ala
     50                  55                  60

Leu Trp Pro Val Ala Glu His Ile Ala Thr Thr Ile Pro Glu Ser Glu
 65                  70                  75                  80

Asn Val Leu Ile His Cys Gln Met Gly Ile Asn Arg Ser Ala Ala Leu
                 85                  90                  95

Met Thr Arg Val Leu Met Leu Arg Asn Asp Cys Thr Ala Asp Glu Ala
            100                 105                 110

Ile Ala Leu Leu Arg Asp Arg Arg Ser Pro Phe Val Leu Phe Asn Glu
        115                 120                 125

His Phe Val Glu Gln Leu Arg Ala Leu
    130                 135
```

<210> 2411
<211> 687
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(664)
<223> RXA01775

<400> 2411

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gtggaaacca aagacgagga aagtatgtct atttgtttgt ccccaggttg tccacatttg 60

ttttattccc cgagaatgtc ctagaaagga actcgacccc atg tcc tat tca ctc   115
                                               Met Ser Tyr Ser Leu
                                                 1               5
```

```
att att tct aaa gca cca acc cac tcc atg cct ttt aat gag gct gaa   163
Ile Ile Ser Lys Ala Pro Thr His Ser Met Pro Phe Asn Glu Ala Glu
                 10                  15                  20

ctc cta gag ctt gtc gat gaa ctg cac tcc gac aac acc gtg aaa aag   211
Leu Leu Glu Leu Val Asp Glu Leu His Ser Asp Asn Thr Val Lys Lys
            25                  30                  35

ccg gtt att gtg cca ctc ccc gat gat ttc tcc tac acc gta gat agc   259
Pro Val Ile Val Pro Leu Pro Asp Asp Phe Ser Tyr Thr Val Asp Ser
        40                  45                  50

gcc gtg cga cta cat gat ttg ggt gtt gac cag gaa ctg act gac tgg   307
Ala Val Arg Leu His Asp Leu Gly Val Asp Gln Glu Leu Thr Asp Trp
    55                  60                  65

att act gca caa gtt gct gca gcc tat cca aac cag atc gtc tca gag   355
Ile Thr Ala Gln Val Ala Ala Ala Tyr Pro Asn Gln Ile Val Ser Glu
70                  75                  80                  85

att gct gct gcc cct gat ccg caa gcc aag acc tta ttc tcc gcc aat   403
Ile Ala Ala Ala Pro Asp Pro Gln Ala Lys Thr Leu Phe Ser Ala Asn
                90                  95                 100

gcg tat aac acc agg tct ttt ggt act ttt tgg act gag cac cct att   451
Ala Tyr Asn Thr Arg Ser Phe Gly Thr Phe Trp Thr Glu His Pro Ile
            105                 110                 115

aca cag ctc caa tac aag cgc tgc tac caa att gtc atc gag aac gtt   499
Thr Gln Leu Gln Tyr Lys Arg Cys Tyr Gln Ile Val Ile Glu Asn Val
        120                 125                 130

acg ggt gtc tat cat ccg tta cct gtt gat aac tac cgc tac gta ccc   547
Thr Gly Val Tyr His Pro Leu Pro Val Asp Asn Tyr Arg Tyr Val Pro
    135                 140                 145

cct gtc acg ccc tca ttg cca cag ccg gtc tac cac gaa gct atc gcc   595
Pro Val Thr Pro Ser Leu Pro Gln Pro Val Tyr His Glu Ala Ile Ala
150                 155                 160                 165

tta aat gag tct gat gtc gct gat cac ggt act cgt gca gcc aag cac   643
Leu Asn Glu Ser Asp Val Ala Asp His Gly Thr Arg Ala Ala Lys His
                170                 175                 180

gca atg atc aac cgc aac gta taaccacaca cgccacagat act             687
Ala Met Ile Asn Arg Asn Val
            185
```

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<210> 2412
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 2412

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Met Ser Tyr Ser Leu Ile Ile Ser Lys Ala Pro Thr His Ser Met Pro
  1               5                  10                  15

Phe Asn Glu Ala Glu Leu Leu Glu Leu Val Asp Glu Leu His Ser Asp
            20                  25                  30
```

```
Asn Thr Val Lys Lys Pro Val Ile Val Pro Leu Pro Asp Asp Phe Ser
          35                  40                  45

Tyr Thr Val Asp Ser Ala Val Arg Leu His Asp Leu Gly Val Asp Gln
      50                  55                  60

Glu Leu Thr Asp Trp Ile Thr Ala Gln Val Ala Ala Ala Tyr Pro Asn
 65                  70                  75                  80

Gln Ile Val Ser Glu Ile Ala Ala Ala Pro Asp Pro Gln Ala Lys Thr
                 85                  90                  95

Leu Phe Ser Ala Asn Ala Tyr Asn Thr Arg Ser Phe Gly Thr Phe Trp
            100                 105                 110

Thr Glu His Pro Ile Thr Gln Leu Gln Tyr Lys Arg Cys Tyr Gln Ile
        115                 120                 125

Val Ile Glu Asn Val Thr Gly Val Tyr His Pro Leu Pro Val Asp Asn
    130                 135                 140

Tyr Arg Tyr Val Pro Pro Val Thr Pro Ser Leu Pro Gln Pro Val Tyr
145                 150                 155                 160

His Glu Ala Ile Ala Leu Asn Glu Ser Asp Val Ala Asp His Gly Thr
                165                 170                 175

Arg Ala Ala Lys His Ala Met Ile Asn Arg Asn Val
            180                 185
```

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<210> 2413
<211> 1575
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1552)
<223> RXA01776

<400> 2413

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cgtataacca cacacgccac agatactcag ctatctgtgg cgtgttgttt tacatcaacc 60

tctcacccat cccccatcac tattaaagaa aatcaccatc atg acc cac act gat   115
                                            Met Thr His Thr Asp
                                              1               5

acc cca gcc cct gca cac ggc gta aca ccg agt gaa ttc gct gtt acc   163
Thr Pro Ala Pro Ala His Gly Val Thr Pro Ser Glu Phe Ala Val Thr
                 10                  15                  20

tca cac gaa ctc acc acc tca cca aca cct agt ccg aca cag gtc gct   211
Ser His Glu Leu Thr Thr Ser Pro Thr Pro Ser Pro Thr Gln Val Ala
             25                  30                  35

att gca gcc cag gaa aaa att cgc cag cgc aag ctc gaa gag ctt aaa   259
Ile Ala Ala Gln Glu Lys Ile Arg Gln Arg Lys Leu Glu Glu Leu Lys
         40                  45                  50
```

```
gca aaa aag cgc aca gac acg aca gct caa cca ctt cta cct gca cct   307
Ala Lys Lys Arg Thr Asp Thr Thr Ala Gln Pro Leu Leu Pro Ala Pro
     55                  60                  65

gtg ctg cat aca cgc cca ctc ccc tca ccg aat cca ccg cga cca tct   355
Val Leu His Thr Arg Pro Leu Pro Ser Pro Asn Pro Pro Arg Pro Ser
 70                  75                  80                  85

cca ccg gca cct acc act gga cac tgg gaa ctt ctt att gtc agg tca   403
Pro Pro Ala Pro Thr Thr Gly His Trp Glu Leu Leu Ile Val Arg Sér
                 90                  95                 100

cag cag aag aaa atg acc gca gcc aat ccc ttt ctc aaa ttc ctt cat   451
Gln Gln Lys Lys Met Thr Ala Ala Asn Pro Phe Leu Lys Phe Leu His
            105                 110                 115

ctc ggt aaa gcc ttc aac gtg aaa gac cta ggg ctc acc tgc gat cgc   499
Leu Gly Lys Ala Phe Asn Val Lys Asp Leu Gly Leu Thr Cys Asp Arg
        120                 125                 130

acc act gat gtt gac ctc tca cgg ctt ggc aag ctc aat ccg ccc agc   547
Thr Thr Asp Val Asp Leu Ser Arg Leu Gly Lys Leu Asn Pro Pro Ser
    135                 140                 145

tca ctt atc ctt gaa cta gca acg gca ctt gac ctg cat cca ttc ctc   595
Ser Leu Ile Leu Glu Leu Ala Thr Ala Leu Asp Leu His Pro Phe Leu
150                 155                 160                 165

tca gtc gca ctc tct tcg cac agt gcg gtc aac gcc cgt cgc aac caa   643
Ser Val Ala Leu Ser Ser His Ser Ala Val Asn Ala Arg Arg Asn Gln
                170                 175                 180

ctt gaa tta acc ctg cac aac cat gac act cag ggc aca gca tta ggt   691
Leu Glu Leu Thr Leu His Asn His Asp Thr Gln Gly Thr Ala Leu Gly
            185                 190                 195

cac agc gtt act atg gtc cag cta ccc gag gtc att aat cga gct gct   739
His Ser Val Thr Met Val Gln Leu Pro Glu Val Ile Asn Arg Ala Ala
        200                 205                 210

gta gag ccc tat atc aaa ccc aag ggc tcg ggc aat gac ccg ctt gac   787
Val Glu Pro Tyr Ile Lys Pro Lys Gly Ser Gly Asn Asp Pro Leu Asp
    215                 220                 225

caa agc ctg aac cac cgc gca ccc acc gta agt gac gtg caa aaa gcc   835
Gln Ser Leu Asn His Arg Ala Pro Thr Val Ser Asp Val Gln Lys Ala
230                 235                 240                 245

ctt gtg cag gaa aac aca ggc acg gca aca gac agc aac aac tac ctg   883
Leu Val Gln Glu Asn Thr Gly Thr Ala Thr Asp Ser Asn Asn Tyr Leu
                250                 255                 260

ctt cct ttt gat cct gat tct ggt gca cca aaa acc acc gcg ctt aat   931
Leu Pro Phe Asp Pro Asp Ser Gly Ala Pro Lys Thr Thr Ala Leu Asn
            265                 270                 275

gcg cct aat aag gat ctc cta cag gcc agg cat gag ctt gcc tat att   979
Ala Pro Asn Lys Asp Leu Leu Gln Ala Arg His Glu Leu Ala Tyr Ile
        280                 285                 290

ccc gag atc ccc gcc att gca tcg tgg ctc gat cac ctt gac ccc atc   1027
```

```
Pro Glu Ile Pro Ala Ile Ala Ser Trp Leu Asp His Leu Asp Pro Ile
    295                 300                 305

atg cgt gtg cac cgt agt ctt gcg ctt tca att ttc cca gtg cag ctt   1075
Met Arg Val His Arg Ser Leu Ala Leu Ser Ile Phe Pro Val Gln Leu
310                 315                 320                 325

cta cgt gct gcc gtt gag aat ctc cct cat aac gta acc gat ctg cat   1123
Leu Arg Ala Ala Val Glu Asn Leu Pro His Asn Val Thr Asp Leu His
                330                 335                 340

aat cac ctt gat cct gag gat ctg ctc cct gag gaa ctc acc acc tgg   1171
Asn His Leu Asp Pro Glu Asp Leu Leu Pro Glu Glu Leu Thr Thr Trp
            345                 350                 355

ctc gat cac ctc ttc gat gca gac tta acc gct ctc gct tca tgc cca   1219
Leu Asp His Leu Phe Asp Ala Asp Leu Thr Ala Leu Ala Ser Cys Pro
        360                 365                 370

cag ctt gca cca cct atc gtg cgc agc cac aat cac gcc aaa gcg atc   1267
Gln Leu Ala Pro Pro Ile Val Arg Ser His Asn His Ala Lys Ala Ile
    375                 380                 385

gca gct atc acc gtg acc tct gtc atg gac gct ctc atc gcc aaa act   1315
Ala Ala Ile Thr Val Thr Ser Val Met Asp Ala Leu Ile Ala Lys Thr
390                 395                 400                 405

ctt gat gcg cat gac gat cca ctg ccc tca cta ccg gag ttt gta gaa   1363
Leu Asp Ala His Asp Asp Pro Leu Pro Ser Leu Pro Glu Phe Val Glu
                410                 415                 420

cta ctg cgt gac gct gta gcc cag ctc gca gcg cat ttt aag cag cag   1411
Leu Leu Arg Asp Ala Val Ala Gln Leu Ala Ala His Phe Lys Gln Gln
            425                 430                 435

cgc ggc gag gta cta ccg cag ccc aat ggc ttg cga tac gcc acc gac   1459
Arg Gly Glu Val Leu Pro Gln Pro Asn Gly Leu Arg Tyr Ala Thr Asp
        440                 445                 450

ttt ggc ctg ctc tct tat att gcc gat ggc tta cat gaa tat gca ctt   1507
Phe Gly Leu Leu Ser Tyr Ile Ala Asp Gly Leu His Glu Tyr Ala Leu
    455                 460                 465

gcc atc gac ttc ggg ctg atc tac ccg aat gaa ctc atc acc gag       1552
Ala Ile Asp Phe Gly Leu Ile Tyr Pro Asn Glu Leu Ile Thr Glu
470                 475                 480

taaacccact cctagaaagg tct                                        1575


<210> 2414
<211> 484
<212> PRT
<213> Corynebacterium glutamicum

<400> 2414
Met Thr His Thr Asp Thr Pro Ala Pro Ala His Gly Val Thr Pro Ser
  1               5                  10                  15

Glu Phe Ala Val Thr Ser His Glu Leu Thr Thr Ser Pro Thr Pro Ser
            20                  25                  30
```

```
Pro Thr Gln Val Ala Ile Ala Ala Gln Glu Lys Ile Arg Gln Arg Lys
         35                  40                  45

Leu Glu Glu Leu Lys Ala Lys Lys Arg Thr Asp Thr Thr Ala Gln Pro
     50                  55                  60

Leu Leu Pro Ala Pro Val Leu His Thr Arg Pro Leu Pro Ser Pro Asn
 65                  70                  75                  80

Pro Pro Arg Pro Ser Pro Pro Ala Pro Thr Thr Gly His Trp Glu Leu
                 85                  90                  95

Leu Ile Val Arg Ser Gln Gln Lys Lys Met Thr Ala Ala Asn Pro Phe
            100                 105                 110

Leu Lys Phe Leu His Leu Gly Lys Ala Phe Asn Val Lys Asp Leu Gly
        115                 120                 125

Leu Thr Cys Asp Arg Thr Thr Asp Val Asp Leu Ser Arg Leu Gly Lys
    130                 135                 140

Leu Asn Pro Pro Ser Ser Leu Ile Leu Glu Leu Ala Thr Ala Leu Asp
145                 150                 155                 160

Leu His Pro Phe Leu Ser Val Ala Leu Ser Ser His Ser Ala Val Asn
                165                 170                 175

Ala Arg Arg Asn Gln Leu Glu Leu Thr Leu His Asn His Asp Thr Gln
            180                 185                 190

Gly Thr Ala Leu Gly His Ser Val Thr Met Val Gln Leu Pro Glu Val
        195                 200                 205

Ile Asn Arg Ala Ala Val Glu Pro Tyr Ile Lys Pro Lys Gly Ser Gly
    210                 215                 220

Asn Asp Pro Leu Asp Gln Ser Leu Asn His Arg Ala Pro Thr Val Ser
225                 230                 235                 240

Asp Val Gln Lys Ala Leu Val Gln Glu Asn Thr Gly Thr Ala Thr Asp
                245                 250                 255

Ser Asn Asn Tyr Leu Leu Pro Phe Asp Pro Asp Ser Gly Ala Pro Lys
            260                 265                 270

Thr Thr Ala Leu Asn Ala Pro Asn Lys Asp Leu Leu Gln Ala Arg His
        275                 280                 285

Glu Leu Ala Tyr Ile Pro Glu Ile Pro Ala Ile Ala Ser Trp Leu Asp
    290                 295                 300

His Leu Asp Pro Ile Met Arg Val His Arg Ser Leu Ala Leu Ser Ile
305                 310                 315                 320

Phe Pro Val Gln Leu Leu Arg Ala Ala Val Glu Asn Leu Pro His Asn
                325                 330                 335

Val Thr Asp Leu His Asn His Leu Asp Pro Glu Asp Leu Leu Pro Glu
            340                 345                 350
```

```
Glu Leu Thr Thr Trp Leu Asp His Leu Phe Asp Ala Asp Leu Thr Ala
        355                 360                 365

Leu Ala Ser Cys Pro Gln Leu Ala Pro Pro Ile Val Arg Ser His Asn
    370                 375                 380

His Ala Lys Ala Ile Ala Ala Ile Thr Val Thr Ser Val Met Asp Ala
385                 390                 395                 400

Leu Ile Ala Lys Thr Leu Asp Ala His Asp Asp Pro Leu Pro Ser Leu
                405                 410                 415

Pro Glu Phe Val Glu Leu Leu Arg Asp Ala Val Ala Gln Leu Ala Ala
            420                 425                 430

His Phe Lys Gln Gln Arg Gly Glu Val Leu Pro Gln Pro Asn Gly Leu
        435                 440                 445

Arg Tyr Ala Thr Asp Phe Gly Leu Leu Ser Tyr Ile Ala Asp Gly Leu
    450                 455                 460

His Glu Tyr Ala Leu Ala Ile Asp Phe Gly Leu Ile Tyr Pro Asn Glu
465                 470                 475                 480

Leu Ile Thr Glu
```

<210> 2415
<211> 582
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(559)
<223> RXA01777

<400> 2415

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ccgatggctt acatgaatat gcacttgcca tcgacttcgg gctgatctac ccgaatgaac 60

tcatcaccga gtaaacccac tcctagaaag gtctttaccc atg tct cgt atc atc   115
                                            Met Ser Arg Ile Ile
                                              1               5

act gct ccc gtc cac aag cct tat att att gct cgt gaa gtc aag ggg   163
Thr Ala Pro Val His Lys Pro Tyr Ile Ile Ala Arg Glu Val Lys Gly
                  10                  15                  20

gtc tcc cat gtc cac gac act gtt ggc ggc aag tgg cag gcc acc ttg   211
Val Ser His Val His Asp Thr Val Gly Gly Lys Trp Gln Ala Thr Leu
              25                  30                  35

cac aca ctt aaa ccg ggg ccc tcc tgg ccg aaa ccg tca cag ttc act   259
His Thr Leu Lys Pro Gly Pro Ser Trp Pro Lys Pro Ser Gln Phe Thr
          40                  45                  50

gcg cct aaa tcc acg tcc atc tgg ttt att gcg gta gca acc cac cca   307
Ala Pro Lys Ser Thr Ser Ile Trp Phe Ile Ala Val Ala Thr His Pro
      55                  60                  65
```

```
cgt aac cca cgg gca cgc aaa ggt acc cta ctt ggt cgc ggt ggt ctt   355
Arg Asn Pro Arg Ala Arg Lys Gly Thr Leu Leu Gly Arg Gly Gly Leu
 70                  75                  80                  85

tac gaa ctc aaa gac act gat ctg aac ttt ctc aca gag cga cag gat   403
Tyr Glu Leu Lys Asp Thr Asp Leu Asn Phe Leu Thr Glu Arg Gln Asp
                 90                  95                 100

ttg ctc gcc aca tct acc tct cgt gac cca gag gat tgc cgt tta cgc   451
Leu Leu Ala Thr Ser Thr Ser Arg Asp Pro Glu Asp Cys Arg Leu Arg
            105                 110                 115

ttt aat tcg cgt cac gat gca gca gca ttt tta cat gct aac gcc cgc   499
Phe Asn Ser Arg His Asp Ala Ala Ala Phe Leu His Ala Asn Ala Arg
        120                 125                 130

cac atc aac aag ctt ttt cat cca gca cta ggt cat gct cgc tac gat   547
His Ile Asn Lys Leu Phe His Pro Ala Leu Gly His Ala Arg Tyr Asp
    135                 140                 145

ctc ata gat gtg taagcacaac gcttagctta tga                        582
Leu Ile Asp Val
150
```

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<210> 2416
<211> 153
<212> PRT
<213> Corynebacterium glutamicum

<400> 2416

```
Met Ser Arg Ile Ile Thr Ala Pro Val His Lys Pro Tyr Ile Ile Ala
  1               5                  10                  15

Arg Glu Val Lys Gly Val Ser His Val His Asp Thr Val Gly Gly Lys
             20                  25                  30

Trp Gln Ala Thr Leu His Thr Leu Lys Pro Gly Pro Ser Trp Pro Lys
         35                  40                  45

Pro Ser Gln Phe Thr Ala Pro Lys Ser Thr Ser Ile Trp Phe Ile Ala
     50                  55                  60

Val Ala Thr His Pro Arg Asn Pro Arg Ala Arg Lys Gly Thr Leu Leu
 65                  70                  75                  80

Gly Arg Gly Gly Leu Tyr Glu Leu Lys Asp Thr Asp Leu Asn Phe Leu
                 85                  90                  95

Thr Glu Arg Gln Asp Leu Leu Ala Thr Ser Thr Ser Arg Asp Pro Glu
            100                 105                 110

Asp Cys Arg Leu Arg Phe Asn Ser Arg His Asp Ala Ala Ala Phe Leu
        115                 120                 125

His Ala Asn Ala Arg His Ile Asn Lys Leu Phe His Pro Ala Leu Gly
    130                 135                 140

His Ala Arg Tyr Asp Leu Ile Asp Val
145                 150
```

<210> 2417
<211> 1260
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1237)
<223> RXA01778

<400> 2417
ctactacccc ctccgggtgt ggggtagctg taacaactac cccacaatct tagccggtct 60

tccatacata actgcgaaat tggttagagt ctttttcatg atg ctc tac caa cac 115
Met Leu Tyr Gln His
1 5

acc aca cgc ggg ctg atc att agt gac gcg atc atc gcg aaa atc agc 163
Thr Thr Arg Gly Leu Ile Ile Ser Asp Ala Ile Ile Ala Lys Ile Ser
10 15 20

caa gtc aac caa ctg ctg cta cta aga ccc acg ctg ttg caa gac aaa 211
Gln Val Asn Gln Leu Leu Leu Leu Arg Pro Thr Leu Leu Gln Asp Lys
25 30 35

gat atg cac cat gcg aca ttg agt agc gac acc cca tca att cgc agt 259
Asp Met His His Ala Thr Leu Ser Ser Asp Thr Pro Ser Ile Arg Ser
40 45 50

cgc cgt cgc tcc tat cgc gag aat aaa gcc gcc tat gcg acc acg agc 307
Arg Arg Arg Ser Tyr Arg Glu Asn Lys Ala Ala Tyr Ala Thr Thr Ser
55 60 65

acc atc aga aac cgt gag acc ttt ttc agc aca tct gat att gat ttc 355
Thr Ile Arg Asn Arg Glu Thr Phe Phe Ser Thr Ser Asp Ile Asp Phe
70 75 80 85

gcc ata ctc atg att cag gac gta caa gaa tct ctc gta tct ttt gac 403
Ala Ile Leu Met Ile Gln Asp Val Gln Glu Ser Leu Val Ser Phe Asp
90 95 100

ccc acc ttg gct caa gat atg aag cca aga acc aac gca gtc att tct 451
Pro Thr Leu Ala Gln Asp Met Lys Pro Arg Thr Asn Ala Val Ile Ser
105 110 115

gca ctc aat gag cta cgc gag cca ctg gat acc ttc tac cgt gcc cat 499
Ala Leu Asn Glu Leu Arg Glu Pro Leu Asp Thr Phe Tyr Arg Ala His
120 125 130

gaa tac ggt gac atc atc agc gat ggt gct tat gag ttc gat cat gct 547
Glu Tyr Gly Asp Ile Ile Ser Asp Gly Ala Tyr Glu Phe Asp His Ala
135 140 145

gcc att gat gca caa cac agc ctt agt gaa ctc gtt gcc ggt ctg cat 595
Ala Ile Asp Ala Gln His Ser Leu Ser Glu Leu Val Ala Gly Leu His
150 155 160 165

aat tat gac aac ctc atg ttt ccc cag gaa acc gct ccg ttg atg agt 643
Asn Tyr Asp Asn Leu Met Phe Pro Gln Glu Thr Ala Pro Leu Met Ser
170 175 180

```
gaa tcc aat ggc att cag ctg gct cag tac tat aag tcc acc aaa ctc   691
Glu Ser Asn Gly Ile Gln Leu Ala Gln Tyr Tyr Lys Ser Thr Lys Leu
            185                 190                 195

gat gag tca caa ttg acg gtg gaa cct aat gag cct ggt atc agc att   739
Asp Glu Ser Gln Leu Thr Val Glu Pro Asn Glu Pro Gly Ile Ser Ile
        200                 205                 210

atg tgg cac gcc cat gat ttc acc tgg tct tgc cta gtg cgc tat gac   787
Met Trp His Ala His Asp Phe Thr Trp Ser Cys Leu Val Arg Tyr Asp
    215                 220                 225

gac atg aac cgt tac cct gag cat ttc agc att tct ttt aaa gac atg   835
Asp Met Asn Arg Tyr Pro Glu His Phe Ser Ile Ser Phe Lys Asp Met
230                 235                 240                 245

ctg atc cct gaa cag atc tat act ttc cac ttc acc cca cgt gag gca   883
Leu Ile Pro Glu Gln Ile Tyr Thr Phe His Phe Thr Pro Arg Glu Ala
                250                 255                 260

atg caa ctg cgc aag gga ctt ttt aat gcc atc gct gcc tac aag tct   931
Met Gln Leu Arg Lys Gly Leu Phe Asn Ala Ile Ala Ala Tyr Lys Ser
            265                 270                 275

cag aca tgg ggt gat gag aac act gat ctc acc aag gct gaa ctc gaa   979
Gln Thr Trp Gly Asp Glu Asn Thr Asp Leu Thr Lys Ala Glu Leu Glu
        280                 285                 290

ttt ggt ggc acc tcc atg acc ttc cgc gcc ggc ctc tca cag ctt agc   1027
Phe Gly Gly Thr Ser Met Thr Phe Arg Ala Gly Leu Ser Gln Leu Ser
    295                 300                 305

gtc acc gga cct cct gat cac cgc cag gtg ttc tgc ttg tcg tct tct   1075
Val Thr Gly Pro Pro Asp His Arg Gln Val Phe Cys Leu Ser Ser Ser
310                 315                 320                 325

ggt cgt gag gat cac aac acc ccg cca aac atg cga gac gga cat gtc   1123
Gly Arg Glu Asp His Asn Thr Pro Pro Asn Met Arg Asp Gly His Val
                330                 335                 340

att gat att gcg gtt act caa ttg tcc acc ctg cgt aac ctc att cgg   1171
Ile Asp Ile Ala Val Thr Gln Leu Ser Thr Leu Arg Asn Leu Ile Arg
            345                 350                 355

gta ctg tgc acc act cac ccg gat cat tca cca gca ctg cta cct tat   1219
Val Leu Cys Thr Thr His Pro Asp His Ser Pro Ala Leu Leu Pro Tyr
        360                 365                 370

ggt cag cag tac acc atc taacatgctc taactcgacc ccg                 1260
Gly Gln Gln Tyr Thr Ile
    375
```

<210> 2418
<211> 379
<212> PRT
<213> Corynebacterium glutamicum

<400> 2418
Met Leu Tyr Gln His Thr Thr Arg Gly Leu Ile Ile Ser Asp Ala Ile

```
  1               5                  10                  15

Ile Ala Lys Ile Ser Gln Val Asn Gln Leu Leu Leu Leu Arg Pro Thr
            20                  25                  30

Leu Leu Gln Asp Lys Asp Met His His Ala Thr Leu Ser Ser Asp Thr
        35                  40                  45

Pro Ser Ile Arg Ser Arg Arg Arg Ser Tyr Arg Glu Asn Lys Ala Ala
    50                  55                  60

Tyr Ala Thr Thr Ser Thr Ile Arg Asn Arg Glu Thr Phe Phe Ser Thr
65                  70                  75                  80

Ser Asp Ile Asp Phe Ala Ile Leu Met Ile Gln Asp Val Gln Glu Ser
                85                  90                  95

Leu Val Ser Phe Asp Pro Thr Leu Ala Gln Asp Met Lys Pro Arg Thr
            100                 105                 110

Asn Ala Val Ile Ser Ala Leu Asn Glu Leu Arg Glu Pro Leu Asp Thr
        115                 120                 125

Phe Tyr Arg Ala His Glu Tyr Gly Asp Ile Ile Ser Asp Gly Ala Tyr
    130                 135                 140

Glu Phe Asp His Ala Ala Ile Asp Ala Gln His Ser Leu Ser Glu Leu
145                 150                 155                 160

Val Ala Gly Leu His Asn Tyr Asp Asn Leu Met Phe Pro Gln Glu Thr
                165                 170                 175

Ala Pro Leu Met Ser Glu Ser Asn Gly Ile Gln Leu Ala Gln Tyr Tyr
            180                 185                 190

Lys Ser Thr Lys Leu Asp Glu Ser Gln Leu Thr Val Glu Pro Asn Glu
        195                 200                 205

Pro Gly Ile Ser Ile Met Trp His Ala His Asp Phe Thr Trp Ser Cys
    210                 215                 220

Leu Val Arg Tyr Asp Asp Met Asn Arg Tyr Pro Glu His Phe Ser Ile
225                 230                 235                 240

Ser Phe Lys Asp Met Leu Ile Pro Glu Gln Ile Tyr Thr Phe His Phe
                245                 250                 255

Thr Pro Arg Glu Ala Met Gln Leu Arg Lys Gly Leu Phe Asn Ala Ile
            260                 265                 270

Ala Ala Tyr Lys Ser Gln Thr Trp Gly Asp Glu Asn Thr Asp Leu Thr
        275                 280                 285

Lys Ala Glu Leu Glu Phe Gly Gly Thr Ser Met Thr Phe Arg Ala Gly
    290                 295                 300

Leu Ser Gln Leu Ser Val Thr Gly Pro Pro Asp His Arg Gln Val Phe
305                 310                 315                 320

Cys Leu Ser Ser Ser Gly Arg Glu Asp His Asn Thr Pro Pro Asn Met
                325                 330                 335
```

```
Arg Asp Gly His Val Ile Asp Ile Ala Val Thr Gln Leu Ser Thr Leu
            340                 345                 350

Arg Asn Leu Ile Arg Val Leu Cys Thr Thr His Pro Asp His Ser Pro
        355                 360                 365

Ala Leu Leu Pro Tyr Gly Gln Gln Tyr Thr Ile
    370                 375


<210> 2419
<211> 1542
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1519)
<223> RXA01779

<400> 2419
ttagtattta gtcaattagc caactacgat aaaactagtg aataaacata ctagttcact 60

ttgtcgcgct taaaatacta gaaagtaata taaaaaactc atg cgt tat act ccc   115
                                            Met Arg Tyr Thr Pro
                                              1               5

cgt acc cac cgc gca ctc gga ctt gct gca ctt acc gct aca gct ctc   163
Arg Thr His Arg Ala Leu Gly Leu Ala Ala Leu Thr Ala Thr Ala Leu
                  10                  15                  20

cta ctg agc tca tgc tcg acc acc gct gac ctt ctc ggc gcc gat tct   211
Leu Leu Ser Ser Cys Ser Thr Thr Ala Asp Leu Leu Gly Ala Asp Ser
             25                  30                  35

gtg gcg cag gct gtc acc gat ggt ggc tct gcc ctt gat ccc act gca   259
Val Ala Gln Ala Val Thr Asp Gly Gly Ser Ala Leu Asp Pro Thr Ala
         40                  45                  50

gct cat gtg ctc acc atc acc aat gcc act gca atg act ctt gct gag   307
Ala His Val Leu Thr Ile Thr Asn Ala Thr Ala Met Thr Leu Ala Glu
     55                  60                  65

cta cca gaa aac acc gac cct gac gca gcc aat aac acg gag cca aca   355
Leu Pro Glu Asn Thr Asp Pro Asp Ala Ala Asn Asn Thr Glu Pro Thr
 70                  75                  80                  85

atg gcc caa agc gcc ctc aag cgt att tac ggt ctc gaa att gcc gcc   403
Met Ala Gln Ser Ala Leu Lys Arg Ile Tyr Gly Leu Glu Ile Ala Ala
                 90                  95                 100

gat ggc act ctg att gct gtc gca gcg cca tta acc tcg cga aat agt   451
Asp Gly Thr Leu Ile Ala Val Ala Ala Pro Leu Thr Ser Arg Asn Ser
            105                 110                 115

ggt tct gag cag cct act gtc gca gca atg gct gat cca gaa aac aat   499
Gly Ser Glu Gln Pro Thr Val Ala Ala Met Ala Asp Pro Glu Asn Asn
        120                 125                 130

gct gaa ctc acc aca gca cat att ctt gag atc gac cca gcc aca gga   547
```

```
Ala Glu Leu Thr Thr Ala His Ile Leu Glu Ile Asp Pro Ala Thr Gly
    135                 140                 145

act gcc aca cca cgt caa gat att gct ctg act gaa gat ttt cag acc   595
Thr Ala Thr Pro Arg Gln Asp Ile Ala Leu Thr Glu Asp Phe Gln Thr
150                 155                 160                 165

atg gct agc tct ttt agc cag atc cgt aat ggc tgg ggt act acc caa   643
Met Ala Ser Ser Phe Ser Gln Ile Arg Asn Gly Trp Gly Thr Thr Gln
                170                 175                 180

ctc atc gga caa cac cct gat gat ccc aag caa cct att cgt tca gct   691
Leu Ile Gly Gln His Pro Asp Asp Pro Lys Gln Pro Ile Arg Ser Ala
            185                 190                 195

gat acc tgg act gtc acc ggc tcc act cag atc acc ggc ttt aac acc   739
Asp Thr Trp Thr Val Thr Gly Ser Thr Gln Ile Thr Gly Phe Asn Thr
        200                 205                 210

aac acc cca acg gga acc gaa gat gct gcc tac acc atg ccg gcg act   787
Asn Thr Pro Thr Gly Thr Glu Asp Ala Ala Tyr Thr Met Pro Ala Thr
    215                 220                 225

gag cca gct gtg gga ctg tgc gct cta gaa tca ggc tcc gat gca cca   835
Glu Pro Ala Val Gly Leu Cys Ala Leu Glu Ser Gly Ser Asp Ala Pro
230                 235                 240                 245

ctg gat gaa cac cgt gag ctc agc acc agt gca ttg cgt acc gca tca   883
Leu Asp Glu His Arg Glu Leu Ser Thr Ser Ala Leu Arg Thr Ala Ser
                250                 255                 260

gta ttg tcg agc tct gga tct gcc acc ctc aag ctg cat gat cct atg   931
Val Leu Ser Ser Ser Gly Ser Ala Thr Leu Lys Leu His Asp Pro Met
            265                 270                 275

gtc atg tct gct act ggc att gtc caa gca cgc gcc tat gtc gat ggc   979
Val Met Ser Ala Thr Gly Ile Val Gln Ala Arg Ala Tyr Val Asp Gly
        280                 285                 290

gaa gtc att aac cag cac gag att ggc gat ctc cgc gag cag ctc ggt   1027
Glu Val Ile Asn Gln His Glu Ile Gly Asp Leu Arg Glu Gln Leu Gly
    295                 300                 305

atc acc atc gaa gaa tct gag gct gct caa gca gaa tcg gat gcc caa   1075
Ile Thr Ile Glu Glu Ser Glu Ala Ala Gln Ala Glu Ser Asp Ala Gln
310                 315                 320                 325

gca gcc acc gat cac cca ctt gca gcc ctg ggc tta agc aac ccc acc   1123
Ala Ala Thr Asp His Pro Leu Ala Ala Leu Gly Leu Ser Asn Pro Thr
                330                 335                 340

agc tca gcg ttg gtt cca ggt ctt gct gag ctt gat tgt ctc agt gct   1171
Ser Ser Ala Leu Val Pro Gly Leu Ala Glu Leu Asp Cys Leu Ser Ala
            345                 350                 355

gac cag gct gcc acc tgg cat aac cgc gac acc agc att ggc acc ggt   1219
Asp Gln Ala Ala Thr Trp His Asn Arg Asp Thr Ser Ile Gly Thr Gly
        360                 365                 370

aag ccc agc gtg ctt gct gtc atc aac gcg gaa atg gcc gat gac ttt   1267
Lys Pro Ser Val Leu Ala Val Ile Asn Ala Glu Met Ala Asp Asp Phe
```

```
    375                 380                 385

acc ctg cag ctg ttg agc tca ggt gcc acc act gcc gaa acg cag ctt   1315
Thr Leu Gln Leu Leu Ser Ser Gly Ala Thr Thr Ala Glu Thr Gln Leu
390                 395                 400                 405

gcc cag ctg ccg gat gaa acc gcg ttc gtg ctc att gac cca tca tct   1363
Ala Gln Leu Pro Asp Glu Thr Ala Phe Val Leu Ile Asp Pro Ser Ser
                410                 415                 420

ggt gct gtt act gac ctg ttc ttt atc caa agt ctc aac act gat ctg   1411
Gly Ala Val Thr Asp Leu Phe Phe Ile Gln Ser Leu Asn Thr Asp Leu
        425                 430                 435

ccg gca cca aca acc cag att aat tct att gct gtt gat gag cgc gac   1459
Pro Ala Pro Thr Thr Gln Ile Asn Ser Ile Ala Val Asp Glu Arg Asp
    440                 445                 450

ccc aac atc atc tac gcc act ttt agc ggc gat gac cac ctg tac caa   1507
Pro Asn Ile Ile Tyr Ala Thr Phe Ser Gly Asp Asp His Leu Tyr Gln
455                 460                 465

atg atg ctg ggt tagttacaca actaactaac cag                        1542
Met Met Leu Gly
470
```

<210> 2420
<211> 473
<212> PRT
<213> Corynebacterium glutamicum

<400> 2420

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Met Arg Tyr Thr Pro Arg Thr His Arg Ala Leu Gly Leu Ala Ala Leu
  1               5                  10                  15

Thr Ala Thr Ala Leu Leu Leu Ser Ser Cys Ser Thr Thr Ala Asp Leu
             20                  25                  30

Leu Gly Ala Asp Ser Val Ala Gln Ala Val Thr Asp Gly Gly Ser Ala
         35                  40                  45

Leu Asp Pro Thr Ala Ala His Val Leu Thr Ile Thr Asn Ala Thr Ala
     50                  55                  60

Met Thr Leu Ala Glu Leu Pro Glu Asn Thr Asp Pro Asp Ala Ala Asn
 65                  70                  75                  80

Asn Thr Glu Pro Thr Met Ala Gln Ser Ala Leu Lys Arg Ile Tyr Gly
                 85                  90                  95

Leu Glu Ile Ala Ala Asp Gly Thr Leu Ile Ala Val Ala Ala Pro Leu
            100                 105                 110

Thr Ser Arg Asn Ser Gly Ser Glu Gln Pro Thr Val Ala Ala Met Ala
        115                 120                 125

Asp Pro Glu Asn Asn Ala Glu Leu Thr Thr Ala His Ile Leu Glu Ile
    130                 135                 140

Asp Pro Ala Thr Gly Thr Ala Thr Pro Arg Gln Asp Ile Ala Leu Thr
```

```
145                 150                 155                 160

Glu Asp Phe Gln Thr Met Ala Ser Ser Phe Ser Gln Ile Arg Asn Gly
                165                 170                 175

Trp Gly Thr Thr Gln Leu Ile Gly Gln His Pro Asp Asp Pro Lys Gln
            180                 185                 190

Pro Ile Arg Ser Ala Asp Thr Trp Thr Val Thr Gly Ser Thr Gln Ile
        195                 200                 205

Thr Gly Phe Asn Thr Asn Thr Pro Thr Gly Thr Glu Asp Ala Ala Tyr
    210                 215                 220

Thr Met Pro Ala Thr Glu Pro Ala Val Gly Leu Cys Ala Leu Glu Ser
225                 230                 235                 240

Gly Ser Asp Ala Pro Leu Asp Glu His Arg Glu Leu Ser Thr Ser Ala
                245                 250                 255

Leu Arg Thr Ala Ser Val Leu Ser Ser Ser Gly Ser Ala Thr Leu Lys
            260                 265                 270

Leu His Asp Pro Met Val Met Ser Ala Thr Gly Ile Val Gln Ala Arg
        275                 280                 285

Ala Tyr Val Asp Gly Glu Val Ile Asn Gln His Glu Ile Gly Asp Leu
    290                 295                 300

Arg Glu Gln Leu Gly Ile Thr Ile Glu Glu Ser Glu Ala Ala Gln Ala
305                 310                 315                 320

Glu Ser Asp Ala Gln Ala Ala Thr Asp His Pro Leu Ala Ala Leu Gly
                325                 330                 335

Leu Ser Asn Pro Thr Ser Ser Ala Leu Val Pro Gly Leu Ala Glu Leu
            340                 345                 350

Asp Cys Leu Ser Ala Asp Gln Ala Ala Thr Trp His Asn Arg Asp Thr
        355                 360                 365

Ser Ile Gly Thr Gly Lys Pro Ser Val Leu Ala Val Ile Asn Ala Glu
    370                 375                 380

Met Ala Asp Asp Phe Thr Leu Gln Leu Leu Ser Ser Gly Ala Thr Thr
385                 390                 395                 400

Ala Glu Thr Gln Leu Ala Gln Leu Pro Asp Glu Thr Ala Phe Val Leu
                405                 410                 415

Ile Asp Pro Ser Ser Gly Ala Val Thr Asp Leu Phe Phe Ile Gln Ser
            420                 425                 430

Leu Asn Thr Asp Leu Pro Ala Pro Thr Thr Gln Ile Asn Ser Ile Ala
        435                 440                 445

Val Asp Glu Arg Asp Pro Asn Ile Ile Tyr Ala Thr Phe Ser Gly Asp
    450                 455                 460

Asp His Leu Tyr Gln Met Met Leu Gly
465                 470
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<210> 2421
<211> 498
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(475)
<223> RXA01780

<400> 2421
ccacttttag cggcgatgac cacctgtacc aaatgatgct gggttagtta cacaactaac 60

taaccaggca ccaacatttt cttaaagaaa cacccttatc atg act ttt ctc cac 115
Met Thr Phe Leu His
1 5

ccc aag gct gcg ttc tac cct ctc acc atg gat cat ctt acc gat ctc 163
Pro Lys Ala Ala Phe Tyr Pro Leu Thr Met Asp His Leu Thr Asp Leu
10 15 20

ggt ctt gat cct gag caa ctc att aat gag ttg ccg acg att acc tac 211
Gly Leu Asp Pro Glu Gln Leu Ile Asn Glu Leu Pro Thr Ile Thr Tyr
25 30 35

gac gtt caa cca cac aat gtc ttt gtt cta cag ttc agc acc gcc gat 259
Asp Val Gln Pro His Asn Val Phe Val Leu Gln Phe Ser Thr Ala Asp
40 45 50

gtg cgc gtc tac cag gaa ggt aat acc ctt ttt atc cgc agt gct gaa 307
Val Arg Val Tyr Gln Glu Gly Asn Thr Leu Phe Ile Arg Ser Ala Glu
55 60 65

tta atc aac cct gaa cta cga caa cga cag cgc aca cag ctc aac gac 355
Leu Ile Asn Pro Glu Leu Arg Gln Arg Gln Arg Thr Gln Leu Asn Asp
70 75 80 85

gat ctc aac aac cct gct tca ctt cgc gtc tgt gat gag atc agt ggc 403
Asp Leu Asn Asn Pro Ala Ser Leu Arg Val Cys Asp Glu Ile Ser Gly
90 95 100

cgc agc acc gtg ttc ctc aaa gac aaa agt gtt gtc act cac gat cac 451
Arg Ser Thr Val Phe Leu Lys Asp Lys Ser Val Val Thr His Asp His
105 110 115

ggg acc aat tgc tgt gat tcc gca taatcctgat gaagccagcg cca 498
Gly Thr Asn Cys Cys Asp Ser Ala
120 125

<210> 2422
<211> 125
<212> PRT
<213> Corynebacterium glutamicum

<400> 2422
Met Thr Phe Leu His Pro Lys Ala Ala Phe Tyr Pro Leu Thr Met Asp
1 5 10 15

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His Leu Thr Asp Leu Gly Leu Asp Pro Glu Gln Leu Ile Asn Glu Leu
            20                  25                  30

Pro Thr Ile Thr Tyr Asp Val Gln Pro His Asn Val Phe Val Leu Gln
        35                  40                  45

Phe Ser Thr Ala Asp Val Arg Val Tyr Gln Glu Gly Asn Thr Leu Phe
    50                  55                  60

Ile Arg Ser Ala Glu Leu Ile Asn Pro Glu Leu Arg Gln Arg Gln Arg
65                  70                  75                  80

Thr Gln Leu Asn Asp Asp Leu Asn Asn Pro Ala Ser Leu Arg Val Cys
                85                  90                  95

Asp Glu Ile Ser Gly Arg Ser Thr Val Phe Leu Lys Asp Lys Ser Val
            100                 105                 110

Val Thr His Asp His Gly Thr Asn Cys Cys Asp Ser Ala
        115                 120                 125
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<210> 2423
<211> 384
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(361)
<223> RXA01781

<400> 2423

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cgacagcgca cacagctcaa cgacgatctc aacaaccctg cttcacttcg cgtctgtgat 60

gagatcagtg gccgcagcac cgtgttcctc aaagacaaaa gtg ttg tca ctc acg   115
                                            Val Leu Ser Leu Thr
                                              1               5

atc acg gga cca att gct gtg att ccg cat aat cct gat gaa gcc agc   163
Ile Thr Gly Pro Ile Ala Val Ile Pro His Asn Pro Asp Glu Ala Ser
                10                  15                  20

gcc aag gct gtc gct acc aaa cat aag cac acc ttg tcc ggc gct acc   211
Ala Lys Ala Val Ala Thr Lys His Lys His Thr Leu Ser Gly Ala Thr
            25                  30                  35

tct gat cac cct tat gcc ggc atg acg ctt aaa gac atg att gaa cag   259
Ser Asp His Pro Tyr Ala Gly Met Thr Leu Lys Asp Met Ile Glu Gln
        40                  45                  50

ggc ttt acg ctc aca ccg ctg gaa ttc ccg ctc tgt gct gtc gat gat   307
Gly Phe Thr Leu Thr Pro Leu Glu Phe Pro Leu Cys Ala Val Asp Asp
    55                  60                  65

cca aca gat tct gat cgc acc atg cac gtg atc aat gtt cgc gag cac   355
Pro Thr Asp Ser Asp Arg Thr Met His Val Ile Asn Val Arg Glu His
70                  75                  80                  85

agt atg tagattctaa agtgcggtac aac                                384
Ser Met
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<210> 2424
<211> 87
<212> PRT
<213> Corynebacterium glutamicum

<400> 2424
Val Leu Ser Leu Thr Ile Thr Gly Pro Ile Ala Val Ile Pro His Asn
1 5 10 15

Pro Asp Glu Ala Ser Ala Lys Ala Val Ala Thr Lys His Lys His Thr
20 25 30

Leu Ser Gly Ala Thr Ser Asp His Pro Tyr Ala Gly Met Thr Leu Lys
35 40 45

Asp Met Ile Glu Gln Gly Phe Thr Leu Thr Pro Leu Glu Phe Pro Leu
50 55 60

Cys Ala Val Asp Asp Pro Thr Asp Ser Asp Arg Thr Met His Val Ile
65 70 75 80

Asn Val Arg Glu His Ser Met
85

<210> 2425
<211> 519
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(496)
<223> RXA01782

<400> 2425
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cccacacaat tccacccttt aagaaaagga cttagccatc atg acc acc ttc gcc 115
Met Thr Thr Phe Ala
1 5

ctt att gct agc ccc aac aat gtt gat ccc act gct gag tcc cca ctc 163
Leu Ile Ala Ser Pro Asn Asn Val Asp Pro Thr Ala Glu Ser Pro Leu
10 15 20

gcc att gaa atc cat acc gat gag gac agc agc tat cca cta ggg ctt 211
Ala Ile Glu Ile His Thr Asp Glu Asp Ser Ser Tyr Pro Leu Gly Leu
25 30 35

att gac tca gac cac ctg gtt cct gct gtg att tac ggc gat atg gtg 259
Ile Asp Ser Asp His Leu Val Pro Ala Val Ile Tyr Gly Asp Met Val
40 45 50

atc tac acc aaa aca ctg ctc gca cag acc cca cca gat gat gtg tcc 307
Ile Tyr Thr Lys Thr Leu Leu Ala Gln Thr Pro Pro Asp Asp Val Ser
55 60 65

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act gct agc gcc ttc ttc gac aaa ctc acc gca ctt gac gct cag ggt   355
Thr Ala Ser Ala Phe Phe Asp Lys Leu Thr Ala Leu Asp Ala Gln Gly
 70                  75                  80                  85

cgc acc cgt gat ctg gtc tac agc gcc acc tac agc caa ctt gtt att   403
Arg Thr Arg Asp Leu Val Tyr Ser Ala Thr Tyr Ser Gln Leu Val Ile
                 90                  95                 100

gcc ggc cac aac cgc act gta tta act gac gac tca gag ttc tac gat   451
Ala Gly His Asn Arg Thr Val Leu Thr Asp Asp Ser Glu Phe Tyr Asp
            105                 110                 115

gag ttt tac cag gtt att gag gct gct cct ggg gtg atc ttg aaa       496
Glu Phe Tyr Gln Val Ile Glu Ala Ala Pro Gly Val Ile Leu Lys
        120                 125                 130

tgatgtttat cgggcaacac ctc                                        519


<210> 2426
<211> 132
<212> PRT
<213> Corynebacterium glutamicum

<400> 2426
Met Thr Thr Phe Ala Leu Ile Ala Ser Pro Asn Asn Val Asp Pro Thr
  1               5                  10                  15

Ala Glu Ser Pro Leu Ala Ile Glu Ile His Thr Asp Glu Asp Ser Ser
             20                  25                  30

Tyr Pro Leu Gly Leu Ile Asp Ser Asp His Leu Val Pro Ala Val Ile
         35                  40                  45

Tyr Gly Asp Met Val Ile Tyr Thr Lys Thr Leu Leu Ala Gln Thr Pro
     50                  55                  60

Pro Asp Asp Val Ser Thr Ala Ser Ala Phe Phe Asp Lys Leu Thr Ala
 65                  70                  75                  80

Leu Asp Ala Gln Gly Arg Thr Arg Asp Leu Val Tyr Ser Ala Thr Tyr
                 85                  90                  95

Ser Gln Leu Val Ile Ala Gly His Asn Arg Thr Val Leu Thr Asp Asp
            100                 105                 110

Ser Glu Phe Tyr Asp Glu Phe Tyr Gln Val Ile Glu Ala Ala Pro Gly
        115                 120                 125

Val Ile Leu Lys
    130


<210> 2427
<211> 360
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(337)
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<223> RXA01783

<400> 2427
accaggttat tgaggctgct cctggggtga tcttgaaatg atgtttatcg ggcaacacct 60

cacacttagg ctaggtctct aacatgaagc agatagcgcc atg atc aat ctt ttt 115
Met Ile Asn Leu Phe
1 5

gct gca gcc ctg ccc gca ttc gag cct ttg agt att acc tcc ata ctc 163
Ala Ala Ala Leu Pro Ala Phe Glu Pro Leu Ser Ile Thr Ser Ile Leu
10 15 20

gtg ctc ggt gct gtg gca ttg atc tgt ggc ctc cct gtt ttt ctc gca 211
Val Leu Gly Ala Val Ala Leu Ile Cys Gly Leu Pro Val Phe Leu Ala
25 30 35

ctg gaa aaa agc gct gag ctc gat gat ctc ttc gca gca ctc atc atc 259
Leu Glu Lys Ser Ala Glu Leu Asp Asp Leu Phe Ala Ala Leu Ile Ile
40 45 50

gct gta ctt tta ggt ttt gct gct tat acg ttt gtg ctc ccc aag ctc 307
Ala Val Leu Leu Gly Phe Ala Ala Tyr Thr Phe Val Leu Pro Lys Leu
55 60 65

gtt gaa ttg ggc tgt act att tgc cag ctc tgactagcga cacttacact 357
Val Glu Leu Gly Cys Thr Ile Cys Gln Leu
70 75

ttc 360

<210> 2428
<211> 79
<212> PRT
<213> Corynebacterium glutamicum

<400> 2428
Met Ile Asn Leu Phe Ala Ala Ala Leu Pro Ala Phe Glu Pro Leu Ser
1 5 10 15

Ile Thr Ser Ile Leu Val Leu Gly Ala Val Ala Leu Ile Cys Gly Leu
20 25 30

Pro Val Phe Leu Ala Leu Glu Lys Ser Ala Glu Leu Asp Asp Leu Phe
35 40 45

Ala Ala Leu Ile Ile Ala Val Leu Leu Gly Phe Ala Ala Tyr Thr Phe
50 55 60

Val Leu Pro Lys Leu Val Glu Leu Gly Cys Thr Ile Cys Gln Leu
65 70 75

<210> 2429
<211> 699
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(676)
<223> RXA01785

<400> 2429

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tgactacgca tctaaggcgg cgcacattag tgatgcaact gtg gat cag ttc gtt   115
                                            Val Asp Gln Phe Val
                                              1               5

gag ttc ggc ggt gga caa gca aac att aac cct gat gga tca gcg acc   163
Glu Phe Gly Gly Gly Gln Ala Asn Ile Asn Pro Asp Gly Ser Ala Thr
                 10                  15                  20

gtt gat tgg gag ggt tct ttc agc atc aac ttc tac gat ggt ttg gtg   211
Val Asp Trp Glu Gly Ser Phe Ser Ile Asn Phe Tyr Asp Gly Leu Val
             25                  30                  35

ccg ttt acc atc acg aat ccg cac ctc gag gtt tct gta gct ggt act   259
Pro Phe Thr Ile Thr Asn Pro His Leu Glu Val Ser Val Ala Gly Thr
         40                  45                  50

ggt gtt ttg act ggt gac ctc act agc tat gca gtg gag atg tcg aac   307
Gly Val Leu Thr Gly Asp Leu Thr Ser Tyr Ala Val Glu Met Ser Asn
     55                  60                  65

ccg aat gag aaa acc ccg ttg act gac ttg tat gag gat gtc acg atc   355
Pro Asn Glu Lys Thr Pro Leu Thr Asp Leu Tyr Glu Asp Val Thr Ile
 70                  75                  80                  85

aca acg ttt ggg gga gtg aac ctt gat cct gaa ggt gtt gtg aca agc   403
Thr Thr Phe Gly Gly Val Asn Leu Asp Pro Glu Gly Val Val Thr Ser
                 90                  95                 100

aat cct gat tat gac gga gtg att gtt gat gtc cca ctg gat gcc acc   451
Asn Pro Asp Tyr Asp Gly Val Ile Val Asp Val Pro Leu Asp Ala Thr
            105                 110                 115

tct cag gtt act tcc ggt gca ggt tgg gga gcg tgg ccg cag ggc ttc   499
Ser Gln Val Thr Ser Gly Ala Gly Trp Gly Ala Trp Pro Gln Gly Phe
        120                 125                 130

ctt gat ttc cac ttt gat acc aac ttg cct tcc tac tgg tat tcc tca   547
Leu Asp Phe His Phe Asp Thr Asn Leu Pro Ser Tyr Trp Tyr Ser Ser
    135                 140                 145

gat ggc gca ggt gat cct aag aag gcg cct atg agc ttt aat gtt gat   595
Asp Gly Ala Gly Asp Pro Lys Lys Ala Pro Met Ser Phe Asn Val Asp
150                 155                 160                 165

ttc act aat ggt cca ggt ctg gtg aac agc caa ttg ctc cac agg caa   643
Phe Thr Asn Gly Pro Gly Leu Val Asn Ser Gln Leu Leu His Arg Gln
                170                 175                 180

gtg atc tca atg ccg gaa acc aag gca gtc tcg tagttccatc ggaggcagaa 696
Val Ile Ser Met Pro Glu Thr Lys Ala Val Ser
            185                 190

gct                                                               699
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<210> 2430
<211> 192
<212> PRT
<213> Corynebacterium glutamicum

<400> 2430
Val Asp Gln Phe Val Glu Phe Gly Gly Gly Gln Ala Asn Ile Asn Pro
1 5 10 15

Asp Gly Ser Ala Thr Val Asp Trp Glu Gly Ser Phe Ser Ile Asn Phe
20 25 30

Tyr Asp Gly Leu Val Pro Phe Thr Ile Thr Asn Pro His Leu Glu Val
35 40 45

Ser Val Ala Gly Thr Gly Val Leu Thr Gly Asp Leu Thr Ser Tyr Ala
50 55 60

Val Glu Met Ser Asn Pro Asn Glu Lys Thr Pro Leu Thr Asp Leu Tyr
65 70 75 80

Glu Asp Val Thr Ile Thr Thr Phe Gly Gly Val Asn Leu Asp Pro Glu
85 90 95

Gly Val Val Thr Ser Asn Pro Asp Tyr Asp Gly Val Ile Val Asp Val
100 105 110

Pro Leu Asp Ala Thr Ser Gln Val Thr Ser Gly Ala Gly Trp Gly Ala
115 120 125

Trp Pro Gln Gly Phe Leu Asp Phe His Phe Asp Thr Asn Leu Pro Ser
130 135 140

Tyr Trp Tyr Ser Ser Asp Gly Ala Gly Asp Pro Lys Lys Ala Pro Met
145 150 155 160

Ser Phe Asn Val Asp Phe Thr Asn Gly Pro Gly Leu Val Asn Ser Gln
165 170 175

Leu Leu His Arg Gln Val Ile Ser Met Pro Glu Thr Lys Ala Val Ser
180 185 190

<210> 2431
<211> 564
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(541)
<223> RXA01788

<400> 2431
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cggaaactaa tcccgacgat gagaaagcag gacgctagcc atg tct cgc agc tac 115
Met Ser Arg Ser Tyr

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                                                    1               5

ccc atc tac atc att tct ttt gcc cca gcg gat gat ctc cac ggc gtt   163
Pro Ile Tyr Ile Ile Ser Phe Ala Pro Ala Asp Asp Leu His Gly Val
                 10                  15                  20

gga gga ttc gag tgg gtt cca gca tca aca cca gaa aac aaa gct gcc   211
Gly Gly Phe Glu Trp Val Pro Ala Ser Thr Pro Glu Asn Lys Ala Ala
             25                  30                  35

gcc ttc acg acc ttt gat cgt caa ttc gat gat tct cgt aac aat ggt   259
Ala Phe Thr Thr Phe Asp Arg Gln Phe Asp Asp Ser Arg Asn Asn Gly
         40                  45                  50

ggc tcg cat att gtg cgt cta ctc aat atc tct gat ccc aat atc aca   307
Gly Ser His Ile Val Arg Leu Leu Asn Ile Ser Asp Pro Asn Ile Thr
     55                  60                  65

gcg gat atg acc caa gac gat att acc gcg tac ctc gac tca aac atc   355
Ala Asp Met Thr Gln Asp Asp Ile Thr Ala Tyr Leu Asp Ser Asn Ile
 70                  75                  80                  85

gac cgc tgg gaa tcc acg gaa cat gcg ctc aag cag ttt gtc cca ctt   403
Asp Arg Trp Glu Ser Thr Glu His Ala Leu Lys Gln Phe Val Pro Leu
                 90                  95                 100

aac gcg ggt gct gat cgc gta cct acc ggt ggt gcc gac gag cac att   451
Asn Ala Gly Ala Asp Arg Val Pro Thr Gly Gly Ala Asp Glu His Ile
             105                 110                 115

acc cac gcc tgc cgc ata ata act gtg cag cgt agc tgc aca cgg att   499
Thr His Ala Cys Arg Ile Ile Thr Val Gln Arg Ser Cys Thr Arg Ile
         120                 125                 130

cac ctg cgc tgt gga tgc atc cca aca cca caa cac cgc ccc           541
His Leu Arg Cys Gly Cys Ile Pro Thr Pro Gln His Arg Pro
     135                 140                 145

tagtgccata aatgctaggg gtg                                        564
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<210> 2432
<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 2432

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Met Ser Arg Ser Tyr Pro Ile Tyr Ile Ile Ser Phe Ala Pro Ala Asp
  1               5                  10                  15

Asp Leu His Gly Val Gly Gly Phe Glu Trp Val Pro Ala Ser Thr Pro
             20                  25                  30

Glu Asn Lys Ala Ala Ala Phe Thr Thr Phe Asp Arg Gln Phe Asp Asp
         35                  40                  45

Ser Arg Asn Asn Gly Gly Ser His Ile Val Arg Leu Leu Asn Ile Ser
     50                  55                  60

Asp Pro Asn Ile Thr Ala Asp Met Thr Gln Asp Asp Ile Thr Ala Tyr
 65                  70                  75                  80
```



```
Leu Asp Ser Asn Ile Asp Arg Trp Glu Ser Thr Glu His Ala Leu Lys
                 85                  90                  95

Gln Phe Val Pro Leu Asn Ala Gly Ala Asp Arg Val Pro Thr Gly Gly
            100                 105                 110

Ala Asp Glu His Ile Thr His Ala Cys Arg Ile Ile Thr Val Gln Arg
        115                 120                 125

Ser Cys Thr Arg Ile His Leu Arg Cys Gly Cys Ile Pro Thr Pro Gln
    130                 135                 140

His Arg Pro
145


<210> 2433
<211> 765
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(742)
<223> RXA01789

<400> 2433
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acccacaaca ccgttcttct ctagaaagag actcgatact atg cct cat aac ccc   115
                                            Met Pro His Asn Pro
                                              1               5

atc gaa ctt cac act aat gat gta ctc gat gct ctc gac att gac gcc   163
Ile Glu Leu His Thr Asn Asp Val Leu Asp Ala Leu Asp Ile Asp Ala
                 10                  15                  20

atc tgc gac gat gtg ttt ctc tac acc gac ttc gag cac acc cca ggt   211
Ile Cys Asp Asp Val Phe Leu Tyr Thr Asp Phe Glu His Thr Pro Gly
             25                  30                  35

cag ctt gat cgc ttc gag caa ctc gcc ttc aca aaa atc tac gac atg   259
Gln Leu Asp Arg Phe Glu Gln Leu Ala Phe Thr Lys Ile Tyr Asp Met
         40                  45                  50

ctg gaa aca gct gct gaa aaa ttc cca gat gta gca att aat gac act   307
Leu Glu Thr Ala Ala Glu Lys Phe Pro Asp Val Ala Ile Asn Asp Thr
     55                  60                  65

tta agc act ggc aac cac gct gct gaa cag tac ttt ctt gcc aat ccc   355
Leu Ser Thr Gly Asn His Ala Ala Glu Gln Tyr Phe Leu Ala Asn Pro
 70                  75                  80                  85

ggc aac atc atc gtg ctg acc agc ttc gcg ctc aat cag acc gat ctc   403
Gly Asn Ile Ile Val Leu Thr Ser Phe Ala Leu Asn Gln Thr Asp Leu
                 90                  95                 100

cgc gac ctc ata atc tca ccg tgc att aag tac aca gca cat gca cga   451
Arg Asp Leu Ile Ile Ser Pro Cys Ile Lys Tyr Thr Ala His Ala Arg
            105                 110                 115
```

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gca ctc atg cgt gcg gtg aca cga aca ttg tgc act gca aac aac cct   499
Ala Leu Met Arg Ala Val Thr Arg Thr Leu Cys Thr Ala Asn Asn Pro
        120                 125                 130

gta gaa cgc gcg act atc ttc cct gtg tct gtc gct aat gcc tta agc   547
Val Glu Arg Ala Thr Ile Phe Pro Val Ser Val Ala Asn Ala Leu Ser
    135                 140                 145

atc gaa gcg ctg tgt tcc gaa tat cat gcg ttc cgc acc aag cag gtg   595
Ile Glu Ala Leu Cys Ser Glu Tyr His Ala Phe Arg Thr Lys Gln Val
150                 155                 160                 165

ctc aac act gct gca ctc atc aat cct gat aac act ctt ata ccc atg   643
Leu Asn Thr Ala Ala Leu Ile Asn Pro Asp Asn Thr Leu Ile Pro Met
                170                 175                 180

ttg ttg agc aaa gcg tat gag gca tac gcc tgg cac aag ggt gtc gaa   691
Leu Leu Ser Lys Ala Tyr Glu Ala Tyr Ala Trp His Lys Gly Val Glu
            185                 190                 195

tcc gcg caa cga ggt agc aac cta gct cgt gag tac tac gca gga ctt   739
Ser Ala Gln Arg Gly Ser Asn Leu Ala Arg Glu Tyr Tyr Ala Gly Leu
        200                 205                 210

atc tgaaaattca ctactcaact ctg                                    765
Ile
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<210> 2434
<211> 214
<212> PRT
<213> Corynebacterium glutamicum

<400> 2434

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Met Pro His Asn Pro Ile Glu Leu His Thr Asn Asp Val Leu Asp Ala
  1               5                  10                  15

Leu Asp Ile Asp Ala Ile Cys Asp Asp Val Phe Leu Tyr Thr Asp Phe
             20                  25                  30

Glu His Thr Pro Gly Gln Leu Asp Arg Phe Glu Gln Leu Ala Phe Thr
         35                  40                  45

Lys Ile Tyr Asp Met Leu Glu Thr Ala Ala Glu Lys Phe Pro Asp Val
     50                  55                  60

Ala Ile Asn Asp Thr Leu Ser Thr Gly Asn His Ala Ala Glu Gln Tyr
 65                  70                  75                  80

Phe Leu Ala Asn Pro Gly Asn Ile Ile Val Leu Thr Ser Phe Ala Leu
                 85                  90                  95

Asn Gln Thr Asp Leu Arg Asp Leu Ile Ile Ser Pro Cys Ile Lys Tyr
            100                 105                 110

Thr Ala His Ala Arg Ala Leu Met Arg Ala Val Thr Arg Thr Leu Cys
        115                 120                 125

Thr Ala Asn Asn Pro Val Glu Arg Ala Thr Ile Phe Pro Val Ser Val
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130 135 140

Ala Asn Ala Leu Ser Ile Glu Ala Leu Cys Ser Glu Tyr His Ala Phe
145 150 155 160

Arg Thr Lys Gln Val Leu Asn Thr Ala Ala Leu Ile Asn Pro Asp Asn
165 170 175

Thr Leu Ile Pro Met Leu Leu Ser Lys Ala Tyr Glu Ala Tyr Ala Trp
180 185 190

His Lys Gly Val Glu Ser Ala Gln Arg Gly Ser Asn Leu Ala Arg Glu
195 200 205

Tyr Tyr Ala Gly Leu Ile
210

<210> 2435
<211> 183
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(160)
<223> RXA01790

<400> 2435
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tgatgatgat tcccctgatc tcgatgagga cgataacacc gtg ctc atc gcc gaa 115
Val Leu Ile Ala Glu
1 5

gac atc cgt gat atg gat gac tat ggc gaa gat cat cct gat ctt 160
Asp Ile Arg Asp Met Asp Asp Tyr Gly Glu Asp His Pro Asp Leu
10 15 20

taaagctcac tgttaagccc gca 183

<210> 2436
<211> 20
<212> PRT
<213> Corynebacterium glutamicum

<400> 2436
Val Leu Ile Ala Glu Asp Ile Arg Asp Met Asp Asp Tyr Gly Glu Asp
1 5 10 15

His Pro Asp Leu
20

<210> 2437
<211> 486
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(463)
<223> RXA01791

<400> 2437
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caacactatc cggtccaaat ctagaaaaga gacaaccccc atg acc tcc ccc acc 115
Met Thr Ser Pro Thr
1 5

acg tta aag ccc tgg tct att cgc gga ccc atc gac ggt gaa tac acc 163
Thr Leu Lys Pro Trp Ser Ile Arg Gly Pro Ile Asp Gly Glu Tyr Thr
10 15 20

atg ctt gag gca tat ccg ttt cag tat gta gca aat act cgc ccg gcc 211
Met Leu Glu Ala Tyr Pro Phe Gln Tyr Val Ala Asn Thr Arg Pro Ala
25 30 35

atc atg ctc tac gca ctc gat gaa aac ggt gta ccg gaa caa tat gcc 259
Ile Met Leu Tyr Ala Leu Asp Glu Asn Gly Val Pro Glu Gln Tyr Ala
40 45 50

gac ctc acc atc aac ctt gcc gat gtg gag ctc aag caa ctt aac cac 307
Asp Leu Thr Ile Asn Leu Ala Asp Val Glu Leu Lys Gln Leu Asn His
55 60 65

gtc atc att aac cca gat ctg cac gct gat gtt acc gaa ctg tgc att 355
Val Ile Ile Asn Pro Asp Leu His Ala Asp Val Thr Glu Leu Cys Ile
70 75 80 85

agc gcc ggc ctg ctg cga cct ggt gtt ctg ggc cag cac caa gtc ggt 403
Ser Ala Gly Leu Leu Arg Pro Gly Val Leu Gly Gln His Gln Val Gly
90 95 100

agc acc acc gcc aag gtc tac cga ctc act gag cgt gct gat ggc tgg 451
Ser Thr Thr Ala Lys Val Tyr Arg Leu Thr Glu Arg Ala Asp Gly Trp
105 110 115

cta cag ctg ttt tagcagctac ctgcgcctaa tcc 486
Leu Gln Leu Phe
120

<210> 2438
<211> 121
<212> PRT
<213> Corynebacterium glutamicum

<400> 2438
Met Thr Ser Pro Thr Thr Leu Lys Pro Trp Ser Ile Arg Gly Pro Ile
1 5 10 15

Asp Gly Glu Tyr Thr Met Leu Glu Ala Tyr Pro Phe Gln Tyr Val Ala
20 25 30

Asn Thr Arg Pro Ala Ile Met Leu Tyr Ala Leu Asp Glu Asn Gly Val
35 40 45

Pro Glu Gln Tyr Ala Asp Leu Thr Ile Asn Leu Ala Asp Val Glu Leu
50 55 60



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Lys Gln Leu Asn His Val Ile Ile Asn Pro Asp Leu His Ala Asp Val
 65                  70                  75                  80

Thr Glu Leu Cys Ile Ser Ala Gly Leu Leu Arg Pro Gly Val Leu Gly
                 85                  90                  95

Gln His Gln Val Gly Ser Thr Thr Ala Lys Val Tyr Arg Leu Thr Glu
            100                 105                 110

Arg Ala Asp Gly Trp Leu Gln Leu Phe
        115                 120


<210> 2439
<211> 396
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(373)
<223> RXA01792

<400> 2439
gactcactga gcgtgctgat ggctggctac agctgtttta gcagctacct gcgcctaatc 60

cccccaccca tactcactcc aaaacaagaa agtagtcatc atg cct cag tac acc   115
                                              Met Pro Gln Tyr Thr
                                                1               5

atc aca atc acc gac gag cag aaa gct gtt cta cac agc ctc acc aac   163
Ile Thr Ile Thr Asp Glu Gln Lys Ala Val Leu His Ser Leu Thr Asn
                10                  15                  20

ccc cat atc gcc act gct gaa cac ggc gct atc acc gca atc gag att   211
Pro His Ile Ala Thr Ala Glu His Gly Ala Ile Thr Ala Ile Glu Ile
            25                  30                  35

cat gac gac cac gat gtt gtt gtc tat cac gtt caa cca gac ggc aca   259
His Asp Asp His Asp Val Val Val Tyr His Val Gln Pro Asp Gly Thr
        40                  45                  50

cta act tac gag cgc ctt gtt gaa ggc ttc cat tac ggc tgg aca cgt   307
Leu Thr Tyr Glu Arg Leu Val Glu Gly Phe His Tyr Gly Trp Thr Arg
    55                  60                  65

ttt gac agc gaa ggt ttt gag atc gac tcc gac aat aac cgc gtt gta   355
Phe Asp Ser Glu Gly Phe Glu Ile Asp Ser Asp Asn Asn Arg Val Val
 70                  75                  80                  85

gac gga ctc cgc gac gaa tagttaacaa caacgaccgc aca                396
Asp Gly Leu Arg Asp Glu
                90


<210> 2440
<211> 91
<212> PRT
<213> Corynebacterium glutamicum
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<400> 2440
Met Pro Gln Tyr Thr Ile Thr Ile Thr Asp Glu Gln Lys Ala Val Leu
1 5 10 15

His Ser Leu Thr Asn Pro His Ile Ala Thr Ala Glu His Gly Ala Ile
20 25 30

Thr Ala Ile Glu Ile His Asp Asp His Asp Val Val Val Tyr His Val
35 40 45

Gln Pro Asp Gly Thr Leu Thr Tyr Glu Arg Leu Val Glu Gly Phe His
50 55 60

Tyr Gly Trp Thr Arg Phe Asp Ser Glu Gly Phe Glu Ile Asp Ser Asp
65 70 75 80

Asn Asn Arg Val Val Asp Gly Leu Arg Asp Glu
85 90

<210> 2441
<211> 357
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(334)
<223> RXA01793

<400> 2441
ccttctctgc aggctacgca gtgctgcgcc tagttcgcag cctgcgccga cttttgcagc 60

gccactaaac acccaaacac aacaagaaag aaacaccact atg gca caa tac cgc 115
Met Ala Gln Tyr Arg
1 5

gtc agt ttt atc gcg ctc gcc gag tca acc atc gag gtc gaa gca gac 163
Val Ser Phe Ile Ala Leu Ala Glu Ser Thr Ile Glu Val Glu Ala Asp
10 15 20

agt cct gaa gaa gca ctc gac cta gcc aat gca gaa ttt gac tac ccg 211
Ser Pro Glu Glu Ala Leu Asp Leu Ala Asn Ala Glu Phe Asp Tyr Pro
25 30 35

gtc acc ttg gcc ggc gat ccc tat gag ctg cac gac tgg gaa gca cgc 259
Val Thr Leu Ala Gly Asp Pro Tyr Glu Leu His Asp Trp Glu Ala Arg
40 45 50

gct gaa att gaa tgg ctc gat acc agc tcg acc ccg cag caa cgc ctt 307
Ala Glu Ile Glu Trp Leu Asp Thr Ser Ser Thr Pro Gln Gln Arg Leu
55 60 65

gga gaa cat gtc gtc aag atc gaa gat taaactcgat cattaaacac 354
Gly Glu His Val Val Lys Ile Glu Asp
70 75

act 357

<210> 2442

<211> 78
<212> PRT
<213> Corynebacterium glutamicum

<400> 2442
Met Ala Gln Tyr Arg Val Ser Phe Ile Ala Leu Ala Glu Ser Thr Ile
1 5 10 15

Glu Val Glu Ala Asp Ser Pro Glu Glu Ala Leu Asp Leu Ala Asn Ala
20 25 30

Glu Phe Asp Tyr Pro Val Thr Leu Ala Gly Asp Pro Tyr Glu Leu His
35 40 45

Asp Trp Glu Ala Arg Ala Glu Ile Glu Trp Leu Asp Thr Ser Ser Thr
50 55 60

Pro Gln Gln Arg Leu Gly Glu His Val Val Lys Ile Glu Asp
65 70 75

<210> 2443
<211> 357
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(334)
<223> RXA01794

<400> 2443
ataccagctc gaccccgcag caacgccttg gagaacatgt cgtcaagatc gaagattaaa 60

ctcgatcatt aaacacactc ttaagataag gacactaatt atg gca acc cac cgc 115
Met Ala Thr His Arg
1 5

gtt cat ttt gtc gca acc gca tcc gcc tac atc gac gtt gag gca gat 163
Val His Phe Val Ala Thr Ala Ser Ala Tyr Ile Asp Val Glu Ala Asp
10 15 20

tcc ccc gaa gat gct ata gaa aaa gcg tat gat ctc gcc ggt gat ctg 211
Ser Pro Glu Asp Ala Ile Glu Lys Ala Tyr Asp Leu Ala Gly Asp Leu
25 30 35

ccc ggc ctc atc gcc gac aac gaa ttt gat ctc ggt gaa tgg gag gta 259
Pro Gly Leu Ile Ala Asp Asn Glu Phe Asp Leu Gly Glu Trp Glu Val
40 45 50

cag gcc gat gtc cag tgg cct gat aac tct gta cct cgc gag caa cgc 307
Gln Ala Asp Val Gln Trp Pro Asp Asn Ser Val Pro Arg Glu Gln Arg
55 60 65

ctt gaa gag ggc gtt gac ctg ctc gat taaacagaat taactcaaac 354
Leu Glu Glu Gly Val Asp Leu Leu Asp
70 75

ccc 357

<210> 2444
<211> 78
<212> PRT
<213> Corynebacterium glutamicum

<400> 2444
Met Ala Thr His Arg Val His Phe Val Ala Thr Ala Ser Ala Tyr Ile
1 5 10 15

Asp Val Glu Ala Asp Ser Pro Glu Asp Ala Ile Glu Lys Ala Tyr Asp
20 25 30

Leu Ala Gly Asp Leu Pro Gly Leu Ile Ala Asp Asn Glu Phe Asp Leu
35 40 45

Gly Glu Trp Glu Val Gln Ala Asp Val Gln Trp Pro Asp Asn Ser Val
50 55 60

Pro Arg Glu Gln Arg Leu Glu Glu Gly Val Asp Leu Leu Asp
65 70 75

<210> 2445
<211> 1317
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1294)
<223> RXA01799

<400> 2445
tattttgggc atgcactcgt catatcttca cagacgtatg gttttgtaac aacctccccc 60

aaaatcccca tagtttcccc cggtgcatat ccttaaaggt atg gaa att ccg ctg 115
Met Glu Ile Pro Leu
1 5

ccc aca tcc ctt atc gat gtc atc act gat ggt gcc ctc ggc caa acc 163
Pro Thr Ser Leu Ile Asp Val Ile Thr Asp Gly Ala Leu Gly Gln Thr
10 15 20

tgc att gat cag gca ttt gct gcc caa ttg ggg cga gtt act gga gtc 211
Cys Ile Asp Gln Ala Phe Ala Ala Gln Leu Gly Arg Val Thr Gly Val
25 30 35

gaa ttc aac ctt tct gac gat aaa acc gcg gct gaa gtg agg atc aat 259
Glu Phe Asn Leu Ser Asp Asp Lys Thr Ala Ala Glu Val Arg Ile Asn
40 45 50

aag gcg tcg ggg agt cct ttt gat acc acc ggt gaa gtc att gcg tgg 307
Lys Ala Ser Gly Ser Pro Phe Asp Thr Thr Gly Glu Val Ile Ala Trp
55 60 65

att aat aat cag gaa ttt gag tgg gtc agc acg cgc ggt gag gat ttg 355
Ile Asn Asn Gln Glu Phe Glu Trp Val Ser Thr Arg Gly Glu Asp Leu
70 75 80 85

gga ctg cct gaa ttg cag ggc att cag ccg ctc gac gat gat ctg atc 403
Gly Leu Pro Glu Leu Gln Gly Ile Gln Pro Leu Asp Asp Asp Leu Ile

```
                    90                  95                  100

acc gcc gca cgc acg ctg tat agc aat gcg ccg gcg ttc atc gcc ccg   451
Thr Ala Ala Arg Thr Leu Tyr Ser Asn Ala Pro Ala Phe Ile Ala Pro
            105                 110                 115

ttg cgc gat ggt cgc agg gcg ttg gtt gcg atc aat cac acg cca aaa   499
Leu Arg Asp Gly Arg Arg Ala Leu Val Ala Ile Asn His Thr Pro Lys
        120                 125                 130

ctg gtt ggt atc cgt cgc acg ctc atc gaa ggc ctg cag gcg ctg aag   547
Leu Val Gly Ile Arg Arg Thr Leu Ile Glu Gly Leu Gln Ala Leu Lys
    135                 140                 145

cct gga act gac ctc aaa cgg gca ttg act tca ttt gct gca ttc tgc   595
Pro Gly Thr Asp Leu Lys Arg Ala Leu Thr Ser Phe Ala Ala Phe Cys
150                 155                 160                 165

gaa ctg ggc atc cga ttc gat gac aac cgc atc tcc ttc agc gat ggc   643
Glu Leu Gly Ile Arg Phe Asp Asp Asn Arg Ile Ser Phe Ser Asp Gly
                170                 175                 180

acc tcg ctg ttg ctt cgt ggc ggc aaa gtc atc gaa atc gca ggc ggg   691
Thr Ser Leu Leu Leu Arg Gly Gly Lys Val Ile Glu Ile Ala Gly Gly
            185                 190                 195

ctg agc ttg cgc gac gta cgc gcg gat gcg gcg ttc atg tcc gct gag   739
Leu Ser Leu Arg Asp Val Arg Ala Asp Ala Ala Phe Met Ser Ala Glu
        200                 205                 210

cat caa ttg ctt ttc gac gcc atc tcc tcg tct cac aac gtc acc ttt   787
His Gln Leu Leu Phe Asp Ala Ile Ser Ser Ser His Asn Val Thr Phe
    215                 220                 225

gac cca cac acc aac gtg gcg acc gtg gca aac gaa cac caa gtt cac   835
Asp Pro His Thr Asn Val Ala Thr Val Ala Asn Glu His Gln Val His
230                 235                 240                 245

gcc atc ccc ctt gct gtt atc gac ggc acg cgt tgg gta tgg aca tgg   883
Ala Ile Pro Leu Ala Val Ile Asp Gly Thr Arg Trp Val Trp Thr Trp
                250                 255                 260

tct tta aaa gaa ctc aat ggt caa gca act gaa ggc ctt gcc cgc ttt   931
Ser Leu Lys Glu Leu Asn Gly Gln Ala Thr Glu Gly Leu Ala Arg Phe
            265                 270                 275

ggt ttc gat aac ggc cta cta ctg ctc acc aat gca gag atc ctt gct   979
Gly Phe Asp Asn Gly Leu Leu Leu Leu Thr Asn Ala Glu Ile Leu Ala
        280                 285                 290

gag gaa gcc acc gca ttc aac ctg att gat gtg gct aaa cag gtg ctc   1027
Glu Glu Ala Thr Ala Phe Asn Leu Ile Asp Val Ala Lys Gln Val Leu
    295                 300                 305

aac act tgg acg cac acc atc gtg cag caa cct gat ggc acc gga att   1075
Asn Thr Trp Thr His Thr Ile Val Gln Gln Pro Asp Gly Thr Gly Ile
310                 315                 320                 325

gtc ctg ctg ctg gat cat cct cgg ctg cag ctt ccg cca gca tca cat   1123
Val Leu Leu Leu Asp His Pro Arg Leu Gln Leu Pro Pro Ala Ser His
                330                 335                 340
```

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gca gct gtt gag gcc acg ctg tat cac cag cta cca ggc gat att gat   1171
Ala Ala Val Glu Ala Thr Leu Tyr His Gln Leu Pro Gly Asp Ile Asp
            345                 350                 355

gcc cgc cgc gcg gtg gcg tcc tat gca gct cac cga cag ctt cct ttt   1219
Ala Arg Arg Ala Val Ala Ser Tyr Ala Ala His Arg Gln Leu Pro Phe
        360                 365                 370

gat ggc tac gca ctc acc gtt gag ggc caa caa gtc ggc gtg act ttt   1267
Asp Gly Tyr Ala Leu Thr Val Glu Gly Gln Gln Val Gly Val Thr Phe
    375                 380                 385

gac ggc gag cat tta aca aag gtg ggc tagttttcta gcaaaaccca         1314
Asp Gly Glu His Leu Thr Lys Val Gly
390                 395

acc                                                               1317
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<210> 2446
<211> 398
<212> PRT
<213> Corynebacterium glutamicum

<400> 2446

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Met Glu Ile Pro Leu Pro Thr Ser Leu Ile Asp Val Ile Thr Asp Gly
  1               5                  10                  15

Ala Leu Gly Gln Thr Cys Ile Asp Gln Ala Phe Ala Ala Gln Leu Gly
             20                  25                  30

Arg Val Thr Gly Val Glu Phe Asn Leu Ser Asp Asp Lys Thr Ala Ala
         35                  40                  45

Glu Val Arg Ile Asn Lys Ala Ser Gly Ser Pro Phe Asp Thr Thr Gly
     50                  55                  60

Glu Val Ile Ala Trp Ile Asn Asn Gln Glu Phe Glu Trp Val Ser Thr
 65                  70                  75                  80

Arg Gly Glu Asp Leu Gly Leu Pro Glu Leu Gln Gly Ile Gln Pro Leu
                 85                  90                  95

Asp Asp Asp Leu Ile Thr Ala Ala Arg Thr Leu Tyr Ser Asn Ala Pro
            100                 105                 110

Ala Phe Ile Ala Pro Leu Arg Asp Gly Arg Arg Ala Leu Val Ala Ile
        115                 120                 125

Asn His Thr Pro Lys Leu Val Gly Ile Arg Arg Thr Leu Ile Glu Gly
    130                 135                 140

Leu Gln Ala Leu Lys Pro Gly Thr Asp Leu Lys Arg Ala Leu Thr Ser
145                 150                 155                 160

Phe Ala Ala Phe Cys Glu Leu Gly Ile Arg Phe Asp Asp Asn Arg Ile
                165                 170                 175

Ser Phe Ser Asp Gly Thr Ser Leu Leu Leu Arg Gly Gly Lys Val Ile
            180                 185                 190
```

```
Glu Ile Ala Gly Gly Leu Ser Leu Arg Asp Val Arg Ala Asp Ala Ala
        195                 200                 205

Phe Met Ser Ala Glu His Gln Leu Leu Phe Asp Ala Ile Ser Ser Ser
    210                 215                 220

His Asn Val Thr Phe Asp Pro His Thr Asn Val Ala Thr Val Ala Asn
225                 230                 235                 240

Glu His Gln Val His Ala Ile Pro Leu Ala Val Ile Asp Gly Thr Arg
                245                 250                 255

Trp Val Trp Thr Trp Ser Leu Lys Glu Leu Asn Gly Gln Ala Thr Glu
            260                 265                 270

Gly Leu Ala Arg Phe Gly Phe Asp Asn Gly Leu Leu Leu Leu Thr Asn
        275                 280                 285

Ala Glu Ile Leu Ala Glu Glu Ala Thr Ala Phe Asn Leu Ile Asp Val
    290                 295                 300

Ala Lys Gln Val Leu Asn Thr Trp Thr His Thr Ile Val Gln Gln Pro
305                 310                 315                 320

Asp Gly Thr Gly Ile Val Leu Leu Leu Asp His Pro Arg Leu Gln Leu
                325                 330                 335

Pro Pro Ala Ser His Ala Ala Val Glu Ala Thr Leu Tyr His Gln Leu
            340                 345                 350

Pro Gly Asp Ile Asp Ala Arg Arg Ala Val Ala Ser Tyr Ala Ala His
        355                 360                 365

Arg Gln Leu Pro Phe Asp Gly Tyr Ala Leu Thr Val Glu Gly Gln Gln
    370                 375                 380

Val Gly Val Thr Phe Asp Gly Glu His Leu Thr Lys Val Gly
385                 390                 395
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<210> 2447
<211> 843
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(820)
<223> RXA01800

<400> 2447
ccagcgcagt tcataaaacc gccaaacttt tgatagcgta gcaatggccc tttcggtgga 60

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tggggccatg tttgcacaat gcttgaagaa gggtagggca gtg aag ccg ctg ggc   115
                                               Val Lys Pro Leu Gly
                                                 1               5

aag atc gcc gtt cct tgg act tgg tac ctg gga att gtt ggg gtc atc   163
Lys Ile Ala Val Pro Trp Thr Trp Tyr Leu Gly Ile Val Gly Val Ile
                 10                  15                  20
```

```
ata ttt gat gtg gtg gca gca ata acg atg ctc acc ctc gtg ccc aac   211
Ile Phe Asp Val Val Ala Ala Ile Thr Met Leu Thr Leu Val Pro Asn
             25                  30                  35

aaa atg ccc gaa aga gtc aac agt ggg ctt gtc gcg ctg ggt gga tcg   259
Lys Met Pro Glu Arg Val Asn Ser Gly Leu Val Ala Leu Gly Gly Ser
         40                  45                  50

tat gca ccc ccg atg agc cgg gaa aca ctc att gcc aga gtc att gcc   307
Tyr Ala Pro Pro Met Ser Arg Glu Thr Leu Ile Ala Arg Val Ile Ala
     55                  60                  65

ggt gca gtg ctg gtt ctg gtg att tct tta ggt att tcg ctg ctg att   355
Gly Ala Val Leu Val Leu Val Ile Ser Leu Gly Ile Ser Leu Leu Ile
 70                  75                  80                  85

tcc gcg cag tcc aag aac ctc gcg tcc gat cac ccg gat gca tct gcc   403
Ser Ala Gln Ser Lys Asn Leu Ala Ser Asp His Pro Asp Ala Ser Ala
                 90                  95                 100

att cag att gct cgg cgt tgg gcg ttt ttg aac aat att caa agc tgt   451
Ile Gln Ile Ala Arg Arg Trp Ala Phe Leu Asn Asn Ile Gln Ser Cys
            105                 110                 115

atc ggc tgg ttt agt ttc ttc ctc gca gcg att ttg agc atc tca tcg   499
Ile Gly Trp Phe Ser Phe Phe Leu Ala Ala Ile Leu Ser Ile Ser Ser
        120                 125                 130

cta aga ctc aac ggc cca ggt gcc acc acg cat ctt gag atg gcc gtt   547
Leu Arg Leu Asn Gly Pro Gly Ala Thr Thr His Leu Glu Met Ala Val
    135                 140                 145

tac atc atc gct gtg tcg gtg ttg gct tgg gcg ttg atg att tcc ttg   595
Tyr Ile Ile Ala Val Ser Val Leu Ala Trp Ala Leu Met Ile Ser Leu
150                 155                 160                 165

cga cgc ggc cag gtg gcg att gat cgt gcc att cca att cgg gaa gat   643
Arg Arg Gly Gln Val Ala Ile Asp Arg Ala Ile Pro Ile Arg Glu Asp
                170                 175                 180

gat tcc gaa ctg aaa tgg ggc atg atc tac cac gat gct tca gac aaa   691
Asp Ser Glu Leu Lys Trp Gly Met Ile Tyr His Asp Ala Ser Asp Lys
            185                 190                 195

cga gtt ttc gtg gaa ctc gat gat ggc cac acg acc gtc atc aac atg   739
Arg Val Phe Val Glu Leu Asp Asp Gly His Thr Thr Val Ile Asn Met
        200                 205                 210

gcg cgc ggg gga gcg tgg ctg ctc atc gca gtg atg gtg ctg cct gcg   787
Ala Arg Gly Gly Ala Trp Leu Leu Ile Ala Val Met Val Leu Pro Ala
    215                 220                 225

ctg gcc atc gtc ggt tgg gtt ttg cta gaa aac tagcccacct ttgttaaatg 840
Leu Ala Ile Val Gly Trp Val Leu Leu Glu Asn
230                 235                 240

ctc                                                               843
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<210> 2448

<211> 240
<212> PRT
<213> Corynebacterium glutamicum

<400> 2448

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Val Lys Pro Leu Gly Lys Ile Ala Val Pro Trp Thr Trp Tyr Leu Gly
  1               5                  10                  15

Ile Val Gly Val Ile Ile Phe Asp Val Val Ala Ala Ile Thr Met Leu
             20                  25                  30

Thr Leu Val Pro Asn Lys Met Pro Glu Arg Val Asn Ser Gly Leu Val
         35                  40                  45

Ala Leu Gly Gly Ser Tyr Ala Pro Pro Met Ser Arg Glu Thr Leu Ile
     50                  55                  60

Ala Arg Val Ile Ala Gly Ala Val Leu Val Leu Val Ile Ser Leu Gly
 65                  70                  75                  80

Ile Ser Leu Leu Ile Ser Ala Gln Ser Lys Asn Leu Ala Ser Asp His
                 85                  90                  95

Pro Asp Ala Ser Ala Ile Gln Ile Ala Arg Arg Trp Ala Phe Leu Asn
            100                 105                 110

Asn Ile Gln Ser Cys Ile Gly Trp Phe Ser Phe Phe Leu Ala Ala Ile
        115                 120                 125

Leu Ser Ile Ser Ser Leu Arg Leu Asn Gly Pro Gly Ala Thr Thr His
    130                 135                 140

Leu Glu Met Ala Val Tyr Ile Ile Ala Val Ser Val Leu Ala Trp Ala
145                 150                 155                 160

Leu Met Ile Ser Leu Arg Arg Gly Gln Val Ala Ile Asp Arg Ala Ile
            165                 170                 175

Pro Ile Arg Glu Asp Asp Ser Glu Leu Lys Trp Gly Met Ile Tyr His
            180                 185                 190

Asp Ala Ser Asp Lys Arg Val Phe Val Glu Leu Asp Asp Gly His Thr
        195                 200                 205

Thr Val Ile Asn Met Ala Arg Gly Gly Ala Trp Leu Leu Ile Ala Val
    210                 215                 220

Met Val Leu Pro Ala Leu Ala Ile Val Gly Trp Val Leu Leu Glu Asn
225                 230                 235                 240
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<210> 2449
<211> 444
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(421)
<223> RXA01804

<400> 2449
agtgggaccg catggcagag ttcgcagtca actaaaatat gacctttgct ggttggctaa 60

ttttgggtca aagttttgtg aaacgaagta agcttaagtt atg cat atc gtc aac 115
Met His Ile Val Asn
1 5

att cgc ttc aag ccc aag gct aag tac gtg gat aca ttc cgc tac aca 163
Ile Arg Phe Lys Pro Lys Ala Lys Tyr Val Asp Thr Phe Arg Tyr Thr
10 15 20

gtc gac aaa ttc act gag tca acc agg aca gag gaa ggc tgt ctc tac 211
Val Asp Lys Phe Thr Glu Ser Thr Arg Thr Glu Glu Gly Cys Leu Tyr
25 30 35

ttt gat tgg ttc cgc aac acc gat tac cca ggc gag tac ctt gta att 259
Phe Asp Trp Phe Arg Asn Thr Asp Tyr Pro Gly Glu Tyr Leu Val Ile
40 45 50

ggt gtg tgg acg gat gaa ggt gcg acg gaa cat aag aag agc gag cac 307
Gly Val Trp Thr Asp Glu Gly Ala Thr Glu His Lys Lys Ser Glu His
55 60 65

ttc ttg cga gct caa gaa aca ctt cca ccg ttg ctg caa caa act cca 355
Phe Leu Arg Ala Gln Glu Thr Leu Pro Pro Leu Leu Gln Gln Thr Pro
70 75 80 85

atg att att cag agt gag ttt tcc aag aag aag ggt tgg gaa cgt ttc 403
Met Ile Ile Gln Ser Glu Phe Ser Lys Lys Lys Gly Trp Glu Arg Phe
90 95 100

agc gat ttc acc gtc tac taaggagccc gcaaaagctt tgt 444
Ser Asp Phe Thr Val Tyr
105

<210> 2450
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

<400> 2450
Met His Ile Val Asn Ile Arg Phe Lys Pro Lys Ala Lys Tyr Val Asp
1 5 10 15

Thr Phe Arg Tyr Thr Val Asp Lys Phe Thr Glu Ser Thr Arg Thr Glu
20 25 30

Glu Gly Cys Leu Tyr Phe Asp Trp Phe Arg Asn Thr Asp Tyr Pro Gly
35 40 45

Glu Tyr Leu Val Ile Gly Val Trp Thr Asp Glu Gly Ala Thr Glu His
50 55 60

Lys Lys Ser Glu His Phe Leu Arg Ala Gln Glu Thr Leu Pro Pro Leu
65 70 75 80

Leu Gln Gln Thr Pro Met Ile Ile Gln Ser Glu Phe Ser Lys Lys Lys

```
                85                  90                  95

Gly Trp Glu Arg Phe Ser Asp Phe Thr Val Tyr
            100                 105


<210> 2451
<211> 453
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(430)
<223> RXA01805

<400> 2451
ggcattgtcg agcgaactca tggtttaact cccttcatga aatgtgtgcg gggtcactgg 60

ttcccagcct agtctgaact ggctaaacaa gatcggtaca gtg gtg gtc gtg att   115
                                            Val Val Val Val Ile
                                              1               5

ttg att aat gtg aaa ttc aag cca ttg cca gaa tat gta gac acc ttc   163
Leu Ile Asn Val Lys Phe Lys Pro Leu Pro Glu Tyr Val Asp Thr Phe
                10                  15                  20

cgc gag cag gta gcg gag ttt aca gaa aag acc cgt gcg gaa gaa gga   211
Arg Glu Gln Val Ala Glu Phe Thr Glu Lys Thr Arg Ala Glu Glu Gly
            25                  30                  35

aac atc ttc ttc gat tgg tca att aac acc gac aac cca aac gag ttc   259
Asn Ile Phe Phe Asp Trp Ser Ile Asn Thr Asp Asn Pro Asn Glu Phe
        40                  45                  50

atc ctc atc gaa gca ttc cag gac gac gct gcc gaa gct cac gtc aac   307
Ile Leu Ile Glu Ala Phe Gln Asp Asp Ala Ala Glu Ala His Val Asn
    55                  60                  65

agc gac cac ttc aag gcg gcc tgt gag ctg ttc cca acc atc ctg tct   355
Ser Asp His Phe Lys Ala Ala Cys Glu Leu Phe Pro Thr Ile Leu Ser
70                  75                  80                  85

gag acc cca gag atc atc aac acc ctt atc gag ggc aag act gag tgg   403
Glu Thr Pro Glu Ile Ile Asn Thr Leu Ile Glu Gly Lys Thr Glu Trp
                90                  95                  100

gac cgc atg gca gag ttc gca gtc aac taaaatatga cctttgctgg         450
Asp Arg Met Ala Glu Phe Ala Val Asn
            105                 110

ttg                                                               453


<210> 2452
<211> 110
<212> PRT
<213> Corynebacterium glutamicum

<400> 2452
Val Val Val Val Ile Leu Ile Asn Val Lys Phe Lys Pro Leu Pro Glu
```

```
  1               5                  10                  15

Tyr Val Asp Thr Phe Arg Glu Gln Val Ala Glu Phe Thr Glu Lys Thr
             20                  25                  30

Arg Ala Glu Glu Gly Asn Ile Phe Phe Asp Trp Ser Ile Asn Thr Asp
         35                  40                  45

Asn Pro Asn Glu Phe Ile Leu Ile Glu Ala Phe Gln Asp Asp Ala Ala
     50                  55                  60

Glu Ala His Val Asn Ser Asp His Phe Lys Ala Ala Cys Glu Leu Phe
 65                  70                  75                  80

Pro Thr Ile Leu Ser Glu Thr Pro Glu Ile Ile Asn Thr Leu Ile Glu
                 85                  90                  95

Gly Lys Thr Glu Trp Asp Arg Met Ala Glu Phe Ala Val Asn
            100                 105                 110
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<210> 2453
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> RXA01806

<400> 2453

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aatcaaaatc acgaccacca ctgtaccgat cttgtttagc cagttcagac taggctggga 60

accagtgacc ccgcacacat ttcatgaagg gagttaaacc atg agt tcg ctc gac   115
                                            Met Ser Ser Leu Asp
                                              1               5

aat gcc ccg ctg ctg gaa ttg gat gtt cag gaa tgg gta aac cac gaa   163
Asn Ala Pro Leu Leu Glu Leu Asp Val Gln Glu Trp Val Asn His Glu
                 10                  15                  20

ggc ttg agc aat gag gac ctg cgc ggc aag gtt gtg gtg gtg gag gtg   211
Gly Leu Ser Asn Glu Asp Leu Arg Gly Lys Val Val Val Val Glu Val
             25                  30                  35

ttt cag atg cta tgc cct gga tgc gtg aat cac ggt gtc cct cag gct   259
Phe Gln Met Leu Cys Pro Gly Cys Val Asn His Gly Val Pro Gln Ala
         40                  45                  50

caa aaa atc cac cgc atg att gat gaa tcc caa gtg caa gtc atc ggg   307
Gln Lys Ile His Arg Met Ile Asp Glu Ser Gln Val Gln Val Ile Gly
     55                  60                  65

ctg cac agc gtg ttt gag cac cat gat gtg atg aca cct gag gct ttg   355
Leu His Ser Val Phe Glu His His Asp Val Met Thr Pro Glu Ala Leu
 70                  75                  80                  85

aaa gtg ttc atc gat gag ttt ggg atc aag ttc ccc gtg gca gtg gat   403
Lys Val Phe Ile Asp Glu Phe Gly Ile Lys Phe Pro Val Ala Val Asp
                 90                  95                 100
```

```
atg ccg agg gaa ggc cag cgg att cct tcg acg atg aaa aag tat cgt   451
Met Pro Arg Glu Gly Gln Arg Ile Pro Ser Thr Met Lys Lys Tyr Arg
            105                 110                 115

ttg gaa gga acg ccc agc atc att ttg gct gat cga aaa gga cgg att   499
Leu Glu Gly Thr Pro Ser Ile Ile Leu Ala Asp Arg Lys Gly Arg Ile
        120                 125                 130

cgt cag gtg cag ttc ggg cag gtt gat gat ttc gtg ctg gga ttg ctg   547
Arg Gln Val Gln Phe Gly Gln Val Asp Asp Phe Val Leu Gly Leu Leu
    135                 140                 145

ctc ggc agt ttg ctg tca gag acg gac gaa acc taaagcgctt tggtctgcag 600
Leu Gly Ser Leu Leu Ser Glu Thr Asp Glu Thr
150                 155                 160

gcc                                                               603
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<210> 2454
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 2454

```
Met Ser Ser Leu Asp Asn Ala Pro Leu Leu Glu Leu Asp Val Gln Glu
  1               5                  10                  15

Trp Val Asn His Glu Gly Leu Ser Asn Glu Asp Leu Arg Gly Lys Val
             20                  25                  30

Val Val Val Glu Val Phe Gln Met Leu Cys Pro Gly Cys Val Asn His
         35                  40                  45

Gly Val Pro Gln Ala Gln Lys Ile His Arg Met Ile Asp Glu Ser Gln
     50                  55                  60

Val Gln Val Ile Gly Leu His Ser Val Phe Glu His His Asp Val Met
 65                  70                  75                  80

Thr Pro Glu Ala Leu Lys Val Phe Ile Asp Glu Phe Gly Ile Lys Phe
                85                  90                  95

Pro Val Ala Val Asp Met Pro Arg Glu Gly Gln Arg Ile Pro Ser Thr
            100                 105                 110

Met Lys Lys Tyr Arg Leu Glu Gly Thr Pro Ser Ile Ile Leu Ala Asp
        115                 120                 125

Arg Lys Gly Arg Ile Arg Gln Val Gln Phe Gly Gln Val Asp Asp Phe
    130                 135                 140

Val Leu Gly Leu Leu Leu Gly Ser Leu Leu Ser Glu Thr Asp Glu Thr
145                 150                 155                 160
```

<210> 2455

<211> 855
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(832)
<223> RXA01816

<400> 2455
ttgggtgtaa cggcgtggga aaataggaaa tgccctcctg aacaggaaga atcaagctta 60

gttagagtcc ttcttcccct gccagaaagg cacctcacag gtg caa tta tta cac 115
Val Gln Leu Leu His
1 5

acc ccc gca gcc ata tcc att tcc ttc gac gac ccc aac ctc atc tct 163
Thr Pro Ala Ala Ile Ser Ile Ser Phe Asp Asp Pro Asn Leu Ile Ser
10 15 20

acc gca ggg ctg gtc ccg acc atg gcc ctg gcc gag gac cgg tta aca 211
Thr Ala Gly Leu Val Pro Thr Met Ala Leu Ala Glu Asp Arg Leu Thr
25 30 35

gta cca acc gac aaa ggt gct aac cca ggt gcc aaa atc acg acc ctc 259
Val Pro Thr Asp Lys Gly Ala Asn Pro Gly Ala Lys Ile Thr Thr Leu
40 45 50

att gcg ggg atg gtc gcc ggt gcc gac tcc atc gac gat atc gat gca 307
Ile Ala Gly Met Val Ala Gly Ala Asp Ser Ile Asp Asp Ile Asp Ala
55 60 65

ctc cgc cac ggc ggt atg cac cga ctc ttt gac tgg atc tac gcc ccc 355
Leu Arg His Gly Gly Met His Arg Leu Phe Asp Trp Ile Tyr Ala Pro
70 75 80 85

tcc acg ttg ggg tcg ttc ctc cgg gcc ttt acc ttc ggg cat gtc cgc 403
Ser Thr Leu Gly Ser Phe Leu Arg Ala Phe Thr Phe Gly His Val Arg
90 95 100

caa ctc gac gct gtg gcc tcc cgg ttc ctg gtg ggt ctg gca aca cag 451
Gln Leu Asp Ala Val Ala Ser Arg Phe Leu Val Gly Leu Ala Thr Gln
105 110 115

gcc ccg gcc ctg gtc ccg gtt gat gct tct acc agt gat tac gtc ttc 499
Ala Pro Ala Leu Val Pro Val Asp Ala Ser Thr Ser Asp Tyr Val Phe
120 125 130

atc gat gtt gat gac acc atc att aag gtc cac gga cat cag aaa caa 547
Ile Asp Val Asp Asp Thr Ile Ile Lys Val His Gly His Gln Lys Gln
135 140 145

ggc gct ggt ttt ggt tac tcc ggt atc cgt gga ctc aac gcc ctg ctg 595
Gly Ala Gly Phe Gly Tyr Ser Gly Ile Arg Gly Leu Asn Ala Leu Leu
150 155 160 165

gcc aca gtg acc aca cca gag tca gca cca gtg gtc gtg gcc caa cga 643
Ala Thr Val Thr Thr Pro Glu Ser Ala Pro Val Val Val Ala Gln Arg
170 175 180

tta cgg aaa gga tcg tgc ggt tcc ccg cgg ggt gca ggc cgg ttg att 691

```
Leu Arg Lys Gly Ser Cys Gly Ser Pro Arg Gly Ala Gly Arg Leu Ile
            185                 190                 195

gct gat gcg gtg gct acc acc cgg cgt ttg ccg ggg atg gag gat gag   739
Ala Asp Ala Val Ala Thr Thr Arg Arg Leu Pro Gly Met Glu Asp Glu
        200                 205                 210

aag atc ctt tta cgc gcg gat tct gcc ttt tat ggc cat ccc agt atc   787
Lys Ile Leu Leu Arg Ala Asp Ser Ala Phe Tyr Gly His Pro Ser Ile
    215                 220                 225

agt gct gcg atc aag gca ggg gcg gat gtg tct tca cgg tgc gga       832
Ser Ala Ala Ile Lys Ala Gly Ala Asp Val Ser Ser Arg Cys Gly
230                 235                 240

tgacccccaa tgtcaagaaa gcg                                        855


<210> 2456
<211> 244
<212> PRT
<213> Corynebacterium glutamicum

<400> 2456
Val Gln Leu Leu His Thr Pro Ala Ala Ile Ser Ile Ser Phe Asp Asp
  1               5                  10                  15

Pro Asn Leu Ile Ser Thr Ala Gly Leu Val Pro Thr Met Ala Leu Ala
             20                  25                  30

Glu Asp Arg Leu Thr Val Pro Thr Asp Lys Gly Ala Asn Pro Gly Ala
         35                  40                  45

Lys Ile Thr Thr Leu Ile Ala Gly Met Val Ala Gly Ala Asp Ser Ile
     50                  55                  60

Asp Asp Ile Asp Ala Leu Arg His Gly Gly Met His Arg Leu Phe Asp
 65                  70                  75                  80

Trp Ile Tyr Ala Pro Ser Thr Leu Gly Ser Phe Leu Arg Ala Phe Thr
                 85                  90                  95

Phe Gly His Val Arg Gln Leu Asp Ala Val Ala Ser Arg Phe Leu Val
            100                 105                 110

Gly Leu Ala Thr Gln Ala Pro Ala Leu Val Pro Val Asp Ala Ser Thr
        115                 120                 125

Ser Asp Tyr Val Phe Ile Asp Val Asp Asp Thr Ile Ile Lys Val His
    130                 135                 140

Gly His Gln Lys Gln Gly Ala Gly Phe Gly Tyr Ser Gly Ile Arg Gly
145                 150                 155                 160

Leu Asn Ala Leu Leu Ala Thr Val Thr Thr Pro Glu Ser Ala Pro Val
                165                 170                 175

Val Val Ala Gln Arg Leu Arg Lys Gly Ser Cys Gly Ser Pro Arg Gly
            180                 185                 190

Ala Gly Arg Leu Ile Ala Asp Ala Val Ala Thr Thr Arg Arg Leu Pro
```

```
        195                 200                 205

Gly Met Glu Asp Glu Lys Ile Leu Leu Arg Ala Asp Ser Ala Phe Tyr
    210                 215                 220

Gly His Pro Ser Ile Ser Ala Ala Ile Lys Ala Gly Ala Asp Val Ser
225                 230                 235                 240

Ser Arg Cys Gly
```

<210> 2457
<211> 756
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)
<223> RXA01817

<400> 2457

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aggatgagaa gatcctttta cgcgcggatt ctgcctttta tggccatccc agtatcagtg 60

ctgcgatcaa ggcaggggcg gatgtgtctt cacggtgcgg atg acc ccc aat gtc   115
                                              Met Thr Pro Asn Val
                                                1               5

aag aaa gcg atc gcc cag gtt cct gat gat gcg tgg cag aca att aag   163
Lys Lys Ala Ile Ala Gln Val Pro Asp Asp Ala Trp Gln Thr Ile Lys
                10                  15                  20

tac acc aac gcg atc ttc gac gag gac acc ggg cgc tgg atc tcg gtg   211
Tyr Thr Asn Ala Ile Phe Asp Glu Asp Thr Gly Arg Trp Ile Ser Val
            25                  30                  35

gcc gag gtc gcc gag ata ccg ttc acc gca ttt acc tcc cgg aag aaa   259
Ala Glu Val Ala Glu Ile Pro Phe Thr Ala Phe Thr Ser Arg Lys Lys
        40                  45                  50

acc gac cac atc ccc gga ctg ctg gtg gta cgc cgg ata ccg gag ctg   307
Thr Asp His Ile Pro Gly Leu Leu Val Val Arg Arg Ile Pro Glu Leu
    55                  60                  65

aat aac aag gat gtg gat cag ccg ggg ttg ttt gat cta cac cgc ttc   355
Asn Asn Lys Asp Val Asp Gln Pro Gly Leu Phe Asp Leu His Arg Phe
70                  75                  80                  85

cat gcg gtg ttc acc acc gcc gac cca ggc atc ctc gat act gtt gct   403
His Ala Val Phe Thr Thr Ala Asp Pro Gly Ile Leu Asp Thr Val Ala
                90                  95                  100

gcg gat aaa acc cac cgt caa cac gca atc atc gaa caa gtc aac gcg   451
Ala Asp Lys Thr His Arg Gln His Ala Ile Ile Glu Gln Val Asn Ala
            105                 110                 115

gac gta aag gcc agt gcg ttg gcg cat atg cca tca ggt gta ttc acc   499
Asp Val Lys Ala Ser Ala Leu Ala His Met Pro Ser Gly Val Phe Thr
        120                 125                 130
```

```
gcc aac agc gcc tgg ttg gtg tgt gcg gtc atg gcg ttc aac ctc acc   547
Ala Asn Ser Ala Trp Leu Val Cys Ala Val Met Ala Phe Asn Leu Thr
    135                 140                 145

cgc aca gcc ggt gtg atc gct gca ggc gcg atg gcc agg gcc acc acc   595
Arg Thr Ala Gly Val Ile Ala Ala Gly Ala Met Ala Arg Ala Thr Thr
150                 155                 160                 165

gca acg atc cgg cgg aaa ctt gtg gcc gtt ccg gcc agg att gca cgc   643
Ala Thr Ile Arg Arg Lys Leu Val Ala Val Pro Ala Arg Ile Ala Arg
                170                 175                 180

agc gcc cgg aga ttg att ctt cac ttg cca cgg aac tgg cgg tgg gaa   691
Ser Ala Arg Arg Leu Ile Leu His Leu Pro Arg Asn Trp Arg Trp Glu
            185                 190                 195

acc cag tgg tca aga ttg tgt gat cac ggc cgt tta cca ccg           733
Thr Gln Trp Ser Arg Leu Cys Asp His Gly Arg Leu Pro Pro
        200                 205                 210

taaccggtag ctccctgact acc                                        756
```

<210> 2458
<211> 211
<212> PRT
<213> Corynebacterium glutamicum

<400> 2458

```
Met Thr Pro Asn Val Lys Lys Ala Ile Ala Gln Val Pro Asp Asp Ala
  1               5                  10                  15

Trp Gln Thr Ile Lys Tyr Thr Asn Ala Ile Phe Asp Glu Asp Thr Gly
             20                  25                  30

Arg Trp Ile Ser Val Ala Glu Val Ala Glu Ile Pro Phe Thr Ala Phe
         35                  40                  45

Thr Ser Arg Lys Lys Thr Asp His Ile Pro Gly Leu Leu Val Val Arg
     50                  55                  60

Arg Ile Pro Glu Leu Asn Asn Lys Asp Val Asp Gln Pro Gly Leu Phe
 65                  70                  75                  80

Asp Leu His Arg Phe His Ala Val Phe Thr Thr Ala Asp Pro Gly Ile
                 85                  90                  95

Leu Asp Thr Val Ala Ala Asp Lys Thr His Arg Gln His Ala Ile Ile
            100                 105                 110

Glu Gln Val Asn Ala Asp Val Lys Ala Ser Ala Leu Ala His Met Pro
        115                 120                 125

Ser Gly Val Phe Thr Ala Asn Ser Ala Trp Leu Val Cys Ala Val Met
    130                 135                 140

Ala Phe Asn Leu Thr Arg Thr Ala Gly Val Ile Ala Ala Gly Ala Met
145                 150                 155                 160

Ala Arg Ala Thr Thr Ala Thr Ile Arg Arg Lys Leu Val Ala Val Pro
                165                 170                 175
```

```
Ala Arg Ile Ala Arg Ser Ala Arg Arg Leu Ile Leu His Leu Pro Arg
            180                 185                 190

Asn Trp Arg Trp Glu Thr Gln Trp Ser Arg Leu Cys Asp His Gly Arg
        195                 200                 205

Leu Pro Pro
    210


<210> 2459
<211> 1497
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1474)
<223> RXA01820

<400> 2459
aaatgccctc ctgaactgga agaatcaagc ttgcttagag tcctgattca cctgccagaa 60

aggcacctca caggtgcaat tattacacaa ccccacagcg atg tcc gca tcc ttt   115
                                              Met Ser Ala Ser Phe
                                                1               5

gat gac ccc aac ctc atc tcg ctt gct gga ctg gtt cca acc atg cac   163
Asp Asp Pro Asn Leu Ile Ser Leu Ala Gly Leu Val Pro Thr Met His
                10                  15                  20

tta gcc gat gct gcc agc ctg tcc acc ttg gcc cag gac cgg ttg agc   211
Leu Ala Asp Ala Ala Ser Leu Ser Thr Leu Ala Gln Asp Arg Leu Ser
            25                  30                  35

atc acc ggt gat aaa ggt gcc aat gct ggt gcg aag atc gcc tcc cta   259
Ile Thr Gly Asp Lys Gly Ala Asn Ala Gly Ala Lys Ile Ala Ser Leu
        40                  45                  50

gtc gcg ggc atg gtc gcc ggt gct gat tcc atc gat gac atg gat gta   307
Val Ala Gly Met Val Ala Gly Ala Asp Ser Ile Asp Asp Met Asp Val
    55                  60                  65

ctc cgc cac gga ggt atg cgc cga ctt ttc gac cgg atc tac gcc cca   355
Leu Arg His Gly Gly Met Arg Arg Leu Phe Asp Arg Ile Tyr Ala Pro
70                  75                  80                  85

tcc aca ttg ggg tct ttt ctg cgg gcc ttc act ttc ggc cac gta cgc   403
Ser Thr Leu Gly Ser Phe Leu Arg Ala Phe Thr Phe Gly His Val Arg
                90                  95                  100

caa ctc gat gct gtg gcc tcc cga ttc ctg gtc aac ctg gcc agg cag   451
Gln Leu Asp Ala Val Ala Ser Arg Phe Leu Val Asn Leu Ala Arg Gln
            105                 110                 115

gca cca cac ctg gtg cca cca cca ccg gca ggc agt ggc ggt aac ggg   499
Ala Pro His Leu Val Pro Pro Pro Pro Ala Gly Ser Gly Gly Asn Gly
        120                 125                 130

tat gtg ttc gtt gat gtt gat gac acc atc att gaa gtc cac ggc cac   547
```

```
Tyr Val Phe Val Asp Val Asp Asp Thr Ile Ile Glu Val His Gly His
    135                 140                 145

acc aaa caa ggt gcc ggc ttt ggt tac tcc ggt atc cgt gga ctc aac   595
Thr Lys Gln Gly Ala Gly Phe Gly Tyr Ser Gly Ile Arg Gly Leu Asn
150                 155                 160                 165

gcc ttg ctg gcc acg gtc acc acc gca cag tcc gcc ccc atc att gtg   643
Ala Leu Leu Ala Thr Val Thr Thr Ala Gln Ser Ala Pro Ile Ile Val
                170                 175                 180

ggc caa cga ttg cgg aaa gga tcg tgt ggt tcc cca cga ggg gcc cac   691
Gly Gln Arg Leu Arg Lys Gly Ser Cys Gly Ser Pro Arg Gly Ala His
            185                 190                 195

cgc ctg atc gcc gat gcg atg acc acc acc agg cgc ctg ccc ggg atg   739
Arg Leu Ile Ala Asp Ala Met Thr Thr Thr Arg Arg Leu Pro Gly Met
        200                 205                 210

gag gat aag aaa atc ctc gtc cgg gca gat tcg gcg tat tat ggt cat   787
Glu Asp Lys Lys Ile Leu Val Arg Ala Asp Ser Ala Tyr Tyr Gly His
    215                 220                 225

ccc agt gtc agt gtg gcc cta agg tcc ggt gcg gat gtg tcc gtc acg   835
Pro Ser Val Ser Val Ala Leu Arg Ser Gly Ala Asp Val Ser Val Thr
230                 235                 240                 245

gtg cgg atg acc ccg aac gtc aag aaa gcg atc gtc gcg atc ccg gaa   883
Val Arg Met Thr Pro Asn Val Lys Lys Ala Ile Val Ala Ile Pro Glu
                250                 255                 260

gat gcg tgg cag acg att cag tac acc gat gcg atc ttc gat gag gca   931
Asp Ala Trp Gln Thr Ile Gln Tyr Thr Asp Ala Ile Phe Asp Glu Ala
            265                 270                 275

tca caa tcg tgg atc tcc tta gcc cag gtc gcc gaa gtg cct ttc acc   979
Ser Gln Ser Trp Ile Ser Leu Ala Gln Val Ala Glu Val Pro Phe Thr
        280                 285                 290

gcg ttt acc tcc cgg aag aag gcc gac cat gtt ccc gga cgc ttg gtg   1027
Ala Phe Thr Ser Arg Lys Lys Ala Asp His Val Pro Gly Arg Leu Val
    295                 300                 305

gta cgc cgg att cct gag ctg aat aag aag gat gtg tat cag ccg ggc   1075
Val Arg Arg Ile Pro Glu Leu Asn Lys Lys Asp Val Tyr Gln Pro Gly
310                 315                 320                 325

ttg ttt gat ctt cac cgc ttc cat gcg gtc ttc acc acc gcc gac cca   1123
Leu Phe Asp Leu His Arg Phe His Ala Val Phe Thr Thr Ala Asp Pro
                330                 335                 340

ggc gtg ctg gat act gtt gct gcg gat aaa acc cac cgt cag cac gcg   1171
Gly Val Leu Asp Thr Val Ala Ala Asp Lys Thr His Arg Gln His Ala
            345                 350                 355

atc att gaa cag gtc aac gca gac ttg aag gca agc gcg ttg gcg cat   1219
Ile Ile Glu Gln Val Asn Ala Asp Leu Lys Ala Ser Ala Leu Ala His
        360                 365                 370

ctg ccg tcg ggg acg ttc acc gcc aac agt gcc tgg ctc gta tgc gcg   1267
Leu Pro Ser Gly Thr Phe Thr Ala Asn Ser Ala Trp Leu Val Cys Ala
```

```
    375                 380                 385

gtc atg gcg ttt aat ctc acc cgt gcc acc ggg gtt atc gct gca ggc   1315
Val Met Ala Phe Asn Leu Thr Arg Ala Thr Gly Val Ile Ala Ala Gly
390                 395                 400                 405

ggg atg gcc aag gcc acc acc gcg acg atc cgg cgg aca ctg atg gcc   1363
Gly Met Ala Lys Ala Thr Thr Ala Thr Ile Arg Arg Thr Leu Met Ala
                410                 415                 420

gtt cca gcc cgg gtc gcc cgc agg tcc cgc cga ctg gtg ctc cac ctt   1411
Val Pro Ala Arg Val Ala Arg Arg Ser Arg Arg Leu Val Leu His Leu
            425                 430                 435

ccc gag ggg tgg acg tgg caa cca cag tgg cag aaa ctg ttt gat cac   1459
Pro Glu Gly Trp Thr Trp Gln Pro Gln Trp Gln Lys Leu Phe Asp His
        440                 445                 450

ggc cat tca cca ccg taaccggtag ctccctgacc acc                     1497
Gly His Ser Pro Pro
    455
```

20050170204

<210> 2460
<211> 458
<212> PRT
<213> Corynebacterium glutamicum

<400> 2460

```
Met Ser Ala Ser Phe Asp Asp Pro Asn Leu Ile Ser Leu Ala Gly Leu
  1               5                  10                  15

Val Pro Thr Met His Leu Ala Asp Ala Ala Ser Leu Ser Thr Leu Ala
             20                  25                  30

Gln Asp Arg Leu Ser Ile Thr Gly Asp Lys Gly Ala Asn Ala Gly Ala
         35                  40                  45

Lys Ile Ala Ser Leu Val Ala Gly Met Val Ala Gly Ala Asp Ser Ile
     50                  55                  60

Asp Asp Met Asp Val Leu Arg His Gly Gly Met Arg Arg Leu Phe Asp
 65                  70                  75                  80

Arg Ile Tyr Ala Pro Ser Thr Leu Gly Ser Phe Leu Arg Ala Phe Thr
                 85                  90                  95

Phe Gly His Val Arg Gln Leu Asp Ala Val Ala Ser Arg Phe Leu Val
            100                 105                 110

Asn Leu Ala Arg Gln Ala Pro His Leu Val Pro Pro Pro Pro Ala Gly
        115                 120                 125

Ser Gly Gly Asn Gly Tyr Val Phe Val Asp Val Asp Asp Thr Ile Ile
    130                 135                 140

Glu Val His Gly His Thr Lys Gln Gly Ala Gly Phe Gly Tyr Ser Gly
145                 150                 155                 160

Ile Arg Gly Leu Asn Ala Leu Leu Ala Thr Val Thr Thr Ala Gln Ser
                165                 170                 175
```

```
Ala Pro Ile Ile Val Gly Gln Arg Leu Arg Lys Gly Ser Cys Gly Ser
            180                 185                 190

Pro Arg Gly Ala His Arg Leu Ile Ala Asp Ala Met Thr Thr Thr Arg
        195                 200                 205

Arg Leu Pro Gly Met Glu Asp Lys Lys Ile Leu Val Arg Ala Asp Ser
    210                 215                 220

Ala Tyr Tyr Gly His Pro Ser Val Ser Val Ala Leu Arg Ser Gly Ala
225                 230                 235                 240

Asp Val Ser Val Thr Val Arg Met Thr Pro Asn Val Lys Lys Ala Ile
                245                 250                 255

Val Ala Ile Pro Glu Asp Ala Trp Gln Thr Ile Gln Tyr Thr Asp Ala
            260                 265                 270

Ile Phe Asp Glu Ala Ser Gln Ser Trp Ile Ser Leu Ala Gln Val Ala
        275                 280                 285

Glu Val Pro Phe Thr Ala Phe Thr Ser Arg Lys Lys Ala Asp His Val
    290                 295                 300

Pro Gly Arg Leu Val Val Arg Arg Ile Pro Glu Leu Asn Lys Lys Asp
305                 310                 315                 320

Val Tyr Gln Pro Gly Leu Phe Asp Leu His Arg Phe His Ala Val Phe
                325                 330                 335

Thr Thr Ala Asp Pro Gly Val Leu Asp Thr Val Ala Ala Asp Lys Thr
            340                 345                 350

His Arg Gln His Ala Ile Ile Glu Gln Val Asn Ala Asp Leu Lys Ala
        355                 360                 365

Ser Ala Leu Ala His Leu Pro Ser Gly Thr Phe Thr Ala Asn Ser Ala
    370                 375                 380

Trp Leu Val Cys Ala Val Met Ala Phe Asn Leu Thr Arg Ala Thr Gly
385                 390                 395                 400

Val Ile Ala Ala Gly Gly Met Ala Lys Ala Thr Thr Ala Thr Ile Arg
                405                 410                 415

Arg Thr Leu Met Ala Val Pro Ala Arg Val Ala Arg Arg Ser Arg Arg
            420                 425                 430

Leu Val Leu His Leu Pro Glu Gly Trp Thr Trp Gln Pro Gln Trp Gln
        435                 440                 445

Lys Leu Phe Asp His Gly His Ser Pro Pro
    450                 455
```

<210> 2461
<211> 1041
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1018)
<223> RXA01842

<400> 2461
cacgtcatgg tctcgcggtg atcatcttcc taccgtgaca ggcaaggccg caaacggccg 60

tgaccacagg aaagaaattc acgaggagag gaagcacacg atg tcg aag gta tac 115
Met Ser Lys Val Tyr
1 5

gtg tcc aac gag tac ggc ggc ccg gaa aac cag gaa ctg atc acc cgc 163
Val Ser Asn Glu Tyr Gly Gly Pro Glu Asn Gln Glu Leu Ile Thr Arg
10 15 20

aac acc ccc cag cca ggc ccg gga gaa ctc ggg gtc aag gtc cac gcg 211
Asn Thr Pro Gln Pro Gly Pro Gly Glu Leu Gly Val Lys Val His Ala
25 30 35

gcc ggg gtc aac ccg ctt gat tgg aag gtc cgt tcc ggg gtt gcc gga 259
Ala Gly Val Asn Pro Leu Asp Trp Lys Val Arg Ser Gly Val Ala Gly
40 45 50

acc ccg cga gag ctt ccg gca ccc ctg ggc gag gag gcc tcc ggg atc 307
Thr Pro Arg Glu Leu Pro Ala Pro Leu Gly Glu Glu Ala Ser Gly Ile
55 60 65

gtc acc gcc gtt gga gac ggt gtg gag ggc ttc gcg gtc ggc gat ccg 355
Val Thr Ala Val Gly Asp Gly Val Glu Gly Phe Ala Val Gly Asp Pro
70 75 80 85

gtg ctc ggc ctg gtg gcc ccc ggc gtc ggc gga tat gcc gag gac acc 403
Val Leu Gly Leu Val Ala Pro Gly Val Gly Gly Tyr Ala Glu Asp Thr
90 95 100

ctg ctg gtg gca gag agt acc gtg cta aag ccg gag gag atc tcg ttc 451
Leu Leu Val Ala Glu Ser Thr Val Leu Lys Pro Glu Glu Ile Ser Phe
105 110 115

acc gac gcc gcc gcg atc ccg gtc gct ggg gcg agc gcc tac gcc ggc 499
Thr Asp Ala Ala Ala Ile Pro Val Ala Gly Ala Ser Ala Tyr Ala Gly
120 125 130

act cac cag gtc gag ctt gaa cca ggc cag tcg ttg ctg atc aat ggg 547
Thr His Gln Val Glu Leu Glu Pro Gly Gln Ser Leu Leu Ile Asn Gly
135 140 145

gcc ggt ggt ggg gtc ggg ctg atg gcc gcg cag atc gga cgg gtc cac 595
Ala Gly Gly Gly Val Gly Leu Met Ala Ala Gln Ile Gly Arg Val His
150 155 160 165

aag ttc cag gtc gtc ggc gtt gac cac gag gac aag cgc gag ctc atc 643
Lys Phe Gln Val Val Gly Val Asp His Glu Asp Lys Arg Glu Leu Ile
170 175 180

gaa tcc acc ggt gct atc ttc gtc gcc acc ggc gac gcc gtc gcg gag 691
Glu Ser Thr Gly Ala Ile Phe Val Ala Thr Gly Asp Ala Val Ala Glu
185 190 195

cag gtg cgt gcg ctg ctc cct gac ggt gtg gac gta gtc ttc gac cta 739

```
Gln Val Arg Ala Leu Leu Pro Asp Gly Val Asp Val Val Phe Asp Leu
        200                 205                 210

gtc ggc ggg gag gcg ttg cgg gtg gtt gct ccc tta gcg aag aat ccg   787
Val Gly Gly Glu Ala Leu Arg Val Val Ala Pro Leu Ala Lys Asn Pro
    215                 220                 225

gcg cac gtg atc tcg gcg gct gat gct gcc acc gtg gga gaa ctc ggt   835
Ala His Val Ile Ser Ala Ala Asp Ala Ala Thr Val Gly Glu Leu Gly
230                 235                 240                 245

gga cag gtg ctg cgc cgc acc ccg gaa atg gtc gga cag atc acc ggg   883
Gly Gln Val Leu Arg Arg Thr Pro Glu Met Val Gly Gln Ile Thr Gly
                250                 255                 260

gtg gtc cag tac ggg ctg gtc gac ccg aag gtc gat acg acc tac ccg   931
Val Val Gln Tyr Gly Leu Val Asp Pro Lys Val Asp Thr Thr Tyr Pro
            265                 270                 275

ctg gaa cag gcc ggt aag gcc ctg gcc cac gtt gag cag ggc cac gcc   979
Leu Glu Gln Ala Gly Lys Ala Leu Ala His Val Glu Gln Gly His Ala
        280                 285                 290

cgc ggc aag atc gtc ctc gag ctc atc acc tcc cag gac taaccagaca   1028
Arg Gly Lys Ile Val Leu Glu Leu Ile Thr Ser Gln Asp
    295                 300                 305

acgcggtgac ctc                                                  1041
```

<210> 2462
<211> 306
<212> PRT
<213> Corynebacterium glutamicum

<400> 2462

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Met Ser Lys Val Tyr Val Ser Asn Glu Tyr Gly Gly Pro Glu Asn Gln
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Glu Leu Ile Thr Arg Asn Thr Pro Gln Pro Gly Pro Gly Glu Leu Gly
             20                  25                  30

Val Lys Val His Ala Ala Gly Val Asn Pro Leu Asp Trp Lys Val Arg
         35                  40                  45

Ser Gly Val Ala Gly Thr Pro Arg Glu Leu Pro Ala Pro Leu Gly Glu
     50                  55                  60

Glu Ala Ser Gly Ile Val Thr Ala Val Gly Asp Gly Val Glu Gly Phe
 65                  70                  75                  80

Ala Val Gly Asp Pro Val Leu Gly Leu Val Ala Pro Gly Val Gly Gly
                 85                  90                  95

Tyr Ala Glu Asp Thr Leu Leu Val Ala Glu Ser Thr Val Leu Lys Pro
            100                 105                 110

Glu Glu Ile Ser Phe Thr Asp Ala Ala Ala Ile Pro Val Ala Gly Ala
        115                 120                 125

Ser Ala Tyr Ala Gly Thr His Gln Val Glu Leu Glu Pro Gly Gln Ser
```

```
    130                 135                 140

Leu Leu Ile Asn Gly Ala Gly Gly Gly Val Gly Leu Met Ala Ala Gln
145                 150                 155                 160

Ile Gly Arg Val His Lys Phe Gln Val Val Gly Val Asp His Glu Asp
                165                 170                 175

Lys Arg Glu Leu Ile Glu Ser Thr Gly Ala Ile Phe Val Ala Thr Gly
            180                 185                 190

Asp Ala Val Ala Glu Gln Val Arg Ala Leu Leu Pro Asp Gly Val Asp
        195                 200                 205

Val Val Phe Asp Leu Val Gly Gly Glu Ala Leu Arg Val Val Ala Pro
    210                 215                 220

Leu Ala Lys Asn Pro Ala His Val Ile Ser Ala Ala Asp Ala Ala Thr
225                 230                 235                 240

Val Gly Glu Leu Gly Gly Gln Val Leu Arg Arg Thr Pro Glu Met Val
                245                 250                 255

Gly Gln Ile Thr Gly Val Val Gln Tyr Gly Leu Val Asp Pro Lys Val
            260                 265                 270

Asp Thr Thr Tyr Pro Leu Glu Gln Ala Gly Lys Ala Leu Ala His Val
        275                 280                 285

Glu Gln Gly His Ala Arg Gly Lys Ile Val Leu Glu Leu Ile Thr Ser
    290                 295                 300

Gln Asp
305
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CURRENT SEQUENCE LISTING

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<210> 2463
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<213> Corynebacterium glutamicum

<220>
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<222> (101)..(280)
<223> RXA01844

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gacctcggcc agggcctcga cgggcaggta gagcgcgcag gtg gtc tca atc gcc   115
                                            Val Val Ser Ile Ala
                                              1               5

cag gag ttg gag atc att gag gac ggc acg ggt gcg gtg ctc gtc tcg   163
Gln Glu Leu Glu Ile Ile Glu Asp Gly Thr Gly Ala Val Leu Val Ser
                 10                  15                  20

gag cag gca acc acc ttc gac aac ggg ttc atc ggc tac tcc tac ttc   211
Glu Gln Ala Thr Thr Phe Asp Asn Gly Phe Ile Gly Tyr Ser Tyr Phe
             25                  30                  35
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acc acc ggt acg gac gga gcc acc tgc atc acc gac ctt cgc ctc agg   259
Thr Thr Gly Thr Asp Gly Ala Thr Cys Ile Thr Asp Leu Arg Leu Arg
         40                  45                  50

gcc tcc cca ctg ccg cag gtt taaccggtac tagccggttt ttc            303
Ala Ser Pro Leu Pro Gln Val
     55                  60


<210> 2464
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<212> PRT
<213> Corynebacterium glutamicum

<400> 2464
Val Val Ser Ile Ala Gln Glu Leu Glu Ile Ile Glu Asp Gly Thr Gly
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Ala Val Leu Val Ser Glu Gln Ala Thr Thr Phe Asp Asn Gly Phe Ile
             20                  25                  30

Gly Tyr Ser Tyr Phe Thr Thr Gly Thr Asp Gly Ala Thr Cys Ile Thr
         35                  40                  45

Asp Leu Arg Leu Arg Ala Ser Pro Leu Pro Gln Val
     50                  55                  60


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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> RXA01845

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ggctccgtcc gtaccggtgg tgaagtagga gtagccgatg aacccgttgt cgaaggtggt 60

tgcctgctcc gagacgagca ccgcacccgt gccgtcctca atg atc tcc aac tcc   115
                                        Met Ile Ser Asn Ser
                                          1               5

tgg gcg att gag acc acc tgc gcg ctc tac ctg ccc gtc gag gcc ctg   163
Trp Ala Ile Glu Thr Thr Cys Ala Leu Tyr Leu Pro Val Glu Ala Leu
                 10                  15                  20

gcc gag gtc gtg gac gcc tac ccg caa ctg gcg ttg gcg atc atg cgg   211
Ala Glu Val Val Asp Ala Tyr Pro Gln Leu Ala Leu Ala Ile Met Arg
             25                  30                  35

atg cag cag gac caa ttg gtc cgg tcc cgg gaa cgc gag acc gca cag   259
Met Gln Gln Asp Gln Leu Val Arg Ser Arg Glu Arg Glu Thr Ala Gln
         40                  45                  50

acc acc tcg act gtc gag cag cgc gtg gcc gcc gcc ctc caa cac ctg   307
Thr Thr Ser Thr Val Glu Gln Arg Val Ala Ala Ala Leu Gln His Leu
     55                  60                  65
```

```
gac gcc aag ctc ggg caa atc cga caa gac gga tcc agc ctg ctg cag   355
Asp Ala Lys Leu Gly Gln Ile Arg Gln Asp Gly Ser Ser Leu Leu Gln
 70                  75                  80                  85

gtc cgc ctg cgc cgc gac gac gtg gcc ggc acc acc gtc gag tcc gcc   403
Val Arg Leu Arg Arg Asp Asp Val Ala Gly Thr Thr Val Glu Ser Ala
                 90                  95                 100

tcc cgg gca atg gcg cgg atg aag aaa acc ggt gtc atc gac tcc ggc   451
Ser Arg Ala Met Ala Arg Met Lys Lys Thr Gly Val Ile Asp Ser Gly
            105                 110                 115

cgc gaa tgg atc gcc att acc aac cac cag gcc ctg gcc gac ctg gtc   499
Arg Glu Trp Ile Ala Ile Thr Asn His Gln Ala Leu Ala Asp Leu Val
        120                 125                 130

gcc ggc ctc taaacgccca catccctctc tct                            531
Ala Gly Leu
    135
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<210> 2466
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 2466

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Met Ile Ser Asn Ser Trp Ala Ile Glu Thr Thr Cys Ala Leu Tyr Leu
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Pro Val Glu Ala Leu Ala Glu Val Val Asp Ala Tyr Pro Gln Leu Ala
             20                  25                  30

Leu Ala Ile Met Arg Met Gln Gln Asp Gln Leu Val Arg Ser Arg Glu
         35                  40                  45

Arg Glu Thr Ala Gln Thr Thr Ser Thr Val Glu Gln Arg Val Ala Ala
     50                  55                  60

Ala Leu Gln His Leu Asp Ala Lys Leu Gly Gln Ile Arg Gln Asp Gly
 65                  70                  75                  80

Ser Ser Leu Leu Gln Val Arg Leu Arg Arg Asp Asp Val Ala Gly Thr
                 85                  90                  95

Thr Val Glu Ser Ala Ser Arg Ala Met Ala Arg Met Lys Lys Thr Gly
            100                 105                 110

Val Ile Asp Ser Gly Arg Glu Trp Ile Ala Ile Thr Asn His Gln Ala
        115                 120                 125

Leu Ala Asp Leu Val Ala Gly Leu
    130                 135
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<210> 2467
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<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(646)
<223> RXA01856

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gttgtagctg cttctgcgtg gctagtaaaa taattggcta atg aat cct ttt ctt 115
Met Asn Pro Phe Leu
1 5

tcg gac acg ttg att gtc cag cag acc tct tcc ttc ctg tct aac aac 163
Ser Asp Thr Leu Ile Val Gln Gln Thr Ser Ser Phe Leu Ser Asn Asn
10 15 20

ttt gag atc tac aat cca gac ggc gaa gtt gtt atc aga atc aaa act 211
Phe Glu Ile Tyr Asn Pro Asp Gly Glu Val Val Ile Arg Ile Lys Thr
25 30 35

gaa ggg tcg ttg ggc tct cgg ctg gtc aag ggc gac cgc aga ttc aca 259
Glu Gly Ser Leu Gly Ser Arg Leu Val Lys Gly Asp Arg Arg Phe Thr
40 45 50

ctg gaa gac gcc ttc ggc acc cca ttg atg cag gtg cgc gat ccc atg 307
Leu Glu Asp Ala Phe Gly Thr Pro Leu Met Gln Val Arg Asp Pro Met
55 60 65

aac ttt gtt cgc gac acc tat gaa att gat gat cca aat ggc aat ccc 355
Asn Phe Val Arg Asp Thr Tyr Glu Ile Asp Asp Pro Asn Gly Asn Pro
70 75 80 85

att gct cat gtg cgg aag cgt ttc acc ttc ttc aac aag cgg atg gac 403
Ile Ala His Val Arg Lys Arg Phe Thr Phe Phe Asn Lys Arg Met Asp
90 95 100

atc gaa cta cca ggt gac cgc gtt att gaa atg cac ggt aac ttc ctt 451
Ile Glu Leu Pro Gly Asp Arg Val Ile Glu Met His Gly Asn Phe Leu
105 110 115

gga ttt gaa ttt gag ttc cgc atg ggc gat cgg att cct gcg aaa gta 499
Gly Phe Glu Phe Glu Phe Arg Met Gly Asp Arg Ile Pro Ala Lys Val
120 125 130

acc cga aaa tgg tcc ggc gct ggc aac gga tac cta ggc cga agc acc 547
Thr Arg Lys Trp Ser Gly Ala Gly Asn Gly Tyr Leu Gly Arg Ser Thr
135 140 145

tac gcc ctt att ttc gat gaa gaa gcc cct gat gaa atc aga aaa gtc 595
Tyr Ala Leu Ile Phe Asp Glu Glu Ala Pro Asp Glu Ile Arg Lys Val
150 155 160 165

atc att gga ggc atg gtc gcg cta gat ctg atc cgg gag aag gaa cgt 643
Ile Ile Gly Gly Met Val Ala Leu Asp Leu Ile Arg Glu Lys Glu Arg
170 175 180

aat taagccaccc ccgtttcatg tct 669
Asn

<210> 2468

<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 2468
Met Asn Pro Phe Leu Ser Asp Thr Leu Ile Val Gln Gln Thr Ser Ser
1 5 10 15

Phe Leu Ser Asn Asn Phe Glu Ile Tyr Asn Pro Asp Gly Glu Val Val
20 25 30

Ile Arg Ile Lys Thr Glu Gly Ser Leu Gly Ser Arg Leu Val Lys Gly
35 40 45

Asp Arg Arg Phe Thr Leu Glu Asp Ala Phe Gly Thr Pro Leu Met Gln
50 55 60

Val Arg Asp Pro Met Asn Phe Val Arg Asp Thr Tyr Glu Ile Asp Asp
65 70 75 80

Pro Asn Gly Asn Pro Ile Ala His Val Arg Lys Arg Phe Thr Phe Phe
85 90 95

Asn Lys Arg Met Asp Ile Glu Leu Pro Gly Asp Arg Val Ile Glu Met
100 105 110

His Gly Asn Phe Leu Gly Phe Glu Phe Glu Phe Arg Met Gly Asp Arg
115 120 125

Ile Pro Ala Lys Val Thr Arg Lys Trp Ser Gly Ala Gly Asn Gly Tyr
130 135 140

Leu Gly Arg Ser Thr Tyr Ala Leu Ile Phe Asp Glu Glu Ala Pro Asp
145 150 155 160

Glu Ile Arg Lys Val Ile Ile Gly Gly Met Val Ala Leu Asp Leu Ile
165 170 175

Arg Glu Lys Glu Arg Asn
180

<210> 2469
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(751)
<223> RXA01857

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tcgtactaat ctaacttaat ctctccctag gagttctccc atg gct tca cgc cgt 115
Met Ala Ser Arg Arg
1 5

ttc cgt atg atg ctc acc gca agc atc acc gca gct tcc ctt ggt ttt 163
Phe Arg Met Met Leu Thr Ala Ser Ile Thr Ala Ala Ser Leu Gly Phe

```
                  10                  15                  20

tcc ctc acc cca gca atc gcc gat gaa gct gta acc gtt gct acg gca   211
Ser Leu Thr Pro Ala Ile Ala Asp Glu Ala Val Thr Val Ala Thr Ala
            25                  30                  35

ccc tcc gtc gga ttc gat tcc ggc gtc gaa cgc gat gca cca ttc acc   259
Pro Ser Val Gly Phe Asp Ser Gly Val Glu Arg Asp Ala Pro Phe Thr
        40                  45                  50

gca gtt cca cac gac gta gtt ctc ggc gtt gga gcg acc cag tcc gag   307
Ala Val Pro His Asp Val Val Leu Gly Val Gly Ala Thr Gln Ser Glu
    55                  60                  65

ctc att ttc aac tgg atc acc gcg cag ggc cta acc ggc cag gtt gca   355
Leu Ile Phe Asn Trp Ile Thr Ala Gln Gly Leu Thr Gly Gln Val Ala
70                  75                  80                  85

cag atc tcc ctg gac gat acc ttc gca tcc cca atc acc gtt gat gca   403
Gln Ile Ser Leu Asp Asp Thr Phe Ala Ser Pro Ile Thr Val Asp Ala
                90                  95                  100

gtt tct gaa aac gtc agc atc gtg aac acc gaa ggc gat tcc cgc gac   451
Val Ser Glu Asn Val Ser Ile Val Asn Thr Glu Gly Asp Ser Arg Asp
            105                 110                 115

cga gct gaa ggt gaa tac gtt gaa tac cgc gat ggc gca gtc aac cgc   499
Arg Ala Glu Gly Glu Tyr Val Glu Tyr Arg Asp Gly Ala Val Asn Arg
        120                 125                 130

gca acc gta gat agc ctc gca gaa aac acc acc tac tcc tac cgc gtc   547
Ala Thr Val Asp Ser Leu Ala Glu Asn Thr Thr Tyr Ser Tyr Arg Val
    135                 140                 145

ggc tcc gaa gct gac ggc tgg tcc gaa gtg caa acc ttc aac acc ggc   595
Gly Ser Glu Ala Asp Gly Trp Ser Glu Val Gln Thr Phe Asn Thr Gly
150                 155                 160                 165

acc tac ggt gac aac tgg aac ttc ctc ttc ttc ggc gac acc cag ctg   643
Thr Tyr Gly Asp Asn Trp Asn Phe Leu Phe Phe Gly Asp Thr Gln Leu
                170                 175                 180

tac aac acc cac tcc aac cgt gca gaa gaa gtc cag aac tgg gca aac   691
Tyr Asn Thr His Ser Asn Arg Ala Glu Glu Val Gln Asn Trp Ala Asn
            185                 190                 195

aac ctg gaa cgg cgg ccc acc aat cga aaa ccc agg aac ctc ctt cat   739
Asn Leu Glu Arg Arg Pro Thr Asn Arg Lys Pro Arg Asn Leu Leu His
        200                 205                 210

cct ctc cgc ggg tgatcaggca aaccactcca gct                        774
Pro Leu Arg Gly
    215
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<210> 2470
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 2470

```
Met Ala Ser Arg Arg Phe Arg Met Met Leu Thr Ala Ser Ile Thr Ala
  1               5                  10                  15

Ala Ser Leu Gly Phe Ser Leu Thr Pro Ala Ile Ala Asp Glu Ala Val
             20                  25                  30

Thr Val Ala Thr Ala Pro Ser Val Gly Phe Asp Ser Gly Val Glu Arg
         35                  40                  45

Asp Ala Pro Phe Thr Ala Val Pro His Asp Val Val Leu Gly Val Gly
     50                  55                  60

Ala Thr Gln Ser Glu Leu Ile Phe Asn Trp Ile Thr Ala Gln Gly Leu
 65                  70                  75                  80

Thr Gly Gln Val Ala Gln Ile Ser Leu Asp Asp Thr Phe Ala Ser Pro
                 85                  90                  95

Ile Thr Val Asp Ala Val Ser Glu Asn Val Ser Ile Val Asn Thr Glu
            100                 105                 110

Gly Asp Ser Arg Asp Arg Ala Glu Gly Glu Tyr Val Glu Tyr Arg Asp
        115                 120                 125

Gly Ala Val Asn Arg Ala Thr Val Asp Ser Leu Ala Glu Asn Thr Thr
    130                 135                 140

Tyr Ser Tyr Arg Val Gly Ser Glu Ala Asp Gly Trp Ser Glu Val Gln
145                 150                 155                 160

Thr Phe Asn Thr Gly Thr Tyr Gly Asp Asn Trp Asn Phe Leu Phe Phe
                165                 170                 175

Gly Asp Thr Gln Leu Tyr Asn Thr His Ser Asn Arg Ala Glu Glu Val
            180                 185                 190

Gln Asn Trp Ala Asn Asn Leu Glu Arg Arg Pro Thr Asn Arg Lys Pro
        195                 200                 205

Arg Asn Leu Leu His Pro Leu Arg Gly
    210                 215
```

<210> 2471
<211> 673
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(673)
<223> RXA01858

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gcggaatcac gcgggacatt gatccccgga cgtaaagccg atg ttt atg aca ccg 115
                                                Met Phe Met Thr Pro
                                                  1   5

cgg gcg ttg acc gaa gat aat gag ttg acc ctg gct ttg aaa tca ctc 163

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Arg Ala Leu Thr Glu Asp Asn Glu Leu Thr Leu Ala Leu Lys Ser Leu
                 10                  15                  20

gga ggg ctt atg gtg tca ccc aat gag tgc tca gta gtg aca gaa gtg   211
Gly Gly Leu Met Val Ser Pro Asn Glu Cys Ser Val Val Thr Glu Val
            25                  30                  35

atg ccg act tgg aga gaa tta tgg cat caa agg ctt cga tgg caa cgc   259
Met Pro Thr Trp Arg Glu Leu Trp His Gln Arg Leu Arg Trp Gln Arg
        40                  45                  50

ggt gcg ctg gaa aac ctc ggt gct tat ggc atc aca cca caa acg aca   307
Gly Ala Leu Glu Asn Leu Gly Ala Tyr Gly Ile Thr Pro Gln Thr Thr
    55                  60                  65

cgg tat tgg ttc cag cag ctg gga atc ggt tac ggc gca tta gcc ttg   355
Arg Tyr Trp Phe Gln Gln Leu Gly Ile Gly Tyr Gly Ala Leu Ala Leu
70                  75                  80                  85

gtc gcc tat ttc gca gtc att atc att acg ttt ctc gcc cgc gat caa   403
Val Ala Tyr Phe Ala Val Ile Ile Ile Thr Phe Leu Ala Arg Asp Gln
                90                  95                 100

tgg atc tgg tat cca ttc tgg atg ctg ctg gga ctg ttg ttc atg att   451
Trp Ile Trp Tyr Pro Phe Trp Met Leu Leu Gly Leu Leu Phe Met Ile
            105                 110                 115

gaa cgc gtg cta acg gtg tgg aga tcc aca tgg ttt gcc agg ttt gtt   499
Glu Arg Val Leu Thr Val Trp Arg Ser Thr Trp Phe Ala Arg Phe Val
        120                 125                 130

gct gcg tta tta atc cca gag ctc atc tac gcc agc tat ctc aac ctg   547
Ala Ala Leu Leu Ile Pro Glu Leu Ile Tyr Ala Ser Tyr Leu Asn Leu
    135                 140                 145

gta ttt ctc aaa ggc gtt gtg gat att cta ttg gcc aag caa gct cac   595
Val Phe Leu Lys Gly Val Val Asp Ile Leu Leu Ala Lys Gln Ala His
150                 155                 160                 165

tgg ggt gag cat ggt gac aag aca atg cag gta gcc gat gca gct gcc   643
Trp Gly Glu His Gly Asp Lys Thr Met Gln Val Ala Asp Ala Ala Ala
                170                 175                 180

gaa att aac gat gaa ggg gag gaa cgc cga                          673
Glu Ile Asn Asp Glu Gly Glu Glu Arg Arg
            185                 190
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<210> 2472
<211> 191
<212> PRT
<213> Corynebacterium glutamicum

<400> 2472

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Met Phe Met Thr Pro Arg Ala Leu Thr Glu Asp Asn Glu Leu Thr Leu
  1               5                  10                  15

Ala Leu Lys Ser Leu Gly Gly Leu Met Val Ser Pro Asn Glu Cys Ser
            20                  25                  30

Val Val Thr Glu Val Met Pro Thr Trp Arg Glu Leu Trp His Gln Arg
```

```
         35                  40                  45

Leu Arg Trp Gln Arg Gly Ala Leu Glu Asn Leu Gly Ala Tyr Gly Ile
     50                  55                  60

Thr Pro Gln Thr Thr Arg Tyr Trp Phe Gln Gln Leu Gly Ile Gly Tyr
 65                  70                  75                  80

Gly Ala Leu Ala Leu Val Ala Tyr Phe Ala Val Ile Ile Ile Thr Phe
                 85                  90                  95

Leu Ala Arg Asp Gln Trp Ile Trp Tyr Pro Phe Trp Met Leu Leu Gly
            100                 105                 110

Leu Leu Phe Met Ile Glu Arg Val Leu Thr Val Trp Arg Ser Thr Trp
        115                 120                 125

Phe Ala Arg Phe Val Ala Ala Leu Leu Ile Pro Glu Leu Ile Tyr Ala
    130                 135                 140

Ser Tyr Leu Asn Leu Val Phe Leu Lys Gly Val Val Asp Ile Leu Leu
145                 150                 155                 160

Ala Lys Gln Ala His Trp Gly Glu His Gly Asp Lys Thr Met Gln Val
                165                 170                 175

Ala Asp Ala Ala Ala Glu Ile Asn Asp Glu Gly Glu Glu Arg Arg
            180                 185                 190


<210> 2473
<211> 798
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> RXA01870

<400> 2473
ggatcatgtc caccccagaa ggtagcctgt cagtgtgagc gtaatcgagg gcaagtacca 60

gctgaaacct caaggccgag gtggcctgtg gtggtcaatc gtg ggt gtg gca gtt   115
                                            Val Gly Val Ala Val
                                              1               5

gtt ttg ttg ctg ctt cca acg ttg atc aac ctg gtg gtt ccg gat aaa   163
Val Leu Leu Leu Leu Pro Thr Leu Ile Asn Leu Val Val Pro Asp Lys
                 10                  15                  20

gcc aat gac tac aag cag cta gaa atc gat ctt ctg ggt gtg gat tgg   211
Ala Asn Asp Tyr Lys Gln Leu Glu Ile Asp Leu Leu Gly Val Asp Trp
             25                  30                  35

tca gtg cca atc acc acg gag gaa tcc gct gcg gtg ctg tgt gag gaa   259
Ser Val Pro Ile Thr Thr Glu Glu Ser Ala Ala Val Leu Cys Glu Glu
         40                  45                  50

aca tct gat gaa atc aca cag aag tat tgg gac tgc aac ggg gac acc   307
Thr Ser Asp Glu Ile Thr Gln Lys Tyr Trp Asp Cys Asn Gly Asp Thr
```

```
     55                  60                  65

acg gtg gtg acc atg atc gtc gag ggc gtg aaa gat ccg tcc aat acg   355
Thr Val Val Thr Met Ile Val Glu Gly Val Lys Asp Pro Ser Asn Thr
 70                  75                  80                  85

ttg cgt cgc atg gtg ggt tca tcg ctg ata acc agt gtg gat gac agc   403
Leu Arg Arg Met Val Gly Ser Ser Leu Ile Thr Ser Val Asp Asp Ser
                 90                  95                 100

cta gag gca gta tct agc gaa gat ggc cgt gcg cat gcg ttg tat gtg   451
Leu Glu Ala Val Ser Ser Glu Asp Gly Arg Ala His Ala Leu Tyr Val
            105                 110                 115

cca ggt cag caa gaa gga tct ttg tgg acg ctg cct atc gtg gca ctg   499
Pro Gly Gln Gln Glu Gly Ser Leu Trp Thr Leu Pro Ile Val Ala Leu
        120                 125                 130

agc gtg cag ggt tcg ggt gat tat gaa gac ctc aca gcg atc gca att   547
Ser Val Gln Gly Ser Gly Asp Tyr Glu Asp Leu Thr Ala Ile Ala Ile
    135                 140                 145

atc aac ggc acc tcg ttg gat tat tac agc acc cac att tgg tcc agc   595
Ile Asn Gly Thr Ser Leu Asp Tyr Tyr Ser Thr His Ile Trp Ser Ser
150                 155                 160                 165

atg gcc gct gac cgc ggg ttg ccg tac cag cag gac ttc ccc ctg atg   643
Met Ala Ala Asp Arg Gly Leu Pro Tyr Gln Gln Asp Phe Pro Leu Met
                170                 175                 180

ctg gaa gag gag cca tgg caa gac acc ccc ggc ggg gat cgt ccc ttc   691
Leu Glu Glu Glu Pro Trp Gln Asp Thr Pro Gly Gly Asp Arg Pro Phe
            185                 190                 195

gag ctg ccc aat gat ttc ttt gat cag tac ccc gat ctt ttt ggc cca   739
Glu Leu Pro Asn Asp Phe Phe Asp Gln Tyr Pro Asp Leu Phe Gly Pro
        200                 205                 210

ggc tcc gtc att ccc aac ctt gaa gga gaa tcc cta tgagtcgcat        785
Gly Ser Val Ile Pro Asn Leu Glu Gly Glu Ser Leu
    215                 220                 225

gtttagcatc acc                                                   798
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<210> 2474
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 2474

```
Val Gly Val Ala Val Val Leu Leu Leu Leu Pro Thr Leu Ile Asn Leu
  1               5                  10                  15

Val Val Pro Asp Lys Ala Asn Asp Tyr Lys Gln Leu Glu Ile Asp Leu
             20                  25                  30

Leu Gly Val Asp Trp Ser Val Pro Ile Thr Thr Glu Glu Ser Ala Ala
         35                  40                  45

Val Leu Cys Glu Glu Thr Ser Asp Glu Ile Thr Gln Lys Tyr Trp Asp
```

```
     50                  55                  60

Cys Asn Gly Asp Thr Thr Val Val Thr Met Ile Val Glu Gly Val Lys
 65                  70                  75                  80

Asp Pro Ser Asn Thr Leu Arg Arg Met Val Gly Ser Ser Leu Ile Thr
                 85                  90                  95

Ser Val Asp Asp Ser Leu Glu Ala Val Ser Ser Glu Asp Gly Arg Ala
            100                 105                 110

His Ala Leu Tyr Val Pro Gly Gln Gln Glu Gly Ser Leu Trp Thr Leu
        115                 120                 125

Pro Ile Val Ala Leu Ser Val Gln Gly Ser Gly Asp Tyr Glu Asp Leu
    130                 135                 140

Thr Ala Ile Ala Ile Ile Asn Gly Thr Ser Leu Asp Tyr Tyr Ser Thr
145                 150                 155                 160

His Ile Trp Ser Ser Met Ala Ala Asp Arg Gly Leu Pro Tyr Gln Gln
                165                 170                 175

Asp Phe Pro Leu Met Leu Glu Glu Glu Pro Trp Gln Asp Thr Pro Gly
            180                 185                 190

Gly Asp Arg Pro Phe Glu Leu Pro Asn Asp Phe Phe Asp Gln Tyr Pro
        195                 200                 205

Asp Leu Phe Gly Pro Gly Ser Val Ile Pro Asn Leu Glu Gly Glu Ser
    210                 215                 220

Leu
225
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<210> 2475
<211> 1086
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1063)
<223> RXA01871

<400> 2475

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gcggggatcg tcccttcgag ctgcccaatg atttctttga tcagtacccc gatcttttttg 60

gcccaggctc cgtcattccc aaccttgaag gagaatccct atg agt cgc atg ttt   115
                                              Met Ser Arg Met Phe
                                                1               5

agc atc acc ttg tgg gtt gcc atc ctc ctc tca acc ccg gcg ctg ttt   163
Ser Ile Thr Leu Trp Val Ala Ile Leu Leu Ser Thr Pro Ala Leu Phe
                10                  15                  20

ttg agc ttg gcc acg ttc atc ttc gtg gat ggc atc tct gtc ctc gtg   211
Leu Ser Leu Ala Thr Phe Ile Phe Val Asp Gly Ile Ser Val Leu Val
            25                  30                  35
```

```
aat ata gtg ttc gcg gtg ctc tac ttg gta gtc att gtt ttc ctg tta   259
Asn Ile Val Phe Ala Val Leu Tyr Leu Val Val Ile Val Phe Leu Leu
         40                  45                  50

agt cgc acc ccg ctg tgg cca cgt ttt aaa ggc tcc ggc agc aag aag   307
Ser Arg Thr Pro Leu Trp Pro Arg Phe Lys Gly Ser Gly Ser Lys Lys
     55                  60                  65

gga ggc gga ttc gcg tgg gcg gcg tca tca ttg ttg tgg ggc gcg ttc   355
Gly Gly Gly Phe Ala Trp Ala Ala Ser Ser Leu Leu Trp Gly Ala Phe
 70                  75                  80                  85

gtt ggt ttc ggc atc gtc atg ttg ttt gcc ggt ccg gtc atg gat ctc   403
Val Gly Phe Gly Ile Val Met Leu Phe Ala Gly Pro Val Met Asp Leu
                 90                  95                 100

acg gac aaa ctc ggc tgg gat ttc gtt gcc atg agt ttc acc gga gcg   451
Thr Asp Lys Leu Gly Trp Asp Phe Val Ala Met Ser Phe Thr Gly Ala
            105                 110                 115

tat cca gaa gaa atc gcc aaa gcg tta ggc gtt gcc atc atc ttg ttg   499
Tyr Pro Glu Glu Ile Ala Lys Ala Leu Gly Val Ala Ile Ile Leu Leu
        120                 125                 130

agc ttc cgc caa ctc aac cgt ccg tgg cat gga ttt atc acc ggc gcg   547
Ser Phe Arg Gln Leu Asn Arg Pro Trp His Gly Phe Ile Thr Gly Ala
    135                 140                 145

cta gtg ggc tta ggt ttt gag gtc aac gaa aac ctc ctc tat ggc gcc   595
Leu Val Gly Leu Gly Phe Glu Val Asn Glu Asn Leu Leu Tyr Gly Ala
150                 155                 160                 165

acc ggt gca atc atg gac ccc aac gct gac ctc gac ggc gtc ctt atg   643
Thr Gly Ala Ile Met Asp Pro Asn Ala Asp Leu Asp Gly Val Leu Met
                170                 175                 180

atg tgg caa tac cgc acc atg ttg ggc cca ctc atc cat acg ttg ctc   691
Met Trp Gln Tyr Arg Thr Met Leu Gly Pro Leu Ile His Thr Leu Leu
            185                 190                 195

acc gga ttc gca ggt tac ggc atc gcg ttg gca ttc ttc cgc gca cga   739
Thr Gly Phe Ala Gly Tyr Gly Ile Ala Leu Ala Phe Phe Arg Ala Arg
        200                 205                 210

aaa aca gtc gcc tgg cgc tgg ggc gtg gcg atc ggt tgg act ctc atc   787
Lys Thr Val Ala Trp Arg Trp Gly Val Ala Ile Gly Trp Thr Leu Ile
    215                 220                 225

gcc ttc gca ctg cat ttt tca tgg aac ctg atg tgg gaa aac gta atc   835
Ala Phe Ala Leu His Phe Ser Trp Asn Leu Met Trp Glu Asn Val Ile
230                 235                 240                 245

ggt tcc tat gtc acc atc atc gtg gtc agc gtt gtc atg tac ggt ctg   883
Gly Ser Tyr Val Thr Ile Ile Val Val Ser Val Val Met Tyr Gly Leu
                250                 255                 260

gct atc tac atc ctc tgg agt aat tgg gcc gaa gcc cgc aac gac tcc   931
Ala Ile Tyr Ile Leu Trp Ser Asn Trp Ala Glu Ala Arg Asn Asp Ser
            265                 270                 275

agc tac gct ttc gtc ccg gga atc atc aca aac acc aaa gat tta tcg   979
```

```
Ser Tyr Ala Phe Val Pro Gly Ile Ile Thr Asn Thr Lys Asp Leu Ser
        280                 285                 290

ctt ctt gac gcc ccc att cca gta ggc gct gag gtt ccc gag tcg cgc   1027
Leu Leu Asp Ala Pro Ile Pro Val Gly Ala Glu Val Pro Glu Ser Arg
    295                 300                 305

att ccc caa cag ata gag gaa ccc aag gcg gag aac tagctttcac       1073
Ile Pro Gln Gln Ile Glu Glu Pro Lys Ala Glu Asn
310                 315                 320

tcgctctcca tcc                                                   1086
```

<210> 2476
<211> 321
<212> PRT
<213> Corynebacterium glutamicum

<400> 2476

```
Met Ser Arg Met Phe Ser Ile Thr Leu Trp Val Ala Ile Leu Leu Ser
  1               5                  10                  15

Thr Pro Ala Leu Phe Leu Ser Leu Ala Thr Phe Ile Phe Val Asp Gly
             20                  25                  30

Ile Ser Val Leu Val Asn Ile Val Phe Ala Val Leu Tyr Leu Val Val
         35                  40                  45

Ile Val Phe Leu Leu Ser Arg Thr Pro Leu Trp Pro Arg Phe Lys Gly
     50                  55                  60

Ser Gly Ser Lys Lys Gly Gly Gly Phe Ala Trp Ala Ala Ser Ser Leu
 65                  70                  75                  80

Leu Trp Gly Ala Phe Val Gly Phe Gly Ile Val Met Leu Phe Ala Gly
                 85                  90                  95

Pro Val Met Asp Leu Thr Asp Lys Leu Gly Trp Asp Phe Val Ala Met
            100                 105                 110

Ser Phe Thr Gly Ala Tyr Pro Glu Glu Ile Ala Lys Ala Leu Gly Val
        115                 120                 125

Ala Ile Ile Leu Leu Ser Phe Arg Gln Leu Asn Arg Pro Trp His Gly
    130                 135                 140

Phe Ile Thr Gly Ala Leu Val Gly Leu Gly Phe Glu Val Asn Glu Asn
145                 150                 155                 160

Leu Leu Tyr Gly Ala Thr Gly Ala Ile Met Asp Pro Asn Ala Asp Leu
                165                 170                 175

Asp Gly Val Leu Met Met Trp Gln Tyr Arg Thr Met Leu Gly Pro Leu
            180                 185                 190

Ile His Thr Leu Leu Thr Gly Phe Ala Gly Tyr Gly Ile Ala Leu Ala
        195                 200                 205

Phe Phe Arg Ala Arg Lys Thr Val Ala Trp Arg Trp Gly Val Ala Ile
    210                 215                 220
```

```
Gly Trp Thr Leu Ile Ala Phe Ala Leu His Phe Ser Trp Asn Leu Met
225                 230                 235                 240

Trp Glu Asn Val Ile Gly Ser Tyr Val Thr Ile Ile Val Val Ser Val
                245                 250                 255

Val Met Tyr Gly Leu Ala Ile Tyr Ile Leu Trp Ser Asn Trp Ala Glu
            260                 265                 270

Ala Arg Asn Asp Ser Ser Tyr Ala Phe Val Pro Gly Ile Ile Thr Asn
        275                 280                 285

Thr Lys Asp Leu Ser Leu Leu Asp Ala Pro Ile Pro Val Gly Ala Glu
    290                 295                 300

Val Pro Glu Ser Arg Ile Pro Gln Gln Ile Glu Glu Pro Lys Ala Glu
305                 310                 315                 320

Asn
```

<210> 2477
<211> 302
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(279)
<223> RXA01903

<400> 2477

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gct cac ctt gat gac cgt ggc atc tat atc atc cca gct caa tat cct   48
Ala His Leu Asp Asp Arg Gly Ile Tyr Ile Ile Pro Ala Gln Tyr Pro
  1               5                  10                  15

tgg gga tac gag gaa atc att aac cta ccg gca cgc gct acc tct aca   96
Trp Gly Tyr Glu Glu Ile Ile Asn Leu Pro Ala Arg Ala Thr Ser Thr
             20                  25                  30

cct gct gtt gct cct cgc act gag gct gct cca gct aca gta tct gat   144
Pro Ala Val Ala Pro Arg Thr Glu Ala Ala Pro Ala Thr Val Ser Asp
         35                  40                  45

gct gag gtc cag agc ctg ctt gag tac ttg cgt act aat gct ttc gta   192
Ala Glu Val Gln Ser Leu Leu Glu Tyr Leu Arg Thr Asn Ala Phe Val
     50                  55                  60

agt cgt cac gac ggc gac acc acg aag gcc gac atc ttc aac aag cac   240
Ser Arg His Asp Gly Asp Thr Thr Lys Ala Asp Ile Phe Asn Lys His
 65                  70                  75                  80

gcg gat act gtc aac aag ctt gca gca cta cgt gca ccc taaacccaca    289
Ala Asp Thr Val Asn Lys Leu Ala Ala Leu Arg Ala Pro
                 85                  90

ccgcataacc ccc                                                   302
```

<210> 2478
<211> 93
<212> PRT
<213> Corynebacterium glutamicum

<400> 2478
Ala His Leu Asp Asp Arg Gly Ile Tyr Ile Ile Pro Ala Gln Tyr Pro
1 5 10 15

Trp Gly Tyr Glu Glu Ile Ile Asn Leu Pro Ala Arg Ala Thr Ser Thr
20 25 30

Pro Ala Val Ala Pro Arg Thr Glu Ala Ala Pro Ala Thr Val Ser Asp
35 40 45

Ala Glu Val Gln Ser Leu Leu Glu Tyr Leu Arg Thr Asn Ala Phe Val
50 55 60

Ser Arg His Asp Gly Asp Thr Thr Lys Ala Asp Ile Phe Asn Lys His
65 70 75 80

Ala Asp Thr Val Asn Lys Leu Ala Ala Leu Arg Ala Pro
85 90

<210> 2479
<211> 546
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(523)
<223> RXA01904

<400> 2479
attagttttt attcgcaagg gtggtctaaa ttttttacta ctgcgtcgtg tccaccggat 60

acacttgagg taatacagtt acgaggctaa ggagtatgta atg agc att tcg ccg 115
Met Ser Ile Ser Pro
1 5

aag aat tcc ggt aca cca aac gag aac gcc gca gca gcg cag gtg gca 163
Lys Asn Ser Gly Thr Pro Asn Glu Asn Ala Ala Ala Ala Gln Val Ala
10 15 20

gca aat ctg gct aat tta acg tcg cag gct aca ggg tcc atg gac gaa 211
Ala Asn Leu Ala Asn Leu Thr Ser Gln Ala Thr Gly Ser Met Asp Glu
25 30 35

act aat gag caa gtc att aaa agt aac gag cat ggc tct gat gct tat 259
Thr Asn Glu Gln Val Ile Lys Ser Asn Glu His Gly Ser Asp Ala Tyr
40 45 50

ttg gcg gat att aaa gcc agt cga gag atg tgg gca aaa att gcg ctc 307
Leu Ala Asp Ile Lys Ala Ser Arg Glu Met Trp Ala Lys Ile Ala Leu
55 60 65

gat ccg aat caa tct gaa gaa act agg aaa gaa gct cgg gag aat atg 355
Asp Pro Asn Gln Ser Glu Glu Thr Arg Lys Glu Ala Arg Glu Asn Met
70 75 80 85

```
gcg cgg ata gat gag tac gct cgt gag cac gat aaa gac aac aag ggt   403
Ala Arg Ile Asp Glu Tyr Ala Arg Glu His Asp Lys Asp Asn Lys Gly
                 90                  95                 100

ttg ttg cag aag tta gcg aaa aac aaa gca gag ctc atc ggg act gtt   451
Leu Leu Gln Lys Leu Ala Lys Asn Lys Ala Glu Leu Ile Gly Thr Val
            105                 110                 115

gcg gtt gca acc tta ggt gta gtg gca gcc att gct aac aat ggc aag   499
Ala Val Ala Thr Leu Gly Val Val Ala Ala Ile Ala Asn Asn Gly Lys
        120                 125                 130

ata ccg atg att cag ttg aaa aaa taacccccgc acaggctgga cat         546
Ile Pro Met Ile Gln Leu Lys Lys
    135                 140
```

<210> 2480
<211> 141
<212> PRT
<213> Corynebacterium glutamicum

<400> 2480

```
Met Ser Ile Ser Pro Lys Asn Ser Gly Thr Pro Asn Glu Asn Ala Ala
  1               5                  10                  15

Ala Ala Gln Val Ala Ala Asn Leu Ala Asn Leu Thr Ser Gln Ala Thr
             20                  25                  30

Gly Ser Met Asp Glu Thr Asn Glu Gln Val Ile Lys Ser Asn Glu His
         35                  40                  45

Gly Ser Asp Ala Tyr Leu Ala Asp Ile Lys Ala Ser Arg Glu Met Trp
     50                  55                  60

Ala Lys Ile Ala Leu Asp Pro Asn Gln Ser Glu Glu Thr Arg Lys Glu
 65                  70                  75                  80

Ala Arg Glu Asn Met Ala Arg Ile Asp Glu Tyr Ala Arg Glu His Asp
                 85                  90                  95

Lys Asp Asn Lys Gly Leu Leu Gln Lys Leu Ala Lys Asn Lys Ala Glu
            100                 105                 110

Leu Ile Gly Thr Val Ala Val Ala Thr Leu Gly Val Val Ala Ala Ile
        115                 120                 125

Ala Asn Asn Gly Lys Ile Pro Met Ile Gln Leu Lys Lys
    130                 135                 140
```

<210> 2481
<211> 654
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(631)
<223> RXA01905

<400> 2481
aaatgaaagt cacaaacttt gttggggttt ctttaaagta aaatacagaa gtttctctgg 60

caaaaaacct cactactttc tacagaaagg cgtcttcctc atg aag gct tct cag 115
Met Lys Ala Ser Gln
1 5

acc ctc acc cgc aac act cgt gca cgc aag ctc ggc atg ggt att ctc 163
Thr Leu Thr Arg Asn Thr Arg Ala Arg Lys Leu Gly Met Gly Ile Leu
10 15 20

gca gca act att atg gct acc ggt gca ctt gct ggc act gct cca cag 211
Ala Ala Thr Ile Met Ala Thr Gly Ala Leu Ala Gly Thr Ala Pro Gln
25 30 35

gcg aca gca gca gta gat acc act gcg cca tac gtg tcc tat gtc gtt 259
Ala Thr Ala Ala Val Asp Thr Thr Ala Pro Tyr Val Ser Tyr Val Val
40 45 50

gac att cct ggc aag gtt ggt gaa cca atc aag cct cag tac ctc acc 307
Asp Ile Pro Gly Lys Val Gly Glu Pro Ile Lys Pro Gln Tyr Leu Thr
55 60 65

atc tcc gat cag tcc gcc tac acc gtg acc ttc aag tac atg cca tcc 355
Ile Ser Asp Gln Ser Ala Tyr Thr Val Thr Phe Lys Tyr Met Pro Ser
70 75 80 85

tgg ttg aag tac gac gca aac aag aag atg ctg tac ggt acc cca acc 403
Trp Leu Lys Tyr Asp Ala Asn Lys Lys Met Leu Tyr Gly Thr Pro Thr
90 95 100

gag gtt gat gtc tgg act cct gag gta cat gtt gtt gat gct cat ggc 451
Glu Val Asp Val Trp Thr Pro Glu Val His Val Val Asp Ala His Gly
105 110 115

aac aag act gtc cgt tac ttc acc gtt gta gca gtc cca gca aac act 499
Asn Lys Thr Val Arg Tyr Phe Thr Val Val Ala Val Pro Ala Asn Thr
120 125 130

gga cca acc acc acc acg cca tct act tca aag cca tct acc ccg cag 547
Gly Pro Thr Thr Thr Thr Pro Ser Thr Ser Lys Pro Ser Thr Pro Gln
135 140 145

gtg acc acc cca act act ccg aag gcg cct acc ttg cca aag tcc acc 595
Val Thr Thr Pro Thr Thr Pro Lys Ala Pro Thr Leu Pro Lys Ser Thr
150 155 160 165

ttc gac tgg acc ttg tgg ggc tcc atc ttt ggt ttc tagttctcac 641
Phe Asp Trp Thr Leu Trp Gly Ser Ile Phe Gly Phe
170 175

tagcacctca aaa 654

<210> 2482
<211> 177
<212> PRT
<213> Corynebacterium glutamicum

<400> 2482

```
Met Lys Ala Ser Gln Thr Leu Thr Arg Asn Thr Arg Ala Arg Lys Leu
  1               5                  10                  15

Gly Met Gly Ile Leu Ala Ala Thr Ile Met Ala Thr Gly Ala Leu Ala
             20                  25                  30

Gly Thr Ala Pro Gln Ala Thr Ala Ala Val Asp Thr Thr Ala Pro Tyr
         35                  40                  45

Val Ser Tyr Val Val Asp Ile Pro Gly Lys Val Gly Glu Pro Ile Lys
     50                  55                  60

Pro Gln Tyr Leu Thr Ile Ser Asp Gln Ser Ala Tyr Thr Val Thr Phe
 65                  70                  75                  80

Lys Tyr Met Pro Ser Trp Leu Lys Tyr Asp Ala Asn Lys Lys Met Leu
                 85                  90                  95

Tyr Gly Thr Pro Thr Glu Val Asp Val Trp Thr Pro Glu Val His Val
            100                 105                 110

Val Asp Ala His Gly Asn Lys Thr Val Arg Tyr Phe Thr Val Val Ala
        115                 120                 125

Val Pro Ala Asn Thr Gly Pro Thr Thr Thr Thr Pro Ser Thr Ser Lys
    130                 135                 140

Pro Ser Thr Pro Gln Val Thr Thr Pro Thr Thr Pro Lys Ala Pro Thr
145                 150                 155                 160

Leu Pro Lys Ser Thr Phe Asp Trp Thr Leu Trp Gly Ser Ile Phe Gly
                165                 170                 175

Phe
```

<210> 2483
<211> 588
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(565)
<223> RXA01906

<400> 2483

```
gcgttcgggt aaacccgtga caatcgcacg gggcttgttt acctgacact caagccccgt 60

gcaccacaac aacccacctt aaagaaaggt ttttccaccc atg tcc gaa ttc cct   115
                                              Met Ser Glu Phe Pro
                                                1               5

aca cct acg act ttt cac gtc gaa cca gaa acg ctt agc tcc gcc acc   163
Thr Pro Thr Thr Phe His Val Glu Pro Glu Thr Leu Ser Ser Ala Thr
                10                  15                  20

gat ctc act gtt gat gca cat aaa atc gca gaa ctg ctg ctc agc acc   211
Asp Leu Thr Val Asp Ala His Lys Ile Ala Glu Leu Leu Leu Ser Thr
            25                  30                  35
```

```
act gat tac cgt gtg ttc tac atg ccg cgt ctc gcc ggt gtg act cct   259
Thr Asp Tyr Arg Val Phe Tyr Met Pro Arg Leu Ala Gly Val Thr Pro
         40                  45                  50

atc gtg tcc tac ctc tat gtc tac gat ggt gaa aac ttc ctc att gtt   307
Ile Val Ser Tyr Leu Tyr Val Tyr Asp Gly Glu Asn Phe Leu Ile Val
     55                  60                  65

ggt cgc tcc act cat gtg ccg tgg gag tac tac gtt cac tac ccc atc   355
Gly Arg Ser Thr His Val Pro Trp Glu Tyr Tyr Val His Tyr Pro Ile
 70                  75                  80                  85

aag cca tca cgt gaa ttt ggc tct gct att gct gtg cct ctc gat gat   403
Lys Pro Ser Arg Glu Phe Gly Ser Ala Ile Ala Val Pro Leu Asp Asp
                 90                  95                 100

tct gat gac cct tat gat gca gca gaa gtt gtt gct cta gta aag cag   451
Ser Asp Asp Pro Tyr Asp Ala Ala Glu Val Val Ala Leu Val Lys Gln
            105                 110                 115

tac atg acg ccc acg ctc act cct ggt gag ggt tat atg cag ggc ttt   499
Tyr Met Thr Pro Thr Leu Thr Pro Gly Glu Gly Tyr Met Gln Gly Phe
        120                 125                 130

tac aag ggt ctc acc ttc acc aac cac ctc gat ata cat cga cca ctg   547
Tyr Lys Gly Leu Thr Phe Thr Asn His Leu Asp Ile His Arg Pro Leu
    135                 140                 145

acc cag att atc tca gac taacagctat attcacccac cta                 588
Thr Gln Ile Ile Ser Asp
150                 155
```

EP1108790A2

<210> 2484
<211> 155
<212> PRT
<213> Corynebacterium glutamicum

<400> 2484

```
Met Ser Glu Phe Pro Thr Pro Thr Thr Phe His Val Glu Pro Glu Thr
  1               5                  10                  15

Leu Ser Ser Ala Thr Asp Leu Thr Val Asp Ala His Lys Ile Ala Glu
             20                  25                  30

Leu Leu Leu Ser Thr Thr Asp Tyr Arg Val Phe Tyr Met Pro Arg Leu
         35                  40                  45

Ala Gly Val Thr Pro Ile Val Ser Tyr Leu Tyr Val Tyr Asp Gly Glu
     50                  55                  60

Asn Phe Leu Ile Val Gly Arg Ser Thr His Val Pro Trp Glu Tyr Tyr
 65                  70                  75                  80

Val His Tyr Pro Ile Lys Pro Ser Arg Glu Phe Gly Ser Ala Ile Ala
                 85                  90                  95

Val Pro Leu Asp Asp Ser Asp Asp Pro Tyr Asp Ala Ala Glu Val Val
            100                 105                 110
```

```
Ala Leu Val Lys Gln Tyr Met Thr Pro Thr Leu Thr Pro Gly Glu Gly
        115                 120                 125

Tyr Met Gln Gly Phe Tyr Lys Gly Leu Thr Phe Thr Asn His Leu Asp
    130                 135                 140

Ile His Arg Pro Leu Thr Gln Ile Ile Ser Asp
145                 150                 155


<210> 2485
<211> 735
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(712)
<223> RXA01907

<400> 2485
ttcgttttac ccacaccagc acgtcaccct cttgcatcac gccgagaggg tgacgtgctt 60

ttttcctact tttcctcata actacagaag ggacgccctc atg tct gct ttt gat   115
                                              Met Ser Ala Phe Asp
                                                1               5

gaa ctc cgc aag aac tac cgc tac aag ttc act gac acc tgg ccg gcc   163
Glu Leu Arg Lys Asn Tyr Arg Tyr Lys Phe Thr Asp Thr Trp Pro Ala
                10                  15                  20

aac gct gtt acc ggc acc ggc tac tac gcc aac cca gct ttt atc atc   211
Asn Ala Val Thr Gly Thr Gly Tyr Tyr Ala Asn Pro Ala Phe Ile Ile
            25                  30                  35

atc tcc gct gat gcc atg acg cag aac acc cat gcc gat tcc aat ctc   259
Ile Ser Ala Asp Ala Met Thr Gln Asn Thr His Ala Asp Ser Asn Leu
        40                  45                  50

atc acg gtt aaa gag cac ctt aac acc ctg ttt ccg tac agc gta caa   307
Ile Thr Val Lys Glu His Leu Asn Thr Leu Phe Pro Tyr Ser Val Gln
    55                  60                  65

cgc aag gat cgt gcc ttt gtc tct gag atc tac acc cct att aac ctg   355
Arg Lys Asp Arg Ala Phe Val Ser Glu Ile Tyr Thr Pro Ile Asn Leu
70                  75                  80                  85

ctc gaa gat aat cca gaa cta gct caa gaa ata ctc gat gtg ctc gac   403
Leu Glu Asp Asn Pro Glu Leu Ala Gln Glu Ile Leu Asp Val Leu Asp
                90                  95                  100

acc ctg agc aac aac gct gtt ttt aac gat gcg cac tac agc gag ctt   451
Thr Leu Ser Asn Asn Ala Val Phe Asn Asp Ala His Tyr Ser Glu Leu
            105                 110                 115

gaa cta gag cgc ctc aat gaa tat gtc atc gac acc ttg gcc tat gac   499
Glu Leu Glu Arg Leu Asn Glu Tyr Val Ile Asp Thr Leu Ala Tyr Asp
        120                 125                 130

atg aag tcc gac atg atg cgc gcc ctc gtt aag gcc cga cca gag gcc   547
Met Lys Ser Asp Met Met Arg Ala Leu Val Lys Ala Arg Pro Glu Ala
```

```
    135                 140                 145

gat ctt gag gcg atg gaa gaa ctc gac att gcc aat atc cag agc tgg   595
Asp Leu Glu Ala Met Glu Glu Leu Asp Ile Ala Asn Ile Gln Ser Trp
150                 155                 160                 165

att aat ctc cac tcc tcc act gtg agc gaa cac aac gat ggc agc gtt   643
Ile Asn Leu His Ser Ser Thr Val Ser Glu His Asn Asp Gly Ser Val
                170                 175                 180

gat gat gca ccg ttt aat tct ctc gca tta gct gag att tat ttg caa   691
Asp Asp Ala Pro Phe Asn Ser Leu Ala Leu Ala Glu Ile Tyr Leu Gln
            185                 190                 195

cag ctt gca gac cac act gtc taagcacgct gtgtaactac cac            735
Gln Leu Ala Asp His Thr Val
        200
```

<210> 2486
<211> 204
<212> PRT
<213> Corynebacterium glutamicum

<400> 2486

```
Met Ser Ala Phe Asp Glu Leu Arg Lys Asn Tyr Arg Tyr Lys Phe Thr
  1               5                  10                  15

Asp Thr Trp Pro Ala Asn Ala Val Thr Gly Thr Gly Tyr Tyr Ala Asn
             20                  25                  30

Pro Ala Phe Ile Ile Ile Ser Ala Asp Ala Met Thr Gln Asn Thr His
         35                  40                  45

Ala Asp Ser Asn Leu Ile Thr Val Lys Glu His Leu Asn Thr Leu Phe
     50                  55                  60

Pro Tyr Ser Val Gln Arg Lys Asp Arg Ala Phe Val Ser Glu Ile Tyr
 65                  70                  75                  80

Thr Pro Ile Asn Leu Leu Glu Asp Asn Pro Glu Leu Ala Gln Glu Ile
                 85                  90                  95

Leu Asp Val Leu Asp Thr Leu Ser Asn Asn Ala Val Phe Asn Asp Ala
            100                 105                 110

His Tyr Ser Glu Leu Glu Leu Glu Arg Leu Asn Glu Tyr Val Ile Asp
        115                 120                 125

Thr Leu Ala Tyr Asp Met Lys Ser Asp Met Met Arg Ala Leu Val Lys
    130                 135                 140

Ala Arg Pro Glu Ala Asp Leu Glu Ala Met Glu Glu Leu Asp Ile Ala
145                 150                 155                 160

Asn Ile Gln Ser Trp Ile Asn Leu His Ser Ser Thr Val Ser Glu His
                165                 170                 175

Asn Asp Gly Ser Val Asp Asp Ala Pro Phe Asn Ser Leu Ala Leu Ala
            180                 185                 190
```

```
Glu Ile Tyr Leu Gln Gln Leu Ala Asp His Thr Val
        195                 200


<210> 2487
<211> 529
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> RXA01923

<400> 2487
ccaaagtgaa taccccgact gcagcagcgc aaaagttcaa gtactttggg atgcaaatct 60

agtagcacgt cccatgtttc tcacactctc aggagctgac atg tct gca ctt att   115
                                           Met Ser Ala Leu Ile
                                             1               5

aaa ggt tca gga cct cat cat gtg gtt gtc tta aat ggt tgg ttt ggt   163
Lys Gly Ser Gly Pro His His Val Val Val Leu Asn Gly Trp Phe Gly
                  10                  15                  20

cat gct gcg ggc tgg gga gct ttc gct gac tat ctt gac ctc ggc aac   211
His Ala Ala Gly Trp Gly Ala Phe Ala Asp Tyr Leu Asp Leu Gly Asn
              25                  30                  35

tac acc tgg cac ttt tgg gat tac cga ggt tac ggc aac aga aaa gac   259
Tyr Thr Trp His Phe Trp Asp Tyr Arg Gly Tyr Gly Asn Arg Lys Asp
          40                  45                  50

gac gca gga gaa ttt act ctg gag gaa att tca gcg gat atc gtt gca   307
Asp Ala Gly Glu Phe Thr Leu Glu Glu Ile Ser Ala Asp Ile Val Ala
      55                  60                  65

tac atc gac tcg att gag gca gaa aag gtt tcc atc ctg ggc cat tcc   355
Tyr Ile Asp Ser Ile Glu Ala Glu Lys Val Ser Ile Leu Gly His Ser
  70                  75                  80                  85

atg ggt gga gtg ttc atg cag aaa gtc ctt gca gac agc gcc acc ccc   403
Met Gly Gly Val Phe Met Gln Lys Val Leu Ala Asp Ser Ala Thr Pro
                  90                  95                 100

atc gct tca ctg gtt gga att tct gcc gtt gct gca gct gga aca cca   451
Ile Ala Ser Leu Val Gly Ile Ser Ala Val Ala Ala Ala Gly Thr Pro
             105                 110                 115

ttc gat gag gat tct cgg aag ctt ttc acc tca gca ggg cac aac ccg   499
Phe Asp Glu Asp Ser Arg Lys Leu Phe Thr Ser Ala Gly His Asn Pro
         120                 125                 130

gac tcg agg cga gcc atc atc gat ttc acc                          529
Asp Ser Arg Arg Ala Ile Ile Asp Phe Thr
    135                 140


<210> 2488
<211> 143
<212> PRT
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<213> Corynebacterium glutamicum

<400> 2488

```
Met Ser Ala Leu Ile Lys Gly Ser Gly Pro His His Val Val Val Leu
  1               5                  10                  15

Asn Gly Trp Phe Gly His Ala Ala Gly Trp Gly Ala Phe Ala Asp Tyr
             20                  25                  30

Leu Asp Leu Gly Asn Tyr Thr Trp His Phe Trp Asp Tyr Arg Gly Tyr
         35                  40                  45

Gly Asn Arg Lys Asp Asp Ala Gly Glu Phe Thr Leu Glu Glu Ile Ser
     50                  55                  60

Ala Asp Ile Val Ala Tyr Ile Asp Ser Ile Glu Ala Glu Lys Val Ser
 65                  70                  75                  80

Ile Leu Gly His Ser Met Gly Gly Val Phe Met Gln Lys Val Leu Ala
                 85                  90                  95

Asp Ser Ala Thr Pro Ile Ala Ser Leu Val Gly Ile Ser Ala Val Ala
            100                 105                 110

Ala Ala Gly Thr Pro Phe Asp Glu Asp Ser Arg Lys Leu Phe Thr Ser
        115                 120                 125

Ala Gly His Asn Pro Asp Ser Arg Arg Ala Ile Ile Asp Phe Thr
    130                 135                 140
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<210> 2489
<211> 777
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(754)
<223> RXA01931

<400> 2489

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tcgataggca tggcgccgat tctaggtcga actgatctaa agtcccacca cgcaaaagta 60

accaaggcgt acatctaccc ggcactttaa gatcagtggc atg agc act tct ttt   115
                                            Met Ser Thr Ser Phe
                                              1               5

gag tcc att ccc gga gtt act atc tcc gct cga aaa gcc ttg agc act   163
Glu Ser Ile Pro Gly Val Thr Ile Ser Ala Arg Lys Ala Leu Ser Thr
                 10                  15                  20

gcg ggg ttt aaa gat ctg gaa tcg ctt gca ggt acc aat tac gaa gaa   211
Ala Gly Phe Lys Asp Leu Glu Ser Leu Ala Gly Thr Asn Tyr Glu Glu
             25                  30                  35

gtg gct ggt ctg tca gga att ggc gca cgt act ttg gag cga ttg caa   259
Val Ala Gly Leu Ser Gly Ile Gly Ala Arg Thr Leu Glu Arg Leu Gln
         40                  45                  50

gca gcg ctg gtg gag aag aga atg agc ttt ggc ggt aaa gtg cca gag   307
```

```
Ala Ala Leu Val Glu Lys Arg Met Ser Phe Gly Gly Lys Val Pro Glu
     55                  60                  65

gca gaa cag cgc acc gcg acg tgg aca acg cta gat tct gca gca cca   355
Ala Glu Gln Arg Thr Ala Thr Trp Thr Thr Leu Asp Ser Ala Ala Pro
 70                  75                  80                  85

gag gca aca gaa acc tca gaa tcc cca gag tac ttc att caa aac cta   403
Glu Ala Thr Glu Thr Ser Glu Ser Pro Glu Tyr Phe Ile Gln Asn Leu
                 90                  95                 100

gac att cct cgc aga att acc cac ggc cgg ttg ttg ttg gaa att ttc   451
Asp Ile Pro Arg Arg Ile Thr His Gly Arg Leu Leu Leu Glu Ile Phe
            105                 110                 115

aac aga gcg aca ggc cag aaa cct tat gta gca ggg tct tcg att gtt   499
Asn Arg Ala Thr Gly Gln Lys Pro Tyr Val Ala Gly Ser Ser Ile Val
        120                 125                 130

ggt tat ggg cga gtt cat tat cgc tat gcc acg ggt agg gaa ggg atc   547
Gly Tyr Gly Arg Val His Tyr Arg Tyr Ala Thr Gly Arg Glu Gly Ile
    135                 140                 145

act att cgt gtg ggt ttc agt ccg cga aag gca aag att tca ctt tat   595
Thr Ile Arg Val Gly Phe Ser Pro Arg Lys Ala Lys Ile Ser Leu Tyr
150                 155                 160                 165

gga cta acc agt gcg cct gcg tct cga gaa ctt ctg aag aaa ttg ggt   643
Gly Leu Thr Ser Ala Pro Ala Ser Arg Glu Leu Leu Lys Lys Leu Gly
                170                 175                 180

aag cat tct gtt ggt gtg tcc tgc cta tat atc aac aaa cca gag gat   691
Lys His Ser Val Gly Val Ser Cys Leu Tyr Ile Asn Lys Pro Glu Asp
            185                 190                 195

gtt gat ctt gag gtg ctt gag gaa atg atc cgt att tct tgg gaa gcg   739
Val Asp Leu Glu Val Leu Glu Glu Met Ile Arg Ile Ser Trp Glu Ala
        200                 205                 210

gaa cct ggc gaa tgt taaatctcaa cctttaacaa agt                    777
Glu Pro Gly Glu Cys
    215
```

EFS Web 2.0.15 - Build 6

<210> 2490
<211> 218
<212> PRT
<213> Corynebacterium glutamicum

<400> 2490

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Met Ser Thr Ser Phe Glu Ser Ile Pro Gly Val Thr Ile Ser Ala Arg
  1               5                  10                  15

Lys Ala Leu Ser Thr Ala Gly Phe Lys Asp Leu Glu Ser Leu Ala Gly
             20                  25                  30

Thr Asn Tyr Glu Glu Val Ala Gly Leu Ser Gly Ile Gly Ala Arg Thr
         35                  40                  45

Leu Glu Arg Leu Gln Ala Ala Leu Val Glu Lys Arg Met Ser Phe Gly
     50                  55                  60
```

```
Gly Lys Val Pro Glu Ala Glu Gln Arg Thr Ala Thr Trp Thr Thr Leu
 65                  70                  75                  80

Asp Ser Ala Ala Pro Glu Ala Thr Glu Thr Ser Glu Ser Pro Glu Tyr
                 85                  90                  95

Phe Ile Gln Asn Leu Asp Ile Pro Arg Arg Ile Thr His Gly Arg Leu
            100                 105                 110

Leu Leu Glu Ile Phe Asn Arg Ala Thr Gly Gln Lys Pro Tyr Val Ala
        115                 120                 125

Gly Ser Ser Ile Val Gly Tyr Gly Arg Val His Tyr Arg Tyr Ala Thr
    130                 135                 140

Gly Arg Glu Gly Ile Thr Ile Arg Val Gly Phe Ser Pro Arg Lys Ala
145                 150                 155                 160

Lys Ile Ser Leu Tyr Gly Leu Thr Ser Ala Pro Ala Ser Arg Glu Leu
                165                 170                 175

Leu Lys Lys Leu Gly Lys His Ser Val Gly Val Ser Cys Leu Tyr Ile
            180                 185                 190

Asn Lys Pro Glu Asp Val Asp Leu Glu Val Leu Glu Glu Met Ile Arg
        195                 200                 205

Ile Ser Trp Glu Ala Glu Pro Gly Glu Cys
    210                 215
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US20050153417A1

<210> 2491
<211> 558
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(535)
<223> RXA01941

<400> 2491

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ccggacttgc cgctggttta gtcacttttt gctcacgacg gtatttattg gtcgatttca 60

ccagcgcagc gttgaaaaac gttgggcgcc agtcacccac atg gcc ttg act tca   115
                                              Met Ala Leu Thr Ser
                                                1               5

ctt ttg cac cag ctt gca gat aaa aaa cac agt gac ctc agc cgg gaa   163
Leu Leu His Gln Leu Ala Asp Lys Lys His Ser Asp Leu Ser Arg Glu
                10                  15                  20

gac atc gta ccg cgg gcc ttt act gtc ccg acc tct act gac gcc cac   211
Asp Ile Val Pro Arg Ala Phe Thr Val Pro Thr Ser Thr Asp Ala His
            25                  30                  35

gct att cat caa gac ttg gaa aaa ctc cga aac tcc gta ctc aaa gag   259
Ala Ile His Gln Asp Leu Glu Lys Leu Arg Asn Ser Val Leu Lys Glu
        40                  45                  50
```

```
caa aat cac cta acc act gtg ttg gga act tgg tca gaa ttc ctc acc   307
Gln Asn His Leu Thr Thr Val Leu Gly Thr Trp Ser Glu Phe Leu Thr
     55                  60                  65

tcc aac agc gat aac tcc gac att ttg cgt tcc tcc gct gaa ctt ggg   355
Ser Asn Ser Asp Asn Ser Asp Ile Leu Arg Ser Ser Ala Glu Leu Gly
 70                  75                  80                  85

ctc caa ttg gag cag gtc cgc gat aaa gca ctc gaa gtg gaa cag cgt   403
Leu Gln Leu Glu Gln Val Arg Asp Lys Ala Leu Glu Val Glu Gln Arg
                 90                  95                 100

atc aaa gcc tct gct cag gtg gat ctt acg gac ctg gct cat gag att   451
Ile Lys Ala Ser Ala Gln Val Asp Leu Thr Asp Leu Ala His Glu Ile
            105                 110                 115

gag atc tgc aat caa cac cac gca acc ctc atc agt gcg att cag gta   499
Glu Ile Cys Asn Gln His His Ala Thr Leu Ile Ser Ala Ile Gln Val
        120                 125                 130

aga ctg caa tcg cat act gct gag ctt cgg gct ggg tgatttctta        545
Arg Leu Gln Ser His Thr Ala Glu Leu Arg Ala Gly
    135                 140                 145

agactgacct agt                                                   558


<210> 2492
<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 2492
Met Ala Leu Thr Ser Leu Leu His Gln Leu Ala Asp Lys Lys His Ser
  1               5                  10                  15

Asp Leu Ser Arg Glu Asp Ile Val Pro Arg Ala Phe Thr Val Pro Thr
             20                  25                  30

Ser Thr Asp Ala His Ala Ile His Gln Asp Leu Glu Lys Leu Arg Asn
         35                  40                  45

Ser Val Leu Lys Glu Gln Asn His Leu Thr Thr Val Leu Gly Thr Trp
     50                  55                  60

Ser Glu Phe Leu Thr Ser Asn Ser Asp Asn Ser Asp Ile Leu Arg Ser
 65                  70                  75                  80

Ser Ala Glu Leu Gly Leu Gln Leu Glu Gln Val Arg Asp Lys Ala Leu
                 85                  90                  95

Glu Val Glu Gln Arg Ile Lys Ala Ser Ala Gln Val Asp Leu Thr Asp
            100                 105                 110

Leu Ala His Glu Ile Glu Ile Cys Asn Gln His His Ala Thr Leu Ile
        115                 120                 125

Ser Ala Ile Gln Val Arg Leu Gln Ser His Thr Ala Glu Leu Arg Ala
    130                 135                 140

Gly
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145

<210> 2493
<211> 723
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(700)
<223> RXA01942

<400> 2493
gccgcgaaat tcggtgaaat tgaaggtatt cctgcagatc aggcaaattc ttccacgact 60

gtgatcaagg tcaacggcaa gaacgagtaa cctgggatcc atg ttg cgc att gga 115
Met Leu Arg Ile Gly
1 5

cta aca gga ggg atc ggc agc ggt aaa tct acc gtt gcc gat ctt ttg 163
Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr Val Ala Asp Leu Leu
10 15 20

tca tct gaa gga ttt ctc atc gtc gac gcg gac caa gtt gcc cgc gat 211
Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp Gln Val Ala Arg Asp
25 30 35

atc gtc gaa ccc gga caa ccg gca tta gca gag cta gct gaa gct ttt 259
Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu Leu Ala Glu Ala Phe
40 45 50

ggc caa gac atc tta aaa ccc gac ggc act cta gac cgc gcg gga tta 307
Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu Asp Arg Ala Gly Leu
55 60 65

gca gcc aaa gca ttt gtc agc gaa gaa caa aca gcg ctg ctc aat gcc 355
Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr Ala Leu Leu Asn Ala
70 75 80 85

att acc cac cct cgt atc gcc gaa gag tca gct cgt cga ttc aac gaa 403
Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala Arg Arg Phe Asn Glu
90 95 100

gcc gaa gat caa ggc gcc aaa gtt gcg gtt tat gac atg cct ttg ctt 451
Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr Asp Met Pro Leu Leu
105 110 115

gta gaa aaa ggc ctt gac cgc aag atg gac ctt gtc gtc gta gtt gat 499
Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu Val Val Val Val Asp
120 125 130

gtt gac gta gag gaa cgc gtc cgc aga ctt gtg gaa aaa cgt ggc ctc 547
Val Asp Val Glu Glu Arg Val Arg Arg Leu Val Glu Lys Arg Gly Leu
135 140 145

aca gag gac gac gtg cgg cgt cga atc gct tct caa gtg ccc gac gac 595
Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser Gln Val Pro Asp Asp
150 155 160 165

gtc aga ctt aaa gcc gct gac atc gtt gtg gac aat aac ggc acg cta 643

```
Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp Asn Asn Gly Thr Leu
                170                 175                 180

gag gac ctt cat gct gaa gca agc aag ctg att gct gag att ctt agt   691
Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile Ala Glu Ile Leu Ser
            185                 190                 195

cgc gtg aat tagcactaaa acatcgtcaa agt                             723
Arg Val Asn
        200


<210> 2494
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 2494
Met Leu Arg Ile Gly Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr
  1               5                  10                  15

Val Ala Asp Leu Leu Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp
             20                  25                  30

Gln Val Ala Arg Asp Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu
         35                  40                  45

Leu Ala Glu Ala Phe Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu
     50                  55                  60

Asp Arg Ala Gly Leu Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr
 65                  70                  75                  80

Ala Leu Leu Asn Ala Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala
                85                  90                  95

Arg Arg Phe Asn Glu Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr
            100                 105                 110

Asp Met Pro Leu Leu Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu
        115                 120                 125

Val Val Val Val Asp Val Asp Val Glu Glu Arg Val Arg Arg Leu Val
    130                 135                 140

Glu Lys Arg Gly Leu Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser
145                 150                 155                 160

Gln Val Pro Asp Asp Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp
                165                 170                 175

Asn Asn Gly Thr Leu Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile
            180                 185                 190

Ala Glu Ile Leu Ser Arg Val Asn
        195                 200


<210> 2495
<211> 585
<212> DNA
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<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> RXA01957

<400> 2495
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gaccgacaaa cactaaaacc tccacaacaa ggacatcatc atg act act cgc acc 115
Met Thr Thr Arg Thr
1 5

gta tct act tct gca ccc cat gtc act gtc aac atc aat acc gcg cac 163
Val Ser Thr Ser Ala Pro His Val Thr Val Asn Ile Asn Thr Ala His
10 15 20

aac aaa aca cgc act gtt acc aat ggc gcc aga aaa act aat gca gag 211
Asn Lys Thr Arg Thr Val Thr Asn Gly Ala Arg Lys Thr Asn Ala Glu
25 30 35

cgt ggc aag agc tgc atc tca ttt cgt gta ggg cca gaa ttg ttt gat 259
Arg Gly Lys Ser Cys Ile Ser Phe Arg Val Gly Pro Glu Leu Phe Asp
40 45 50

gaa ttc aaa gcg acc tgc atc gac aac gat att tcc atg acc aag gcg 307
Glu Phe Lys Ala Thr Cys Ile Asp Asn Asp Ile Ser Met Thr Lys Ala
55 60 65

ttt gag aaa gag ctt cgc acc tgg gtt gat gag cac aac gct ggt gca 355
Phe Glu Lys Glu Leu Arg Thr Trp Val Asp Glu His Asn Ala Gly Ala
70 75 80 85

aca aag aaa aga aac acc cat cgc acc tac gta caa gca ccc gtt ggt 403
Thr Lys Lys Arg Asn Thr His Arg Thr Tyr Val Gln Ala Pro Val Gly
90 95 100

act gtc gcc acc agc tct att cca ggt ctt ggg tta ttt act gtg ttc 451
Thr Val Ala Thr Ser Ser Ile Pro Gly Leu Gly Leu Phe Thr Val Phe
105 110 115

aag aag agc tct gat cag atg tgg tac gac ctg gaa agc agc ccg ctg 499
Lys Lys Ser Ser Asp Gln Met Trp Tyr Asp Leu Glu Ser Ser Pro Leu
120 125 130

atc gca caa gag ccc atg tcg aat atg gac atg cat cgt aac ggc tct 547
Ile Ala Gln Glu Pro Met Ser Asn Met Asp Met His Arg Asn Gly Ser
135 140 145

ttt gag ctg cac ctg tagatctctc tctcgaccac aca 585
Phe Glu Leu His Leu
150

<210> 2496
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 2496

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Met Thr Thr Arg Thr Val Ser Thr Ser Ala Pro His Val Thr Val Asn
  1               5                  10                  15

Ile Asn Thr Ala His Asn Lys Thr Arg Thr Val Thr Asn Gly Ala Arg
             20                  25                  30

Lys Thr Asn Ala Glu Arg Gly Lys Ser Cys Ile Ser Phe Arg Val Gly
         35                  40                  45

Pro Glu Leu Phe Asp Glu Phe Lys Ala Thr Cys Ile Asp Asn Asp Ile
     50                  55                  60

Ser Met Thr Lys Ala Phe Glu Lys Glu Leu Arg Thr Trp Val Asp Glu
 65                  70                  75                  80

His Asn Ala Gly Ala Thr Lys Lys Arg Asn Thr His Arg Thr Tyr Val
                 85                  90                  95

Gln Ala Pro Val Gly Thr Val Ala Thr Ser Ser Ile Pro Gly Leu Gly
            100                 105                 110

Leu Phe Thr Val Phe Lys Lys Ser Ser Asp Gln Met Trp Tyr Asp Leu
        115                 120                 125

Glu Ser Ser Pro Leu Ile Ala Gln Glu Pro Met Ser Asn Met Asp Met
    130                 135                 140

His Arg Asn Gly Ser Phe Glu Leu His Leu
145                 150


<210> 2497
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(607)
<223> RXA01958

<400> 2497
atatggacat gcatcgtaac ggctcttttg agctgcacct gtagatctct ctctcgacca 60

cacacagctc tcaccacctc ctagaaagga cggtttcacc atg tct aaa aaa cgc   115
                                            Met Ser Lys Lys Arg
                                              1               5

gac cac ctc acc gtc att cct gac ctt gag tca cgc acc cat cac agc   163
Asp His Leu Thr Val Ile Pro Asp Leu Glu Ser Arg Thr His His Ser
                 10                  15                  20

cgc agt aca caa ccg cca act acg ctg ccc gca cca cag ctg act att   211
Arg Ser Thr Gln Pro Pro Thr Thr Leu Pro Ala Pro Gln Leu Thr Ile
             25                  30                  35

atc acc gca cca gac aag cat caa cca cag ctt cgg gtt gtt aaa aac   259
Ile Thr Ala Pro Asp Lys His Gln Pro Gln Leu Arg Val Val Lys Asn
         40                  45                  50

acc acc acc cca tct tct gtg cag ccc tcg ccg atc aac tac agc ttt   307
```

```
Thr Thr Thr Pro Ser Ser Val Gln Pro Ser Pro Ile Asn Tyr Ser Phe
     55                  60                  65

act gat cct gta ctt cgc gag gct cac tat gca ttc cag cac agc gaa   355
Thr Asp Pro Val Leu Arg Glu Ala His Tyr Ala Phe Gln His Ser Glu
 70                  75                  80                  85

ctt gcc agg cca aca gtc ctg gac tca cac tgg gtt cgt cgc gca caa   403
Leu Ala Arg Pro Thr Val Leu Asp Ser His Trp Val Arg Arg Ala Gln
                 90                  95                 100

gaa gaa ttc gac act gag cat aat gct gcc tat gtc cgt gcc gct gac   451
Glu Glu Phe Asp Thr Glu His Asn Ala Ala Tyr Val Arg Ala Ala Asp
            105                 110                 115

cag ctc tta tcc cct ttt gat gcc tac atc ctc gac aac ggc gat gtt   499
Gln Leu Leu Ser Pro Phe Asp Ala Tyr Ile Leu Asp Asn Gly Asp Val
        120                 125                 130

tac acc aag acc cca cgt gcc atc agt gct gct gaa caa gaa gaa ata   547
Tyr Thr Lys Thr Pro Arg Ala Ile Ser Ala Ala Glu Gln Glu Glu Ile
    135                 140                 145

ctt gag cac ttg cac gaa cac cat atc tgc tgg gac gaa gaa gct gaa   595
Leu Glu His Leu His Glu His His Ile Cys Trp Asp Glu Glu Ala Glu
150                 155                 160                 165

ttc ctg ctg cgc taaaggttgc cactggtttc agg                        630
Phe Leu Leu Arg
```

<210> 2498
<211> 169
<212> PRT
<213> Corynebacterium glutamicum

<400> 2498

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Met Ser Lys Lys Arg Asp His Leu Thr Val Ile Pro Asp Leu Glu Ser
  1               5                  10                  15

Arg Thr His His Ser Arg Ser Thr Gln Pro Pro Thr Thr Leu Pro Ala
             20                  25                  30

Pro Gln Leu Thr Ile Ile Thr Ala Pro Asp Lys His Gln Pro Gln Leu
         35                  40                  45

Arg Val Val Lys Asn Thr Thr Thr Pro Ser Ser Val Gln Pro Ser Pro
     50                  55                  60

Ile Asn Tyr Ser Phe Thr Asp Pro Val Leu Arg Glu Ala His Tyr Ala
 65                  70                  75                  80

Phe Gln His Ser Glu Leu Ala Arg Pro Thr Val Leu Asp Ser His Trp
                 85                  90                  95

Val Arg Arg Ala Gln Glu Glu Phe Asp Thr Glu His Asn Ala Ala Tyr
            100                 105                 110

Val Arg Ala Ala Asp Gln Leu Leu Ser Pro Phe Asp Ala Tyr Ile Leu
        115                 120                 125
```

```
Asp Asn Gly Asp Val Tyr Thr Lys Thr Pro Arg Ala Ile Ser Ala Ala
    130                 135                 140

Glu Gln Glu Glu Ile Leu Glu His Leu His Glu His His Ile Cys Trp
145                 150                 155                 160

Asp Glu Glu Ala Glu Phe Leu Leu Arg
                165
```

<210> 2499
<211> 481
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(481)
<223> RXA01959

<400> 2499

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cccaactact atgcacagcc cgtaaccatc gagccggcta aaatctatca acagaaaaac 60

cactgcctat ttgaccattc ttgtgcaaga aagtacacct atg ccc cac gac gtt   115
                                            Met Pro His Asp Val
                                              1               5

tac gat gtc gaa cac atc att tcc aag caa cct ttc tgc tcc atc ttt   163
Tyr Asp Val Glu His Ile Ile Ser Lys Gln Pro Phe Cys Ser Ile Phe
                 10                  15                  20

ttc cag ctc ccc gct gca gcg ctg aaa cct act att caa aaa gct gcc   211
Phe Gln Leu Pro Ala Ala Ala Leu Lys Pro Thr Ile Gln Lys Ala Ala
             25                  30                  35

acc aac cgc gac ctt act aag ctc aac acc gaa cag atc gct gag aac   259
Thr Asn Arg Asp Leu Thr Lys Leu Asn Thr Glu Gln Ile Ala Glu Asn
         40                  45                  50

cta cag cgc tac ctc gac acc tac agt gtc atg tct cac cag cgt gtc   307
Leu Gln Arg Tyr Leu Asp Thr Tyr Ser Val Met Ser His Gln Arg Val
     55                  60                  65

acc att gaa gag gtc act cat gtg cgc aac cct cat gag cct gat tat   355
Thr Ile Glu Glu Val Thr His Val Arg Asn Pro His Glu Pro Asp Tyr
 70                  75                  80                  85

gag ttt tca cca cag tac ggt gca cat atc tcg ctc atc ggt gag tct   403
Glu Phe Ser Pro Gln Tyr Gly Ala His Ile Ser Leu Ile Gly Glu Ser
                 90                  95                 100

tat gct gtg aac acg gcc acc aac gag cct tat gcc acc gac tcc gag   451
Tyr Ala Val Asn Thr Ala Thr Asn Glu Pro Tyr Ala Thr Asp Ser Glu
            105                 110                 115

ggc cat cct ctc gca ctg tat ttt gaa atg                          481
Gly His Pro Leu Ala Leu Tyr Phe Glu Met
        120                 125
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<210> 2500
<211> 127
<212> PRT
<213> Corynebacterium glutamicum

<400> 2500
Met Pro His Asp Val Tyr Asp Val Glu His Ile Ile Ser Lys Gln Pro
1 5 10 15

Phe Cys Ser Ile Phe Phe Gln Leu Pro Ala Ala Ala Leu Lys Pro Thr
20 25 30

Ile Gln Lys Ala Ala Thr Asn Arg Asp Leu Thr Lys Leu Asn Thr Glu
35 40 45

Gln Ile Ala Glu Asn Leu Gln Arg Tyr Leu Asp Thr Tyr Ser Val Met
50 55 60

Ser His Gln Arg Val Thr Ile Glu Glu Val Thr His Val Arg Asn Pro
65 70 75 80

His Glu Pro Asp Tyr Glu Phe Ser Pro Gln Tyr Gly Ala His Ile Ser
85 90 95

Leu Ile Gly Glu Ser Tyr Ala Val Asn Thr Ala Thr Asn Glu Pro Tyr
100 105 110

Ala Thr Asp Ser Glu Gly His Pro Leu Ala Leu Tyr Phe Glu Met
115 120 125

<210> 2501
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> RXA01961

<400> 2501
aacacccagc tagtgcctgt gcttgagcta ccaaagttca atccttttga ggcacttgct 60

atccaccttg aagccgccaa caactaagaa agcatccttc atg act gac aac gct 115
Met Thr Asp Asn Ala
1 5

gac aac acc aca gat aac gta acc aat aac tca gac acc aat ctc gat 163
Asp Asn Thr Thr Asp Asn Val Thr Asn Asn Ser Asp Thr Asn Leu Asp
10 15 20

tac agc ttc gac ccg ctc cct gac gag ccc tat gcc tac ggc ttt gaa 211
Tyr Ser Phe Asp Pro Leu Pro Asp Glu Pro Tyr Ala Tyr Gly Phe Glu
25 30 35

ctg gtc gct gct gat gca cac tct gac tca aca aca acc agc acc gat 259
Leu Val Ala Ala Asp Ala His Ser Asp Ser Thr Thr Thr Ser Thr Asp
40 45 50

acc cca gag act gtc gct gtg gca ctt aaa acc cgc gag gac act atc 307

```
Thr Pro Glu Thr Val Ala Val Ala Leu Lys Thr Arg Glu Asp Thr Ile
     55                  60                  65

aac tgg gtc aac acc cag cgt gcc gaa ggt aaa ccc gat gaa att cgt   355
Asn Trp Val Asn Thr Gln Arg Ala Glu Gly Lys Pro Asp Glu Ile Arg
 70                  75                  80                  85

atc aat aac cca att cga tca gag cgt att gct gag ttt gtc cac gaa   403
Ile Asn Asn Pro Ile Arg Ser Glu Arg Ile Ala Glu Phe Val His Glu
                 90                  95                 100

atg atc atg cat cac ggc ctc gta gcc tgc atg gaa gat ctc gca ata   451
Met Ile Met His His Gly Leu Val Ala Cys Met Glu Asp Leu Ala Ile
            105                 110                 115

ctt atc aag cgc gac aag ctc acc cag ctg gaa gcc gaa aac gct atc   499
Leu Ile Lys Arg Asp Lys Leu Thr Gln Leu Glu Ala Glu Asn Ala Ile
        120                 125                 130

aca gcc tgg cac aac ctc acc aaa gaa tcc ctt ggt cag atc atg ggg   547
Thr Ala Trp His Asn Leu Thr Lys Glu Ser Leu Gly Gln Ile Met Gly
    135                 140                 145

ctc ttc tat cag tac gtc gaa aac aac aca aaa taggaaagaa gaaacaccat 600
Leu Phe Tyr Gln Tyr Val Glu Asn Asn Thr Lys
150                 155                 160

cat                                                               603
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CONFIDENTIAL

<210> 2502
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 2502

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Met Thr Asp Asn Ala Asp Asn Thr Thr Asp Asn Val Thr Asn Asn Ser
  1               5                  10                  15

Asp Thr Asn Leu Asp Tyr Ser Phe Asp Pro Leu Pro Asp Glu Pro Tyr
             20                  25                  30

Ala Tyr Gly Phe Glu Leu Val Ala Ala Asp Ala His Ser Asp Ser Thr
         35                  40                  45

Thr Thr Ser Thr Asp Thr Pro Glu Thr Val Ala Val Ala Leu Lys Thr
     50                  55                  60

Arg Glu Asp Thr Ile Asn Trp Val Asn Thr Gln Arg Ala Glu Gly Lys
 65                  70                  75                  80

Pro Asp Glu Ile Arg Ile Asn Asn Pro Ile Arg Ser Glu Arg Ile Ala
                 85                  90                  95

Glu Phe Val His Glu Met Ile Met His His Gly Leu Val Ala Cys Met
            100                 105                 110

Glu Asp Leu Ala Ile Leu Ile Lys Arg Asp Lys Leu Thr Gln Leu Glu
        115                 120                 125

Ala Glu Asn Ala Ile Thr Ala Trp His Asn Leu Thr Lys Glu Ser Leu
```

```
    130                 135                 140

Gly Gln Ile Met Gly Leu Phe Tyr Gln Tyr Val Glu Asn Asn Thr Lys
145                 150                 155                 160
```

<210> 2503
<211> 693
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(670)
<223> RXA01962

<400> 2503

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agcctggcac aacctcacca aagaatccct tggtcagatc atggggctct tctatcagta 60

cgtcgaaaac aacacaaaat aggaaagaag aaacaccatc atg tct gac aac act   115
                                              Met Ser Asp Asn Thr
                                                1               5

cag gac aac cct ttc tcc atc cgc tac gca cac cct gac cac cag ctc   163
Gln Asp Asn Pro Phe Ser Ile Arg Tyr Ala His Pro Asp His Gln Leu
                10                  15                  20

gct ctt aat gag ctt gtt gat act gcc gat cta cct gca cca aca agc   211
Ala Leu Asn Glu Leu Val Asp Thr Ala Asp Leu Pro Ala Pro Thr Ser
            25                  30                  35

tat atg aaa aat ccc tgg tcc ggg gac aac acg cct atc gcc gag tgg   259
Tyr Met Lys Asn Pro Trp Ser Gly Asp Asn Thr Pro Ile Ala Glu Trp
        40                  45                  50

cga cgc gag cgc atc acc cag tgg cag cgc acc gag atc att gtc aat   307
Arg Arg Glu Arg Ile Thr Gln Trp Gln Arg Thr Glu Ile Ile Val Asn
    55                  60                  65

caa cgc gat gat gac gat ctc att cac gtc agc ttc ccg aag ctc ggc   355
Gln Arg Asp Asp Asp Asp Leu Ile His Val Ser Phe Pro Lys Leu Gly
70                  75                  80                  85

cag cac att cag ctc aac acc gac gat att ctc gca ttg gtc gca gcc   403
Gln His Ile Gln Leu Asn Thr Asp Asp Ile Leu Ala Leu Val Ala Ala
                90                  95                  100

tgc gtc aca ccc act gct aac gac att gag gca act atc gaa gaa aat   451
Cys Val Thr Pro Thr Ala Asn Asp Ile Glu Ala Thr Ile Glu Glu Asn
            105                 110                 115

ctc cac tca tat ccg cac gat acg gtc atc atg ttt aac gca gat gat   499
Leu His Ser Tyr Pro His Asp Thr Val Ile Met Phe Asn Ala Asp Asp
        120                 125                 130

cta gat gat gcc ctt ggt ctc gtt gtt gcc gtc aaa gac gcg agc ggg   547
Leu Asp Asp Ala Leu Gly Leu Val Val Ala Val Lys Asp Ala Ser Gly
    135                 140                 145
```

```
gaa cac tca ccg cgc gct gtc tgg cgc acc aac acc gat cat gga gct   595
Glu His Ser Pro Arg Ala Val Trp Arg Thr Asn Thr Asp His Gly Ala
150                 155                 160                 165

ctt gac gag act gaa ctc gcg cgg ctc att ctc aaa ttc ggt ggc agc   643
Leu Asp Glu Thr Glu Leu Ala Arg Leu Ile Leu Lys Phe Gly Gly Ser
                170                 175                 180

ttc gat gac tac ggc gtg ctg caa cat taaaccgact cactaagcac         690
Phe Asp Asp Tyr Gly Val Leu Gln His
            185                 190

cgc                                                               693
```

<210> 2504
<211> 190
<212> PRT
<213> Corynebacterium glutamicum

<400> 2504

```
Met Ser Asp Asn Thr Gln Asp Asn Pro Phe Ser Ile Arg Tyr Ala His
  1               5                  10                  15

Pro Asp His Gln Leu Ala Leu Asn Glu Leu Val Asp Thr Ala Asp Leu
             20                  25                  30

Pro Ala Pro Thr Ser Tyr Met Lys Asn Pro Trp Ser Gly Asp Asn Thr
         35                  40                  45

Pro Ile Ala Glu Trp Arg Arg Glu Arg Ile Thr Gln Trp Gln Arg Thr
     50                  55                  60

Glu Ile Ile Val Asn Gln Arg Asp Asp Asp Asp Leu Ile His Val Ser
 65                  70                  75                  80

Phe Pro Lys Leu Gly Gln His Ile Gln Leu Asn Thr Asp Asp Ile Leu
                 85                  90                  95

Ala Leu Val Ala Ala Cys Val Thr Pro Thr Ala Asn Asp Ile Glu Ala
            100                 105                 110

Thr Ile Glu Glu Asn Leu His Ser Tyr Pro His Asp Thr Val Ile Met
        115                 120                 125

Phe Asn Ala Asp Asp Leu Asp Asp Ala Leu Gly Leu Val Val Ala Val
    130                 135                 140

Lys Asp Ala Ser Gly Glu His Ser Pro Arg Ala Val Trp Arg Thr Asn
145                 150                 155                 160

Thr Asp His Gly Ala Leu Asp Glu Thr Glu Leu Ala Arg Leu Ile Leu
                165                 170                 175

Lys Phe Gly Gly Ser Phe Asp Asp Tyr Gly Val Leu Gln His
            180                 185                 190
```

<210> 2505
<211> 784

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(784)
<223> RXA01963

<400> 2505
cagattttct ctgtgtgagc tggggttttc tgcatttccc acttgttttt ctccaacact 60

ccacacacac accttcaaag aagaaagttc gaaagattct atg aaa aac cgt aaa 115
Met Lys Asn Arg Lys
1 5

aaa atc atg tct acc ctc acc act gtc tgc gcc gta ctg ggt ata gtt 163
Lys Ile Met Ser Thr Leu Thr Thr Val Cys Ala Val Leu Gly Ile Val
10 15 20

gca gct cat cca ttc cac gcc tct gct gtc atc ggc ggc tct gtc cca 211
Ala Ala His Pro Phe His Ala Ser Ala Val Ile Gly Gly Ser Val Pro
25 30 35

tca act gat tcc gtt gcc aac gct gtc gca aaa atc gga cca ggc gca 259
Ser Thr Asp Ser Val Ala Asn Ala Val Ala Lys Ile Gly Pro Gly Ala
40 45 50

ttg aac tgc agc ggt gtc atg atc tca cca tcg tgg gca ctc acc gca 307
Leu Asn Cys Ser Gly Val Met Ile Ser Pro Ser Trp Ala Leu Thr Ala
55 60 65

cgc cac tgt gtc gat gac atc aac ata ctc ggc gac atc gac acc atc 355
Arg His Cys Val Asp Asp Ile Asn Ile Leu Gly Asp Ile Asp Thr Ile
70 75 80 85

acg cct att act cca ggt att cat cgc aat gaa ggt aac tat atg ggt 403
Thr Pro Ile Thr Pro Gly Ile His Arg Asn Glu Gly Asn Tyr Met Gly
90 95 100

gag gtt tac cgc gca ccg tcc ggt gat cta gcg ctc att aat atc aac 451
Glu Val Tyr Arg Ala Pro Ser Gly Asp Leu Ala Leu Ile Asn Ile Asn
105 110 115

ggc gtg cac aag ggc acc att gcg cag ctc ccc aca caa gaa tat cca 499
Gly Val His Lys Gly Thr Ile Ala Gln Leu Pro Thr Gln Glu Tyr Pro
120 125 130

ctg gga acc gct gca cag tca gtc ggt ttt ggt ggc ggt ggt gtc aat 547
Leu Gly Thr Ala Ala Gln Ser Val Gly Phe Gly Gly Gly Gly Val Asn
135 140 145

atc cgc acc gct gaa tcg gtc aac atg att ctc acc gac ata tat agc 595
Ile Arg Thr Ala Glu Ser Val Asn Met Ile Leu Thr Asp Ile Tyr Ser
150 155 160 165

gtg agg tca ggg aaa ttc cat cac ggt gtc ggt cga tca cac tat ctc 643
Val Arg Ser Gly Lys Phe His His Gly Val Gly Arg Ser His Tyr Leu
170 175 180

ctc ttt gat tat gac agt gct gaa act ggt cga atc cac aaa ggt gat 691
Leu Phe Asp Tyr Asp Ser Ala Glu Thr Gly Arg Ile His Lys Gly Asp

```
            185                 190                 195

tct ggg ggc ccc atc ttc att ggt gac gag gtt gtg ggc att atg tct   739
Ser Gly Gly Pro Ile Phe Ile Gly Asp Glu Val Val Gly Ile Met Ser
        200                 205                 210

cac ggc aca ata aat aag aac gac ggg tct ttt gat gac gaa tcc       784
His Gly Thr Ile Asn Lys Asn Asp Gly Ser Phe Asp Asp Glu Ser
    215                 220                 225


<210> 2506
<211> 228
<212> PRT
<213> Corynebacterium glutamicum

<400> 2506
Met Lys Asn Arg Lys Lys Ile Met Ser Thr Leu Thr Thr Val Cys Ala
  1               5                  10                  15

Val Leu Gly Ile Val Ala Ala His Pro Phe His Ala Ser Ala Val Ile
             20                  25                  30

Gly Gly Ser Val Pro Ser Thr Asp Ser Val Ala Asn Ala Val Ala Lys
         35                  40                  45

Ile Gly Pro Gly Ala Leu Asn Cys Ser Gly Val Met Ile Ser Pro Ser
     50                  55                  60

Trp Ala Leu Thr Ala Arg His Cys Val Asp Asp Ile Asn Ile Leu Gly
 65                  70                  75                  80

Asp Ile Asp Thr Ile Thr Pro Ile Thr Pro Gly Ile His Arg Asn Glu
                 85                  90                  95

Gly Asn Tyr Met Gly Glu Val Tyr Arg Ala Pro Ser Gly Asp Leu Ala
            100                 105                 110

Leu Ile Asn Ile Asn Gly Val His Lys Gly Thr Ile Ala Gln Leu Pro
        115                 120                 125

Thr Gln Glu Tyr Pro Leu Gly Thr Ala Ala Gln Ser Val Gly Phe Gly
    130                 135                 140

Gly Gly Gly Val Asn Ile Arg Thr Ala Glu Ser Val Asn Met Ile Leu
145                 150                 155                 160

Thr Asp Ile Tyr Ser Val Arg Ser Gly Lys Phe His His Gly Val Gly
                165                 170                 175

Arg Ser His Tyr Leu Leu Phe Asp Tyr Asp Ser Ala Glu Thr Gly Arg
            180                 185                 190

Ile His Lys Gly Asp Ser Gly Gly Pro Ile Phe Ile Gly Asp Glu Val
        195                 200                 205

Val Gly Ile Met Ser His Gly Thr Ile Asn Lys Asn Asp Gly Ser Phe
    210                 215                 220

Asp Asp Glu Ser
225
```

<210> 2507
<211> 1426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1426)
<223> RXA01964

<400> 2507
agagccagat gatggctttg atatggatga tgtcatgggc caagcgttcg gtcgctagct 60

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catacctttgt tacaacgaca ctttttaagg gaagaagatt atg acc agc gct gtg   115
                                            Met Thr Ser Ala Val
                                              1               5

aat gtg cag aag aag acc aca cag aaa gta ctt aag ccc att aat acg   163
Asn Val Gln Lys Lys Thr Thr Gln Lys Val Leu Lys Pro Ile Asn Thr
                  10                  15                  20

aag aat tac tct gcg aca gat gca gta cag aca ggc cag cac gga tct   211
Lys Asn Tyr Ser Ala Thr Asp Ala Val Gln Thr Gly Gln His Gly Ser
              25                  30                  35

gct tta ggc tcg aat atc ggt gtc tac acc tat acc gct gga ctc gat   259
Ala Leu Gly Ser Asn Ile Gly Val Tyr Thr Tyr Thr Ala Gly Leu Asp
          40                  45                  50

att gga aac ggt tat gtc aag ggc att atc gag gca acc ggt gat acg   307
Ile Gly Asn Gly Tyr Val Lys Gly Ile Ile Glu Ala Thr Gly Asp Thr
      55                  60                  65

act ggc acg tct gtt gat gtt att gat atg ccc tct gca gca acg cgc   355
Thr Gly Thr Ser Val Asp Val Ile Asp Met Pro Ser Ala Ala Thr Arg
  70                  75                  80                  85

atg agc cgg cca acg gaa gtt ccc gaa cca gat gac acc gct gtt gct   403
Met Ser Arg Pro Thr Glu Val Pro Glu Pro Asp Asp Thr Ala Val Ala
                  90                  95                 100

gtc acc ggt gcg gat ttc ttc aac cac att gat acc aat ttc aat tcg   451
Val Thr Gly Ala Asp Phe Phe Asn His Ile Asp Thr Asn Phe Asn Ser
             105                 110                 115

cct atg gtg aaa ggt aat tat cgt tac ctt tgt ggc acg cgc agc ttg   499
Pro Met Val Lys Gly Asn Tyr Arg Tyr Leu Cys Gly Thr Arg Ser Leu
         120                 125                 130

tct gca cga ggt agc ttg gag gaa ttt gat ctg gtg ggt aac cgc tcc   547
Ser Ala Arg Gly Ser Leu Glu Glu Phe Asp Leu Val Gly Asn Arg Ser
     135                 140                 145

aag gcg gaa caa gaa ctg agc aag gtg ctg gtc atg gca gta ctt gcg   595
Lys Ala Glu Gln Glu Leu Ser Lys Val Leu Val Met Ala Val Leu Ala
150                 155                 160                 165

gcc aag gct gtg aaa gac ttt gtg gca gca cat ggt cga atc cca cag   643
Ala Lys Ala Val Lys Asp Phe Val Ala Ala His Gly Arg Ile Pro Gln
```

```
                    170                 175                 180

gtt gct gtt gag ggt gat ccc ggt gtg ctg cgt gtg cat acg tat ctt   691
Val Ala Val Glu Gly Asp Pro Gly Val Leu Arg Val His Thr Tyr Leu
            185                 190                 195

gca ctt gcg tta ccg att aat gaa tat gtg ggt cac cgt cat ggg tat   739
Ala Leu Ala Leu Pro Ile Asn Glu Tyr Val Gly His Arg His Gly Tyr
        200                 205                 210

aag gca cag ttt atg ggt gat ggg gca gcg aac ccg gct gtg cat gtg   787
Lys Ala Gln Phe Met Gly Asp Gly Ala Ala Asn Pro Ala Val His Val
    215                 220                 225

gtg acg gtt aac aac ttt gaa acc cca gca acg gtg cag ctc atc ttt   835
Val Thr Val Asn Asn Phe Glu Thr Pro Ala Thr Val Gln Leu Ile Phe
230                 235                 240                 245

gag cgt gtc gag gtc att gcc gag ggc gca tcg gca cag tat gcc att   883
Glu Arg Val Glu Val Ile Ala Glu Gly Ala Ser Ala Gln Tyr Ala Ile
                250                 255                 260

acc gca ggt ggc gaa gta ctt atg aac gga atg ctc gcc gat gta cgc   931
Thr Ala Gly Gly Glu Val Leu Met Asn Gly Met Leu Ala Asp Val Arg
            265                 270                 275

tcc aaa ggg ctt gct cta gag ggc gtg aca gca ggt gat gtg cta caa   979
Ser Lys Gly Leu Ala Leu Glu Gly Val Thr Ala Gly Asp Val Leu Gln
        280                 285                 290

gct cgc cac aca atc ggt gtg gat gtg ggt gaa ggt act gtg aat ttc   1027
Ala Arg His Thr Ile Gly Val Asp Val Gly Glu Gly Thr Val Asn Phe
    295                 300                 305

cca gtc ttt acg gat ggg cgg ttt aat cat gat gct tca cgc gcc tat   1075
Pro Val Phe Thr Asp Gly Arg Phe Asn His Asp Ala Ser Arg Ala Tyr
310                 315                 320                 325

gac aag ggt tat ggc acc gtc ttg gag tcg gcg att cag gct atg gac   1123
Asp Lys Gly Tyr Gly Thr Val Leu Glu Ser Ala Ile Gln Ala Met Asp
                330                 335                 340

gat gct ggg ttg gca cac aac ttt aac tcg cgt aag cag ttg gct gat   1171
Asp Ala Gly Leu Ala His Asn Phe Asn Ser Arg Lys Gln Leu Ala Asp
            345                 350                 355

tat ttg cag cga cca ccg agt gca ctc aag cgg aat ttc tat acc cgc   1219
Tyr Leu Gln Arg Pro Pro Ser Ala Leu Lys Arg Asn Phe Tyr Thr Arg
        360                 365                 370

gtg gaa cag cat gtt gat cag gag gca gtg ttc ttt gtt cag gat gtg   1267
Val Glu Gln His Val Asp Gln Glu Ala Val Phe Phe Val Gln Asp Val
    375                 380                 385

gct gca gag ttc gca cga gtg ttg agc gac gtg ggt gct ctt acc gaa   1315
Ala Ala Glu Phe Ala Arg Val Leu Ser Asp Val Gly Ala Leu Thr Glu
390                 395                 400                 405

gta gcc ttt gtc tac ggc ggt ggt tcc ggc ccg ctg cgt gat cga ctg   1363
Val Ala Phe Val Tyr Gly Gly Gly Ser Gly Pro Leu Arg Asp Arg Leu
                410                 415                 420
```

```
cat gaa gcg ttg ctg att aag gca gcg gag atg ggt tcg gaa gat acg   1411
His Glu Ala Leu Leu Ile Lys Ala Ala Glu Met Gly Ser Glu Asp Thr
            425                 430                 435

ttc ccg gtg ctg tat                                           1426
Phe Pro Val Leu Tyr
        440
```

<210> 2508
<211> 442
<212> PRT
<213> Corynebacterium glutamicum

<400> 2508

```
Met Thr Ser Ala Val Asn Val Gln Lys Lys Thr Thr Gln Lys Val Leu
  1               5                  10                  15

Lys Pro Ile Asn Thr Lys Asn Tyr Ser Ala Thr Asp Ala Val Gln Thr
             20                  25                  30

Gly Gln His Gly Ser Ala Leu Gly Ser Asn Ile Gly Val Tyr Thr Tyr
         35                  40                  45

Thr Ala Gly Leu Asp Ile Gly Asn Gly Tyr Val Lys Gly Ile Ile Glu
     50                  55                  60

Ala Thr Gly Asp Thr Thr Gly Thr Ser Val Asp Val Ile Asp Met Pro
 65                  70                  75                  80

Ser Ala Ala Thr Arg Met Ser Arg Pro Thr Glu Val Pro Glu Pro Asp
                 85                  90                  95

Asp Thr Ala Val Ala Val Thr Gly Ala Asp Phe Phe Asn His Ile Asp
            100                 105                 110

Thr Asn Phe Asn Ser Pro Met Val Lys Gly Asn Tyr Arg Tyr Leu Cys
        115                 120                 125

Gly Thr Arg Ser Leu Ser Ala Arg Gly Ser Leu Glu Glu Phe Asp Leu
    130                 135                 140

Val Gly Asn Arg Ser Lys Ala Glu Gln Glu Leu Ser Lys Val Leu Val
145                 150                 155                 160

Met Ala Val Leu Ala Ala Lys Ala Val Lys Asp Phe Val Ala Ala His
                165                 170                 175

Gly Arg Ile Pro Gln Val Ala Val Glu Gly Asp Pro Gly Val Leu Arg
            180                 185                 190

Val His Thr Tyr Leu Ala Leu Ala Leu Pro Ile Asn Glu Tyr Val Gly
        195                 200                 205

His Arg His Gly Tyr Lys Ala Gln Phe Met Gly Asp Gly Ala Ala Asn
    210                 215                 220

Pro Ala Val His Val Val Thr Val Asn Asn Phe Glu Thr Pro Ala Thr
225                 230                 235                 240
```

```
Val Gln Leu Ile Phe Glu Arg Val Glu Val Ile Ala Glu Gly Ala Ser
                245                 250                 255

Ala Gln Tyr Ala Ile Thr Ala Gly Gly Glu Val Leu Met Asn Gly Met
            260                 265                 270

Leu Ala Asp Val Arg Ser Lys Gly Leu Ala Leu Glu Gly Val Thr Ala
        275                 280                 285

Gly Asp Val Leu Gln Ala Arg His Thr Ile Gly Val Asp Val Gly Glu
    290                 295                 300

Gly Thr Val Asn Phe Pro Val Phe Thr Asp Gly Arg Phe Asn His Asp
305                 310                 315                 320

Ala Ser Arg Ala Tyr Asp Lys Gly Tyr Gly Thr Val Leu Glu Ser Ala
                325                 330                 335

Ile Gln Ala Met Asp Asp Ala Gly Leu Ala His Asn Phe Asn Ser Arg
            340                 345                 350

Lys Gln Leu Ala Asp Tyr Leu Gln Arg Pro Pro Ser Ala Leu Lys Arg
        355                 360                 365

Asn Phe Tyr Thr Arg Val Glu Gln His Val Asp Gln Glu Ala Val Phe
    370                 375                 380

Phe Val Gln Asp Val Ala Ala Glu Phe Ala Arg Val Leu Ser Asp Val
385                 390                 395                 400

Gly Ala Leu Thr Glu Val Ala Phe Val Tyr Gly Gly Gly Ser Gly Pro
                405                 410                 415

Leu Arg Asp Arg Leu His Glu Ala Leu Leu Ile Lys Ala Ala Glu Met
            420                 425                 430

Gly Ser Glu Asp Thr Phe Pro Val Leu Tyr
        435                 440
```

<210> 2509
<211> 684
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(661)
<223> RXA01965

<400> 2509

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acttctatgt tactattaaa ttagtcaata acgttagtca taaacaatgc agttattgaa 60

gagaaacttc ccgacacaat gtacgaaatg ggggtcacac atg gct caa aaa cag   115
                                            Met Ala Gln Lys Gln
                                              1               5

gac acg aca cat gta tca gag gac gat gcc ccg tgg cgt aat gtg cgt   163
Asp Thr Thr His Val Ser Glu Asp Asp Ala Pro Trp Arg Asn Val Arg
                 10                  15                  20
```

```
atg cgc ttc cca gaa aca gac gct atc gtt gag cgg ttt ttg gaa aca   211
Met Arg Phe Pro Glu Thr Asp Ala Ile Val Glu Arg Phe Leu Glu Thr
             25                  30                  35

cag ggt gct cgt ggc atc tcg ctt gcg atg cga cag ctg atc tat ttg   259
Gln Gly Ala Arg Gly Ile Ser Leu Ala Met Arg Gln Leu Ile Tyr Leu
         40                  45                  50

ttt gtc gct gaa tac ggt gat gta gag gtt gct acc gtt att ggc ctc   307
Phe Val Ala Glu Tyr Gly Asp Val Glu Val Ala Thr Val Ile Gly Leu
     55                  60                  65

aag ctg gtg gaa agc ctg cag gca ggg gct gag ggt agt gat ctt ttt   355
Lys Leu Val Glu Ser Leu Gln Ala Gly Ala Glu Gly Ser Asp Leu Phe
 70                  75                  80                  85

gct cag ctc gcg gcc ggg gtt gct gac gta gac gct gtg act aca cgc   403
Ala Gln Leu Ala Ala Gly Val Ala Asp Val Asp Ala Val Thr Thr Arg
                 90                  95                 100

aag aag gca ccg cag cag ata gca ccg cca tcg acc aca acc cgt gca   451
Lys Lys Ala Pro Gln Gln Ile Ala Pro Pro Ser Thr Thr Thr Arg Ala
             105                 110                 115

cct gat cag gta aat gag ttt gtt gcc gag gcg gag agt cag ccg gtt   499
Pro Asp Gln Val Asn Glu Phe Val Ala Glu Ala Glu Ser Gln Pro Val
         120                 125                 130

gag gag tca gtt gtt gag gcc aaa gta ccc aag cag cag gta gca cca   547
Glu Glu Ser Val Val Glu Ala Lys Val Pro Lys Gln Gln Val Ala Pro
     135                 140                 145

cag ccg gca cag aag ccg gag caa aaa cca gaa caa aag tcg gcg caa   595
Gln Pro Ala Gln Lys Pro Glu Gln Lys Pro Glu Gln Lys Ser Ala Gln
150                 155                 160                 165

cca gca cag tca gag cca gat gat ggc ttt gat atg gat gat gtc atg   643
Pro Ala Gln Ser Glu Pro Asp Asp Gly Phe Asp Met Asp Asp Val Met
                170                 175                 180

ggc caa gcg ttc ggt cgc tagctcatac cttgttacaa cga                684
Gly Gln Ala Phe Gly Arg
             185
```

<210> 2510
<211> 187
<212> PRT
<213> Corynebacterium glutamicum

<400> 2510

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Met Ala Gln Lys Gln Asp Thr Thr His Val Ser Glu Asp Asp Ala Pro
  1               5                  10                  15

Trp Arg Asn Val Arg Met Arg Phe Pro Glu Thr Asp Ala Ile Val Glu
             20                  25                  30

Arg Phe Leu Glu Thr Gln Gly Ala Arg Gly Ile Ser Leu Ala Met Arg
         35                  40                  45

Gln Leu Ile Tyr Leu Phe Val Ala Glu Tyr Gly Asp Val Glu Val Ala
```

```
     50                  55                  60

Thr Val Ile Gly Leu Lys Leu Val Glu Ser Leu Gln Ala Gly Ala Glu
 65                  70                  75                  80

Gly Ser Asp Leu Phe Ala Gln Leu Ala Ala Gly Val Ala Asp Val Asp
                 85                  90                  95

Ala Val Thr Thr Arg Lys Lys Ala Pro Gln Gln Ile Ala Pro Pro Ser
            100                 105                 110

Thr Thr Thr Arg Ala Pro Asp Gln Val Asn Glu Phe Val Ala Glu Ala
        115                 120                 125

Glu Ser Gln Pro Val Glu Glu Ser Val Val Glu Ala Lys Val Pro Lys
    130                 135                 140

Gln Gln Val Ala Pro Gln Pro Ala Gln Lys Pro Glu Gln Lys Pro Glu
145                 150                 155                 160

Gln Lys Ser Ala Gln Pro Ala Gln Ser Glu Pro Asp Asp Gly Phe Asp
                165                 170                 175

Met Asp Asp Val Met Gly Gln Ala Phe Gly Arg
            180                 185


<210> 2511
<211> 726
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (47)..(703)
<223> RXA01966

<400> 2511
ccctgttatg ggctgggttt ataagaagat gggttagttt ttaaaagtg tct gaa tct 58
                                                    Val Ser Glu Ser
                                                      1

gaa aac aac aca aca cca gca gtc gca gct cgc gat gac cgt ctg gtc   106
Glu Asn Asn Thr Thr Pro Ala Val Ala Ala Arg Asp Asp Arg Leu Val
  5                  10                  15                  20

tgg gtc gat ctg gaa atg act ggt cta gat ttg aag cgc cac gtg atc   154
Trp Val Asp Leu Glu Met Thr Gly Leu Asp Leu Lys Arg His Val Ile
                 25                  30                  35

gtg gag gtt gcg gcg ttg gtc act gac gct aac ctc aac gtt ttg ggc   202
Val Glu Val Ala Ala Leu Val Thr Asp Ala Asn Leu Asn Val Leu Gly
             40                  45                  50

gag ggc gtg gac ttg gtt gtt cac gca act gaa gaa gag ctc gcg cag   250
Glu Gly Val Asp Leu Val Val His Ala Thr Glu Glu Glu Leu Ala Gln
         55                  60                  65

atg gat gat ttt gtc acc aac atg cac gaa tcc tct ggg ctg act gag   298
Met Asp Asp Phe Val Thr Asn Met His Glu Ser Ser Gly Leu Thr Glu
     70                  75                  80
```

```
cag atc cgg gaa tcc gcg gtc acg ttg aag gaa gcc gaa gat gct gtg   346
Gln Ile Arg Glu Ser Ala Val Thr Leu Lys Glu Ala Glu Asp Ala Val
 85                  90                  95                 100

ctc gca ttg att gaa aag cac tgc gat cca gcc cat cct gca ccg cta   394
Leu Ala Leu Ile Glu Lys His Cys Asp Pro Ala His Pro Ala Pro Leu
                105                 110                 115

gct ggt aac tcc att gcc act gac cgc gcg ttt atc cgc gaa cat atg   442
Ala Gly Asn Ser Ile Ala Thr Asp Arg Ala Phe Ile Arg Glu His Met
            120                 125                 130

cca cgt ctt gat gag gcc ctg cat tac cgc atg gtg gat gtg tcc tcg   490
Pro Arg Leu Asp Glu Ala Leu His Tyr Arg Met Val Asp Val Ser Ser
        135                 140                 145

gtg aag gaa ttg gcg cgt cgc tgg tac cca cgc gtg tac tac aag cag   538
Val Lys Glu Leu Ala Arg Arg Trp Tyr Pro Arg Val Tyr Tyr Lys Gln
    150                 155                 160

ccg gag aag ggt ttg gcg cac cgc gcg ttg gcg gac att gtg gag tcg   586
Pro Glu Lys Gly Leu Ala His Arg Ala Leu Ala Asp Ile Val Glu Ser
165                 170                 175                 180

att cgg gag ttg gat tac tac cgt cgc tca ttt ttt gtt gca gag cct   634
Ile Arg Glu Leu Asp Tyr Tyr Arg Arg Ser Phe Phe Val Ala Glu Pro
                185                 190                 195

ggt cct acc tct gag cag tgc gca gat gat gcg cag gca gcg gtg gac   682
Gly Pro Thr Ser Glu Gln Cys Ala Asp Asp Ala Gln Ala Ala Val Asp
            200                 205                 210

cgt ttt gca ccc tac ttt gat tagagggttt taagcagcct ggt            726
Arg Phe Ala Pro Tyr Phe Asp
        215
```

EFS Version 5.00.00 Build 5.00.00.00

<210> 2512
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

<400> 2512

```
Val Ser Glu Ser Glu Asn Asn Thr Thr Pro Ala Val Ala Ala Arg Asp
  1               5                  10                  15

Asp Arg Leu Val Trp Val Asp Leu Glu Met Thr Gly Leu Asp Leu Lys
             20                  25                  30

Arg His Val Ile Val Glu Val Ala Ala Leu Val Thr Asp Ala Asn Leu
         35                  40                  45

Asn Val Leu Gly Glu Gly Val Asp Leu Val Val His Ala Thr Glu Glu
     50                  55                  60

Glu Leu Ala Gln Met Asp Asp Phe Val Thr Asn Met His Glu Ser Ser
 65                  70                  75                  80

Gly Leu Thr Glu Gln Ile Arg Glu Ser Ala Val Thr Leu Lys Glu Ala
                 85                  90                  95
```

```
Glu Asp Ala Val Leu Ala Leu Ile Glu Lys His Cys Asp Pro Ala His
            100                 105                 110

Pro Ala Pro Leu Ala Gly Asn Ser Ile Ala Thr Asp Arg Ala Phe Ile
        115                 120                 125

Arg Glu His Met Pro Arg Leu Asp Glu Ala Leu His Tyr Arg Met Val
    130                 135                 140

Asp Val Ser Ser Val Lys Glu Leu Ala Arg Arg Trp Tyr Pro Arg Val
145                 150                 155                 160

Tyr Tyr Lys Gln Pro Glu Lys Gly Leu Ala His Arg Ala Leu Ala Asp
                165                 170                 175

Ile Val Glu Ser Ile Arg Glu Leu Asp Tyr Tyr Arg Arg Ser Phe Phe
            180                 185                 190

Val Ala Glu Pro Gly Pro Thr Ser Glu Gln Cys Ala Asp Asp Ala Gln
        195                 200                 205

Ala Ala Val Asp Arg Phe Ala Pro Tyr Phe Asp
    210                 215
```

20050208

<210> 2513
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1258)
<223> RXA01968

<400> 2513

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gaactggcgc tttttaagtt gtggcaattt tgccagaagg gcgtaacagg tgcgggtttt 60

tcgtggtagg cgcggagcag tagcaggatc ttttcttgca gtg ctg gca att ggt   115
                                              Val Leu Ala Ile Gly
                                                1               5

tca ctg gcg ctt acg ggt tgc aca att gaa cga agc gat gcg cag gag   163
Ser Leu Ala Leu Thr Gly Cys Thr Ile Glu Arg Ser Asp Ala Gln Glu
                10                  15                  20

caa tcc tcg cag caa agt aca gaa gtt gaa gct gaa gaa gct caa gct   211
Gln Ser Ser Gln Gln Ser Thr Glu Val Glu Ala Glu Glu Ala Gln Ala
            25                  30                  35

cct gtg att tct gtt gat gat ggt gat gag gat gtg gac cct tcg gaa   259
Pro Val Ile Ser Val Asp Asp Gly Asp Glu Asp Val Asp Pro Ser Glu
        40                  45                  50

tct gtc atc gta aag tcg atg ggt gac ggt ctg agc aag gtc acc atg   307
Ser Val Ile Val Lys Ser Met Gly Asp Gly Leu Ser Lys Val Thr Met
    55                  60                  65

act aat gaa gaa ggc tat gag gtt gag tca gag ctt tct gac gat ggc   355
Thr Asn Glu Glu Gly Tyr Glu Val Glu Ser Glu Leu Ser Asp Asp Gly
```

```
 70                  75                  80                  85

cgt agc tgg acc act gcg gaa acc ctt ggc tac aac cgc acg tac acc   403
Arg Ser Trp Thr Thr Ala Glu Thr Leu Gly Tyr Asn Arg Thr Tyr Thr
                 90                  95                 100

att aag gca acc gat aag aac ggc gag acc gct act gcg tct ttt agt   451
Ile Lys Ala Thr Asp Lys Asn Gly Glu Thr Ala Thr Ala Ser Phe Ser
            105                 110                 115

act gca acc cct gca gct acc aca aac gtg gcg ctt tct ccg ctg gct   499
Thr Ala Thr Pro Ala Ala Thr Thr Asn Val Ala Leu Ser Pro Leu Ala
        120                 125                 130

gat tct gtc gtt ggt gtt ggc cag act atc ggt ttc cgt ttt ggt tcc   547
Asp Ser Val Val Gly Val Gly Gln Thr Ile Gly Phe Arg Phe Gly Ser
    135                 140                 145

cct gtg aag gat cgc aag gcg gct cag gat gct att act gtg aca act   595
Pro Val Lys Asp Arg Lys Ala Ala Gln Asp Ala Ile Thr Val Thr Thr
150                 155                 160                 165

tca cca aag gtg gag ggt ggc ttt tac tgg ttg aac aac agt gag ttg   643
Ser Pro Lys Val Glu Gly Gly Phe Tyr Trp Leu Asn Asn Ser Glu Leu
                170                 175                 180

cgc tgg cgt cca gcg gag tac tgg gag cca ggt act gaa gtt acg gtc   691
Arg Trp Arg Pro Ala Glu Tyr Trp Glu Pro Gly Thr Glu Val Thr Val
            185                 190                 195

gag gct gac att tac ggc aag gat ctc ggc ggc ggt gtc tgg ggc gaa   739
Glu Ala Asp Ile Tyr Gly Lys Asp Leu Gly Gly Gly Val Trp Gly Glu
        200                 205                 210

act gat aac gcc acc aac ttc acc att ggt gac aag gtt gag gct gtg   787
Thr Asp Asn Ala Thr Asn Phe Thr Ile Gly Asp Lys Val Glu Ala Val
    215                 220                 225

gca gat gat gcc acc aag acc atg agt gtg tac aag aac ggt gag ttg   835
Ala Asp Asp Ala Thr Lys Thr Met Ser Val Tyr Lys Asn Gly Glu Leu
230                 235                 240                 245

ctg cgc act atg ccg gta tcc ttt ggt cgt gac acc tct gag tgg gca   883
Leu Arg Thr Met Pro Val Ser Phe Gly Arg Asp Thr Ser Glu Trp Ala
                250                 255                 260

acg cca aac ggt acc tac atc att ggt gat cgc aat gag tcg atg atc   931
Thr Pro Asn Gly Thr Tyr Ile Ile Gly Asp Arg Asn Glu Ser Met Ile
            265                 270                 275

atg gac tcc acc acc ttc ggt ctg gga tat gag gag ggt ggc tac cgc   979
Met Asp Ser Thr Thr Phe Gly Leu Gly Tyr Glu Glu Gly Gly Tyr Arg
        280                 285                 290

act ccg gtg aag tac gcg acc cag atg tcc tat tct gga att tac gtg   1027
Thr Pro Val Lys Tyr Ala Thr Gln Met Ser Tyr Ser Gly Ile Tyr Val
    295                 300                 305

cac gca gca ccg tgg tct gta ggt gcg caa ggt agc tac aac acc tca   1075
His Ala Ala Pro Trp Ser Val Gly Ala Gln Gly Ser Tyr Asn Thr Ser
310                 315                 320                 325
```

```
cat ggt tgc atc aat gta tcc acc gaa aat gct cag tgg ttc cag gag   1123
His Gly Cys Ile Asn Val Ser Thr Glu Asn Ala Gln Trp Phe Gln Glu
                330                 335                 340

gcc gtg aag cgc ggt gac att gtg acc gtg aaa aac acc atc ggt gag   1171
Ala Val Lys Arg Gly Asp Ile Val Thr Val Lys Asn Thr Ile Gly Glu
            345                 350                 355

act ttg agt ggc tac gac gga ctg ggg gac tgg aac att cca tgg tct   1219
Thr Leu Ser Gly Tyr Asp Gly Leu Gly Asp Trp Asn Ile Pro Trp Ser
        360                 365                 370

gaa tgg agc aag ggg aac gcg gat caa act tcg gcg tgg taactgcgga    1268
Glu Trp Ser Lys Gly Asn Ala Asp Gln Thr Ser Ala Trp
    375                 380                 385

agtcgcaggt aaa                                                   1281
```

<210> 2514
<211> 386
<212> PRT
<213> Corynebacterium glutamicum

<400> 2514

```
Val Leu Ala Ile Gly Ser Leu Ala Leu Thr Gly Cys Thr Ile Glu Arg
  1               5                  10                  15

Ser Asp Ala Gln Glu Gln Ser Ser Gln Gln Ser Thr Glu Val Glu Ala
             20                  25                  30

Glu Glu Ala Gln Ala Pro Val Ile Ser Val Asp Asp Gly Asp Glu Asp
         35                  40                  45

Val Asp Pro Ser Glu Ser Val Ile Val Lys Ser Met Gly Asp Gly Leu
     50                  55                  60

Ser Lys Val Thr Met Thr Asn Glu Glu Gly Tyr Glu Val Glu Ser Glu
 65                  70                  75                  80

Leu Ser Asp Asp Gly Arg Ser Trp Thr Thr Ala Glu Thr Leu Gly Tyr
                85                  90                  95

Asn Arg Thr Tyr Thr Ile Lys Ala Thr Asp Lys Asn Gly Glu Thr Ala
            100                 105                 110

Thr Ala Ser Phe Ser Thr Ala Thr Pro Ala Ala Thr Thr Asn Val Ala
        115                 120                 125

Leu Ser Pro Leu Ala Asp Ser Val Val Gly Val Gly Gln Thr Ile Gly
    130                 135                 140

Phe Arg Phe Gly Ser Pro Val Lys Asp Arg Lys Ala Ala Gln Asp Ala
145                 150                 155                 160

Ile Thr Val Thr Thr Ser Pro Lys Val Glu Gly Gly Phe Tyr Trp Leu
                165                 170                 175

Asn Asn Ser Glu Leu Arg Trp Arg Pro Ala Glu Tyr Trp Glu Pro Gly
            180                 185                 190
```

```
Thr Glu Val Thr Val Glu Ala Asp Ile Tyr Gly Lys Asp Leu Gly Gly
        195                 200                 205

Gly Val Trp Gly Glu Thr Asp Asn Ala Thr Asn Phe Thr Ile Gly Asp
    210                 215                 220

Lys Val Glu Ala Val Ala Asp Asp Ala Thr Lys Thr Met Ser Val Tyr
225                 230                 235                 240

Lys Asn Gly Glu Leu Leu Arg Thr Met Pro Val Ser Phe Gly Arg Asp
                245                 250                 255

Thr Ser Glu Trp Ala Thr Pro Asn Gly Thr Tyr Ile Ile Gly Asp Arg
            260                 265                 270

Asn Glu Ser Met Ile Met Asp Ser Thr Thr Phe Gly Leu Gly Tyr Glu
        275                 280                 285

Glu Gly Gly Tyr Arg Thr Pro Val Lys Tyr Ala Thr Gln Met Ser Tyr
    290                 295                 300

Ser Gly Ile Tyr Val His Ala Ala Pro Trp Ser Val Gly Ala Gln Gly
305                 310                 315                 320

Ser Tyr Asn Thr Ser His Gly Cys Ile Asn Val Ser Thr Glu Asn Ala
                325                 330                 335

Gln Trp Phe Gln Glu Ala Val Lys Arg Gly Asp Ile Val Thr Val Lys
            340                 345                 350

Asn Thr Ile Gly Glu Thr Leu Ser Gly Tyr Asp Gly Leu Gly Asp Trp
        355                 360                 365

Asn Ile Pro Trp Ser Glu Trp Ser Lys Gly Asn Ala Asp Gln Thr Ser
    370                 375                 380

Ala Trp
385
```

<210> 2515
<211> 497
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(474)
<223> RXA01969

<400> 2515

```
aaa tgc cag cgt cgt ggt tta agc cag gat ccg ttg tat aaa aac cgg   48
Lys Cys Gln Arg Arg Gly Leu Ser Gln Asp Pro Leu Tyr Lys Asn Arg
  1               5                  10                  15

aat tcc ttg ttg acc acg cag aag tgg ttt agt cct cgt cag caa gaa   96
Asn Ser Leu Leu Thr Thr Gln Lys Trp Phe Ser Pro Arg Gln Gln Glu
             20                  25                  30

agc ttg gag cag ttg tgg gcg tat gac aaa gcc tac ggg gcg tta aag   144
```

```
Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys Ala Tyr Gly Ala Leu Lys
         35                  40                  45

ctt gcg tgg ctt gcg tat cag gcg att att gat tgt tat cag atg ggt   192
Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile Asp Cys Tyr Gln Met Gly
     50                  55                  60

aat aag cgt gaa gcg aag aag aaa atg cgg acc att att gat cag ctt   240
Asn Lys Arg Glu Ala Lys Lys Lys Met Arg Thr Ile Ile Asp Gln Leu
 65                  70                  75                  80

cgg gtg ttg aag ggg ccg aat aag gaa ctc gcg cag ttg ggt cgt agt   288
Arg Val Leu Lys Gly Pro Asn Lys Glu Leu Ala Gln Leu Gly Arg Ser
                 85                  90                  95

ttg ttt aaa cga ctt ggt gat gtg ttg gcg tat ttc gat gtt ggt gtc   336
Leu Phe Lys Arg Leu Gly Asp Val Leu Ala Tyr Phe Asp Val Gly Val
            100                 105                 110

tcc aac ggt ccg gtc gaa gcg atc aac gga cgg ttg gag cat ttg cgt   384
Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu Arg
        115                 120                 125

ggg att gct cta ggt ttc cgt aat ttg aac cac tac att ctg cgg tgc   432
Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile Leu Arg Cys
    130                 135                 140

ctt atc cat tca ggg cag ttg gtc cat aag atc aat gca ctc           474
Leu Ile His Ser Gly Gln Leu Val His Lys Ile Asn Ala Leu
145                 150                 155

taaaacagga agagccactt aag                                        497


<210> 2516
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 2516
Lys Cys Gln Arg Arg Gly Leu Ser Gln Asp Pro Leu Tyr Lys Asn Arg
  1               5                  10                  15

Asn Ser Leu Leu Thr Thr Gln Lys Trp Phe Ser Pro Arg Gln Gln Glu
             20                  25                  30

Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys Ala Tyr Gly Ala Leu Lys
         35                  40                  45

Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile Asp Cys Tyr Gln Met Gly
     50                  55                  60

Asn Lys Arg Glu Ala Lys Lys Lys Met Arg Thr Ile Ile Asp Gln Leu
 65                  70                  75                  80

Arg Val Leu Lys Gly Pro Asn Lys Glu Leu Ala Gln Leu Gly Arg Ser
                 85                  90                  95

Leu Phe Lys Arg Leu Gly Asp Val Leu Ala Tyr Phe Asp Val Gly Val
            100                 105                 110
```

```
Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu Arg
        115                 120                 125

Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile Leu Arg Cys
    130                 135                 140

Leu Ile His Ser Gly Gln Leu Val His Lys Ile Asn Ala Leu
145                 150                 155
```

<210> 2517
<211> 605
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(582)
<223> RXA01973

<400> 2517

```
tcc gcg atg tct aaa tcg cag gat gat cga aaa att gca gag ctt gaa   48
Ser Ala Met Ser Lys Ser Gln Asp Asp Arg Lys Ile Ala Glu Leu Glu
  1               5                  10                  15

gca cag ttt cat agt ctt ggt ctt aac aac act gaa cta gtt acc ctt   96
Ala Gln Phe His Ser Leu Gly Leu Asn Asn Thr Glu Leu Val Thr Leu
             20                  25                  30

gat gat gca gcg tcg cta ttg ggt gtg ccg gca ggt att cat cag att   144
Asp Asp Ala Ala Ser Leu Leu Gly Val Pro Ala Gly Ile His Gln Ile
         35                  40                  45

gag gcc gag gtg atg ttg gtg aat ttc ggt gat ggt gca gat ggc atg   192
Glu Ala Glu Val Met Leu Val Asn Phe Gly Asp Gly Ala Asp Gly Met
     50                  55                  60

ggc ggt gac acg acg aag ttt ttg cat tat cag cca gat gag tcg cag   240
Gly Gly Asp Thr Thr Lys Phe Leu His Tyr Gln Pro Asp Glu Ser Gln
 65                  70                  75                  80

cct tac gtc tgg gtg atg aag cgg gtg tat tcc ttt gag gcg atg aaa   288
Pro Tyr Val Trp Val Met Lys Arg Val Tyr Ser Phe Glu Ala Met Lys
                 85                  90                  95

aag ctc atg gtc ggg ttg ttt att ggc ttg tgc ata ctc atc gtg ggt   336
Lys Leu Met Val Gly Leu Phe Ile Gly Leu Cys Ile Leu Ile Val Gly
            100                 105                 110

ggg cca gct tta ggg ctt atg ctc ggt ggt ttt atc ggt gtg ctt att   384
Gly Pro Ala Leu Gly Leu Met Leu Gly Gly Phe Ile Gly Val Leu Ile
        115                 120                 125

ggt cta tgt cta ggt act tcc gca gcc atg att gtt ggc cct ttt ggg   432
Gly Leu Cys Leu Gly Thr Ser Ala Ala Met Ile Val Gly Pro Phe Gly
    130                 135                 140

ctt atg cgg atg aag gcg tat cca cca tgt atg gac agt cca tgg gtg   480
Leu Met Arg Met Lys Ala Tyr Pro Pro Cys Met Asp Ser Pro Trp Val
145                 150                 155                 160
```

```
tat atg tca caa gag cag tgg cgc acc gct atg ggt gcg gca cag cag   528
Tyr Met Ser Gln Glu Gln Trp Arg Thr Ala Met Gly Ala Ala Gln Gln
                165                 170                 175

acc gag gtg tct ttt gtt gag cac tgg gac aat att tac ggg gat aat   576
Thr Glu Val Ser Phe Val Glu His Trp Asp Asn Ile Tyr Gly Asp Asn
            180                 185                 190

ctg cat taacaaatta gttaataaag tgt                                 605
Leu His
```

<210> 2518
<211> 194
<212> PRT
<213> Corynebacterium glutamicum

<400> 2518

```
Ser Ala Met Ser Lys Ser Gln Asp Asp Arg Lys Ile Ala Glu Leu Glu
  1               5                  10                  15

Ala Gln Phe His Ser Leu Gly Leu Asn Asn Thr Glu Leu Val Thr Leu
             20                  25                  30

Asp Asp Ala Ala Ser Leu Leu Gly Val Pro Ala Gly Ile His Gln Ile
         35                  40                  45

Glu Ala Glu Val Met Leu Val Asn Phe Gly Asp Gly Ala Asp Gly Met
     50                  55                  60

Gly Gly Asp Thr Thr Lys Phe Leu His Tyr Gln Pro Asp Glu Ser Gln
 65                  70                  75                  80

Pro Tyr Val Trp Val Met Lys Arg Val Tyr Ser Phe Glu Ala Met Lys
                 85                  90                  95

Lys Leu Met Val Gly Leu Phe Ile Gly Leu Cys Ile Leu Ile Val Gly
            100                 105                 110

Gly Pro Ala Leu Gly Leu Met Leu Gly Gly Phe Ile Gly Val Leu Ile
        115                 120                 125

Gly Leu Cys Leu Gly Thr Ser Ala Ala Met Ile Val Gly Pro Phe Gly
    130                 135                 140

Leu Met Arg Met Lys Ala Tyr Pro Pro Cys Met Asp Ser Pro Trp Val
145                 150                 155                 160

Tyr Met Ser Gln Glu Gln Trp Arg Thr Ala Met Gly Ala Ala Gln Gln
                165                 170                 175

Thr Glu Val Ser Phe Val Glu His Trp Asp Asn Ile Tyr Gly Asp Asn
            180                 185                 190

Leu His
```

<210> 2519
<211> 1552

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1552)
<223> RXA01974

<400> 2519
acaatattta cggggataat ctgcattaac aaattagtta ataaagtgta gtatttaatt 60

aattattaaa ttcaattaac ttttttgtaa aggtgggaag atg acc cag gtt gtg 115
Met Thr Gln Val Val
1 5

gcg ggt acg ttg gtg gga gag tcg att aat cgt gag att gat gaa gac 163
Ala Gly Thr Leu Val Gly Glu Ser Ile Asn Arg Glu Ile Asp Glu Asp
10 15 20

aag tac cct tat ttg agc tcg tat gca gcg cct gtt gct gta ccg gtg 211
Lys Tyr Pro Tyr Leu Ser Ser Tyr Ala Ala Pro Val Ala Val Pro Val
25 30 35

cgt gag att att ggg cgc gaa gaa gaa gtc aat aag att atg gcc gcg 259
Arg Glu Ile Ile Gly Arg Glu Glu Glu Val Asn Lys Ile Met Ala Ala
40 45 50

ctg atg cgt cca gag att tct aat gtc atg ctt gtg ggt cct gct ggt 307
Leu Met Arg Pro Glu Ile Ser Asn Val Met Leu Val Gly Pro Ala Gly
55 60 65

tcg ggt aaa act acg ttg gta cag caa gca ctg gtg aaa gat cca gag 355
Ser Gly Lys Thr Thr Leu Val Gln Gln Ala Leu Val Lys Asp Pro Glu
70 75 80 85

cgt aac tac atc gag gtc gat gta gcg aaa atg gtt gcg gat ttg agc 403
Arg Asn Tyr Ile Glu Val Asp Val Ala Lys Met Val Ala Asp Leu Ser
90 95 100

acc ccg gcg caa atg gct gcg cgt att aaa ggt gtg ttt gag gac gcc 451
Thr Pro Ala Gln Met Ala Ala Arg Ile Lys Gly Val Phe Glu Asp Ala
105 110 115

att gcc tat cgc aag cac gaa ggt cat gaa ttg gtg ctg ttc gtt gat 499
Ile Ala Tyr Arg Lys His Glu Gly His Glu Leu Val Leu Phe Val Asp
120 125 130

gag ttt cac caa att gtg cag ctg tct aat gct gcg gta gag gca atc 547
Glu Phe His Gln Ile Val Gln Leu Ser Asn Ala Ala Val Glu Ala Ile
135 140 145

aag ccg att ttg gcg atg tct ggt gtc ctt ggt gtg cgc gtt atc gct 595
Lys Pro Ile Leu Ala Met Ser Gly Val Leu Gly Val Arg Val Ile Ala
150 155 160 165

gcg aca act ctc gaa gaa ttt cac gaa cac atc agg ccg aac caa gca 643
Ala Thr Thr Leu Glu Glu Phe His Glu His Ile Arg Pro Asn Gln Ala
170 175 180

ttg acg gag cgt ttg cag gaa att cga cta acg ccg acc gat cag aag 691
Leu Thr Glu Arg Leu Gln Glu Ile Arg Leu Thr Pro Thr Asp Gln Lys

```
            185                 190                 195

acc act gtg gcg att ttg cgt ggt atg gca gat cgt tat ggc gta agt   739
Thr Thr Val Ala Ile Leu Arg Gly Met Ala Asp Arg Tyr Gly Val Ser
        200                 205                 210

gat cag ttc tat gac gac cac gtt ttt gag cag att tac tcc acc act   787
Asp Gln Phe Tyr Asp Asp His Val Phe Glu Gln Ile Tyr Ser Thr Thr
    215                 220                 225

gag cgt ttt atg ccg agt tct gtc cag cct cgt aaa tcc att cgt gtc   835
Glu Arg Phe Met Pro Ser Ser Val Gln Pro Arg Lys Ser Ile Arg Val
230                 235                 240                 245

ctt gat gcg atg gtt ggt tgg cat cga ctt tcc ggc aag ccg atg gat   883
Leu Asp Ala Met Val Gly Trp His Arg Leu Ser Gly Lys Pro Met Asp
                250                 255                 260

atg gat ctg ctc ggt gat gtg ctc cac gat gct att ggt gtc gat att   931
Met Asp Leu Leu Gly Asp Val Leu His Asp Ala Ile Gly Val Asp Ile
            265                 270                 275

gca ttc aag gtc gat ggt acg agc att aaa gac aag ctt gat gag aag   979
Ala Phe Lys Val Asp Gly Thr Ser Ile Lys Asp Lys Leu Asp Glu Lys
        280                 285                 290

gta atg gcg caa agt ctt gcc acc act gtg gta gca cgt cgt ttg cag   1027
Val Met Ala Gln Ser Leu Ala Thr Thr Val Val Ala Arg Arg Leu Gln
    295                 300                 305

ctg gtg gtg gcg gat ctt cat gat aaa tca cgg cca ctg tcg aac ttc   1075
Leu Val Val Ala Asp Leu His Asp Lys Ser Arg Pro Leu Ser Asn Phe
310                 315                 320                 325

ttg ttc acc ggg cct act ggt gtc ggt aaa aca gag ctg gtc aag caa   1123
Leu Phe Thr Gly Pro Thr Gly Val Gly Lys Thr Glu Leu Val Lys Gln
                330                 335                 340

cta gca cgg gtg ctc ttt ggt gat gac act ggg cga ttg att cgt ttt   1171
Leu Ala Arg Val Leu Phe Gly Asp Asp Thr Gly Arg Leu Ile Arg Phe
            345                 350                 355

gac atg tca gag ttc gcc tta gaa tca agt ctt gac ctt ttc agg tct   1219
Asp Met Ser Glu Phe Ala Leu Glu Ser Ser Leu Asp Leu Phe Arg Ser
        360                 365                 370

gag ctc act cgt cgt gtc gct gac cag ggt aac gct att gtc ctg ctc   1267
Glu Leu Thr Arg Arg Val Ala Asp Gln Gly Asn Ala Ile Val Leu Leu
    375                 380                 385

gat gag gtt gag aaa gct gat cga gct att gcg cgg ttg tta ctg cag   1315
Asp Glu Val Glu Lys Ala Asp Arg Ala Ile Ala Arg Leu Leu Leu Gln
390                 395                 400                 405

gta ctt gat gat ggc cga cta tct gac gat tac aac cgt gag gtg agt   1363
Val Leu Asp Asp Gly Arg Leu Ser Asp Asp Tyr Asn Arg Glu Val Ser
                410                 415                 420

ttt ctt aat acc tat atc gtc atg aca act aac gct ggt tct gag att   1411
Phe Leu Asn Thr Tyr Ile Val Met Thr Thr Asn Ala Gly Ser Glu Ile
            425                 430                 435
```

```
ttc gag aca att tcg aac tat gcc act gat gac acg ggc gat ggt cgg   1459
Phe Glu Thr Ile Ser Asn Tyr Ala Thr Asp Asp Thr Gly Asp Gly Arg
        440                 445                 450

gcg atc aaa gac ttt gtg aaa aac att cac acg tcg atc aag aat aag   1507
Ala Ile Lys Asp Phe Val Lys Asn Ile His Thr Ser Ile Lys Asn Lys
    455                 460                 465

ggt ttt cca cct gag ctt ctt ggt cgt gta gat gaa att gtg cct       1552
Gly Phe Pro Pro Glu Leu Leu Gly Arg Val Asp Glu Ile Val Pro
470                 475                 480
```

<210> 2520
<211> 484
<212> PRT
<213> Corynebacterium glutamicum

<400> 2520

```
Met Thr Gln Val Val Ala Gly Thr Leu Val Gly Glu Ser Ile Asn Arg
  1               5                  10                  15

Glu Ile Asp Glu Asp Lys Tyr Pro Tyr Leu Ser Ser Tyr Ala Ala Pro
             20                  25                  30

Val Ala Val Pro Val Arg Glu Ile Ile Gly Arg Glu Glu Glu Val Asn
         35                  40                  45

Lys Ile Met Ala Ala Leu Met Arg Pro Glu Ile Ser Asn Val Met Leu
     50                  55                  60

Val Gly Pro Ala Gly Ser Gly Lys Thr Thr Leu Val Gln Gln Ala Leu
 65                  70                  75                  80

Val Lys Asp Pro Glu Arg Asn Tyr Ile Glu Val Asp Val Ala Lys Met
                 85                  90                  95

Val Ala Asp Leu Ser Thr Pro Ala Gln Met Ala Ala Arg Ile Lys Gly
            100                 105                 110

Val Phe Glu Asp Ala Ile Ala Tyr Arg Lys His Glu Gly His Glu Leu
        115                 120                 125

Val Leu Phe Val Asp Glu Phe His Gln Ile Val Gln Leu Ser Asn Ala
    130                 135                 140

Ala Val Glu Ala Ile Lys Pro Ile Leu Ala Met Ser Gly Val Leu Gly
145                 150                 155                 160

Val Arg Val Ile Ala Ala Thr Thr Leu Glu Glu Phe His Glu His Ile
                165                 170                 175

Arg Pro Asn Gln Ala Leu Thr Glu Arg Leu Gln Glu Ile Arg Leu Thr
            180                 185                 190

Pro Thr Asp Gln Lys Thr Thr Val Ala Ile Leu Arg Gly Met Ala Asp
        195                 200                 205

Arg Tyr Gly Val Ser Asp Gln Phe Tyr Asp Asp His Val Phe Glu Gln
    210                 215                 220
```

```
Ile Tyr Ser Thr Thr Glu Arg Phe Met Pro Ser Ser Val Gln Pro Arg
225                 230                 235                 240

Lys Ser Ile Arg Val Leu Asp Ala Met Val Gly Trp His Arg Leu Ser
                245                 250                 255

Gly Lys Pro Met Asp Met Asp Leu Leu Gly Asp Val Leu His Asp Ala
            260                 265                 270

Ile Gly Val Asp Ile Ala Phe Lys Val Asp Gly Thr Ser Ile Lys Asp
        275                 280                 285

Lys Leu Asp Glu Lys Val Met Ala Gln Ser Leu Ala Thr Thr Val Val
    290                 295                 300

Ala Arg Arg Leu Gln Leu Val Val Ala Asp Leu His Asp Lys Ser Arg
305                 310                 315                 320

Pro Leu Ser Asn Phe Leu Phe Thr Gly Pro Thr Gly Val Gly Lys Thr
                325                 330                 335

Glu Leu Val Lys Gln Leu Ala Arg Val Leu Phe Gly Asp Asp Thr Gly
            340                 345                 350

Arg Leu Ile Arg Phe Asp Met Ser Glu Phe Ala Leu Glu Ser Ser Leu
        355                 360                 365

Asp Leu Phe Arg Ser Glu Leu Thr Arg Arg Val Ala Asp Gln Gly Asn
    370                 375                 380

Ala Ile Val Leu Leu Asp Glu Val Glu Lys Ala Asp Arg Ala Ile Ala
385                 390                 395                 400

Arg Leu Leu Leu Gln Val Leu Asp Asp Gly Arg Leu Ser Asp Asp Tyr
                405                 410                 415

Asn Arg Glu Val Ser Phe Leu Asn Thr Tyr Ile Val Met Thr Thr Asn
            420                 425                 430

Ala Gly Ser Glu Ile Phe Glu Thr Ile Ser Asn Tyr Ala Thr Asp Asp
        435                 440                 445

Thr Gly Asp Gly Arg Ala Ile Lys Asp Phe Val Lys Asn Ile His Thr
    450                 455                 460

Ser Ile Lys Asn Lys Gly Phe Pro Pro Glu Leu Leu Gly Arg Val Asp
465                 470                 475                 480

Glu Ile Val Pro
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<210> 2521
<211> 1644
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1621)

<223> RXA01976

<400> 2521

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gtgattccgg gcgtcttcgc ttagagtaaa ttaaaccgta aaaataaact caattaagtt 60

agtatattaa ttacttgatt taattgaagg ggtttatagt atg acg caa aca ctt   115
                                              Met Thr Gln Thr Leu
                                                1               5

gct ggc gag cgc aga atc gtc acc acg gca gag ctt aaa gcg atg ctg   163
Ala Gly Glu Arg Arg Ile Val Thr Thr Ala Glu Leu Lys Ala Met Leu
                  10                  15                  20

gca cga ggg gat aag gtg ttt ctg cct ggt gtc gca gcg cgg gcg cca   211
Ala Arg Gly Asp Lys Val Phe Leu Pro Gly Val Ala Ala Arg Ala Pro
              25                  30                  35

gag atc ctc gac aac ttc gat cca gca gat cgg gca cgt ctc gac gtg   259
Glu Ile Leu Asp Asn Phe Asp Pro Ala Asp Arg Ala Arg Leu Asp Val
          40                  45                  50

ccc gca gca gac aat gaa atc gtc tct gta gaa ttc tcc cgc cgc gat   307
Pro Ala Ala Asp Asn Glu Ile Val Ser Val Glu Phe Ser Arg Arg Asp
      55                  60                  65

acc gtg caa tgc atc agc att gcc gac cgt gac cat ctc tac atc act   355
Thr Val Gln Cys Ile Ser Ile Ala Asp Arg Asp His Leu Tyr Ile Thr
  70                  75                  80                  85

gac gat atg atc ccg acc cac aac acg tcc aac att atc ttc ttg aaa   403
Asp Asp Met Ile Pro Thr His Asn Thr Ser Asn Ile Ile Phe Leu Lys
                  90                  95                 100

tcc aca gac gaa aca atg att aag acg ttg gtg gat tgg tca ggt gag   451
Ser Thr Asp Glu Thr Met Ile Lys Thr Leu Val Asp Trp Ser Gly Glu
              105                 110                 115

cga cat gtt gta cgc aga aat tca aag acc gta acc cgt gac ttg gca   499
Arg His Val Val Arg Arg Asn Ser Lys Thr Val Thr Arg Asp Leu Ala
          120                 125                 130

cag tta gtt atg cgc acc gag ggt aaa gtg tcg tac acg tct gca act   547
Gln Leu Val Met Arg Thr Glu Gly Lys Val Ser Tyr Thr Ser Ala Thr
      135                 140                 145

gaa aaa gag ccg gtg gtg tct tat aat gac cta aat act ctg cca tcg   595
Glu Lys Glu Pro Val Val Ser Tyr Asn Asp Leu Asn Thr Leu Pro Ser
150                 155                 160                 165

cag aac gcc atc gtc ttc cgt gcg ggt cag tat ccg gtg tgg tca cgc   643
Gln Asn Ala Ile Val Phe Arg Ala Gly Gln Tyr Pro Val Trp Ser Arg
                  170                 175                 180

aat gaa acg att tgg ccg atg tcg ttc atg ttg ttt gct aac cag att   691
Asn Glu Thr Ile Trp Pro Met Ser Phe Met Leu Phe Ala Asn Gln Ile
              185                 190                 195

atc caa ccg ggt cgc gaa tac tcg ttg cag act att cca aca ctg tcg   739
Ile Gln Pro Gly Arg Glu Tyr Ser Leu Gln Thr Ile Pro Thr Leu Ser
          200                 205                 210
```

```
agc gct aat gaa ttc gat gtg aat caa aat gca ccg gac ttt atg gcg   787
Ser Ala Asn Glu Phe Asp Val Asn Gln Asn Ala Pro Asp Phe Met Ala
    215                 220                 225

atg ctg gaa aag cgc atg gcg cag tcg att cgt act cag cgt gcc gtc   835
Met Leu Glu Lys Arg Met Ala Gln Ser Ile Arg Thr Gln Arg Ala Val
230                 235                 240                 245

gat att tat aaa aag gcg act ggg ctc gat gac tct gat att gca cgc   883
Asp Ile Tyr Lys Lys Ala Thr Gly Leu Asp Asp Ser Asp Ile Ala Arg
                250                 255                 260

ctg gat atg gat gtg tat tca gca gaa atc atg gac atc gtg gac acg   931
Leu Asp Met Asp Val Tyr Ser Ala Glu Ile Met Asp Ile Val Asp Thr
            265                 270                 275

atg atc gcg aaa gat gag tac gat gac acg ccg gat tat gac gag ggg   979
Met Ile Ala Lys Asp Glu Tyr Asp Asp Thr Pro Asp Tyr Asp Glu Gly
        280                 285                 290

gat gag tct gtc atg aat gct cgt gat ttc atg gag tct gaa tat gac   1027
Asp Glu Ser Val Met Asn Ala Arg Asp Phe Met Glu Ser Glu Tyr Asp
    295                 300                 305

gtt ttt gat gat gag ttc gaa gac agt gct cag ggc ttc ccc gtg gct   1075
Val Phe Asp Asp Glu Phe Glu Asp Ser Ala Gln Gly Phe Pro Val Ala
310                 315                 320                 325

act ggt acg aag gtg aaa aag aaa tct ctg tct gaa gaa gca gag gtc   1123
Thr Gly Thr Lys Val Lys Lys Lys Ser Leu Ser Glu Glu Ala Glu Val
                330                 335                 340

aat gat gaa ttc att cac gat cag gag aat gca gaa cat aag ctc gct   1171
Asn Asp Glu Phe Ile His Asp Gln Glu Asn Ala Glu His Lys Leu Ala
            345                 350                 355

gac atg cgg ttg aag cgt tat gcc gaa ggc aag gtg tca cga gat atg   1219
Asp Met Arg Leu Lys Arg Tyr Ala Glu Gly Lys Val Ser Arg Asp Met
        360                 365                 370

ctg gct gat caa ttc ggc cac atc ctg cag gac tca ctc gaa gat gag   1267
Leu Ala Asp Gln Phe Gly His Ile Leu Gln Asp Ser Leu Glu Asp Glu
    375                 380                 385

ctc act gca gcc tat gat gag agc ctg cac gct ttt gct caa gat ccg   1315
Leu Thr Ala Ala Tyr Asp Glu Ser Leu His Ala Phe Ala Gln Asp Pro
390                 395                 400                 405

aat ttc cgg gtg act gct aac aac ggc ttg gtt aat gct gtc gat ggc   1363
Asn Phe Arg Val Thr Ala Asn Asn Gly Leu Val Asn Ala Val Asp Gly
                410                 415                 420

act gtg ttg att gag gcg ttg tcg cag gaa gat att gca ctt atg cgc   1411
Thr Val Leu Ile Glu Ala Leu Ser Gln Glu Asp Ile Ala Leu Met Arg
            425                 430                 435

gcg caa gca gga gtg gag cag tcg cgt gtc tac tct gag ggt gaa gaa   1459
Ala Gln Ala Gly Val Glu Gln Ser Arg Val Tyr Ser Glu Gly Glu Glu
        440                 445                 450

gct cta tct ggc aca gag gat gat ccg ctg tct gct atg ggt aaa tat   1507
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Ala Leu Ser Gly Thr Glu Asp Asp Pro Leu Ser Ala Met Gly Lys Tyr
    455                 460                 465

aag acc acc cga gca ttc cgc atc atg ctg gtg gag ctt ccg cat tgg   1555
Lys Thr Thr Arg Ala Phe Arg Ile Met Leu Val Glu Leu Pro His Trp
470                 475                 480                 485

cgt gat ctc gcc cag ggt cac ttt gat aaa gaa gtc gcg cga gcc ttt   1603
Arg Asp Leu Ala Gln Gly His Phe Asp Lys Glu Val Ala Arg Ala Phe
                490                 495                 500

agg cgt att gaa gat gct taagtgtcgt gagcgataaa aaa                 1644
Arg Arg Ile Glu Asp Ala
            505
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<210> 2522
<211> 507
<212> PRT
<213> Corynebacterium glutamicum

<400> 2522

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Met Thr Gln Thr Leu Ala Gly Glu Arg Arg Ile Val Thr Thr Ala Glu
  1               5                  10                  15

Leu Lys Ala Met Leu Ala Arg Gly Asp Lys Val Phe Leu Pro Gly Val
             20                  25                  30

Ala Ala Arg Ala Pro Glu Ile Leu Asp Asn Phe Asp Pro Ala Asp Arg
         35                  40                  45

Ala Arg Leu Asp Val Pro Ala Ala Asp Asn Glu Ile Val Ser Val Glu
     50                  55                  60

Phe Ser Arg Arg Asp Thr Val Gln Cys Ile Ser Ile Ala Asp Arg Asp
 65                  70                  75                  80

His Leu Tyr Ile Thr Asp Asp Met Ile Pro Thr His Asn Thr Ser Asn
                 85                  90                  95

Ile Ile Phe Leu Lys Ser Thr Asp Glu Thr Met Ile Lys Thr Leu Val
            100                 105                 110

Asp Trp Ser Gly Glu Arg His Val Val Arg Arg Asn Ser Lys Thr Val
        115                 120                 125

Thr Arg Asp Leu Ala Gln Leu Val Met Arg Thr Glu Gly Lys Val Ser
    130                 135                 140

Tyr Thr Ser Ala Thr Glu Lys Glu Pro Val Val Ser Tyr Asn Asp Leu
145                 150                 155                 160

Asn Thr Leu Pro Ser Gln Asn Ala Ile Val Phe Arg Ala Gly Gln Tyr
                165                 170                 175

Pro Val Trp Ser Arg Asn Glu Thr Ile Trp Pro Met Ser Phe Met Leu
            180                 185                 190

Phe Ala Asn Gln Ile Ile Gln Pro Gly Arg Glu Tyr Ser Leu Gln Thr
        195                 200                 205
```

```
Ile Pro Thr Leu Ser Ser Ala Asn Glu Phe Asp Val Asn Gln Asn Ala
    210                 215                 220

Pro Asp Phe Met Ala Met Leu Glu Lys Arg Met Ala Gln Ser Ile Arg
225                 230                 235                 240

Thr Gln Arg Ala Val Asp Ile Tyr Lys Lys Ala Thr Gly Leu Asp Asp
                245                 250                 255

Ser Asp Ile Ala Arg Leu Asp Met Asp Val Tyr Ser Ala Glu Ile Met
            260                 265                 270

Asp Ile Val Asp Thr Met Ile Ala Lys Asp Glu Tyr Asp Asp Thr Pro
        275                 280                 285

Asp Tyr Asp Glu Gly Asp Glu Ser Val Met Asn Ala Arg Asp Phe Met
    290                 295                 300

Glu Ser Glu Tyr Asp Val Phe Asp Asp Glu Phe Glu Asp Ser Ala Gln
305                 310                 315                 320

Gly Phe Pro Val Ala Thr Gly Thr Lys Val Lys Lys Lys Ser Leu Ser
                325                 330                 335

Glu Glu Ala Glu Val Asn Asp Glu Phe Ile His Asp Gln Glu Asn Ala
            340                 345                 350

Glu His Lys Leu Ala Asp Met Arg Leu Lys Arg Tyr Ala Glu Gly Lys
        355                 360                 365

Val Ser Arg Asp Met Leu Ala Asp Gln Phe Gly His Ile Leu Gln Asp
    370                 375                 380

Ser Leu Glu Asp Glu Leu Thr Ala Ala Tyr Asp Glu Ser Leu His Ala
385                 390                 395                 400

Phe Ala Gln Asp Pro Asn Phe Arg Val Thr Ala Asn Asn Gly Leu Val
                405                 410                 415

Asn Ala Val Asp Gly Thr Val Leu Ile Glu Ala Leu Ser Gln Glu Asp
            420                 425                 430

Ile Ala Leu Met Arg Ala Gln Ala Gly Val Glu Gln Ser Arg Val Tyr
        435                 440                 445

Ser Glu Gly Glu Glu Ala Leu Ser Gly Thr Glu Asp Asp Pro Leu Ser
    450                 455                 460

Ala Met Gly Lys Tyr Lys Thr Thr Arg Ala Phe Arg Ile Met Leu Val
465                 470                 475                 480

Glu Leu Pro His Trp Arg Asp Leu Ala Gln Gly His Phe Asp Lys Glu
                485                 490                 495

Val Ala Arg Ala Phe Arg Arg Ile Glu Asp Ala
            500                 505
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<210> 2523
<211> 699
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(676)
<223> RXA01977

<400> 2523
aagtccagtg actaatacca atagaattga agaccactac ctcaagggcg gacgtggcag 60

gggcacagac gatcctagca atatgcaaat tgcaggaagt atg ttg cgc aca tta 115
Met Leu Arg Thr Leu
1 5

ttc gtc cgc aag att aga gcg ctg ctg ctg gtt ttg atg att gcg cca 163
Phe Val Arg Lys Ile Arg Ala Leu Leu Leu Val Leu Met Ile Ala Pro
10 15 20

act cca ttg gtc gaa ggg cta act tcg act gca atg att gta tcc gta 211
Thr Pro Leu Val Glu Gly Leu Thr Ser Thr Ala Met Ile Val Ser Val
25 30 35

gta atc ctg gcg atc tac atg gcg ata aca atg tat aga gta gtg cac 259
Val Ile Leu Ala Ile Tyr Met Ala Ile Thr Met Tyr Arg Val Val His
40 45 50

ggt cgc cat gag ttc gcg cat atc gca cgt cgc atg gcg ctt tac gtc 307
Gly Arg His Glu Phe Ala His Ile Ala Arg Arg Met Ala Leu Tyr Val
55 60 65

aac aag act tct tct agg ttc agt gtt gtt att gct tat gta gta tta 355
Asn Lys Thr Ser Ser Arg Phe Ser Val Val Ile Ala Tyr Val Val Leu
70 75 80 85

att gct att tat gcg cta cta att ccc gga ctt gtc tac tct gtt aca 403
Ile Ala Ile Tyr Ala Leu Leu Ile Pro Gly Leu Val Tyr Ser Val Thr
90 95 100

ttt gga ttc atc gtc cca agc aca cct aat acg ttt agt gat gca cct 451
Phe Gly Phe Ile Val Pro Ser Thr Pro Asn Thr Phe Ser Asp Ala Pro
105 110 115

gca tgg att atg tgc gta tcg ctg ctg ctc att gca gtc gcc agt ttc 499
Ala Trp Ile Met Cys Val Ser Leu Leu Leu Ile Ala Val Ala Ser Phe
120 125 130

atc aca tca atc atg gat gac ttt att gat ggc ata ctc act gat ttt 547
Ile Thr Ser Ile Met Asp Asp Phe Ile Asp Gly Ile Leu Thr Asp Phe
135 140 145

tat gac gaa gat aat gct gat agc ccc gat agt cct gcc gag gat ata 595
Tyr Asp Glu Asp Asn Ala Asp Ser Pro Asp Ser Pro Ala Glu Asp Ile
150 155 160 165

gcc acc cgt cct gtc gag agc gca aca aca agt gct ctt gct gga ttt 643
Ala Thr Arg Pro Val Glu Ser Ala Thr Thr Ser Ala Leu Ala Gly Phe
170 175 180

gct gtt ggt tat att tgt ggg cgc ttt aat cgc taacacttaa aacacttctc 696
Ala Val Gly Tyr Ile Cys Gly Arg Phe Asn Arg
185 190

aac 699

<210> 2524
<211> 192
<212> PRT
<213> Corynebacterium glutamicum

<400> 2524
Met Leu Arg Thr Leu Phe Val Arg Lys Ile Arg Ala Leu Leu Leu Val
1 5 10 15

Leu Met Ile Ala Pro Thr Pro Leu Val Glu Gly Leu Thr Ser Thr Ala
20 25 30

Met Ile Val Ser Val Val Ile Leu Ala Ile Tyr Met Ala Ile Thr Met
35 40 45

Tyr Arg Val Val His Gly Arg His Glu Phe Ala His Ile Ala Arg Arg
50 55 60

Met Ala Leu Tyr Val Asn Lys Thr Ser Ser Arg Phe Ser Val Val Ile
65 70 75 80

Ala Tyr Val Val Leu Ile Ala Ile Tyr Ala Leu Leu Ile Pro Gly Leu
85 90 95

Val Tyr Ser Val Thr Phe Gly Phe Ile Val Pro Ser Thr Pro Asn Thr
100 105 110

Phe Ser Asp Ala Pro Ala Trp Ile Met Cys Val Ser Leu Leu Leu Ile
115 120 125

Ala Val Ala Ser Phe Ile Thr Ser Ile Met Asp Asp Phe Ile Asp Gly
130 135 140

Ile Leu Thr Asp Phe Tyr Asp Glu Asp Asn Ala Asp Ser Pro Asp Ser
145 150 155 160

Pro Ala Glu Asp Ile Ala Thr Arg Pro Val Glu Ser Ala Thr Thr Ser
165 170 175

Ala Leu Ala Gly Phe Ala Val Gly Tyr Ile Cys Gly Arg Phe Asn Arg
180 185 190

<210> 2525
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1258)
<223> RXA01982

<400> 2525

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cttcacccaa ctcatcatct actgaaagaa ggcttctgct atg gct acc acc agc   115
                                            Met Ala Thr Thr Ser
                                              1               5

ctc ccc acg acg att aca ccg gat tcc gag gag acc gta gaa aag cgt   163
Leu Pro Thr Thr Ile Thr Pro Asp Ser Glu Glu Thr Val Glu Lys Arg
                 10                  15                  20

cac tcc ctg acc ccg atc ctg gat tca ctt ccc tgc gag tca gtt ccc   211
His Ser Leu Thr Pro Ile Leu Asp Ser Leu Pro Cys Glu Ser Val Pro
             25                  30                  35

tat gct ctg gct gca ggt gag gga caa caa cac cag ctt ggc ccc tac   259
Tyr Ala Leu Ala Ala Gly Glu Gly Gln Gln His Gln Leu Gly Pro Tyr
         40                  45                  50

cat ctc aca gtt atg tcc cgt ccc gaa gac aac ggt gga ata ttt tcg   307
His Leu Thr Val Met Ser Arg Pro Glu Asp Asn Gly Gly Ile Phe Ser
     55                  60                  65

ctg gct cgt gtg agc gca ggc aag act ccc gcc acc cgg ttc ttc tct   355
Leu Ala Arg Val Ser Ala Gly Lys Thr Pro Ala Thr Arg Phe Phe Ser
 70                  75                  80                  85

gtc gca gga ccg acg ttc ctc tac atg atg gag ggg cgg ttg act ctc   403
Val Ala Gly Pro Thr Phe Leu Tyr Met Met Glu Gly Arg Leu Thr Leu
                 90                  95                 100

tgg ttc gct gat gga cgt caa gag atc atc gct ggc ggc agt gcc acc   451
Trp Phe Ala Asp Gly Arg Gln Glu Ile Ile Ala Gly Gly Ser Ala Thr
             105                 110                 115

att cct acg aat acg ccc tgg tcc ttc gcc tgt gag ggc cta gta aat   499
Ile Pro Thr Asn Thr Pro Trp Ser Phe Ala Cys Glu Gly Leu Val Asn
         120                 125                 130

tca gct cta gtg tac tac tca tcc tcg aat gca ttc cta cac gcg gca   547
Ser Ala Leu Val Tyr Tyr Ser Ser Ser Asn Ala Phe Leu His Ala Ala
     135                 140                 145

gag aaa ctt ggc acg tcc tcg ttc tcc cac acc ttc cgc gtc agt ggc   595
Glu Lys Leu Gly Thr Ser Ser Phe Ser His Thr Phe Arg Val Ser Gly
150                 155                 160                 165

gag gtc aca ggg att ccc tac gag gaa ctg gag gat tgc gga ttc aca   643
Glu Val Thr Gly Ile Pro Tyr Glu Glu Leu Glu Asp Cys Gly Phe Thr
                 170                 175                 180

ttc tat gag cgg gac cac ctt gcc gag ctc ggg ccg cat ttc gat cgc   691
Phe Tyr Glu Arg Asp His Leu Ala Glu Leu Gly Pro His Phe Asp Arg
             185                 190                 195

ctc cca gaa gat atg aag gcg ttt gcc ctg aac gat ggt gag ggg gac   739
Leu Pro Glu Asp Met Lys Ala Phe Ala Leu Asn Asp Gly Glu Gly Asp
         200                 205                 210

cgg ctt gag cag ttc gag cag atc aac agc ttc gtc tgc cgt ccg aga   787
Arg Leu Glu Gln Phe Glu Gln Ile Asn Ser Phe Val Cys Arg Pro Arg
     215                 220                 225
```

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cac acc gga aat cag ttc ctc gct atg cag acc aag ggt gcc aag acg   835
His Thr Gly Asn Gln Phe Leu Ala Met Gln Thr Lys Gly Ala Lys Thr
230                 235                 240                 245

cct tat ata cct cgt cat ttc cac cgc ctt cac acc gaa aac ttc atc   883
Pro Tyr Ile Pro Arg His Phe His Arg Leu His Thr Glu Asn Phe Ile
                250                 255                 260

tgt ctg gac ggg cgc gtc aaa ctg cac gtc aac ggt caa gag atc atc   931
Cys Leu Asp Gly Arg Val Lys Leu His Val Asn Gly Gln Glu Ile Ile
            265                 270                 275

ctc tcc cgt ggg gat tac gtt cat gcc cca gcc gga acc atc cac tct   979
Leu Ser Arg Gly Asp Tyr Val His Ala Pro Ala Gly Thr Ile His Ser
        280                 285                 290

ttc gcc ttc gca ggg cac aat acc cag atg ctg gga gtg ctc acc aca   1027
Phe Ala Phe Ala Gly His Asn Thr Gln Met Leu Gly Val Leu Thr Thr
    295                 300                 305

gag gta ttc gag aag ttc ttt gac tac ata aac act ccg act aat gct   1075
Glu Val Phe Glu Lys Phe Phe Asp Tyr Ile Asn Thr Pro Thr Asn Ala
310                 315                 320                 325

cga gtt cag ctg gag gac ggg ggg aag cca ttt ttt cct gct gaa gca   1123
Arg Val Gln Leu Glu Asp Gly Gly Lys Pro Phe Phe Pro Ala Glu Ala
                330                 335                 340

ttc gcg aaa gtc caa gct gaa ctc gat gtc gtg gtg gtc ggc ccc cca   1171
Phe Ala Lys Val Gln Ala Glu Leu Asp Val Val Val Val Gly Pro Pro
            345                 350                 355

cga att agt acc ctg gat gtt gtt aca aac tcg cgt ttc gaa cca att   1219
Arg Ile Ser Thr Leu Asp Val Val Thr Asn Ser Arg Phe Glu Pro Ile
        360                 365                 370

aac aga act atc acc tat cgt gcg ctg gac gct aac caa tagtgagtga   1268
Asn Arg Thr Ile Thr Tyr Arg Ala Leu Asp Ala Asn Gln
    375                 380                 385

gccgaaatcc ctg                                                  1281
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Sequence Listing

<210> 2526
<211> 386
<212> PRT
<213> Corynebacterium glutamicum

<400> 2526

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Met Ala Thr Thr Ser Leu Pro Thr Thr Ile Thr Pro Asp Ser Glu Glu
  1               5                  10                  15

Thr Val Glu Lys Arg His Ser Leu Thr Pro Ile Leu Asp Ser Leu Pro
             20                  25                  30

Cys Glu Ser Val Pro Tyr Ala Leu Ala Ala Gly Glu Gly Gln Gln His
         35                  40                  45

Gln Leu Gly Pro Tyr His Leu Thr Val Met Ser Arg Pro Glu Asp Asn
     50                  55                  60
```

```
Gly Gly Ile Phe Ser Leu Ala Arg Val Ser Ala Gly Lys Thr Pro Ala
 65                  70                  75                  80

Thr Arg Phe Phe Ser Val Ala Gly Pro Thr Phe Leu Tyr Met Met Glu
                 85                  90                  95

Gly Arg Leu Thr Leu Trp Phe Ala Asp Gly Arg Gln Glu Ile Ile Ala
            100                 105                 110

Gly Gly Ser Ala Thr Ile Pro Thr Asn Thr Pro Trp Ser Phe Ala Cys
        115                 120                 125

Glu Gly Leu Val Asn Ser Ala Leu Val Tyr Tyr Ser Ser Ser Asn Ala
    130                 135                 140

Phe Leu His Ala Ala Glu Lys Leu Gly Thr Ser Ser Phe Ser His Thr
145                 150                 155                 160

Phe Arg Val Ser Gly Glu Val Thr Gly Ile Pro Tyr Glu Glu Leu Glu
                165                 170                 175

Asp Cys Gly Phe Thr Phe Tyr Glu Arg Asp His Leu Ala Glu Leu Gly
            180                 185                 190

Pro His Phe Asp Arg Leu Pro Glu Asp Met Lys Ala Phe Ala Leu Asn
        195                 200                 205

Asp Gly Glu Gly Asp Arg Leu Glu Gln Phe Glu Gln Ile Asn Ser Phe
    210                 215                 220

Val Cys Arg Pro Arg His Thr Gly Asn Gln Phe Leu Ala Met Gln Thr
225                 230                 235                 240

Lys Gly Ala Lys Thr Pro Tyr Ile Pro Arg His Phe His Arg Leu His
                245                 250                 255

Thr Glu Asn Phe Ile Cys Leu Asp Gly Arg Val Lys Leu His Val Asn
            260                 265                 270

Gly Gln Glu Ile Ile Leu Ser Arg Gly Asp Tyr Val His Ala Pro Ala
        275                 280                 285

Gly Thr Ile His Ser Phe Ala Phe Ala Gly His Asn Thr Gln Met Leu
    290                 295                 300

Gly Val Leu Thr Thr Glu Val Phe Glu Lys Phe Phe Asp Tyr Ile Asn
305                 310                 315                 320

Thr Pro Thr Asn Ala Arg Val Gln Leu Glu Asp Gly Gly Lys Pro Phe
                325                 330                 335

Phe Pro Ala Glu Ala Phe Ala Lys Val Gln Ala Glu Leu Asp Val Val
            340                 345                 350

Val Val Gly Pro Pro Arg Ile Ser Thr Leu Asp Val Val Thr Asn Ser
        355                 360                 365

Arg Phe Glu Pro Ile Asn Arg Thr Ile Thr Tyr Arg Ala Leu Asp Ala
    370                 375                 380
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Asn Gln
385

<210> 2527
<211> 1022
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(999)
<223> RXA01990

<400> 2527

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aca tct gat cat gtg gca cag ttt ggt atg gca act gcg tct gct gcg   48
Thr Ser Asp His Val Ala Gln Phe Gly Met Ala Thr Ala Ser Ala Ala
  1               5                  10                  15

acg ttg ccg gac agt att gtg acc agt gtt tct tat acg ttg aac ggg   96
Thr Leu Pro Asp Ser Ile Val Thr Ser Val Ser Tyr Thr Leu Asn Gly
            20                  25                  30

ctg tca ttt tct gac ccg gtt gag ctg ggt atc agt gac aac gac aag   144
Leu Ser Phe Ser Asp Pro Val Glu Leu Gly Ile Ser Asp Asn Asp Lys
         35                  40                  45

cgt gaa gag ctt cta gga gac atc acc aag ggt gaa ctg cga ttg cag   192
Arg Glu Glu Leu Leu Gly Asp Ile Thr Lys Gly Glu Leu Arg Leu Gln
     50                  55                  60

atg gag ttt tcg atc ccg gat tca gca act gcc gag gat gag tac gtc   240
Met Glu Phe Ser Ile Pro Asp Ser Ala Thr Ala Glu Asp Glu Tyr Val
 65                  70                  75                  80

ttt aat ctc acc ggc gat gga ctt cgg ttt ttc aat tca aac gat cgc   288
Phe Asn Leu Thr Gly Asp Gly Leu Arg Phe Phe Asn Ser Asn Asp Arg
                85                  90                  95

acc gtc cct gta cgc aat gat gca ggt att cgt gtc gca gat ctt ttg   336
Thr Val Pro Val Arg Asn Asp Ala Gly Ile Arg Val Ala Asp Leu Leu
            100                 105                 110

gtg agc aac ggt ggt acg cgc ggt acg ttg aca aac ttt agt tcg gat   384
Val Ser Asn Gly Gly Thr Arg Gly Thr Leu Thr Asn Phe Ser Ser Asp
        115                 120                 125

gct ggc act act tct cgc acc gca gct ctt gat atg gaa ctg tac ggg   432
Ala Gly Thr Thr Ser Arg Thr Ala Ala Leu Asp Met Glu Leu Tyr Gly
    130                 135                 140

tgg gtg agt agc gcc cag cag acg ggt gag cga cca att caa gac tgg   480
Trp Val Ser Ser Ala Gln Gln Thr Gly Glu Arg Pro Ile Gln Asp Trp
145                 150                 155                 160

act gtg ggt aag act gag ggt cag gtt gag aac aag gta gtc cgc tac   528
Thr Val Gly Lys Thr Glu Gly Gln Val Glu Asn Lys Val Val Arg Tyr
                165                 170                 175

ggc gtt gct gga cac ccg tgg att atc agt act gtc cag cac acg tgg   576
Gly Val Ala Gly His Pro Trp Ile Ile Ser Thr Val Gln His Thr Trp
```

```
            180                 185                 190

gtt aag tct acg cag acc gtg tcg cat ttc cga agt gaa caa gac tgg   624
Val Lys Ser Thr Gln Thr Val Ser His Phe Arg Ser Glu Gln Asp Trp
        195                 200                 205

aag att aat caa cca cca gct gtt gat atg ggc gca tta gca tac gca   672
Lys Ile Asn Gln Pro Pro Ala Val Asp Met Gly Ala Leu Ala Tyr Ala
    210                 215                 220

gct cca ctt ggc gtc gtg gtc ggg cac gcc aat gtt gtc att agc aat   720
Ala Pro Leu Gly Val Val Val Gly His Ala Asn Val Val Ile Ser Asn
225                 230                 235                 240

aac aac ggt gct gga ttc cgg ggt gcg ctt gtc aat acc aca ccc acc   768
Asn Asn Gly Ala Gly Phe Arg Gly Ala Leu Val Asn Thr Thr Pro Thr
                245                 250                 255

aca cgc gac gtg ata ctt aat ttc aca gcc gca gac gga gcc act tta   816
Thr Arg Asp Val Ile Leu Asn Phe Thr Ala Ala Asp Gly Ala Thr Leu
            260                 265                 270

cgc gaa cgt tcc gga ggt gga ttt gag gat ttc gac gtt ttc tcg gaa   864
Arg Glu Arg Ser Gly Gly Gly Phe Glu Asp Phe Asp Val Phe Ser Glu
        275                 280                 285

gtt cct cgg gta gag gaa aca tcg acg agg atc agc tat tct tac aaa   912
Val Pro Arg Val Glu Glu Thr Ser Thr Arg Ile Ser Tyr Ser Tyr Lys
    290                 295                 300

aat tca ttt gaa tat gac gaa ttt gtt gcc gca ttt ccc gag tac cga   960
Asn Ser Phe Glu Tyr Asp Glu Phe Val Ala Ala Phe Pro Glu Tyr Arg
305                 310                 315                 320

cgt agc tgc gtg gga acc aac cgt tgt gta ttc agc gga taagaccaca   1009
Arg Ser Cys Val Gly Thr Asn Arg Cys Val Phe Ser Gly
                325                 330

gcaacagcga cgt                                                  1022
```

<210> 2528
<211> 333
<212> PRT
<213> Corynebacterium glutamicum

<400> 2528

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Thr Ser Asp His Val Ala Gln Phe Gly Met Ala Thr Ala Ser Ala Ala
  1               5                  10                  15

Thr Leu Pro Asp Ser Ile Val Thr Ser Val Ser Tyr Thr Leu Asn Gly
            20                  25                  30

Leu Ser Phe Ser Asp Pro Val Glu Leu Gly Ile Ser Asp Asn Asp Lys
        35                  40                  45

Arg Glu Glu Leu Leu Gly Asp Ile Thr Lys Gly Glu Leu Arg Leu Gln
    50                  55                  60

Met Glu Phe Ser Ile Pro Asp Ser Ala Thr Ala Glu Asp Glu Tyr Val
65                  70                  75                  80
```

```
Phe Asn Leu Thr Gly Asp Gly Leu Arg Phe Phe Asn Ser Asn Asp Arg
                 85                  90                  95

Thr Val Pro Val Arg Asn Asp Ala Gly Ile Arg Val Ala Asp Leu Leu
            100                 105                 110

Val Ser Asn Gly Gly Thr Arg Gly Thr Leu Thr Asn Phe Ser Ser Asp
        115                 120                 125

Ala Gly Thr Thr Ser Arg Thr Ala Ala Leu Asp Met Glu Leu Tyr Gly
    130                 135                 140

Trp Val Ser Ser Ala Gln Gln Thr Gly Glu Arg Pro Ile Gln Asp Trp
145                 150                 155                 160

Thr Val Gly Lys Thr Glu Gly Gln Val Glu Asn Lys Val Val Arg Tyr
                165                 170                 175

Gly Val Ala Gly His Pro Trp Ile Ile Ser Thr Val Gln His Thr Trp
            180                 185                 190

Val Lys Ser Thr Gln Thr Val Ser His Phe Arg Ser Glu Gln Asp Trp
        195                 200                 205

Lys Ile Asn Gln Pro Pro Ala Val Asp Met Gly Ala Leu Ala Tyr Ala
    210                 215                 220

Ala Pro Leu Gly Val Val Val Gly His Ala Asn Val Val Ile Ser Asn
225                 230                 235                 240

Asn Asn Gly Ala Gly Phe Arg Gly Ala Leu Val Asn Thr Thr Pro Thr
                245                 250                 255

Thr Arg Asp Val Ile Leu Asn Phe Thr Ala Ala Asp Gly Ala Thr Leu
            260                 265                 270

Arg Glu Arg Ser Gly Gly Gly Phe Glu Asp Phe Asp Val Phe Ser Glu
        275                 280                 285

Val Pro Arg Val Glu Glu Thr Ser Thr Arg Ile Ser Tyr Ser Tyr Lys
    290                 295                 300

Asn Ser Phe Glu Tyr Asp Glu Phe Val Ala Ala Phe Pro Glu Tyr Arg
305                 310                 315                 320

Arg Ser Cys Val Gly Thr Asn Arg Cys Val Phe Ser Gly
                325                 330
```

<210> 2529
<211> 573
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(550)
<223> RXA01992

<400> 2529

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atagatcaat gctggcataa actaaaggca caacagccga ttcacttatt tttaggcgaa 60

tgcttgaagt cgaagtaagt gaggggggaga ggatccgtta gtg tac tgc cca ttt   115
                                              Val Tyr Cys Pro Phe
                                                1               5

tgc caa cat gat cat tca aaa gtc att gac tcc cgc gtc att gac gcc   163
Cys Gln His Asp His Ser Lys Val Ile Asp Ser Arg Val Ile Asp Ala
                  10                  15                  20

gga agc gcc att cgc agg cgc cgc gag tgc agc aaa tgc gaa ggc cgt   211
Gly Ser Ala Ile Arg Arg Arg Arg Glu Cys Ser Lys Cys Glu Gly Arg
             25                  30                  35

ttc acc acc atc gaa aaa gct gtt ctc ctc gtt gtt aaa aga aac ggc   259
Phe Thr Thr Ile Glu Lys Ala Val Leu Leu Val Val Lys Arg Asn Gly
         40                  45                  50

gtc act gaa ccg ttc agt cga gaa aaa gta gtc acc ggt gtc cgt cgt   307
Val Thr Glu Pro Phe Ser Arg Glu Lys Val Val Thr Gly Val Arg Arg
     55                  60                  65

gca tgc caa ggc cgc gac gta tca gat gac gcg ttg aaa cgc cta gct   355
Ala Cys Gln Gly Arg Asp Val Ser Asp Asp Ala Leu Lys Arg Leu Ala
 70                  75                  80                  85

cag caa gtg gaa gaa aca gtc cgc agc aac gga agc tct caa gta cgc   403
Gln Gln Val Glu Glu Thr Val Arg Ser Asn Gly Ser Ser Gln Val Arg
                 90                  95                 100

gct aac gat att ggt tta gcc att ctc gat cca ctg aga gaa ctc gac   451
Ala Asn Asp Ile Gly Leu Ala Ile Leu Asp Pro Leu Arg Glu Leu Asp
            105                 110                 115

gag gta gcg tac cta cgc ttt gcc tct gtg tat aag tct ttt gac agt   499
Glu Val Ala Tyr Leu Arg Phe Ala Ser Val Tyr Lys Ser Phe Asp Ser
        120                 125                 130

gct gac gac ttt gaa aaa gaa atc cgc ctc atg cgc aga cgc gga agg   547
Ala Asp Asp Phe Glu Lys Glu Ile Arg Leu Met Arg Arg Arg Gly Arg
    135                 140                 145

gac tagcagacac aaagtcttaa cta                                    573
Asp
150
```

<210> 2530
<211> 150
<212> PRT
<213> Corynebacterium glutamicum

<400> 2530

```
Val Tyr Cys Pro Phe Cys Gln His Asp His Ser Lys Val Ile Asp Ser
  1               5                  10                  15

Arg Val Ile Asp Ala Gly Ser Ala Ile Arg Arg Arg Arg Glu Cys Ser
             20                  25                  30

Lys Cys Glu Gly Arg Phe Thr Thr Ile Glu Lys Ala Val Leu Leu Val
         35                  40                  45
```

```
Val Lys Arg Asn Gly Val Thr Glu Pro Phe Ser Arg Glu Lys Val Val
     50                  55                  60

Thr Gly Val Arg Arg Ala Cys Gln Gly Arg Asp Val Ser Asp Asp Ala
 65                  70                  75                  80

Leu Lys Arg Leu Ala Gln Gln Val Glu Glu Thr Val Arg Ser Asn Gly
                 85                  90                  95

Ser Ser Gln Val Arg Ala Asn Asp Ile Gly Leu Ala Ile Leu Asp Pro
            100                 105                 110

Leu Arg Glu Leu Asp Glu Val Ala Tyr Leu Arg Phe Ala Ser Val Tyr
        115                 120                 125

Lys Ser Phe Asp Ser Ala Asp Asp Phe Glu Lys Glu Ile Arg Leu Met
    130                 135                 140

Arg Arg Arg Gly Arg Asp
145                 150
```

5000 2500 2000 1500 1000 500

<210> 2531
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXA01999

<400> 2531

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gggtatgtag ttagagacga cagacacaga aatcttcagc ctcgcgaacc gagtgatagc 60

atacttgacc atatcgaatt ctctaccagc tcgaggcatc atg act ctc ccc acc   115
                                            Met Thr Leu Pro Thr
                                              1               5

cct aca cat tcc acc aaa ggc agt tca ggc cgc atg aaa cga atg gcc   163
Pro Thr His Ser Thr Lys Gly Ser Ser Gly Arg Met Lys Arg Met Ala
                 10                  15                  20

ctt atc ggc tcc tcg ctc att att tcc atg gga ctt att act gcg tgc   211
Leu Ile Gly Ser Ser Leu Ile Ile Ser Met Gly Leu Ile Thr Ala Cys
             25                  30                  35

ggt tcg gcc gct gca gaa ccc gaa gcc cct gca cca aca gtt acc gaa   259
Gly Ser Ala Ala Ala Glu Pro Glu Ala Pro Ala Pro Thr Val Thr Glu
         40                  45                  50

act gta aca gcc acg gtg aca acc aca gct aaa gcc agc acg atc acc   307
Thr Val Thr Ala Thr Val Thr Thr Thr Ala Lys Ala Ser Thr Ile Thr
     55                  60                  65

tcg aca gtg acg gaa act acc tcc gcg gaa gat ctt gcc caa gaa att   355
Ser Thr Val Thr Glu Thr Thr Ser Ala Glu Asp Leu Ala Gln Glu Ile
 70                  75                  80                  85

gtg aag cca gcg gcc gtg gag gaa tat tca gag cct cag gta aat acg   403
```

```
Val Lys Pro Ala Ala Val Glu Glu Tyr Ser Glu Pro Gln Val Asn Thr
                 90                  95                 100

cca cag cag ttt gcg gcc atc ccg gaa cct gca ccg gcg gtt gca cca   451
Pro Gln Gln Phe Ala Ala Ile Pro Glu Pro Ala Pro Ala Val Ala Pro
            105                 110                 115

gct caa acg tat tac gcc aac tgc gcg gca gtt cgt gcg gcg ggt gca   499
Ala Gln Thr Tyr Tyr Ala Asn Cys Ala Ala Val Arg Ala Ala Gly Ala
        120                 125                 130

gct ccc ctt tat gcg gga tca cct gga tat agt tcc aag ctt gat cgc   547
Ala Pro Leu Tyr Ala Gly Ser Pro Gly Tyr Ser Ser Lys Leu Asp Arg
    135                 140                 145

gat ggc gac gga att gcc tgc gaa taaataggaa tagttaaaaa cac         594
Asp Gly Asp Gly Ile Ala Cys Glu
150                 155
```

<210> 2532
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 2532

```
Met Thr Leu Pro Thr Pro Thr His Ser Thr Lys Gly Ser Ser Gly Arg
  1               5                  10                  15

Met Lys Arg Met Ala Leu Ile Gly Ser Ser Leu Ile Ile Ser Met Gly
             20                  25                  30

Leu Ile Thr Ala Cys Gly Ser Ala Ala Ala Glu Pro Glu Ala Pro Ala
         35                  40                  45

Pro Thr Val Thr Glu Thr Val Thr Ala Thr Val Thr Thr Thr Ala Lys
     50                  55                  60

Ala Ser Thr Ile Thr Ser Thr Val Thr Glu Thr Thr Ser Ala Glu Asp
 65                  70                  75                  80

Leu Ala Gln Glu Ile Val Lys Pro Ala Ala Val Glu Glu Tyr Ser Glu
                 85                  90                  95

Pro Gln Val Asn Thr Pro Gln Gln Phe Ala Ala Ile Pro Glu Pro Ala
            100                 105                 110

Pro Ala Val Ala Pro Ala Gln Thr Tyr Tyr Ala Asn Cys Ala Ala Val
        115                 120                 125

Arg Ala Ala Gly Ala Ala Pro Leu Tyr Ala Gly Ser Pro Gly Tyr Ser
    130                 135                 140

Ser Lys Leu Asp Arg Asp Gly Asp Gly Ile Ala Cys Glu
145                 150                 155
```

<210> 2533
<211> 572
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(549)
<223> RXA02001

<400> 2533

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acc cgc gac ccc atc gtc gca gcc gtc gga att gtc caa gcg ttt caa   48
Thr Arg Asp Pro Ile Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln
  1               5                  10                  15

acg ata gtc agc cgg aat cac aat ccg gtc gag gac ctt gtc gtg tcg   96
Thr Ile Val Ser Arg Asn His Asn Pro Val Glu Asp Leu Val Val Ser
            20                  25                  30

gtc acg caa atc cac acc ggc agc gcc gat aat atc atc ccc gaa acc  144
Val Thr Gln Ile His Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr
        35                  40                  45

gcc tat atc aac ggc act gtc cgc acc ttc aac aaa gac gtg cag gcc  192
Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala
    50                  55                  60

atg gtc atc acg cgg atg gaa gaa atc gtc gcg ggc caa gct gca gcc  240
Met Val Ile Thr Arg Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala
65                  70                  75                  80

tat ggg gtc gag gcg acg ctg acc tac aac cgc aac tat ccc gcc acc  288
Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr
                85                  90                  95

att aac gac gcc gcc aaa gcc gcc atc gct gcc gaa gtc gcg ggc gag  336
Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu
            100                 105                 110

gtc ggc ctc ggg gtc aac ccg aac ggc tcg cgc ggg atg ggg gcc gag  384
Val Gly Leu Gly Val Asn Pro Asn Gly Ser Arg Gly Met Gly Ala Glu
        115                 120                 125

gat ttc tcg tat ttc ctc gaa aag cgc ccg ggt gcc tac ctg ttc gtc  432
Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro Gly Ala Tyr Leu Phe Val
    130                 135                 140

ggt aat ggc gac agc gcg ggc ctt cac aac ccc gcc tat aat ttc aac  480
Gly Asn Gly Asp Ser Ala Gly Leu His Asn Pro Ala Tyr Asn Phe Asn
145                 150                 155                 160

gac gag gcc gcg ccc tac ggc gca tcg ttc ttg gcc cgc atg gca gaa  528
Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe Leu Ala Arg Met Ala Glu
                165                 170                 175

cgc ccc ttg ccg tta aag ggc tgatccatgg cgctcgaaga tgc            572
Arg Pro Leu Pro Leu Lys Gly
            180
```

<210> 2534
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 2534
Thr Arg Asp Pro Ile Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln
1 5 10 15

Thr Ile Val Ser Arg Asn His Asn Pro Val Glu Asp Leu Val Val Ser
20 25 30

Val Thr Gln Ile His Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr
35 40 45

Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala
50 55 60

Met Val Ile Thr Arg Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala
65 70 75 80

Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr
85 90 95

Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu
100 105 110

Val Gly Leu Gly Val Asn Pro Asn Gly Ser Arg Gly Met Gly Ala Glu
115 120 125

Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro Gly Ala Tyr Leu Phe Val
130 135 140

Gly Asn Gly Asp Ser Ala Gly Leu His Asn Pro Ala Tyr Asn Phe Asn
145 150 155 160

Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe Leu Ala Arg Met Ala Glu
165 170 175

Arg Pro Leu Pro Leu Lys Gly
180

<210> 2535
<211> 230
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(207)
<223> RXA02004

<400> 2535
cgc gtc ggc cgt ctg atg cgt cag aac ggc att ctc atc atc cgc agc 48
Arg Val Gly Arg Leu Met Arg Gln Asn Gly Ile Leu Ile Ile Arg Ser
1 5 10 15

cgg aag ttc aag cgc acg acc ggc agc gat cat acc ttc aac atc gca 96
Arg Lys Phe Lys Arg Thr Thr Gly Ser Asp His Thr Phe Asn Ile Ala
20 25 30

ccg aac ttt ctg cag cag gac ttt atg gcg agc agg ccg aac cag aag 144
Pro Asn Phe Leu Gln Gln Asp Phe Met Ala Ser Arg Pro Asn Gln Lys
35 40 45

```
tgg gcg ggc gac atc acc tat gtc tgg acg cgc gag ggc ctg ggt cta   192
Trp Ala Gly Asp Ile Thr Tyr Val Trp Thr Arg Glu Gly Leu Gly Leu
     50                  55                  60

tct ggc cga cat tct tgacctttat ccccgccggg tga                    230
Ser Gly Arg His Ser
 65
```

<210> 2536
<211> 69
<212> PRT
<213> Corynebacterium glutamicum

<400> 2536
Arg Val Gly Arg Leu Met Arg Gln Asn Gly Ile Leu Ile Ile Arg Ser
  1   5   10   15

Arg Lys Phe Lys Arg Thr Thr Gly Ser Asp His Thr Phe Asn Ile Ala
             20   25   30

Pro Asn Phe Leu Gln Gln Asp Phe Met Ala Ser Arg Pro Asn Gln Lys
         35   40   45

Trp Ala Gly Asp Ile Thr Tyr Val Trp Thr Arg Glu Gly Leu Gly Leu
     50   55   60

Ser Gly Arg His Ser
 65

<210> 2537
<211> 565
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (71)..(565)
<223> RXA02006

<400> 2537
atcatccata catgcagagc acagctttca cacatagaca tcactgcaca tttatctaat 60

```
gggagactca atg aca gtt gca cac aaa cga agt ctg aca tgg atc aag    109
           Met Thr Val Ala His Lys Arg Ser Leu Thr Trp Ile Lys
             1               5                  10

aga cta tct gcg act aca ttt gca gct ttt ctt ggc att cag ctt gtg   157
Arg Leu Ser Ala Thr Thr Phe Ala Ala Phe Leu Gly Ile Gln Leu Val
     15                  20                  25

acc ccc gct cac tca att gaa aac acg acg cag att cca gaa agc gaa   205
Thr Pro Ala His Ser Ile Glu Asn Thr Thr Gln Ile Pro Glu Ser Glu
 30                  35                  40                  45

ttg cac aac ctc ggg ctc aca gac gaa gaa att caa gaa ttc aat caa   253
Leu His Asn Leu Gly Leu Thr Asp Glu Glu Ile Gln Glu Phe Asn Gln
                 50                  55                  60

tat ctc att gac gag tca ctc ttt caa gag act gta gaa acc tct ccg   301
```

```
Tyr Leu Ile Asp Glu Ser Leu Phe Gln Glu Thr Val Glu Thr Ser Pro
            65                  70                  75

atc gta gtc agc gac aat gaa gat gca gcc caa gat ccc ggt ttc ggc   349
Ile Val Val Ser Asp Asn Glu Asp Ala Ala Gln Asp Pro Gly Phe Gly
         80                  85                  90

ctt ttc acc aca aat cct gtg aaa cac aca gat gag cac att ggc gct   397
Leu Phe Thr Thr Asn Pro Val Lys His Thr Asp Glu His Ile Gly Ala
     95                 100                 105

cta tac ttc tcc gac cta cca ggt att tcc aat ctt acg tgc act gcc   445
Leu Tyr Phe Ser Asp Leu Pro Gly Ile Ser Asn Leu Thr Cys Thr Ala
110                 115                 120                 125

aac tac atc ggt gga aaa ttc tgg acc aca gca cat cat tgt gtt gaa   493
Asn Tyr Ile Gly Gly Lys Phe Trp Thr Thr Ala His His Cys Val Glu
                130                 135                 140

ggc cgc agt cgc ttc gtc ggc ttc atc gag cag tcg gac gga caa tat   541
Gly Arg Ser Arg Phe Val Gly Phe Ile Glu Gln Ser Asp Gly Gln Tyr
            145                 150                 155

gca ggc att gag cat gtt tac aca                                  565
Ala Gly Ile Glu His Val Tyr Thr
        160                 165
```

<210> 2538
<211> 165
<212> PRT
<213> Corynebacterium glutamicum

<400> 2538

```
Met Thr Val Ala His Lys Arg Ser Leu Thr Trp Ile Lys Arg Leu Ser
  1               5                  10                  15

Ala Thr Thr Phe Ala Ala Phe Leu Gly Ile Gln Leu Val Thr Pro Ala
             20                  25                  30

His Ser Ile Glu Asn Thr Thr Gln Ile Pro Glu Ser Glu Leu His Asn
         35                  40                  45

Leu Gly Leu Thr Asp Glu Glu Ile Gln Glu Phe Asn Gln Tyr Leu Ile
     50                  55                  60

Asp Glu Ser Leu Phe Gln Glu Thr Val Glu Thr Ser Pro Ile Val Val
 65                  70                  75                  80

Ser Asp Asn Glu Asp Ala Ala Gln Asp Pro Gly Phe Gly Leu Phe Thr
                 85                  90                  95

Thr Asn Pro Val Lys His Thr Asp Glu His Ile Gly Ala Leu Tyr Phe
            100                 105                 110

Ser Asp Leu Pro Gly Ile Ser Asn Leu Thr Cys Thr Ala Asn Tyr Ile
        115                 120                 125

Gly Gly Lys Phe Trp Thr Thr Ala His His Cys Val Glu Gly Arg Ser
    130                 135                 140
```

```
Arg Phe Val Gly Phe Ile Glu Gln Ser Asp Gly Gln Tyr Ala Gly Ile
145                 150                 155                 160

Glu His Val Tyr Thr
                165


<210> 2539
<211> 223
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(223)
<223> RXA02009

<400> 2539
aactgcatca ttgtcgttcc tgaacaagcg ccgtggttta agccagccat catcaaacag 60

gcttaaaaat actcaatcgt cccattcaag aaaagagcac atg acc atg tac aac   115
                                            Met Thr Met Tyr Asn
                                              1               5

gcc gca aag acc ctt gtt ccc cag att gtt gct ttc gat gac aca gca   163
Ala Ala Lys Thr Leu Val Pro Gln Ile Val Ala Phe Asp Asp Thr Ala
                  10                  15                  20

atc atc gca ctc gac caa gcc gcg gaa gat gaa ttc cgc aag gct aac   211
Ile Ile Ala Leu Asp Gln Ala Ala Glu Asp Glu Phe Arg Lys Ala Asn
              25                  30                  35

tac ccc gag gtt                                                  223
Tyr Pro Glu Val
         40


<210> 2540
<211> 41
<212> PRT
<213> Corynebacterium glutamicum

<400> 2540
Met Thr Met Tyr Asn Ala Ala Lys Thr Leu Val Pro Gln Ile Val Ala
  1               5                  10                  15

Phe Asp Asp Thr Ala Ile Ile Ala Leu Asp Gln Ala Ala Glu Asp Glu
             20                  25                  30

Phe Arg Lys Ala Asn Tyr Pro Glu Val
         35                  40


<210> 2541
<211> 649
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
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<223> RXA02013

<400> 2541

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atcaccgcgc tggcgacaat ttcagaaaac tcccacaaag cactgcttgg cctttatttg 60

tccggtctta aacacggcat gatggctaac atcggagaac atg acg gaa agt cct   115
                                          Met Thr Glu Ser Pro
                                            1               5

gat cta gca gtt tcc ttt tta gcc gcc ttc aat gac atc gaa gcg cac   163
Asp Leu Ala Val Ser Phe Leu Ala Ala Phe Asn Asp Ile Glu Ala His
                 10                  15                  20

ctt cga acc cag ctc cgc gct aaa cgc tcc gac agt ttc aga tgg atg   211
Leu Arg Thr Gln Leu Arg Ala Lys Arg Ser Asp Ser Phe Arg Trp Met
             25                  30                  35

gta cgt atc gcc gag aaa cag cat ctg att tcc aaa gaa caa gca gaa   259
Val Arg Ile Ala Glu Lys Gln His Leu Ile Ser Lys Glu Gln Ala Glu
         40                  45                  50

acc ctt gat gct ttt gcg gag ctg cgc aac gca att agc cac ggc caa   307
Thr Leu Asp Ala Phe Ala Glu Leu Arg Asn Ala Ile Ser His Gly Gln
     55                  60                  65

tac aac gat cta cgc ccg att gcc gat ccc cgc ccc gac acc gtg gac   355
Tyr Asn Asp Leu Arg Pro Ile Ala Asp Pro Arg Pro Asp Thr Val Asp
 70                  75                  80                  85

acc att gag aag att cgc tcc ctc ctt ctc aat cct cca att gcg tta   403
Thr Ile Glu Lys Ile Arg Ser Leu Leu Leu Asn Pro Pro Ile Ala Leu
                 90                  95                 100

aac gtc ctc ccg gag caa aag gtc cgc tcc tac tca ctt gaa gat cca   451
Asn Val Leu Pro Glu Gln Lys Val Arg Ser Tyr Ser Leu Glu Asp Pro
            105                 110                 115

gtg agt agg gcc tta gaa gtt gtg cac acc acg gag atc tcc caa ttc   499
Val Ser Arg Ala Leu Glu Val Val His Thr Thr Glu Ile Ser Gln Phe
        120                 125                 130

ccc ata tat aag gga acg gaa tac gtg gca ctg cta act acc aac aca   547
Pro Ile Tyr Lys Gly Thr Glu Tyr Val Ala Leu Leu Thr Thr Asn Thr
    135                 140                 145

atc gct cgc tgg gtt gcc tcc gat tta cat gac aat gcc cag ctg gat   595
Ile Ala Arg Trp Val Ala Ser Asp Leu His Asp Asn Ala Gln Leu Asp
150                 155                 160                 165

gca cgt tct atc aaa gag gtt ctg gat tat gca gaa tcc tct gac act   643
Ala Arg Ser Ile Lys Glu Val Leu Asp Tyr Ala Glu Ser Ser Asp Thr
                170                 175                 180

gca gtt                                                          649
Ala Val
```

<210> 2542
<211> 183
<212> PRT

<213> Corynebacterium glutamicum

<400> 2542

```
Met Thr Glu Ser Pro Asp Leu Ala Val Ser Phe Leu Ala Ala Phe Asn
  1               5                  10                  15

Asp Ile Glu Ala His Leu Arg Thr Gln Leu Arg Ala Lys Arg Ser Asp
             20                  25                  30

Ser Phe Arg Trp Met Val Arg Ile Ala Glu Lys Gln His Leu Ile Ser
         35                  40                  45

Lys Glu Gln Ala Glu Thr Leu Asp Ala Phe Ala Glu Leu Arg Asn Ala
     50                  55                  60

Ile Ser His Gly Gln Tyr Asn Asp Leu Arg Pro Ile Ala Asp Pro Arg
 65                  70                  75                  80

Pro Asp Thr Val Asp Thr Ile Glu Lys Ile Arg Ser Leu Leu Leu Asn
                 85                  90                  95

Pro Pro Ile Ala Leu Asn Val Leu Pro Glu Gln Lys Val Arg Ser Tyr
            100                 105                 110

Ser Leu Glu Asp Pro Val Ser Arg Ala Leu Glu Val Val His Thr Thr
        115                 120                 125

Glu Ile Ser Gln Phe Pro Ile Tyr Lys Gly Thr Glu Tyr Val Ala Leu
    130                 135                 140

Leu Thr Thr Asn Thr Ile Ala Arg Trp Val Ala Ser Asp Leu His Asp
145                 150                 155                 160

Asn Ala Gln Leu Asp Ala Arg Ser Ile Lys Glu Val Leu Asp Tyr Ala
                165                 170                 175

Glu Ser Ser Asp Thr Ala Val
            180
```

<210> 2543
<211> 1071
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1048)
<223> RXA02021

<400> 2543

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ttgggtcgcc gaggagatct aatcctggtt tgagttcaga gttcacaggt ttaagcctac 60

aaaccttagt taaaacatga tggaagcggt cgattaaaaa atg agt gaa aac att   115
                                              Met Ser Glu Asn Ile
                                                1               5

cgc gga gcc caa gca gtt gga atc gca aat atc gcc atg gac ggg acc   163
Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr
                10                  15                  20
```

```
atc ctg gac acg tgg tac cca gaa ccc caa att ttc aac ccg gat cag   211
Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln
             25                  30                  35

tgg gct gaa cgc tac cca ttg gaa gtg ggc acc aca cgc ctc gga gca   259
Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala
         40                  45                  50

aac gaa ctc acc cca cgg atg ctg cag ttg gta aaa ctg gac caa gat   307
Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp
     55                  60                  65

cgc ctc gtc gaa cag gta gca gtc cgc acc gtt atc ccc gat ctg tct   355
Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser
 70                  75                  80                  85

caa cct cca gta gac gcg cac gat gtt tac ctg cgc ctc cac ctg ctt   403
Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu
                 90                  95                 100

tcc cac cgg ctg gtc cgc ccc cac gaa atg cac atg caa aac acc ttg   451
Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu
            105                 110                 115

gag ctg ctg tcc gac gtg gtg tgg aca aac aag ggc cct tgc ctt cct   499
Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro
        120                 125                 130

gaa aac ttt gag tgg gtg cgt ggt gct ctg cgg tcc cgc gga ctc atc   547
Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile
    135                 140                 145

cac gtc tac tgt gtg gac cgt ctt ccc cgc atg gtc gac tat gtg gtt   595
His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val
150                 155                 160                 165

ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca   643
Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala
                170                 175                 180

tac ctt gct ccg ggt acc tct gtg ctg cgt gaa ggt ttc gtg tct ttc   691
Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe
            185                 190                 195

aac tcc ggc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc   739
Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser
        200                 205                 210

ggt gtg gtc atc ggt gaa ggt tcc gag att gga ctg tct tct act att   787
Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile
    215                 220                 225

cag tcc ccg aga gat gaa cag cgc cgc cgt ttg ccg ttg agc atc ggc   835
Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly
230                 235                 240                 245

caa aac tgc aac ttt ggt gtc agc tcc gga atc atc gga gtc agt ctg   883
Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu
                250                 255                 260

gga gac aat tgc gac atc gga aat aac att gtc ttg gat gga gat acc   931
```

```
Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr
            265                 270                 275

ccc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc   979
Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile
        280                 285                 290

gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag   1027
Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu
    295                 300                 305

cca gtt gcc cgc ctc aaa gct tgacccattt tcataaccag tgc             1071
Pro Val Ala Arg Leu Lys Ala
310                 315


<210> 2544
<211> 316
<212> PRT
<213> Corynebacterium glutamicum

<400> 2544
Met Ser Glu Asn Ile Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile
  1               5                  10                  15

Ala Met Asp Gly Thr Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile
             20                  25                  30

Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr
         35                  40                  45

Thr Arg Leu Gly Ala Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val
     50                  55                  60

Lys Leu Asp Gln Asp Arg Leu Val Glu Gln Val Ala Val Arg Thr Val
 65                  70                  75                  80

Ile Pro Asp Leu Ser Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu
                 85                  90                  95

Arg Leu His Leu Leu Ser His Arg Leu Val Arg Pro His Glu Met His
            100                 105                 110

Met Gln Asn Thr Leu Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys
        115                 120                 125

Gly Pro Cys Leu Pro Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg
    130                 135                 140

Ser Arg Gly Leu Ile His Val Tyr Cys Val Asp Arg Leu Pro Arg Met
145                 150                 155                 160

Val Asp Tyr Val Val Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg
                165                 170                 175

Val Arg Leu Gly Ala Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu
            180                 185                 190

Gly Phe Val Ser Phe Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu
        195                 200                 205
```

```
Gly Arg Leu Ser Ser Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly
    210                 215                 220

Leu Ser Ser Thr Ile Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu
225                 230                 235                 240

Pro Leu Ser Ile Gly Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile
                245                 250                 255

Ile Gly Val Ser Leu Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val
            260                 265                 270

Leu Asp Gly Asp Thr Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg
        275                 280                 285

Thr Ile Asp Ser Ile Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu
    290                 295                 300

Ser Gly Phe His Glu Pro Val Ala Arg Leu Lys Ala
305                 310                 315
```

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<210> 2545
<211> 504
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(481)
<223> RXA02036

<400> 2545

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ctaaaatgga aggcaatgga tacccgccgc atgaacctcc gccaatggaa aatcctcgtt 60

gccctcatct ctgctgcagt ggcggctctc ggagggtggt gtg cat att cct ttt   115
                                              Val His Ile Pro Phe
                                                1               5

ggg cac ctc gcc gac acc gtc tcc tgg gac tgc ggg gga ggc agc tgc   163
Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys Gly Gly Gly Ser Cys
               10                  15                  20

gcc acc aac gat ttg gta tcc ctg ttc atg ccg gcc gcc ttc atg agt   211
Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro Ala Ala Phe Met Ser
           25                  30                  35

acc ctc gcc gcc tgc gta ttt ggc gcg tgg gcc ata ggt ttg atc gct   259
Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala Ile Gly Leu Ile Ala
       40                  45                  50

ccc gca cta ttc atc gcg gtg act gcc tgg gca ttt cgc tcc ggc gtg   307
Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala Phe Arg Ser Gly Val
   55                  60                  65

cag gct gcg att gcc gac ggc tac acg tcc gcg act tcc gtc ggc ttc   355
Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala Thr Ser Val Gly Phe
70                  75                  80                  85

gaa atg act gtc tcg ctc att ctt ttc atc atc gca ggt ctg tgc ttt   403
Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile Ala Gly Leu Cys Phe
```

```
                90                  95                  100

ctg ggc tgg atc ccc atg ttc atc aac aac cgc caa gtc gcg cgc aag   451
Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg Gln Val Ala Arg Lys
            105                 110                 115

gtc cgc gag agg gct gcg ggc ttg agc aat taggctctcg cttttcgacg     501
Val Arg Glu Arg Ala Ala Gly Leu Ser Asn
        120                 125

ttt                                                               504
```

<210> 2546
<211> 127
<212> PRT
<213> Corynebacterium glutamicum

<400> 2546

```
Val His Ile Pro Phe Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys
  1               5                  10                  15

Gly Gly Gly Ser Cys Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro
             20                  25                  30

Ala Ala Phe Met Ser Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala
         35                  40                  45

Ile Gly Leu Ile Ala Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala
     50                  55                  60

Phe Arg Ser Gly Val Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala
 65                  70                  75                  80

Thr Ser Val Gly Phe Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile
                 85                  90                  95

Ala Gly Leu Cys Phe Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg
            100                 105                 110

Gln Val Ala Arg Lys Val Arg Glu Arg Ala Ala Gly Leu Ser Asn
        115                 120                 125
```

<210> 2547
<211> 551
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(528)
<223> RXA02040

<400> 2547

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tac ata cct ttt gtc att tgg tcc gat ctc ggt gag gct gcc gaa ggt   48
Tyr Ile Pro Phe Val Ile Trp Ser Asp Leu Gly Glu Ala Ala Glu Gly
  1               5                  10                  15

gag aac ttt gct cgc ttc tgg tcc tgg ctg aaa tcg cgc cgg gac aaa   96
Glu Asn Phe Ala Arg Phe Trp Ser Trp Leu Lys Ser Arg Arg Asp Lys
```

```
             20                  25                  30

gct cgc cag cag gga caa acc ttc ggt gtg ttc tgc tat gcc agc aac   144
Ala Arg Gln Gln Gly Gln Thr Phe Gly Val Phe Cys Tyr Ala Ser Asn
         35                  40                  45

ggc gaa aac cac tgg atg ctc tcc act gct cgc aga ttc ttc ggc aaa   192
Gly Glu Asn His Trp Met Leu Ser Thr Ala Arg Arg Phe Phe Gly Lys
     50                  55                  60

gtc aaa ggt gtg ccc gac gag caa gaa atc cgc agc ttc att agc tct   240
Val Lys Gly Val Pro Asp Glu Gln Glu Ile Arg Ser Phe Ile Ser Ser
 65                  70                  75                  80

gac caa tgg aat gac atg ttt gct gtc gcg cgc tcc caa ctt gtt ggc   288
Asp Gln Trp Asn Asp Met Phe Ala Val Ala Arg Ser Gln Leu Val Gly
                 85                  90                  95

ccc ggt ggt tta ggt ctg aaa caa ctc gcg ccg gca gct gga ttc cat   336
Pro Gly Gly Leu Gly Leu Lys Gln Leu Ala Pro Ala Ala Gly Phe His
            100                 105                 110

tgg gag gaa gaa gac ttc gca ggt gaa gat agc ctc cac gca tat ctc   384
Trp Glu Glu Glu Asp Phe Ala Gly Glu Asp Ser Leu His Ala Tyr Leu
        115                 120                 125

att gct tcc acg gct gcc gaa cca gaa gct gag gcc gct cgt gct caa   432
Ile Ala Ser Thr Ala Ala Glu Pro Glu Ala Glu Ala Ala Arg Ala Gln
    130                 135                 140

ttg ctc agc tac aac ggc gat gat tgc agg gcc acc gca gcg gtt cgc   480
Leu Leu Ser Tyr Asn Gly Asp Asp Cys Arg Ala Thr Ala Ala Val Arg
145                 150                 155                 160

cat tgg ctt cga caa ggt gcg cgc acg gca cct gtg ctg ggg aat att   528
His Trp Leu Arg Gln Gly Ala Arg Thr Ala Pro Val Leu Gly Asn Ile
                165                 170                 175

taaaccaagg aaggattctc cag                                        551
```

<210> 2548
<211> 176
<212> PRT
<213> Corynebacterium glutamicum

<400> 2548

```
Tyr Ile Pro Phe Val Ile Trp Ser Asp Leu Gly Glu Ala Ala Glu Gly
  1               5                  10                  15

Glu Asn Phe Ala Arg Phe Trp Ser Trp Leu Lys Ser Arg Arg Asp Lys
             20                  25                  30

Ala Arg Gln Gln Gly Gln Thr Phe Gly Val Phe Cys Tyr Ala Ser Asn
         35                  40                  45

Gly Glu Asn His Trp Met Leu Ser Thr Ala Arg Arg Phe Phe Gly Lys
     50                  55                  60

Val Lys Gly Val Pro Asp Glu Gln Glu Ile Arg Ser Phe Ile Ser Ser
 65                  70                  75                  80
```

```
Asp Gln Trp Asn Asp Met Phe Ala Val Ala Arg Ser Gln Leu Val Gly
                 85                  90                  95

Pro Gly Gly Leu Gly Leu Lys Gln Leu Ala Pro Ala Ala Gly Phe His
            100                 105                 110

Trp Glu Glu Glu Asp Phe Ala Gly Glu Asp Ser Leu His Ala Tyr Leu
        115                 120                 125

Ile Ala Ser Thr Ala Ala Glu Pro Glu Ala Glu Ala Ala Arg Ala Gln
    130                 135                 140

Leu Leu Ser Tyr Asn Gly Asp Asp Cys Arg Ala Thr Ala Ala Val Arg
145                 150                 155                 160

His Trp Leu Arg Gln Gly Ala Arg Thr Ala Pro Val Leu Gly Asn Ile
                165                 170                 175
```

<210> 2549
<211> 364
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(364)
<223> RXA02046

<400> 2549

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tccgtgccat caccaccggc gagatcactg gcatcgtgga cgcaaaacaa acagcaacag 60

aaattattaa catccgacgc aacgcttcag gagagtcctc atg aaa gag aca ctg  115
                                            Met Lys Glu Thr Leu
                                              1               5

acc acc ggt tta acc cac caa atg acc tac ata gtg cca gca aac cgc  163
Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile Val Pro Ala Asn Arg
                 10                  15                  20

aca gtt ccg cat ctg ctt ccc gaa gca gca gaa ttt gaa acc atg cca  211
Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu Phe Glu Thr Met Pro
             25                  30                  35

gat gtc ctg gcc act gga tat atg gtc ggc atc atc gag tgg gcc tgc  259
Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile Ile Glu Trp Ala Cys
         40                  45                  50

atg gaa ctt ctg cgt ccc cat ttg gac gac ggt gaa atc tcg ctg ggc  307
Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly Glu Ile Ser Leu Gly
     55                  60                  65

act cat gtg aac ttc tcc cac gca gct cca acg gtt cct gga tcc acg  355
Thr His Val Asn Phe Ser His Ala Ala Pro Thr Val Pro Gly Ser Thr
 70                  75                  80                  85

gtc acc atc                                                     364
```

Val Thr Ile

<210> 2550
<211> 88
<212> PRT
<213> Corynebacterium glutamicum

<400> 2550
Met Lys Glu Thr Leu Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile
1 5 10 15

Val Pro Ala Asn Arg Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu
20 25 30

Phe Glu Thr Met Pro Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile
35 40 45

Ile Glu Trp Ala Cys Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly
50 55 60

Glu Ile Ser Leu Gly Thr His Val Asn Phe Ser His Ala Ala Pro Thr
65 70 75 80

Val Pro Gly Ser Thr Val Thr Ile
85

<210> 2551
<211> 621
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(598)
<223> RXA02051

<400> 2551
cgcactgatc ggtgtagtaa ctggcggtat tttgctgcta attaactcgc aaaacggtga 60

gcagacatca tcttcaactc gcacaacagt caatgactcc atg gtc atc aga gct 115
Met Val Ile Arg Ala
1 5

ctc cag cgc gaa gaa gaa atc gtc ctt ctc agc gcc gga gca ctt gga 163
Leu Gln Arg Glu Glu Glu Ile Val Leu Leu Ser Ala Gly Ala Leu Gly
10 15 20

atc cat gag aaa acc gtt gaa cgt aca att cgt gga aaa cgt att cct 211
Ile His Glu Lys Thr Val Glu Arg Thr Ile Arg Gly Lys Arg Ile Pro
25 30 35

ggc acg caa aag acc gtg cac gtc caa tac agc tac acc gga aaa ctc 259
Gly Thr Gln Lys Thr Val His Val Gln Tyr Ser Tyr Thr Gly Lys Leu
40 45 50

gga atc gat gcc tca gat gtt gaa atc aaa tcc gca ggt gac aat aag 307
Gly Ile Asp Ala Ser Asp Val Glu Ile Lys Ser Ala Gly Asp Asn Lys
55 60 65

```
ctt tcc atc act atc cct gag ttc atc ttc atc gga tac gac gat cta   355
Leu Ser Ile Thr Ile Pro Glu Phe Ile Phe Ile Gly Tyr Asp Asp Leu
 70                  75                  80                  85

aag ttt aag acc ata gcc gaa gat gac ggt tgg atc agt ttc agc act   403
Lys Phe Lys Thr Ile Ala Glu Asp Asp Gly Trp Ile Ser Phe Ser Thr
                 90                  95                 100

gac gat atc gat act gca gaa gta gtt tct gag atc atg agc caa gag   451
Asp Asp Ile Asp Thr Ala Glu Val Val Ser Glu Ile Met Ser Gln Glu
            105                 110                 115

aac ttc gtc gag caa gta acc act aac cgg gaa atg ttg gaa gat caa   499
Asn Phe Val Glu Gln Val Thr Thr Asn Arg Glu Met Leu Glu Asp Gln
        120                 125                 130

gcg gtt gat ttc tac aac gac ctg ctc cac gaa ttc acc gag aaa ctc   547
Ala Val Asp Phe Tyr Asn Asp Leu Leu His Glu Phe Thr Glu Lys Leu
    135                 140                 145

gat aca gat cga tac gaa gac acc aag att gag ctc gaa ttc gag ttt   595
Asp Thr Asp Arg Tyr Glu Asp Thr Lys Ile Glu Leu Glu Phe Glu Phe
150                 155                 160                 165

gag tagatagtgc ttcgaagaca gtt                                    621
Glu
```

<210> 2552
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

<400> 2552

```
Met Val Ile Arg Ala Leu Gln Arg Glu Glu Glu Ile Val Leu Leu Ser
  1               5                  10                  15

Ala Gly Ala Leu Gly Ile His Glu Lys Thr Val Glu Arg Thr Ile Arg
            20                  25                  30

Gly Lys Arg Ile Pro Gly Thr Gln Lys Thr Val His Val Gln Tyr Ser
        35                  40                  45

Tyr Thr Gly Lys Leu Gly Ile Asp Ala Ser Asp Val Glu Ile Lys Ser
    50                  55                  60

Ala Gly Asp Asn Lys Leu Ser Ile Thr Ile Pro Glu Phe Ile Phe Ile
65                  70                  75                  80

Gly Tyr Asp Asp Leu Lys Phe Lys Thr Ile Ala Glu Asp Asp Gly Trp
                85                  90                  95

Ile Ser Phe Ser Thr Asp Asp Ile Asp Thr Ala Glu Val Val Ser Glu
            100                 105                 110

Ile Met Ser Gln Glu Asn Phe Val Glu Gln Val Thr Thr Asn Arg Glu
        115                 120                 125

Met Leu Glu Asp Gln Ala Val Asp Phe Tyr Asn Asp Leu Leu His Glu
```

```
    130                 135                 140

Phe Thr Glu Lys Leu Asp Thr Asp Arg Tyr Glu Asp Thr Lys Ile Glu
145                 150                 155                 160

Leu Glu Phe Glu Phe Glu
                165
```

<210> 2553
<211> 702
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(679)
<223> RXA02053

<400> 2553

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aaccagccag aaactatctc caaaagctaa taaaaccctt gcactgacaa ataaggcgac 60

ctaccatgac tctgtttcca acacataaaa aggataaaaa atg tca ctt tca gtc   115
                                            Met Ser Leu Ser Val
                                              1               5

gtc gag gcg att acc aac cgc cgc gcc acc cgc aaa tac acc gat gaa   163
Val Glu Ala Ile Thr Asn Arg Arg Ala Thr Arg Lys Tyr Thr Asp Glu
                 10                  15                  20

gct cct acc cct gag ctg atc gac aaa atc gtt gac ctt gcc ctg gag   211
Ala Pro Thr Pro Glu Leu Ile Asp Lys Ile Val Asp Leu Ala Leu Glu
             25                  30                  35

gca ccc agt gcg ttc aat gcg cag caa cgt gaa att gtt gtg att act   259
Ala Pro Ser Ala Phe Asn Ala Gln Gln Arg Glu Ile Val Val Ile Thr
         40                  45                  50

gat ccc gca cag aag cag aag ctt tac gag gcc tcc cat cag aaa caa   307
Asp Pro Ala Gln Lys Gln Lys Leu Tyr Glu Ala Ser His Gln Lys Gln
     55                  60                  65

ttc ctc acc gca cct gta act ttc att gcg gtt gcc cgc gtg gaa aac   355
Phe Leu Thr Ala Pro Val Thr Phe Ile Ala Val Ala Arg Val Glu Asn
 70                  75                  80                  85

gag cct gag gat ttg gaa gag att ctt ggt acg gaa agg gct gaa cgt   403
Glu Pro Glu Asp Leu Glu Glu Ile Leu Gly Thr Glu Arg Ala Glu Arg
                 90                  95                 100

gtc gcg gga ttc atc aac ggt cgc agc att cag cag gca cgc gaa gca   451
Val Ala Gly Phe Ile Asn Gly Arg Ser Ile Gln Gln Ala Arg Glu Ala
            105                 110                 115

acg ttg agg gat gcc agc ctc gcg gcg gct ttt cta att ctg gct gcc   499
Thr Leu Arg Asp Ala Ser Leu Ala Ala Ala Phe Leu Ile Leu Ala Ala
        120                 125                 130

cag gcg gag ggt ttg agt acc agc ccg act act ggt tgg gat gag gaa   547
Gln Ala Glu Gly Leu Ser Thr Ser Pro Thr Thr Gly Trp Asp Glu Glu
    135                 140                 145
```

```
aaa gtg aag gaa gca atc ggt ctc ggc ggg cgt gag gat cgt gca atc   595
Lys Val Lys Glu Ala Ile Gly Leu Gly Gly Arg Glu Asp Arg Ala Ile
150                 155                 160                 165

gcc ctt gtt att gct acc gga ttc cct aat gaa cag ccg gag cac cct   643
Ala Leu Val Ile Ala Thr Gly Phe Pro Asn Glu Gln Pro Glu His Pro
                170                 175                 180

ggt cgt ttg cag aat agg cgc atc gac aac agc tac taactctgcc        689
Gly Arg Leu Gln Asn Arg Arg Ile Asp Asn Ser Tyr
            185                 190

agctcgcccg gac                                                   702
```

<210> 2554
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 2554

```
Met Ser Leu Ser Val Val Glu Ala Ile Thr Asn Arg Arg Ala Thr Arg
  1               5                  10                  15

Lys Tyr Thr Asp Glu Ala Pro Thr Pro Glu Leu Ile Asp Lys Ile Val
             20                  25                  30

Asp Leu Ala Leu Glu Ala Pro Ser Ala Phe Asn Ala Gln Gln Arg Glu
         35                  40                  45

Ile Val Val Ile Thr Asp Pro Ala Gln Lys Gln Lys Leu Tyr Glu Ala
     50                  55                  60

Ser His Gln Lys Gln Phe Leu Thr Ala Pro Val Thr Phe Ile Ala Val
 65                  70                  75                  80

Ala Arg Val Glu Asn Glu Pro Glu Asp Leu Glu Glu Ile Leu Gly Thr
                 85                  90                  95

Glu Arg Ala Glu Arg Val Ala Gly Phe Ile Asn Gly Arg Ser Ile Gln
            100                 105                 110

Gln Ala Arg Glu Ala Thr Leu Arg Asp Ala Ser Leu Ala Ala Ala Phe
        115                 120                 125

Leu Ile Leu Ala Ala Gln Ala Glu Gly Leu Ser Thr Ser Pro Thr Thr
    130                 135                 140

Gly Trp Asp Glu Glu Lys Val Lys Glu Ala Ile Gly Leu Gly Gly Arg
145                 150                 155                 160

Glu Asp Arg Ala Ile Ala Leu Val Ile Ala Thr Gly Phe Pro Asn Glu
                165                 170                 175

Gln Pro Glu His Pro Gly Arg Leu Gln Asn Arg Arg Ile Asp Asn Ser
            180                 185                 190

Tyr
```

<210> 2555
<211> 654
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(631)
<223> RXA02057

<400> 2555
aagtctttat agtcctgcac tagcctagaa gggccttatg ccgtgtgaat cacacagcat 60

acggcccttt ttgctgccgt ggttgcctaa ggtggaaggt atg aaa cga atc tgt 115
Met Lys Arg Ile Cys
1 5

gcg gtc gcg atc tct tca gta ctt ttg tta agt ggc tgc tcc tcc act 163
Ala Val Ala Ile Ser Ser Val Leu Leu Leu Ser Gly Cys Ser Ser Thr
10 15 20

tcc aca acg cag ctc gag gga ttc gat gga cgc tca gcg cag gag atc 211
Ser Thr Thr Gln Leu Glu Gly Phe Asp Gly Arg Ser Ala Gln Glu Ile
25 30 35

atc aca gaa ctt gat caa acc cca gtc gca gac aga gca act aac ctc 259
Ile Thr Glu Leu Asp Gln Thr Pro Val Ala Asp Arg Ala Thr Asn Leu
40 45 50

atg gcc tcc att cgg gca gat gag tta att ctg tcg gat caa agc gga 307
Met Ala Ser Ile Arg Ala Asp Glu Leu Ile Leu Ser Asp Gln Ser Gly
55 60 65

cag ctc agc att gac atg cct gca gat gag ttc tat atc tcc gca gcc 355
Gln Leu Ser Ile Asp Met Pro Ala Asp Glu Phe Tyr Ile Ser Ala Ala
70 75 80 85

ccg tac acc acc aca acc cac gag tgc ttc tat cac agc ctc acc aca 403
Pro Tyr Thr Thr Thr Thr His Glu Cys Phe Tyr His Ser Leu Thr Thr
90 95 100

tgt act ggt gaa ctc gcc aac acc cca gtg aaa gta acg gtg gtg gca 451
Cys Thr Gly Glu Leu Ala Asn Thr Pro Val Lys Val Thr Val Val Ala
105 110 115

gat aat gga gaa acc atc ctc gaa gag gac acc atc acc tac gat aat 499
Asp Asn Gly Glu Thr Ile Leu Glu Glu Asp Thr Ile Thr Tyr Asp Asn
120 125 130

gga ttt gtt ggg atg tgg ctc ccc cgc aac att gat gcc aca ctc acc 547
Gly Phe Val Gly Met Trp Leu Pro Arg Asn Ile Asp Ala Thr Leu Thr
135 140 145

atc gaa cat gac ggc ctg aaa tcc acc cag ccg atc tct acg ggt gat 595
Ile Glu His Asp Gly Leu Lys Ser Thr Gln Pro Ile Ser Thr Gly Asp
150 155 160 165

gac gcc ccc acg tgc atc acc acg gct gaa cta gcg tgaaaatcct 641
Asp Ala Pro Thr Cys Ile Thr Thr Ala Glu Leu Ala
170 175

ttagacaata aga 654

<210> 2556
<211> 177
<212> PRT
<213> Corynebacterium glutamicum

<400> 2556

```
Met Lys Arg Ile Cys Ala Val Ala Ile Ser Ser Val Leu Leu Leu Ser
  1               5                  10                  15

Gly Cys Ser Ser Thr Ser Thr Thr Gln Leu Glu Gly Phe Asp Gly Arg
             20                  25                  30

Ser Ala Gln Glu Ile Ile Thr Glu Leu Asp Gln Thr Pro Val Ala Asp
         35                  40                  45

Arg Ala Thr Asn Leu Met Ala Ser Ile Arg Ala Asp Glu Leu Ile Leu
     50                  55                  60

Ser Asp Gln Ser Gly Gln Leu Ser Ile Asp Met Pro Ala Asp Glu Phe
 65                  70                  75                  80

Tyr Ile Ser Ala Ala Pro Tyr Thr Thr Thr Thr His Glu Cys Phe Tyr
                 85                  90                  95

His Ser Leu Thr Thr Cys Thr Gly Glu Leu Ala Asn Thr Pro Val Lys
            100                 105                 110

Val Thr Val Val Ala Asp Asn Gly Glu Thr Ile Leu Glu Glu Asp Thr
        115                 120                 125

Ile Thr Tyr Asp Asn Gly Phe Val Gly Met Trp Leu Pro Arg Asn Ile
    130                 135                 140

Asp Ala Thr Leu Thr Ile Glu His Asp Gly Leu Lys Ser Thr Gln Pro
145                 150                 155                 160

Ile Ser Thr Gly Asp Asp Ala Pro Thr Cys Ile Thr Thr Ala Glu Leu
                165                 170                 175

Ala
```

<210> 2557
<211> 675
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(652)
<223> RXA02058

<400> 2557

gaagcggatt ttagtccttg cgcttggtgc ctcggtagcg ggatgctcaa cgctttccca 60

agaaccttca ccacctgttc cgttgggaaa cgttgatact gtg cag att gtc tct 115

```
                                                    Val Gln Ile Val Ser
                                                      1               5

ccc aat ggg gag att gag tct ttt gtg ctg ggg aag ctg tat gag acc   163
Pro Asn Gly Glu Ile Glu Ser Phe Val Leu Gly Lys Leu Tyr Glu Thr
                 10                  15                  20

gca tta gtg gaa cgt ggc aga tct gca tca gtt cag ctg att gac ggc   211
Ala Leu Val Glu Arg Gly Arg Ser Ala Ser Val Gln Leu Ile Asp Gly
             25                  30                  35

gac ttg gat gag caa cta tct atg ctg cga gat gac agc act gat ttg   259
Asp Leu Asp Glu Gln Leu Ser Met Leu Arg Asp Asp Ser Thr Asp Leu
         40                  45                  50

gtg att gct tgc tca gga caa tta ctg gaa tat tac aac cca gat tta   307
Val Ile Ala Cys Ser Gly Gln Leu Leu Glu Tyr Tyr Asn Pro Asp Leu
     55                  60                  65

gcc tcc gag ttt gcc gtc gaa tac gct aat cag aca gcc ttt gat aaa   355
Ala Ser Glu Phe Ala Val Glu Tyr Ala Asn Gln Thr Ala Phe Asp Lys
 70                  75                  80                  85

aac tct ggt gaa tgg cgc gaa aaa gtc tac gat gct ctc caa gga tcg   403
Asn Ser Gly Glu Trp Arg Glu Lys Val Tyr Asp Ala Leu Gln Gly Ser
                 90                  95                 100

ctg ccg gac tcc atc gtg gcc acc gat cct tcc aat gct att ggt tgt   451
Leu Pro Asp Ser Ile Val Ala Thr Asp Pro Ser Asn Ala Ile Gly Cys
            105                 110                 115

aag gac gat acg tcg ctg cct caa aac atc gtg cca att tat aga aag   499
Lys Asp Asp Thr Ser Leu Pro Gln Asn Ile Val Pro Ile Tyr Arg Lys
        120                 125                 130

ccc aat ctg gat agg gac aat cgg gac acc ctg aac ttt gtg agc ggt   547
Pro Asn Leu Asp Arg Asp Asn Arg Asp Thr Leu Asn Phe Val Ser Gly
    135                 140                 145

tct ttg ggt aca agc gat ttg gaa gca ttg gtc aag gac gcc caa aca   595
Ser Leu Gly Thr Ser Asp Leu Glu Ala Leu Val Lys Asp Ala Gln Thr
150                 155                 160                 165

aca ggc aca acc tct gaa act gcg ctg gat ttc tta ttg tct aaa gga   643
Thr Gly Thr Thr Ser Glu Thr Ala Leu Asp Phe Leu Leu Ser Lys Gly
                170                 175                 180

ttt tca cgc tagttcagcc gtggtgatgc acg                             675
Phe Ser Arg
```

<210> 2558
<211> 184
<212> PRT
<213> Corynebacterium glutamicum

<400> 2558

```
Val Gln Ile Val Ser Pro Asn Gly Glu Ile Glu Ser Phe Val Leu Gly
  1               5                  10                  15
```

```
Lys Leu Tyr Glu Thr Ala Leu Val Glu Arg Gly Arg Ser Ala Ser Val
            20                  25                  30

Gln Leu Ile Asp Gly Asp Leu Asp Glu Gln Leu Ser Met Leu Arg Asp
        35                  40                  45

Asp Ser Thr Asp Leu Val Ile Ala Cys Ser Gly Gln Leu Leu Glu Tyr
    50                  55                  60

Tyr Asn Pro Asp Leu Ala Ser Glu Phe Ala Val Glu Tyr Ala Asn Gln
65                  70                  75                  80

Thr Ala Phe Asp Lys Asn Ser Gly Glu Trp Arg Glu Lys Val Tyr Asp
                85                  90                  95

Ala Leu Gln Gly Ser Leu Pro Asp Ser Ile Val Ala Thr Asp Pro Ser
            100                 105                 110

Asn Ala Ile Gly Cys Lys Asp Asp Thr Ser Leu Pro Gln Asn Ile Val
        115                 120                 125

Pro Ile Tyr Arg Lys Pro Asn Leu Asp Arg Asp Asn Arg Asp Thr Leu
    130                 135                 140

Asn Phe Val Ser Gly Ser Leu Gly Thr Ser Asp Leu Glu Ala Leu Val
145                 150                 155                 160

Lys Asp Ala Gln Thr Thr Gly Thr Thr Ser Glu Thr Ala Leu Asp Phe
                165                 170                 175

Leu Leu Ser Lys Gly Phe Ser Arg
            180


<210> 2559
<211> 702
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(679)
<223> RXA02069

<400> 2559
cgccatctgc ttggtgccgt agctgtcgat gacttgctcg accacatgct gccagaagac 60

tggcgcgacg ccggaatccg accaggaaag gagcacaccc atg gct gat ttc aac   115
                                              Met Ala Asp Phe Asn
                                                1               5

cgc tct gaa tta gac agc cca ctt ttt gga tcc cgc aaa cga ttt aaa   163
Arg Ser Glu Leu Asp Ser Pro Leu Phe Gly Ser Arg Lys Arg Phe Lys
                10                  15                  20

ttc gac gat gac acc att ggt gcc tac gcc gaa aaa gta gcc cgg ttc   211
Phe Asp Asp Asp Thr Ile Gly Ala Tyr Ala Glu Lys Val Ala Arg Phe
            25                  30                  35

ttt ggc acg gga cag tac ctg ttt tgg caa acc att ttc gtg gtg gtg   259
Phe Gly Thr Gly Gln Tyr Leu Phe Trp Gln Thr Ile Phe Val Val Val
```

```
         40                  45                  50

tgg att ttc ctc aac atc ggt ggt tgg gcc tgg agt tgg gac ccc tac   307
Trp Ile Phe Leu Asn Ile Gly Gly Trp Ala Trp Ser Trp Asp Pro Tyr
     55                  60                  65

cct ttc atc ctg ctc aac ctg gca ttc tcc acg cag gct gct tat gct   355
Pro Phe Ile Leu Leu Asn Leu Ala Phe Ser Thr Gln Ala Ala Tyr Ala
 70                  75                  80                  85

gct ccg ctg atc ctg ttg gcg caa aac cgt caa gaa gac cgc gat aag   403
Ala Pro Leu Ile Leu Leu Ala Gln Asn Arg Gln Glu Asp Arg Asp Lys
                 90                  95                 100

cac acc att ttg gcg gat cgt cgg cgt gct gaa gag aca aaa gcc gat   451
His Thr Ile Leu Ala Asp Arg Arg Arg Ala Glu Glu Thr Lys Ala Asp
            105                 110                 115

act gaa ttc ctc gca cgg gaa ctc gca ggc gtt cgc tta gcc ttg gga   499
Thr Glu Phe Leu Ala Arg Glu Leu Ala Gly Val Arg Leu Ala Leu Gly
        120                 125                 130

gat act gtc aca cgt gac tat ttg cgc cat gag tta gaa gat ctc cgc   547
Asp Thr Val Thr Arg Asp Tyr Leu Arg His Glu Leu Glu Asp Leu Arg
    135                 140                 145

gga ctt ctt gac cgc att gaa gcc aag ctc gac gac gag gca gcg tcc   595
Gly Leu Leu Asp Arg Ile Glu Ala Lys Leu Asp Asp Glu Ala Ala Ser
150                 155                 160                 165

cgt att gca gac cgc cac gaa cag cac gga tca gga cct caa gat ttg   643
Arg Ile Ala Asp Arg His Glu Gln His Gly Ser Gly Pro Gln Asp Leu
                170                 175                 180

tct gac ccc act cag ggt gat gtt gca gac gaa ttt tagggagtat        689
Ser Asp Pro Thr Gln Gly Asp Val Ala Asp Glu Phe
            185                 190

caaaacttgg gac                                                   702
```

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<210> 2560
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 2560

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Met Ala Asp Phe Asn Arg Ser Glu Leu Asp Ser Pro Leu Phe Gly Ser
  1               5                  10                  15

Arg Lys Arg Phe Lys Phe Asp Asp Asp Thr Ile Gly Ala Tyr Ala Glu
             20                  25                  30

Lys Val Ala Arg Phe Phe Gly Thr Gly Gln Tyr Leu Phe Trp Gln Thr
         35                  40                  45

Ile Phe Val Val Val Trp Ile Phe Leu Asn Ile Gly Gly Trp Ala Trp
     50                  55                  60

Ser Trp Asp Pro Tyr Pro Phe Ile Leu Leu Asn Leu Ala Phe Ser Thr
 65                  70                  75                  80
```

```
Gln Ala Ala Tyr Ala Ala Pro Leu Ile Leu Leu Ala Gln Asn Arg Gln
                 85                  90                  95

Glu Asp Arg Asp Lys His Thr Ile Leu Ala Asp Arg Arg Arg Ala Glu
            100                 105                 110

Glu Thr Lys Ala Asp Thr Glu Phe Leu Ala Arg Glu Leu Ala Gly Val
        115                 120                 125

Arg Leu Ala Leu Gly Asp Thr Val Thr Arg Asp Tyr Leu Arg His Glu
    130                 135                 140

Leu Glu Asp Leu Arg Gly Leu Leu Asp Arg Ile Glu Ala Lys Leu Asp
145                 150                 155                 160

Asp Glu Ala Ala Ser Arg Ile Ala Asp Arg His Glu Gln His Gly Ser
                165                 170                 175

Gly Pro Gln Asp Leu Ser Asp Pro Thr Gln Gly Asp Val Ala Asp Glu
            180                 185                 190

Phe
```

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<210> 2561
<211> 1221
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1198)
<223> RXA02070

<400> 2561

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agcacggatc aggacctcaa gatttgtctg accccactca gggtgatgtt gcagacgaat 60

tttagggagt atcaaaactt gggactacta tcgatacgtg atg act caa gta acc   115
                                        Met Thr Gln Val Thr
                                          1               5

gaa tcc gct gtc cgc agc gcg cta tcc cgc gta gag gat cca gag atc   163
Glu Ser Ala Val Arg Ser Ala Leu Ser Arg Val Glu Asp Pro Glu Ile
                 10                  15                  20

ggt aag ccc atc aca gag ctc ggc atg gtc aaa tca gtg tcc atc gac   211
Gly Lys Pro Ile Thr Glu Leu Gly Met Val Lys Ser Val Ser Ile Asp
             25                  30                  35

ggc tct gat gtc cag gtg gag gtc tac ctg acg atc gcg gct tgc ccg   259
Gly Ser Asp Val Gln Val Glu Val Tyr Leu Thr Ile Ala Ala Cys Pro
         40                  45                  50

atg aaa acc acc att gtc acc aac act gaa gca gct ctc aaa gac atc   307
Met Lys Thr Thr Ile Val Thr Asn Thr Glu Ala Ala Leu Lys Asp Ile
     55                  60                  65

gac ggg gtt ggc caa gtt cat gtc acc acc gat gtc atg agt gat gaa   355
Asp Gly Val Gly Gln Val His Val Thr Thr Asp Val Met Ser Asp Glu
```

```
 70                  75                  80                  85

cag cgc cgt gcg ctc cgc gtc tcc ctg cgc ggt gaa act tct gag cca   403
Gln Arg Arg Ala Leu Arg Val Ser Leu Arg Gly Glu Thr Ser Glu Pro
                90                  95                 100

gtg att cca ttc gct cag cct ggt tcc act acc cgc gtt tac gct gtt   451
Val Ile Pro Phe Ala Gln Pro Gly Ser Thr Thr Arg Val Tyr Ala Val
            105                 110                 115

gct tcc ggc aaa ggt ggc gta gga aaa tcc tcc atg acg gtg aac ttg   499
Ala Ser Gly Lys Gly Gly Val Gly Lys Ser Ser Met Thr Val Asn Leu
        120                 125                 130

gct gca gcc cta gcc aag cgc ggg ctg tct gtg gga att ttg gat gcc   547
Ala Ala Ala Leu Ala Lys Arg Gly Leu Ser Val Gly Ile Leu Asp Ala
    135                 140                 145

gat att tac gga cac tca gtg ccc gga atg ctc ggc tcg gac caa cgc   595
Asp Ile Tyr Gly His Ser Val Pro Gly Met Leu Gly Ser Asp Gln Arg
150                 155                 160                 165

cca cac cag gtc gat gac atg atc atg cct ccc cag gcg cac ggc gtg   643
Pro His Gln Val Asp Asp Met Ile Met Pro Pro Gln Ala His Gly Val
                170                 175                 180

aag atg ata tcc att gct cac ttc acc gaa gga aat gct cct gtg gtg   691
Lys Met Ile Ser Ile Ala His Phe Thr Glu Gly Asn Ala Pro Val Val
            185                 190                 195

tgg cgt gga cca atg ctg cac cgt gcc atc cag caa ttc ctc act gac   739
Trp Arg Gly Pro Met Leu His Arg Ala Ile Gln Gln Phe Leu Thr Asp
        200                 205                 210

gtg ttc tgg ggc gac ctg gat att ttg ctg ctg gat ctt cct cca gga   787
Val Phe Trp Gly Asp Leu Asp Ile Leu Leu Leu Asp Leu Pro Pro Gly
    215                 220                 225

act ggt gac atc gcc atc acc gtt gcc caa ttg atc ccg aat gct gag   835
Thr Gly Asp Ile Ala Ile Thr Val Ala Gln Leu Ile Pro Asn Ala Glu
230                 235                 240                 245

ttg ctc att gtg acc act cct cag gct gcc gca gct gag gtt gcc gag   883
Leu Leu Ile Val Thr Thr Pro Gln Ala Ala Ala Ala Glu Val Ala Glu
                250                 255                 260

cga gca gga acg atc tct gtg cag acc aac cag aag gtt gct ggc gtg   931
Arg Ala Gly Thr Ile Ser Val Gln Thr Asn Gln Lys Val Ala Gly Val
            265                 270                 275

att gaa aac atg tct gcc atg gtg ctt cct gat ggc acc acc atg gat   979
Ile Glu Asn Met Ser Ala Met Val Leu Pro Asp Gly Thr Thr Met Asp
        280                 285                 290

gtt ttc ggc acc ggc ggc ggt caa aag att gct gat cgt ctt acc gct  1027
Val Phe Gly Thr Gly Gly Gly Gln Lys Ile Ala Asp Arg Leu Thr Ala
    295                 300                 305

gtg aca ggt gaa gag gtc aag gtt atc gga tct gtt cca ttg gat ccg  1075
Val Thr Gly Glu Glu Val Lys Val Ile Gly Ser Val Pro Leu Asp Pro
310                 315                 320                 325
```

```
aac ctg cgt atc ggt ggc gat gtg gga aat cct att gcg att tct gaa   1123
Asn Leu Arg Ile Gly Gly Asp Val Gly Asn Pro Ile Ala Ile Ser Glu
                330                 335                 340

cca cac tcc cca acc gct gca gcg atc aat gag atc gct gaa cac cta   1171
Pro His Ser Pro Thr Ala Ala Ala Ile Asn Glu Ile Ala Glu His Leu
            345                 350                 355

gct cac cgc aag gta tcg ccc acc aaa tgacccagaa ccacaccgca         1218
Ala His Arg Lys Val Ser Pro Thr Lys
        360                 365

aac                                                              1221
```

<210> 2562
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

<400> 2562

```
Met Thr Gln Val Thr Glu Ser Ala Val Arg Ser Ala Leu Ser Arg Val
  1               5                  10                  15

Glu Asp Pro Glu Ile Gly Lys Pro Ile Thr Glu Leu Gly Met Val Lys
             20                  25                  30

Ser Val Ser Ile Asp Gly Ser Asp Val Gln Val Glu Val Tyr Leu Thr
         35                  40                  45

Ile Ala Ala Cys Pro Met Lys Thr Thr Ile Val Thr Asn Thr Glu Ala
     50                  55                  60

Ala Leu Lys Asp Ile Asp Gly Val Gly Gln Val His Val Thr Thr Asp
 65                  70                  75                  80

Val Met Ser Asp Glu Gln Arg Arg Ala Leu Arg Val Ser Leu Arg Gly
                 85                  90                  95

Glu Thr Ser Glu Pro Val Ile Pro Phe Ala Gln Pro Gly Ser Thr Thr
            100                 105                 110

Arg Val Tyr Ala Val Ala Ser Gly Lys Gly Gly Val Gly Lys Ser Ser
        115                 120                 125

Met Thr Val Asn Leu Ala Ala Ala Leu Ala Lys Arg Gly Leu Ser Val
    130                 135                 140

Gly Ile Leu Asp Ala Asp Ile Tyr Gly His Ser Val Pro Gly Met Leu
145                 150                 155                 160

Gly Ser Asp Gln Arg Pro His Gln Val Asp Asp Met Ile Met Pro Pro
                165                 170                 175

Gln Ala His Gly Val Lys Met Ile Ser Ile Ala His Phe Thr Glu Gly
            180                 185                 190

Asn Ala Pro Val Val Trp Arg Gly Pro Met Leu His Arg Ala Ile Gln
        195                 200                 205
```

```
Gln Phe Leu Thr Asp Val Phe Trp Gly Asp Leu Asp Ile Leu Leu Leu
    210                 215                 220

Asp Leu Pro Pro Gly Thr Gly Asp Ile Ala Ile Thr Val Ala Gln Leu
225                 230                 235                 240

Ile Pro Asn Ala Glu Leu Leu Ile Val Thr Thr Pro Gln Ala Ala Ala
                245                 250                 255

Ala Glu Val Ala Glu Arg Ala Gly Thr Ile Ser Val Gln Thr Asn Gln
            260                 265                 270

Lys Val Ala Gly Val Ile Glu Asn Met Ser Ala Met Val Leu Pro Asp
        275                 280                 285

Gly Thr Thr Met Asp Val Phe Gly Thr Gly Gly Gly Gln Lys Ile Ala
    290                 295                 300

Asp Arg Leu Thr Ala Val Thr Gly Glu Glu Val Lys Val Ile Gly Ser
305                 310                 315                 320

Val Pro Leu Asp Pro Asn Leu Arg Ile Gly Gly Asp Val Gly Asn Pro
                325                 330                 335

Ile Ala Ile Ser Glu Pro His Ser Pro Thr Ala Ala Ala Ile Asn Glu
            340                 345                 350

Ile Ala Glu His Leu Ala His Arg Lys Val Ser Pro Thr Lys
        355                 360                 365
```

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<210> 2563
<211> 930
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(907)
<223> RXA02080

<400> 2563

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cgtaaattcg aagcgagctt ctaattctag caagcttggt gatggagtat cctgccaaaa 60

tttgtcctgt tgcttattgt gcaggaattc ggaggcggac atg tca atc gag tgg   115
                                              Met Ser Ile Glu Trp
                                                1               5

tta caa att gtt gaa tta gga gcg atc ttt ggt gca ggt ttc ctc gca   163
Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly Ala Gly Phe Leu Ala
                 10                  15                  20

gga agc atc aat gta att gtc gga gca gga aca tta gtg tcg ttt cct   211
Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr Leu Val Ser Phe Pro
             25                  30                  35

att ctc gtg ttc ctg ggc ctt cca ccg ttg act gcc acc atc gcc aac   259
Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr Ala Thr Ile Ala Asn
         40                  45                  50

acc atc ggc atc gtt cct gga agt att tcg ggt gtg gtt gct tat aga   307
```

```
Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly Val Val Ala Tyr Arg
     55                  60                  65

cgt gaa cta cac gcc cat gta aaa acc atc aga ttt ctg ctg cca gca   355
Arg Glu Leu His Ala His Val Lys Thr Ile Arg Phe Leu Leu Pro Ala
 70                  75                  80                  85

tca atc ctc gga ggg atc acc ggc gcc tcg ctc ttg ctg cat ttc tcc   403
Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu Leu Leu His Phe Ser
                 90                  95                 100

gca gat gtt ttt aca gca gta att ccc tgg ctg att gga ttc ggc acg   451
Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu Ile Gly Phe Gly Thr
            105                 110                 115

ctg ttg gtt atc gca ggt cca tca att aag aag cat gtt ggc gct cat   499
Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys His Val Gly Ala His
        120                 125                 130

act tca ggt ggc atc tct gct ggg ttt agg caa ttg cct ttc ccg agc   547
Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln Leu Pro Phe Pro Ser
    135                 140                 145

cga acc acc ttc atc gtc tca gta tgt ggt gcc ctg ttg ctg ggc atg   595
Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala Leu Leu Leu Gly Met
150                 155                 160                 165

tat gga ggg tac ttc agc gca gct caa ggc att ctt ctc atc gca ttg   643
Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile Leu Leu Ile Ala Leu
                170                 175                 180

ctt ggc atc aca tca acg ctg cag atg cag gaa ctc aac gcc atc aaa   691
Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu Leu Asn Ala Ile Lys
            185                 190                 195

aac ctc aca gtg gcg gca gtt aat ctc atc gca gcc agt gtt ttt ata   739
Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala Ala Ser Val Phe Ile
        200                 205                 210

atc atc tcc cct gag ttg atc tcc tgg ccg acc gtt gcc tta atc gcg   787
Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr Val Ala Leu Ile Ala
    215                 220                 225

ctt ggc tca gct tta ggt gga tac atc ggc gga cgg tac gcc cgc cga   835
Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly Arg Tyr Ala Arg Arg
230                 235                 240                 245

ctt cgc ccc agt gtt ttt aga gca ttt gtg gtc atc gtc gga atc acc   883
Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val Ile Val Gly Ile Thr
                250                 255                 260

acg gtc atc gtt atg acg atc ggt taatgcagca gactagtaac ccc         930
Thr Val Ile Val Met Thr Ile Gly
            265
```

<2564>
<211> 269
<212> PRT
<213> Corynebacterium glutamicum

<400> 2564

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Met Ser Ile Glu Trp Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly
  1               5                  10                  15

Ala Gly Phe Leu Ala Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr
             20                  25                  30

Leu Val Ser Phe Pro Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr
         35                  40                  45

Ala Thr Ile Ala Asn Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly
     50                  55                  60

Val Val Ala Tyr Arg Arg Glu Leu His Ala His Val Lys Thr Ile Arg
 65                  70                  75                  80

Phe Leu Leu Pro Ala Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu
                 85                  90                  95

Leu Leu His Phe Ser Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu
            100                 105                 110

Ile Gly Phe Gly Thr Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys
        115                 120                 125

His Val Gly Ala His Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln
    130                 135                 140

Leu Pro Phe Pro Ser Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala
145                 150                 155                 160

Leu Leu Leu Gly Met Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile
                165                 170                 175

Leu Leu Ile Ala Leu Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu
            180                 185                 190

Leu Asn Ala Ile Lys Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala
        195                 200                 205

Ala Ser Val Phe Ile Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr
    210                 215                 220

Val Ala Leu Ile Ala Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly
225                 230                 235                 240

Arg Tyr Ala Arg Arg Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val
                245                 250                 255

Ile Val Gly Ile Thr Thr Val Ile Val Met Thr Ile Gly
            260                 265
```

<210> 2565
<211> 1752
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1729)

<223> RXA02081

<400> 2565

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cctggatgat gtcactgtct taaatccggt atacgcagat gatttgtggg aagatccgga 60

agctcaacat aattttgcgg tgccaccggt acaaaaacat atg acg tta agt ggc   115
                                              Met Thr Leu Ser Gly
                                                1               5

ttg gag ctt tta gag ttc gag cgt cga aca gct gcg atg gaa acc agg   163
Leu Glu Leu Leu Glu Phe Glu Arg Arg Thr Ala Ala Met Glu Thr Arg
                  10                  15                  20

ctt ggt cgg cat aat cgg gga gcg ggt ggc gca ttt cct gag gcg gtg   211
Leu Gly Arg His Asn Arg Gly Ala Gly Gly Ala Phe Pro Glu Ala Val
              25                  30                  35

gtg tct cga agc gtg gag ttg cca ctt ttt gta cag gcc cgg aat ttc   259
Val Ser Arg Ser Val Glu Leu Pro Leu Phe Val Gln Ala Arg Asn Phe
          40                  45                  50

ctc aac aat cag cag atc aga gct caa gtg cat cgc cgt att ttg gag   307
Leu Asn Asn Gln Gln Ile Arg Ala Gln Val His Arg Arg Ile Leu Glu
      55                  60                  65

cag ctt cca acc gag gga gag att gtg ctg ttg ggg cac agt ttg ggg   355
Gln Leu Pro Thr Glu Gly Glu Ile Val Leu Leu Gly His Ser Leu Gly
  70                  75                  80                  85

tcg gta att gct gca gac ctt ttg agg cga ttg ccg cca gag ctt acg   403
Ser Val Ile Ala Ala Asp Leu Leu Arg Arg Leu Pro Pro Glu Leu Thr
                  90                  95                 100

gtg aag gga ttt gtc acc atc ggt agt ccg ttg gca aat ggt caa ttc   451
Val Lys Gly Phe Val Thr Ile Gly Ser Pro Leu Ala Asn Gly Gln Phe
             105                 110                 115

aat gtg gat gat ttg ttt aag ttg ctg cgc acg ccg ttg agc aat gtg   499
Asn Val Asp Asp Leu Phe Lys Leu Leu Arg Thr Pro Leu Ser Asn Val
         120                 125                 130

tcg tgg tgg gtg aat ttt tgg agt gga tct gat cct gtt gca gca aaa   547
Ser Trp Trp Val Asn Phe Trp Ser Gly Ser Asp Pro Val Ala Ala Lys
     135                 140                 145

cgc gga gtg tcg gtg gct gtt ccg tgg gta ttg gat ttt cgt gtg aaa   595
Arg Gly Val Ser Val Ala Val Pro Trp Val Leu Asp Phe Arg Val Lys
150                 155                 160                 165

acc tca ctg gtc cca ggc cct ggg cat tct tcg cgg gaa tac tgt gcc   643
Thr Ser Leu Val Pro Gly Pro Gly His Ser Ser Arg Glu Tyr Cys Ala
                 170                 175                 180

aat gat gca gtg gcg gaa gca att ggg ttt ggg ctg ttc gga tcg cgc   691
Asn Asp Ala Val Ala Glu Ala Ile Gly Phe Gly Leu Phe Gly Ser Arg
             185                 190                 195

agc aaa gaa atc gtc ctt gcg gag aaa aat ctg cag att ccg ctc aat   739
Ser Lys Glu Ile Val Leu Ala Glu Lys Asn Leu Gln Ile Pro Leu Asn
         200                 205                 210
```

```
gac gcg gag att ttt gtg ctg cag gcg ctg cgt tat tgt tac ctc att   787
Asp Ala Glu Ile Phe Val Leu Gln Ala Leu Arg Tyr Cys Tyr Leu Ile
    215                 220                 225

ttg caa cgg ctc aaa ggc gat gaa gcc tta agg tat gag tac gca ctt   835
Leu Gln Arg Leu Lys Gly Asp Glu Ala Leu Arg Tyr Glu Tyr Ala Leu
230                 235                 240                 245

cgg gag act cag gat cgc ctg att gag gag att aaa tcc aga aac gcc   883
Arg Glu Thr Gln Asp Arg Leu Ile Glu Glu Ile Lys Ser Arg Asn Ala
                250                 255                 260

gaa gag ggc cgg ccg att ccg aag gaa atc gca cgc ctg gat ttt gat   931
Glu Glu Gly Arg Pro Ile Pro Lys Glu Ile Ala Arg Leu Asp Phe Asp
            265                 270                 275

aac ggt gat cca aac gca gca gct cct gtt cca ggt ttg agc cca ttt   979
Asn Gly Asp Pro Asn Ala Ala Ala Pro Val Pro Gly Leu Ser Pro Phe
        280                 285                 290

atg ccc aaa gag cag gca att gag cgg ctt tta gag atc att gga cag   1027
Met Pro Lys Glu Gln Ala Ile Glu Arg Leu Leu Glu Ile Ile Gly Gln
    295                 300                 305

aac ctg ctg ctg cct ttt gag atc gag gtg ccg gag aaa att cag cgg   1075
Asn Leu Leu Leu Pro Phe Glu Ile Glu Val Pro Glu Lys Ile Gln Arg
310                 315                 320                 325

gaa gca ctg agg gat ttc acg gcg gaa act caa ttg ggt tcc acc gtg   1123
Glu Ala Leu Arg Asp Phe Thr Ala Glu Thr Gln Leu Gly Ser Thr Val
                330                 335                 340

ggc gct gat att ttt gat gca ttg caa atg gct gtt ggg gtg gtg tcg   1171
Gly Ala Asp Ile Phe Asp Ala Leu Gln Met Ala Val Gly Val Val Ser
            345                 350                 355

gga agc gcg aag agc aat tgg cgc aaa tgg gga gcg ttt ggt gtg ggg   1219
Gly Ser Ala Lys Ser Asn Trp Arg Lys Trp Gly Ala Phe Gly Val Gly
        360                 365                 370

gct gca gct ttg acc gct gca acg ggt ggt ttg gct ttg gcg gct gtg   1267
Ala Ala Ala Leu Thr Ala Ala Thr Gly Gly Leu Ala Leu Ala Ala Val
    375                 380                 385

ccg act gtt gct gga gta gcc act gtt gcc tcg aca ctc gca gca ttt   1315
Pro Thr Val Ala Gly Val Ala Thr Val Ala Ser Thr Leu Ala Ala Phe
390                 395                 400                 405

ggt cca ggt ggg atg atg ggc ggt ttg gtc act gca gga aca ctg ctc   1363
Gly Pro Gly Gly Met Met Gly Gly Leu Val Thr Ala Gly Thr Leu Leu
                410                 415                 420

aca gtt ggt ggc ggc agt tta acc gct ggg gtg ttg agc tcg gtg aac   1411
Thr Val Gly Gly Gly Ser Leu Thr Ala Gly Val Leu Ser Ser Val Asn
            425                 430                 435

acc acg gaa gag atc gaa gcg ctc gtt gta cag aag cta agt ttg gct   1459
Thr Thr Glu Glu Ile Glu Ala Leu Val Val Gln Lys Leu Ser Leu Ala
        440                 445                 450

att ttg tgg cag cgc cat gag ata gat aga act cat gag gtg tgg gaa   1507
```

```
Ile Leu Trp Gln Arg His Glu Ile Asp Arg Thr His Glu Val Trp Glu
    455                 460                 465

gaa ttc gcg gag gca gaa cgt ctg att gtg cgg gag cac acg cgt gtg   1555
Glu Phe Ala Glu Ala Glu Arg Leu Ile Val Arg Glu His Thr Arg Val
470                 475                 480                 485

aaa aac gtg tcg gat agt tct tcg ccc att ttg aaa gct ttc gag cag   1603
Lys Asn Val Ser Asp Ser Ser Ser Pro Ile Leu Lys Ala Phe Glu Gln
                490                 495                 500

cag cgt tcg act att gag cgg gcg ttg aag tat ttg agc gat cat ggg   1651
Gln Arg Ser Thr Ile Glu Arg Ala Leu Lys Tyr Leu Ser Asp His Gly
            505                 510                 515

atg gaa cct ggc tgg ttt gaa gaa ctg gaa cca cca gcc cca aca ccg   1699
Met Glu Pro Gly Trp Phe Glu Glu Leu Glu Pro Pro Ala Pro Thr Pro
        520                 525                 530

ttt cta aaa ctg cgg gct aag aaa act gat taggagaaac acaatggaga     1749
Phe Leu Lys Leu Arg Ala Lys Lys Thr Asp
    535                 540

aag                                                               1752


<210> 2566
<211> 543
<212> PRT
<213> Corynebacterium glutamicum

<400> 2566
Met Thr Leu Ser Gly Leu Glu Leu Leu Glu Phe Glu Arg Arg Thr Ala
  1               5                  10                  15

Ala Met Glu Thr Arg Leu Gly Arg His Asn Arg Gly Ala Gly Gly Ala
             20                  25                  30

Phe Pro Glu Ala Val Val Ser Arg Ser Val Glu Leu Pro Leu Phe Val
         35                  40                  45

Gln Ala Arg Asn Phe Leu Asn Asn Gln Gln Ile Arg Ala Gln Val His
     50                  55                  60

Arg Arg Ile Leu Glu Gln Leu Pro Thr Glu Gly Glu Ile Val Leu Leu
 65                  70                  75                  80

Gly His Ser Leu Gly Ser Val Ile Ala Ala Asp Leu Leu Arg Arg Leu
                 85                  90                  95

Pro Pro Glu Leu Thr Val Lys Gly Phe Val Thr Ile Gly Ser Pro Leu
            100                 105                 110

Ala Asn Gly Gln Phe Asn Val Asp Asp Leu Phe Lys Leu Leu Arg Thr
        115                 120                 125

Pro Leu Ser Asn Val Ser Trp Trp Val Asn Phe Trp Ser Gly Ser Asp
    130                 135                 140

Pro Val Ala Ala Lys Arg Gly Val Ser Val Ala Val Pro Trp Val Leu
145                 150                 155                 160
```

```
Asp Phe Arg Val Lys Thr Ser Leu Val Pro Gly Pro Gly His Ser Ser
                165                 170                 175

Arg Glu Tyr Cys Ala Asn Asp Ala Val Ala Glu Ala Ile Gly Phe Gly
            180                 185                 190

Leu Phe Gly Ser Arg Ser Lys Glu Ile Val Leu Ala Glu Lys Asn Leu
        195                 200                 205

Gln Ile Pro Leu Asn Asp Ala Glu Ile Phe Val Leu Gln Ala Leu Arg
    210                 215                 220

Tyr Cys Tyr Leu Ile Leu Gln Arg Leu Lys Gly Asp Glu Ala Leu Arg
225                 230                 235                 240

Tyr Glu Tyr Ala Leu Arg Glu Thr Gln Asp Arg Leu Ile Glu Glu Ile
                245                 250                 255

Lys Ser Arg Asn Ala Glu Glu Gly Arg Pro Ile Pro Lys Glu Ile Ala
            260                 265                 270

Arg Leu Asp Phe Asp Asn Gly Asp Pro Asn Ala Ala Ala Pro Val Pro
        275                 280                 285

Gly Leu Ser Pro Phe Met Pro Lys Glu Gln Ala Ile Glu Arg Leu Leu
    290                 295                 300

Glu Ile Ile Gly Gln Asn Leu Leu Leu Pro Phe Glu Ile Glu Val Pro
305                 310                 315                 320

Glu Lys Ile Gln Arg Glu Ala Leu Arg Asp Phe Thr Ala Glu Thr Gln
                325                 330                 335

Leu Gly Ser Thr Val Gly Ala Asp Ile Phe Asp Ala Leu Gln Met Ala
            340                 345                 350

Val Gly Val Val Ser Gly Ser Ala Lys Ser Asn Trp Arg Lys Trp Gly
        355                 360                 365

Ala Phe Gly Val Gly Ala Ala Ala Leu Thr Ala Ala Thr Gly Gly Leu
    370                 375                 380

Ala Leu Ala Ala Val Pro Thr Val Ala Gly Val Ala Thr Val Ala Ser
385                 390                 395                 400

Thr Leu Ala Ala Phe Gly Pro Gly Gly Met Met Gly Gly Leu Val Thr
                405                 410                 415

Ala Gly Thr Leu Leu Thr Val Gly Gly Gly Ser Leu Thr Ala Gly Val
            420                 425                 430

Leu Ser Ser Val Asn Thr Thr Glu Glu Ile Glu Ala Leu Val Val Gln
        435                 440                 445

Lys Leu Ser Leu Ala Ile Leu Trp Gln Arg His Glu Ile Asp Arg Thr
    450                 455                 460

His Glu Val Trp Glu Glu Phe Ala Glu Ala Glu Arg Leu Ile Val Arg
465                 470                 475                 480
```

```
Glu His Thr Arg Val Lys Asn Val Ser Asp Ser Ser Ser Pro Ile Leu
                485                 490                 495

Lys Ala Phe Glu Gln Gln Arg Ser Thr Ile Glu Arg Ala Leu Lys Tyr
            500                 505                 510

Leu Ser Asp His Gly Met Glu Pro Gly Trp Phe Glu Glu Leu Glu Pro
        515                 520                 525

Pro Ala Pro Thr Pro Phe Leu Lys Leu Arg Ala Lys Lys Thr Asp
    530                 535                 540


<210> 2567
<211> 468
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(445)
<223> RXA02084

<400> 2567
cgttgatggt tgggtggtgg gtcacagttt agaaaaagtg acttcaaatc acgtcgaaaa 60

gaaattgaaa gtacttaaga aacatgtcac gctaggagac gtg ata atc att gca   115
                                            Val Ile Ile Ile Ala
                                              1               5

agc gtt gtt ttc ctc ctc gtt ggc gca atg ttg gcg aat gct gcc gct   163
Ser Val Val Phe Leu Leu Val Gly Ala Met Leu Ala Asn Ala Ala Ala
                 10                  15                  20

gcg ctc ttt agt gcc agc gag cca ttc gga cga att tcc tac ctc att   211
Ala Leu Phe Ser Ala Ser Glu Pro Phe Gly Arg Ile Ser Tyr Leu Ile
             25                  30                  35

ggc cta cct aac gaa gac gac ttc gtg ccg tac tca cta cgg ttc gtg   259
Gly Leu Pro Asn Glu Asp Asp Phe Val Pro Tyr Ser Leu Arg Phe Val
         40                  45                  50

gcc ttt ttc cca ctg atg ctc tcc gca tcg atg gca gca tcc ttc ttc   307
Ala Phe Phe Pro Leu Met Leu Ser Ala Ser Met Ala Ala Ser Phe Phe
     55                  60                  65

ggg gtg tgg gca gta cta atc att cct ttc ggt tac ttc cca tca ctg   355
Gly Val Trp Ala Val Leu Ile Ile Pro Phe Gly Tyr Phe Pro Ser Leu
 70                  75                  80                  85

atg atg gtt cat aag cac aac aag cag gta cag cga acc tgg gat tcc   403
Met Met Val His Lys His Asn Lys Gln Val Gln Arg Thr Trp Asp Ser
                 90                  95                 100

gtc acc gtt gct gac ttc tac gag gat tcc acc cct ctg gtc           445
Val Thr Val Ala Asp Phe Tyr Glu Asp Ser Thr Pro Leu Val
            105                 110                 115

taatttcgat ttctaaatgt cat                                        468
```

<210> 2568
<211> 115
<212> PRT
<213> Corynebacterium glutamicum

<400> 2568
Val Ile Ile Ile Ala Ser Val Val Phe Leu Leu Val Gly Ala Met Leu
1 5 10 15

Ala Asn Ala Ala Ala Ala Leu Phe Ser Ala Ser Glu Pro Phe Gly Arg
20 25 30

Ile Ser Tyr Leu Ile Gly Leu Pro Asn Glu Asp Asp Phe Val Pro Tyr
35 40 45

Ser Leu Arg Phe Val Ala Phe Phe Pro Leu Met Leu Ser Ala Ser Met
50 55 60

Ala Ala Ser Phe Phe Gly Val Trp Ala Val Leu Ile Ile Pro Phe Gly
65 70 75 80

Tyr Phe Pro Ser Leu Met Met Val His Lys His Asn Lys Gln Val Gln
85 90 95

Arg Thr Trp Asp Ser Val Thr Val Ala Asp Phe Tyr Glu Asp Ser Thr
100 105 110

Pro Leu Val
115

<210> 2569
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXA02089

<400> 2569
ctagctgacc agtattaata ccaataatag aacatattat cgaacaatgt cgcttgggtg 60

ctctacactt cccactatga tcaaacaccg aaaccgccta atg tct tcc atc tac 115
Met Ser Ser Ile Tyr
1 5

tcc gca act cgc tac gcc gcc cac ttc aaa agc gtc ttc ccc acc gcc 163
Ser Ala Thr Arg Tyr Ala Ala His Phe Lys Ser Val Phe Pro Thr Ala
10 15 20

ctg gat gac att caa tcc atg atg cgc cac cct cga tca ctg gcc aga 211
Leu Asp Asp Ile Gln Ser Met Met Arg His Pro Arg Ser Leu Ala Arg
25 30 35

gcc ata ccc acg tgg cgc ccg ccg agc atc ccg cta ccg tca ctt ccc 259
Ala Ile Pro Thr Trp Arg Pro Pro Ser Ile Pro Leu Pro Ser Leu Pro
40 45 50

ggc gaa gat ccc ctc acc ctc acc ttg tca cgt cac cgc gca ggc ccc 307

```
Gly Glu Asp Pro Leu Thr Leu Thr Leu Ser Arg His Arg Ala Gly Pro
     55                  60                  65

gcc gcc cgc caa atc atc cgc gag ttc ggt gag caa cgt gaa ccc gcc   355
Ala Ala Arg Gln Ile Ile Arg Glu Phe Gly Glu Gln Arg Glu Pro Ala
 70                  75                  80                  85

tat ctc atc acc atc cgc atc acc agc cca gag ggc ttc aaa gta tcc   403
Tyr Leu Ile Thr Ile Arg Ile Thr Ser Pro Glu Gly Phe Lys Val Ser
                 90                  95                 100

acc cgc ctc gcc gaa ggc tgg atc cgc gca att ctc agc acc gcg cac   451
Thr Arg Leu Ala Glu Gly Trp Ile Arg Ala Ile Leu Ser Thr Ala His
            105                 110                 115

agc ggc act gtc cac cag ctc acc gat gag ccg gca ccg acg ttt tgc   499
Ser Gly Thr Val His Gln Leu Thr Asp Glu Pro Ala Pro Thr Phe Cys
        120                 125                 130

tgg ctt gtc gac gcc cac ttt gat ccg gtg cgt tcc cct tcc ttc ctt   547
Trp Leu Val Asp Ala His Phe Asp Pro Val Arg Ser Pro Ser Phe Leu
    135                 140                 145

ttc gaa tat tcc aaa agt gca gcc tagaaaatga cgaaaccctg gat         594
Phe Glu Tyr Ser Lys Ser Ala Ala
150                 155


<210> 2570
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 2570
Met Ser Ser Ile Tyr Ser Ala Thr Arg Tyr Ala Ala His Phe Lys Ser
  1               5                  10                  15

Val Phe Pro Thr Ala Leu Asp Asp Ile Gln Ser Met Met Arg His Pro
             20                  25                  30

Arg Ser Leu Ala Arg Ala Ile Pro Thr Trp Arg Pro Pro Ser Ile Pro
         35                  40                  45

Leu Pro Ser Leu Pro Gly Glu Asp Pro Leu Thr Leu Thr Leu Ser Arg
     50                  55                  60

His Arg Ala Gly Pro Ala Ala Arg Gln Ile Ile Arg Glu Phe Gly Glu
 65                  70                  75                  80

Gln Arg Glu Pro Ala Tyr Leu Ile Thr Ile Arg Ile Thr Ser Pro Glu
                 85                  90                  95

Gly Phe Lys Val Ser Thr Arg Leu Ala Glu Gly Trp Ile Arg Ala Ile
            100                 105                 110

Leu Ser Thr Ala His Ser Gly Thr Val His Gln Leu Thr Asp Glu Pro
        115                 120                 125

Ala Pro Thr Phe Cys Trp Leu Val Asp Ala His Phe Asp Pro Val Arg
    130                 135                 140
```

```
Ser Pro Ser Phe Leu Phe Glu Tyr Ser Lys Ser Ala Ala
145                 150                 155


<210> 2571
<211> 924
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(901)
<223> RXA02090

<400> 2571
aggtgaaagg ctaggcgcgg attcgttgtg gacgctaggc ttgtcggcag tgtctttggg 60

ggacgtcccc agcacaaacc agatggaagg tcatcagaac atg agc ttt ttt gag   115
                                            Met Ser Phe Phe Glu
                                              1               5

gac atc gcg gct gga ctt gat agt gac ggt atc gag tcc cgc gta aac   163
Asp Ile Ala Ala Gly Leu Asp Ser Asp Gly Ile Glu Ser Arg Val Asn
                 10                  15                  20

ggc gac aca atg ttc gtt ccg atc acc tct gac ttg gaa atc cag ttc   211
Gly Asp Thr Met Phe Val Pro Ile Thr Ser Asp Leu Glu Ile Gln Phe
             25                  30                  35

gtg gag atc gat tcc ctc cta cct gca gca aac gtt tat atc gct gca   259
Val Glu Ile Asp Ser Leu Leu Pro Ala Ala Asn Val Tyr Ile Ala Ala
         40                  45                  50

gcc aat gtt gat gaa gac gat gat gag ttc gag gca gtt ctc gtt tcg   307
Ala Asn Val Asp Glu Asp Asp Asp Glu Phe Glu Ala Val Leu Val Ser
     55                  60                  65

gtg gtg ttc tct gtt gag gat gct gtc gct gct gtc gca aag cat gtt   355
Val Val Phe Ser Val Glu Asp Ala Val Ala Ala Val Ala Lys His Val
 70                  75                  80                  85

gct act gat cag gtg gtg act gtg ctg cgt gat cta ctt gaa gga act   403
Ala Thr Asp Gln Val Val Thr Val Leu Arg Asp Leu Leu Glu Gly Thr
                 90                  95                 100

gat gaa cgc atc cag gat ttg gag ttt ttc cag gat gca gtg aat gca   451
Asp Glu Arg Ile Gln Asp Leu Glu Phe Phe Gln Asp Ala Val Asn Ala
            105                 110                 115

aat ttg gtt cgt gcg gaa gtc ggc cag aat tct gag ctt cag gtt ttg   499
Asn Leu Val Arg Ala Glu Val Gly Gln Asn Ser Glu Leu Gln Val Leu
        120                 125                 130

gtc gag gtt gaa gac ggc gtc cca acc gca acg gtc aat ttc atc gcg   547
Val Glu Val Glu Asp Gly Val Pro Thr Ala Thr Val Asn Phe Ile Ala
    135                 140                 145

atc ggt gag tcc ttt gaa gat ctg att gat cag gcc att gaa gaa ttg   595
Ile Gly Glu Ser Phe Glu Asp Leu Ile Asp Gln Ala Ile Glu Glu Leu
150                 155                 160                 165
```

```
tgg gaa tcc gac ggc gac gca gtt cta tcg gat gaa gat cgc caa cgc   643
Trp Glu Ser Asp Gly Asp Ala Val Leu Ser Asp Glu Asp Arg Gln Arg
                170                 175                 180

atg ttc gct gat ttg acc tcc gag ttg gaa ttt gtc act gat gaa gtc   691
Met Phe Ala Asp Leu Thr Ser Glu Leu Glu Phe Val Thr Asp Glu Val
            185                 190                 195

ctc gac ttg ggt acc ttc act gat ttt gat cga ctt ttc gat atc ctt   739
Leu Asp Leu Gly Thr Phe Thr Asp Phe Asp Arg Leu Phe Asp Ile Leu
        200                 205                 210

tcc ctc gcc gat gac cag gct gag gat tgg gaa gca cag ctc gtt cct   787
Ser Leu Ala Asp Asp Gln Ala Glu Asp Trp Glu Ala Gln Leu Val Pro
    215                 220                 225

ttt gag gac gag gaa ttt gat gag ccg gat gtt tat gac ctt ttc gtc   835
Phe Glu Asp Glu Glu Phe Asp Glu Pro Asp Val Tyr Asp Leu Phe Val
230                 235                 240                 245

gat gac tct gaa gaa gat gac gac gac ctc gat gat gac gag gac gat   883
Asp Asp Ser Glu Glu Asp Asp Asp Asp Leu Asp Asp Asp Glu Asp Asp
                250                 255                 260

gag gat gat gac gaa gac tagattttag cctttgtcgc ggt                924
Glu Asp Asp Asp Glu Asp
            265
```

<210> 2572
<211> 267
<212> PRT
<213> Corynebacterium glutamicum

<400> 2572

```
Met Ser Phe Phe Glu Asp Ile Ala Ala Gly Leu Asp Ser Asp Gly Ile
  1               5                  10                  15

Glu Ser Arg Val Asn Gly Asp Thr Met Phe Val Pro Ile Thr Ser Asp
             20                  25                  30

Leu Glu Ile Gln Phe Val Glu Ile Asp Ser Leu Leu Pro Ala Ala Asn
         35                  40                  45

Val Tyr Ile Ala Ala Ala Asn Val Asp Glu Asp Asp Asp Glu Phe Glu
     50                  55                  60

Ala Val Leu Val Ser Val Val Phe Ser Val Glu Asp Ala Val Ala Ala
 65                  70                  75                  80

Val Ala Lys His Val Ala Thr Asp Gln Val Val Thr Val Leu Arg Asp
                 85                  90                  95

Leu Leu Glu Gly Thr Asp Glu Arg Ile Gln Asp Leu Glu Phe Phe Gln
            100                 105                 110

Asp Ala Val Asn Ala Asn Leu Val Arg Ala Glu Val Gly Gln Asn Ser
        115                 120                 125

Glu Leu Gln Val Leu Val Glu Val Glu Asp Gly Val Pro Thr Ala Thr
    130                 135                 140
```

```
Val Asn Phe Ile Ala Ile Gly Glu Ser Phe Glu Asp Leu Ile Asp Gln
145                 150                 155                 160

Ala Ile Glu Glu Leu Trp Glu Ser Asp Gly Asp Ala Val Leu Ser Asp
                165                 170                 175

Glu Asp Arg Gln Arg Met Phe Ala Asp Leu Thr Ser Glu Leu Glu Phe
            180                 185                 190

Val Thr Asp Glu Val Leu Asp Leu Gly Thr Phe Thr Asp Phe Asp Arg
        195                 200                 205

Leu Phe Asp Ile Leu Ser Leu Ala Asp Asp Gln Ala Glu Asp Trp Glu
    210                 215                 220

Ala Gln Leu Val Pro Phe Glu Asp Glu Glu Phe Asp Glu Pro Asp Val
225                 230                 235                 240

Tyr Asp Leu Phe Val Asp Asp Ser Glu Glu Asp Asp Asp Asp Leu Asp
                245                 250                 255

Asp Asp Glu Asp Asp Glu Asp Asp Asp Glu Asp
            260                 265


<210> 2573
<211> 774
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> RXA02091

<400> 2573
agatctagcc aacgaacttg atttcatcga gccggaagag acagaagaag agcagcaatt 60

gaagtggctt agccttatgc agtttttgg aagtagataa atg agc atc tgg aaa   115
                                            Met Ser Ile Trp Lys
                                              1               5

cgt ctg tta gtg cag tac ccg cgc ttc gcc gac acc ctc aca gcc ggc   163
Arg Leu Leu Val Gln Tyr Pro Arg Phe Ala Asp Thr Leu Thr Ala Gly
                 10                  15                  20

caa ccc atc acg ctc gag gaa tta gca acc ccg gaa gtg atc ttg gaa   211
Gln Pro Ile Thr Leu Glu Glu Leu Ala Thr Pro Glu Val Ile Leu Glu
             25                  30                  35

gct gtt gcc aaa ggc caa gaa att ttc ggc att gag cag cca aaa cat   259
Ala Val Ala Lys Gly Gln Glu Ile Phe Gly Ile Glu Gln Pro Lys His
         40                  45                  50

gca gca caa ctc tgg ttt cac tcc ctg tgc acc gca att gtc ggc ccc   307
Ala Ala Gln Leu Trp Phe His Ser Leu Cys Thr Ala Ile Val Gly Pro
     55                  60                  65

gcc gtc acc gcc atg gtg gaa ttc gat gtc atc ccc agc ctc gac ata   355
Ala Val Thr Ala Met Val Glu Phe Asp Val Ile Pro Ser Leu Asp Ile
```

```
 70                  75                  80                  85

cgt cga ggt cag ctg cat aac atc gac ggt tac tgg ttc ggc ttc agg   403
Arg Arg Gly Gln Leu His Asn Ile Asp Gly Tyr Trp Phe Gly Phe Arg
                 90                  95                 100

ccg gag gag atg ctt gtc gac gcc tcc ctc cac ctg tcg ggc acc caa   451
Pro Glu Glu Met Leu Val Asp Ala Ser Leu His Leu Ser Gly Thr Gln
            105                 110                 115

ttc ggc gag agt atc cgc gtg gtg att gat gca tta tgc gct gcc acg   499
Phe Gly Glu Ser Ile Arg Val Val Ile Asp Ala Leu Cys Ala Ala Thr
        120                 125                 130

gat ctg cga ccg gca ccc ctg tgg gcg gtt gcc tca gat gcg ttg gga   547
Asp Leu Arg Pro Ala Pro Leu Trp Ala Val Ala Ser Asp Ala Leu Gly
    135                 140                 145

atc gca gct agc ggc gca ggt gtc gag gcc ttt gaa gaa gaa cat gcc   595
Ile Ala Ala Ser Gly Ala Gly Val Glu Ala Phe Glu Glu Glu His Ala
150                 155                 160                 165

cgc gag gtg gcg gaa gcc ctc att gaa gga atg aat agt gtg aac tca   643
Arg Glu Val Ala Glu Ala Leu Ile Glu Gly Met Asn Ser Val Asn Ser
                170                 175                 180

gtt cca tcg ccg cgg ttt aac gac gac gat tat ttc att cga gct gga   691
Val Pro Ser Pro Arg Phe Asn Asp Asp Asp Tyr Phe Ile Arg Ala Gly
            185                 190                 195

tgc tgc atg att ttc cac tca cca cga gct gat ttt tgc acg tcg tgc   739
Cys Cys Met Ile Phe His Ser Pro Arg Ala Asp Phe Cys Thr Ser Cys
        200                 205                 210

cca cag aag agg tgaaaggcta ggcgcggatt cgt                        774
Pro Gln Lys Arg
    215
```

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<210> 2574
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 2574

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Met Ser Ile Trp Lys Arg Leu Leu Val Gln Tyr Pro Arg Phe Ala Asp
  1               5                  10                  15

Thr Leu Thr Ala Gly Gln Pro Ile Thr Leu Glu Glu Leu Ala Thr Pro
             20                  25                  30

Glu Val Ile Leu Glu Ala Val Ala Lys Gly Gln Glu Ile Phe Gly Ile
         35                  40                  45

Glu Gln Pro Lys His Ala Ala Gln Leu Trp Phe His Ser Leu Cys Thr
     50                  55                  60

Ala Ile Val Gly Pro Ala Val Thr Ala Met Val Glu Phe Asp Val Ile
 65                  70                  75                  80

Pro Ser Leu Asp Ile Arg Arg Gly Gln Leu His Asn Ile Asp Gly Tyr
```

```
                 85                  90                  95

Trp Phe Gly Phe Arg Pro Glu Glu Met Leu Val Asp Ala Ser Leu His
            100                 105                 110

Leu Ser Gly Thr Gln Phe Gly Glu Ser Ile Arg Val Val Ile Asp Ala
        115                 120                 125

Leu Cys Ala Ala Thr Asp Leu Arg Pro Ala Pro Leu Trp Ala Val Ala
    130                 135                 140

Ser Asp Ala Leu Gly Ile Ala Ala Ser Gly Ala Gly Val Glu Ala Phe
145                 150                 155                 160

Glu Glu Glu His Ala Arg Glu Val Ala Glu Ala Leu Ile Glu Gly Met
                165                 170                 175

Asn Ser Val Asn Ser Val Pro Ser Pro Arg Phe Asn Asp Asp Asp Tyr
            180                 185                 190

Phe Ile Arg Ala Gly Cys Cys Met Ile Phe His Ser Pro Arg Ala Asp
        195                 200                 205

Phe Cys Thr Ser Cys Pro Gln Lys Arg
    210                 215
```

<210> 2575
<211> 3495
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(3472)
<223> RXA02097

<400> 2575

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ctagaggaaa acgcattttt tgcgcgggga gagtgtatac atg ccg gct ggc atc   115
                                            Met Pro Ala Gly Ile
                                              1               5

gca gac atg aca gat tca ttg ctc gga tgg gca tca caa act gag ctg   163
Ala Asp Met Thr Asp Ser Leu Leu Gly Trp Ala Ser Gln Thr Glu Leu
                  10                  15                  20

gat ctg aac cag cgt ctt gca ggg gta gag tac ttt cca caa att cag   211
Asp Leu Asn Gln Arg Leu Ala Gly Val Glu Tyr Phe Pro Gln Ile Gln
              25                  30                  35

ctg cga cac gat gag ctc gag cgc att cat cgg ttt tac ggc acc ttt   259
Leu Arg His Asp Glu Leu Glu Arg Ile His Arg Phe Tyr Gly Thr Phe
          40                  45                  50

ttg tcc cgc cag gta ggc gcg ggc gca agc ctt ggg gat ctt ttt gaa   307
Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu Gly Asp Leu Phe Glu
      55                  60                  65

atg acc cca tgc ctg aca gtc acc acc ttg gtg tct cgg gcg tca cgg   355
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Met Thr Pro Cys Leu Thr Val Thr Thr Leu Val Ser Arg Ala Ser Arg
 70                  75                  80                  85

atc agc gat cca gca gat ttc ttc ggt gaa tac atc gga gga ctg gga   403
Ile Ser Asp Pro Ala Asp Phe Phe Gly Glu Tyr Ile Gly Gly Leu Gly
                 90                  95                 100

ctt agc gca gaa cac gca gca gtt gtt gaa ggg ttg acc gaa aag ctc   451
Leu Ser Ala Glu His Ala Ala Val Val Glu Gly Leu Thr Glu Lys Leu
            105                 110                 115

ttc gca cag gct ggc ctg ctc gtt cct gag gga att gca tct cca ttg   499
Phe Ala Gln Ala Gly Leu Leu Val Pro Glu Gly Ile Ala Ser Pro Leu
        120                 125                 130

gag ttg tta tcc atc cac gca ggc att agt aac cac gaa gtg gcc gca   547
Glu Leu Leu Ser Ile His Ala Gly Ile Ser Asn His Glu Val Ala Ala
    135                 140                 145

gtg ctg acc gaa gtg gaa aac ggc acc acc gaa tat cca ttc atg ttc   595
Val Leu Thr Glu Val Glu Asn Gly Thr Thr Glu Tyr Pro Phe Met Phe
150                 155                 160                 165

gac gct gtc ctg cgc cta acc cct gag tgg gca cag acc ctt atc ggc   643
Asp Ala Val Leu Arg Leu Thr Pro Glu Trp Ala Gln Thr Leu Ile Gly
                170                 175                 180

gga gtt caa gaa ctc att gaa ttt gcc acc acc cac cga act tct tgg   691
Gly Val Gln Glu Leu Ile Glu Phe Ala Thr Thr His Arg Thr Ser Trp
            185                 190                 195

tca gac cgc cag cgc gaa tcc tca ctg cca gcc atg atc gat gag atc   739
Ser Asp Arg Gln Arg Glu Ser Ser Leu Pro Ala Met Ile Asp Glu Ile
        200                 205                 210

gtt gtg gcg gaa ctt cgg gaa cgc cca gtt ggt act gcc gac cgt gaa   787
Val Val Ala Glu Leu Arg Glu Arg Pro Val Gly Thr Ala Asp Arg Glu
    215                 220                 225

aac tcc gtt ggt gtg gca ctt cgt gag ctt cgc cca cgc ctc atc ctg   835
Asn Ser Val Gly Val Ala Leu Arg Glu Leu Arg Pro Arg Leu Ile Leu
230                 235                 240                 245

gat gca gaa cgc cgc aaa gtc tgc ctg cgt cta cct gaa cag cgc gtc   883
Asp Ala Glu Arg Arg Lys Val Cys Leu Arg Leu Pro Glu Gln Arg Val
                250                 255                 260

agc gac gat gaa atc aac tgg cga gtc agc cta gaa ggc acc acc cgg   931
Ser Asp Asp Glu Ile Asn Trp Arg Val Ser Leu Glu Gly Thr Thr Arg
            265                 270                 275

att ttc tcc acc cgc cga gca tgg ggc gat act tct gga tac tcc gaa   979
Ile Phe Ser Thr Arg Arg Ala Trp Gly Asp Thr Ser Gly Tyr Ser Glu
        280                 285                 290

gcc ctc gac atc act gtc gag cgt caa atc cgc gaa acc acc gtc acc   1027
Ala Leu Asp Ile Thr Val Glu Arg Gln Ile Arg Glu Thr Thr Val Thr
    295                 300                 305

gac acc tca aac caa atc acc tgg gtt gtc cca gtc gtg gac ttc aac   1075
Asp Thr Ser Asn Gln Ile Thr Trp Val Val Pro Val Val Asp Phe Asn
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310                 315                 320                 325

gac cca gtg ctg gtg ttt tcc gcg cgc ggt gaa aac ctc acc gac aag   1123
Asp Pro Val Leu Val Phe Ser Ala Arg Gly Glu Asn Leu Thr Asp Lys
                330                 335                 340

gtc tcc ctg cac cat caa gag att tac gtt ctc gcg cca gcg gaa gca   1171
Val Ser Leu His His Gln Glu Ile Tyr Val Leu Ala Pro Ala Glu Ala
            345                 350                 355

aaa ctc gaa gac atg gtc act ggc cag cca gta cca gtt att gag caa   1219
Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val Pro Val Ile Glu Gln
        360                 365                 370

ttc ctc gta gag ggc tgg aac tca tgg gtg tgc tcc cgc gtg gac gcc   1267
Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys Ser Arg Val Asp Ala
    375                 380                 385

cgt ggc ctg tcc tct ctg aag gtc aac aaa gaa gtc cga tgc att gac   1315
Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu Val Arg Cys Ile Asp
390                 395                 400                 405

cca cgt cga cgc gtt gcc ttc cac cac cca gcc gaa ttg gtc cct cac   1363
Pro Arg Arg Arg Val Ala Phe His His Pro Ala Glu Leu Val Pro His
                410                 415                 420

gta cga tcc att tcc gga ctc ccc gta cac gcg cag tcc ctg atc gcc   1411
Val Arg Ser Ile Ser Gly Leu Pro Val His Ala Gln Ser Leu Ile Ala
            425                 430                 435

gag ttc cca cca acc ctg agc gga caa gac gaa acc tgg atg ctc tcc   1459
Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu Thr Trp Met Leu Ser
        440                 445                 450

atc tcg gct ttc gca ggt gta ggc gct gct ggt gaa gaa atc gcc gag   1507
Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly Glu Glu Ile Ala Glu
    455                 460                 465

cca gag cct ttg gaa gtc cct gcc gac ggt ggc ctt ttc gcc atc ttc   1555
Pro Glu Pro Leu Glu Val Pro Ala Asp Gly Gly Leu Phe Ala Ile Phe
470                 475                 480                 485

gac cca gaa ata tac gac gcc cca tgg gtg ggt gaa tac ctg gtc cga   1603
Asp Pro Glu Ile Tyr Asp Ala Pro Trp Val Gly Glu Tyr Leu Val Arg
                490                 495                 500

ctc cgc ggc cca cgc aat gaa tcc ttc cga ccc gaa ttc gcc atc gtc   1651
Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro Glu Phe Ala Ile Val
            505                 510                 515

gaa gac atg acc acc gaa ttc gaa gtc gcc tca ggt gca tca ttt cga   1699
Glu Asp Met Thr Thr Glu Phe Glu Val Ala Ser Gly Ala Ser Phe Arg
        520                 525                 530

atc cca acc acc act ggt ctc agc gaa gcc agc cta cgc gtg cgt tcc   1747
Ile Pro Thr Thr Thr Gly Leu Ser Glu Ala Ser Leu Arg Val Arg Ser
    535                 540                 545

ggt gaa aag cac ttc acc gca gag cca cgc ctg gtc acc gtt gaa gca   1795
Gly Glu Lys His Phe Thr Ala Glu Pro Arg Leu Val Thr Val Glu Ala
550                 555                 560                 565
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acc gac ccc aac gca tca ttc gtg gtc acc acc gat gaa ggc gat caa   1843
Thr Asp Pro Asn Ala Ser Phe Val Val Thr Thr Asp Glu Gly Asp Gln
                570                 575                 580

atg cca ttg cga ttt gtg cca cca caa atc gcc atc gaa ctt cca ctg   1891
Met Pro Leu Arg Phe Val Pro Pro Gln Ile Ala Ile Glu Leu Pro Leu
            585                 590                 595

acc acc gag cca cca acc tgg cgc gtc acc cgt act gtc tgt gga cca   1939
Thr Thr Glu Pro Pro Thr Trp Arg Val Thr Arg Thr Val Cys Gly Pro
        600                 605                 610

cgc gac ctc gac ggt gca ggc gaa ctc cgc atc cgc acc ggt gtc gat   1987
Arg Asp Leu Asp Gly Ala Gly Glu Leu Arg Ile Arg Thr Gly Val Asp
    615                 620                 625

gtc ggc gat cca aag gtc agt gtg cgc aac cac cac ggt tca cca ctg   2035
Val Gly Asp Pro Lys Val Ser Val Arg Asn His His Gly Ser Pro Leu
630                 635                 640                 645

cga acc gtg aaa atg gtc acc cct gac aac ggc cgt acc tgg att gcc   2083
Arg Thr Val Lys Met Val Thr Pro Asp Asn Gly Arg Thr Trp Ile Ala
                650                 655                 660

agc atg aag gaa atc gca gcc agt acc ttt gtg atg cca cgc gga tcc   2131
Ser Met Lys Glu Ile Ala Ala Ser Thr Phe Val Met Pro Arg Gly Ser
            665                 670                 675

atc gaa ttt gag tgg act gac cgc aag gtt gac cgt cgc gtt tcc gtg   2179
Ile Glu Phe Glu Trp Thr Asp Arg Lys Val Asp Arg Arg Val Ser Val
        680                 685                 690

acg att gct gtc att gac aaa act gag aac ttt act ggc atc acc atc   2227
Thr Ile Ala Val Ile Asp Lys Thr Glu Asn Phe Thr Gly Ile Thr Ile
    695                 700                 705

gaa gat gga aag ctc gta ttc gaa gaa ctc gca gcc ggt cgc caa ctc   2275
Glu Asp Gly Lys Leu Val Phe Glu Glu Leu Ala Ala Gly Arg Gln Leu
710                 715                 720                 725

gct gca tgg gtg tgg cca caa acc gca ccg tgg gta agc gca gtg gaa   2323
Ala Ala Trp Val Trp Pro Gln Thr Ala Pro Trp Val Ser Ala Val Glu
                730                 735                 740

ctt gct gtc acc gga cca gag ctg gaa ctc cct gaa gtt ctc gtc ggc   2371
Leu Ala Val Thr Gly Pro Glu Leu Glu Leu Pro Glu Val Leu Val Gly
            745                 750                 755

gca ggc aac ctg att gtt caa ctc cac acc gct gac cca ttc act acc   2419
Ala Gly Asn Leu Ile Val Gln Leu His Thr Ala Asp Pro Phe Thr Thr
        760                 765                 770

tcc gtg acc cca ctg tca cca gga aaa gct gcg gtc acc gtt gag caa   2467
Ser Val Thr Pro Leu Ser Pro Gly Lys Ala Ala Val Thr Val Glu Gln
    775                 780                 785

gaa ggc tac tac tca gca caa acc gaa gaa tat gca cag ctt tca gca   2515
Glu Gly Tyr Tyr Ser Ala Gln Thr Glu Glu Tyr Ala Gln Leu Ser Ala
790                 795                 800                 805
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```
ttc ttc ggt ggg gaa gta gaa gaa cca cca atc agt gac gct gtg gtc   2563
Phe Phe Gly Gly Glu Val Glu Glu Pro Pro Ile Ser Asp Ala Val Val
                810                 815                 820

ccc gca ctt tgg gat gtt tcc cat atc tgg acc gaa cag gga aac acc   2611
Pro Ala Leu Trp Asp Val Ser His Ile Trp Thr Glu Gln Gly Asn Thr
            825                 830                 835

gag cat ctt cca gta gtc cat gcc gcc ctg cgc tcc tca cca gcc gca   2659
Glu His Leu Pro Val Val His Ala Ala Leu Arg Ser Ser Pro Ala Ala
        840                 845                 850

gca ctg aag ggt ctg tcc gct tcg ctg gtt ccc gca cag gca cta cct   2707
Ala Leu Lys Gly Leu Ser Ala Ser Leu Val Pro Ala Gln Ala Leu Pro
    855                 860                 865

gga aaa gtc att tcc tcc gga ctg gca gcc tca ccg ttc acc acg gaa   2755
Gly Lys Val Ile Ser Ser Gly Leu Ala Ala Ser Pro Phe Thr Thr Glu
870                 875                 880                 885

tca cca gca aca gaa gtg cac cgc acc gca tgg atc gga acc ctg caa   2803
Ser Pro Ala Thr Glu Val His Arg Thr Ala Trp Ile Gly Thr Leu Gln
                890                 895                 900

ctc ctg ggt gca ctg cca agc gca ttc aag gaa gcc gaa gag ctt ggc   2851
Leu Leu Gly Ala Leu Pro Ser Ala Phe Lys Glu Ala Glu Glu Leu Gly
            905                 910                 915

aac cgc aca cca ctg ctg cca atc ctc gga caa ctt gag gaa gtc gcc   2899
Asn Arg Thr Pro Leu Leu Pro Ile Leu Gly Gln Leu Glu Glu Val Ala
        920                 925                 930

ggc aag aac atc ctg tcc acc ctt gca act ggc cgt gac tcc act ttg   2947
Gly Lys Asn Ile Leu Ser Thr Leu Ala Thr Gly Arg Asp Ser Thr Leu
    935                 940                 945

gac acc gca tgc atc gac caa tcc acc gtt gcg att gcc ggc atg aac   2995
Asp Thr Ala Cys Ile Asp Gln Ser Thr Val Ala Ile Ala Gly Met Asn
950                 955                 960                 965

gaa acc cag caa aaa gcc ctg ctg gac atg ttc ttc agc aac gcc gac   3043
Glu Thr Gln Gln Lys Ala Leu Leu Asp Met Phe Phe Ser Asn Ala Asp
                970                 975                 980

atc gtt cct gga cca cta atg gaa gac aac acc cgc ctc atg gca gtg   3091
Ile Val Pro Gly Pro Leu Met Glu Asp Asn Thr Arg Leu Met Ala Val
            985                 990                 995

ttc gaa acc ttc aag aag cgc gat gca ctc cgt gag gtt ctc cag act   3139
Phe Glu Thr Phe Lys Lys Arg Asp Ala Leu Arg Glu Val Leu Gln Thr
        1000                1005                1010

gaa ggc ttg att aag acc gct gta gaa ctt ctt cgt gcc atg cgt gga   3187
Glu Gly Leu Ile Lys Thr Ala Val Glu Leu Leu Arg Ala Met Arg Gly
    1015                1020                1025

acc cag cgt cag ctg tat tcc tcc gca cgt att cga ttc gac aag ctc   3235
Thr Gln Arg Gln Leu Tyr Ser Ser Ala Arg Ile Arg Phe Asp Lys Leu
1030                1035                1040                1045

gat ggt gtc aac act gac aac cca gaa aac atg tgg gca ctc acc cca   3283
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Asp Gly Val Asn Thr Asp Asn Pro Glu Asn Met Trp Ala Leu Thr Pro
                1050                1055                1060

gtt gtg tca ctg gtg ttc gcg ttg tca tcc cgt ttg cat gca cac gaa   3331
Val Val Ser Leu Val Phe Ala Leu Ser Ser Arg Leu His Ala His Glu
            1065                1070                1075

ttg atc ggc aag acc cga act ctc gat cgt gca tct gcc ggt tgg ggt   3379
Leu Ile Gly Lys Thr Arg Thr Leu Asp Arg Ala Ser Ala Gly Trp Gly
        1080                1085                1090

cga atc gct gat ctg gtg cca gac ctt gtc acc ggt gac ttg atc tcc   3427
Arg Ile Ala Asp Leu Val Pro Asp Leu Val Thr Gly Asp Leu Ile Ser
    1095                1100                1105

gcg gag gca atg gtt ttg gga gct cga aac cca gga ctc gtc gat       3472
Ala Glu Ala Met Val Leu Gly Ala Arg Asn Pro Gly Leu Val Asp
1110                1115                1120

tagtccctga tttcatcgga ggg                                        3495
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<210> 2576
<211> 1124
<212> PRT
<213> Corynebacterium glutamicum

<400> 2576

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Met Pro Ala Gly Ile Ala Asp Met Thr Asp Ser Leu Leu Gly Trp Ala
  1               5                  10                  15

Ser Gln Thr Glu Leu Asp Leu Asn Gln Arg Leu Ala Gly Val Glu Tyr
            20                  25                  30

Phe Pro Gln Ile Gln Leu Arg His Asp Glu Leu Glu Arg Ile His Arg
        35                  40                  45

Phe Tyr Gly Thr Phe Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu
    50                  55                  60

Gly Asp Leu Phe Glu Met Thr Pro Cys Leu Thr Val Thr Thr Leu Val
65                  70                  75                  80

Ser Arg Ala Ser Arg Ile Ser Asp Pro Ala Asp Phe Phe Gly Glu Tyr
                85                  90                  95

Ile Gly Gly Leu Gly Leu Ser Ala Glu His Ala Ala Val Val Glu Gly
            100                 105                 110

Leu Thr Glu Lys Leu Phe Ala Gln Ala Gly Leu Leu Val Pro Glu Gly
        115                 120                 125

Ile Ala Ser Pro Leu Glu Leu Leu Ser Ile His Ala Gly Ile Ser Asn
    130                 135                 140

His Glu Val Ala Ala Val Leu Thr Glu Val Glu Asn Gly Thr Thr Glu
145                 150                 155                 160

Tyr Pro Phe Met Phe Asp Ala Val Leu Arg Leu Thr Pro Glu Trp Ala
                165                 170                 175
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Gln Thr Leu Ile Gly Gly Val Gln Glu Leu Ile Glu Phe Ala Thr Thr
            180                 185                 190

His Arg Thr Ser Trp Ser Asp Arg Gln Arg Glu Ser Ser Leu Pro Ala
        195                 200                 205

Met Ile Asp Glu Ile Val Val Ala Glu Leu Arg Glu Arg Pro Val Gly
    210                 215                 220

Thr Ala Asp Arg Glu Asn Ser Val Gly Val Ala Leu Arg Glu Leu Arg
225                 230                 235                 240

Pro Arg Leu Ile Leu Asp Ala Glu Arg Arg Lys Val Cys Leu Arg Leu
                245                 250                 255

Pro Glu Gln Arg Val Ser Asp Asp Glu Ile Asn Trp Arg Val Ser Leu
            260                 265                 270

Glu Gly Thr Thr Arg Ile Phe Ser Thr Arg Arg Ala Trp Gly Asp Thr
        275                 280                 285

Ser Gly Tyr Ser Glu Ala Leu Asp Ile Thr Val Glu Arg Gln Ile Arg
    290                 295                 300

Glu Thr Thr Val Thr Asp Thr Ser Asn Gln Ile Thr Trp Val Val Pro
305                 310                 315                 320

Val Val Asp Phe Asn Asp Pro Val Leu Val Phe Ser Ala Arg Gly Glu
                325                 330                 335

Asn Leu Thr Asp Lys Val Ser Leu His His Gln Glu Ile Tyr Val Leu
            340                 345                 350

Ala Pro Ala Glu Ala Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val
        355                 360                 365

Pro Val Ile Glu Gln Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys
    370                 375                 380

Ser Arg Val Asp Ala Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu
385                 390                 395                 400

Val Arg Cys Ile Asp Pro Arg Arg Arg Val Ala Phe His His Pro Ala
                405                 410                 415

Glu Leu Val Pro His Val Arg Ser Ile Ser Gly Leu Pro Val His Ala
            420                 425                 430

Gln Ser Leu Ile Ala Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu
        435                 440                 445

Thr Trp Met Leu Ser Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly
    450                 455                 460

Glu Glu Ile Ala Glu Pro Glu Pro Leu Glu Val Pro Ala Asp Gly Gly
465                 470                 475                 480

Leu Phe Ala Ile Phe Asp Pro Glu Ile Tyr Asp Ala Pro Trp Val Gly
                485                 490                 495

Glu Tyr Leu Val Arg Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro
```

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            500                 505                 510

Glu Phe Ala Ile Val Glu Asp Met Thr Thr Glu Phe Glu Val Ala Ser
        515                 520                 525

Gly Ala Ser Phe Arg Ile Pro Thr Thr Thr Gly Leu Ser Glu Ala Ser
    530                 535                 540

Leu Arg Val Arg Ser Gly Glu Lys His Phe Thr Ala Glu Pro Arg Leu
545                 550                 555                 560

Val Thr Val Glu Ala Thr Asp Pro Asn Ala Ser Phe Val Val Thr Thr
                565                 570                 575

Asp Glu Gly Asp Gln Met Pro Leu Arg Phe Val Pro Pro Gln Ile Ala
            580                 585                 590

Ile Glu Leu Pro Leu Thr Thr Glu Pro Pro Thr Trp Arg Val Thr Arg
        595                 600                 605

Thr Val Cys Gly Pro Arg Asp Leu Asp Gly Ala Gly Glu Leu Arg Ile
    610                 615                 620

Arg Thr Gly Val Asp Val Gly Asp Pro Lys Val Ser Val Arg Asn His
625                 630                 635                 640

His Gly Ser Pro Leu Arg Thr Val Lys Met Val Thr Pro Asp Asn Gly
                645                 650                 655

Arg Thr Trp Ile Ala Ser Met Lys Glu Ile Ala Ala Ser Thr Phe Val
            660                 665                 670

Met Pro Arg Gly Ser Ile Glu Phe Glu Trp Thr Asp Arg Lys Val Asp
        675                 680                 685

Arg Arg Val Ser Val Thr Ile Ala Val Ile Asp Lys Thr Glu Asn Phe
    690                 695                 700

Thr Gly Ile Thr Ile Glu Asp Gly Lys Leu Val Phe Glu Glu Leu Ala
705                 710                 715                 720

Ala Gly Arg Gln Leu Ala Ala Trp Val Trp Pro Gln Thr Ala Pro Trp
                725                 730                 735

Val Ser Ala Val Glu Leu Ala Val Thr Gly Pro Glu Leu Glu Leu Pro
            740                 745                 750

Glu Val Leu Val Gly Ala Gly Asn Leu Ile Val Gln Leu His Thr Ala
        755                 760                 765

Asp Pro Phe Thr Thr Ser Val Thr Pro Leu Ser Pro Gly Lys Ala Ala
    770                 775                 780

Val Thr Val Glu Gln Glu Gly Tyr Tyr Ser Ala Gln Thr Glu Glu Tyr
785                 790                 795                 800

Ala Gln Leu Ser Ala Phe Phe Gly Gly Glu Val Glu Glu Pro Pro Ile
                805                 810                 815

Ser Asp Ala Val Val Pro Ala Leu Trp Asp Val Ser His Ile Trp Thr
            820                 825                 830
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Glu Gln Gly Asn Thr Glu His Leu Pro Val Val His Ala Ala Leu Arg
        835                 840                 845

Ser Ser Pro Ala Ala Ala Leu Lys Gly Leu Ser Ala Ser Leu Val Pro
    850                 855                 860

Ala Gln Ala Leu Pro Gly Lys Val Ile Ser Ser Gly Leu Ala Ala Ser
865                 870                 875                 880

Pro Phe Thr Thr Glu Ser Pro Ala Thr Glu Val His Arg Thr Ala Trp
                885                 890                 895

Ile Gly Thr Leu Gln Leu Leu Gly Ala Leu Pro Ser Ala Phe Lys Glu
            900                 905                 910

Ala Glu Glu Leu Gly Asn Arg Thr Pro Leu Leu Pro Ile Leu Gly Gln
        915                 920                 925

Leu Glu Glu Val Ala Gly Lys Asn Ile Leu Ser Thr Leu Ala Thr Gly
    930                 935                 940

Arg Asp Ser Thr Leu Asp Thr Ala Cys Ile Asp Gln Ser Thr Val Ala
945                 950                 955                 960

Ile Ala Gly Met Asn Glu Thr Gln Gln Lys Ala Leu Leu Asp Met Phe
                965                 970                 975

Phe Ser Asn Ala Asp Ile Val Pro Gly Pro Leu Met Glu Asp Asn Thr
            980                 985                 990

Arg Leu Met Ala Val Phe Glu Thr Phe Lys Lys Arg Asp Ala Leu Arg
        995                 1000                1005

Glu Val Leu Gln Thr Glu Gly Leu Ile Lys Thr Ala Val Glu Leu Leu
    1010                1015                1020

Arg Ala Met Arg Gly Thr Gln Arg Gln Leu Tyr Ser Ser Ala Arg Ile
1025                1030                1035                1040

Arg Phe Asp Lys Leu Asp Gly Val Asn Thr Asp Asn Pro Glu Asn Met
                1045                1050                1055

Trp Ala Leu Thr Pro Val Val Ser Leu Val Phe Ala Leu Ser Ser Arg
            1060                1065                1070

Leu His Ala His Glu Leu Ile Gly Lys Thr Arg Thr Leu Asp Arg Ala
        1075                1080                1085

Ser Ala Gly Trp Gly Arg Ile Ala Asp Leu Val Pro Asp Leu Val Thr
    1090                1095                1100

Gly Asp Leu Ile Ser Ala Glu Ala Met Val Leu Gly Ala Arg Asn Pro
1105                1110                1115                1120

Gly Leu Val Asp
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<210> 2577
<211> 1281

<212> DNA
<213> Corynebacterium glutamicum

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<221> CDS
<222> (101)..(1258)
<223> RXA02102

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tcttcggcat aacaccacag tagacaatag ccttggtgtt atg act agc ccc cat   115
                                            Met Thr Ser Pro His
                                              1               5

tct ttt tct gtc acc ccc att cgc acc atg gct gac ggc acg atc aaa   163
Ser Phe Ser Val Thr Pro Ile Arg Thr Met Ala Asp Gly Thr Ile Lys
                  10                  15                  20

cag att cac cct ttc aca ggc acc gaa gtg tgg acg gtc cct ggg cgt   211
Gln Ile His Pro Phe Thr Gly Thr Glu Val Trp Thr Val Pro Gly Arg
             25                  30                  35

gga aat cga cct ctg tca cat ccc gct tct acg atc gtc gaa cta tct   259
Gly Asn Arg Pro Leu Ser His Pro Ala Ser Thr Ile Val Glu Leu Ser
         40                  45                  50

gca cac gat cac acc tct tac tgt gca ttt tgt tcc gac aat atg ctc   307
Ala His Asp His Thr Ser Tyr Cys Ala Phe Cys Ser Asp Asn Met Leu
     55                  60                  65

tcc act ccg cct gag aaa tcg cgc atc atc att gat agc tcc ggc gac   355
Ser Thr Pro Pro Glu Lys Ser Arg Ile Ile Ile Asp Ser Ser Gly Asp
 70                  75                  80                  85

ttt gac atc ctt ccc gga gca ttg cct ggt gag ctt tca gaa acc act   403
Phe Asp Ile Leu Pro Gly Ala Leu Pro Gly Glu Leu Ser Glu Thr Thr
                 90                  95                 100

ccg gaa ttt cga cga gtc ccc aat ctg ttt gag att gtc tct ttt gac   451
Pro Glu Phe Arg Arg Val Pro Asn Leu Phe Glu Ile Val Ser Phe Asp
            105                 110                 115

tac tgg cac cag aat ttt ggt ttc gat atg gat tca gaa acc gcc atg   499
Tyr Trp His Gln Asn Phe Gly Phe Asp Met Asp Ser Glu Thr Ala Met
        120                 125                 130

cgc atg gcg caa tac ttg gcg att cca gaa ggt cgc gaa cat gtt tta   547
Arg Met Ala Gln Tyr Leu Ala Ile Pro Glu Gly Arg Glu His Val Leu
    135                 140                 145

gcc att gtg cgc acc cga ctt tct gcc gct ggt gaa gat ccc gcg cac   595
Ala Ile Val Arg Thr Arg Leu Ser Ala Ala Gly Glu Asp Pro Ala His
150                 155                 160                 165

atg acc gat ggc gag ttg tta gaa aaa gct ccc agc tac ttt gct ggt   643
Met Thr Asp Gly Glu Leu Leu Glu Lys Ala Pro Ser Tyr Phe Ala Gly
                170                 175                 180

ggt cat gac gtc atc atc gga cgc cga cac ttt gtc gat gac gca acc   691
Gly His Asp Val Ile Ile Gly Arg Arg His Phe Val Asp Asp Ala Thr
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            185                 190                 195

acc agt gat caa ttg gcc tca tct gga aca ctg acc gtt aaa gag cat   739
Thr Ser Asp Gln Leu Ala Ser Ser Gly Thr Leu Thr Val Lys Glu His
        200                 205                 210

gag gcg ttc atc cgc ctg act gtc gat ggc atc agg gat ttg tac cac   787
Glu Ala Phe Ile Arg Leu Thr Val Asp Gly Ile Arg Asp Leu Tyr His
    215                 220                 225

cgc aac cgt tac gca ccg tat gta gtg gcg ttt caa aac tgg ttg aaa   835
Arg Asn Arg Tyr Ala Pro Tyr Val Val Ala Phe Gln Asn Trp Leu Lys
230                 235                 240                 245

ccc gcc ggc gcg tct ttt gac cat ctt cat aaa cag ctc gtc gcc att   883
Pro Ala Gly Ala Ser Phe Asp His Leu His Lys Gln Leu Val Ala Ile
                250                 255                 260

gat gaa cgc ggc cga ctt att gcc gat gaa ctg cat cat cta cgt ggc   931
Asp Glu Arg Gly Arg Leu Ile Ala Asp Glu Leu His His Leu Arg Gly
            265                 270                 275

aat ccc aat atg tac aac gaa ctt gct gtt gat tac gcc gga tac cac   979
Asn Pro Asn Met Tyr Asn Glu Leu Ala Val Asp Tyr Ala Gly Tyr His
        280                 285                 290

aac ctg atc atc gcg gaa aac gat cac gcc gtg gcc ttc gca ggt ttc   1027
Asn Leu Ile Ile Ala Glu Asn Asp His Ala Val Ala Phe Ala Gly Phe
    295                 300                 305

ggt cac cgc tac ccc acc att gag att tac tct aag tcc gct att cct   1075
Gly His Arg Tyr Pro Thr Ile Glu Ile Tyr Ser Lys Ser Ala Ile Pro
310                 315                 320                 325

gaa ccc tgg ctt caa agc gac gag gaa atc caa gcg atg agc aac ctc   1123
Glu Pro Trp Leu Gln Ser Asp Glu Glu Ile Gln Ala Met Ser Asn Leu
                330                 335                 340

atc cat gca tgc cat gct gca acc ggc gca gat gta ccc tgc aat gag   1171
Ile His Ala Cys His Ala Ala Thr Gly Ala Asp Val Pro Cys Asn Glu
            345                 350                 355

gga tgg gta cac aaa cca atc gat gtt gat atg cca atg ccc tgg cat   1219
Gly Trp Val His Lys Pro Ile Asp Val Asp Met Pro Met Pro Trp His
        360                 365                 370

gtg atg atc aaa tgg cgt gtt tct acc ctg gca ggt ttt tgaaggtggc   1268
Val Met Ile Lys Trp Arg Val Ser Thr Leu Ala Gly Phe
    375                 380                 385

accaaggtgt atc                                                  1281


<210> 2578
<211> 386
<212> PRT
<213> Corynebacterium glutamicum

<400> 2578
Met Thr Ser Pro His Ser Phe Ser Val Thr Pro Ile Arg Thr Met Ala
  1               5                  10                  15
```

```
Asp Gly Thr Ile Lys Gln Ile His Pro Phe Thr Gly Thr Glu Val Trp
             20                  25                  30

Thr Val Pro Gly Arg Gly Asn Arg Pro Leu Ser His Pro Ala Ser Thr
         35                  40                  45

Ile Val Glu Leu Ser Ala His Asp His Thr Ser Tyr Cys Ala Phe Cys
     50                  55                  60

Ser Asp Asn Met Leu Ser Thr Pro Pro Glu Lys Ser Arg Ile Ile Ile
 65                  70                  75                  80

Asp Ser Ser Gly Asp Phe Asp Ile Leu Pro Gly Ala Leu Pro Gly Glu
                 85                  90                  95

Leu Ser Glu Thr Thr Pro Glu Phe Arg Arg Val Pro Asn Leu Phe Glu
            100                 105                 110

Ile Val Ser Phe Asp Tyr Trp His Gln Asn Phe Gly Phe Asp Met Asp
        115                 120                 125

Ser Glu Thr Ala Met Arg Met Ala Gln Tyr Leu Ala Ile Pro Glu Gly
    130                 135                 140

Arg Glu His Val Leu Ala Ile Val Arg Thr Arg Leu Ser Ala Ala Gly
145                 150                 155                 160

Glu Asp Pro Ala His Met Thr Asp Gly Glu Leu Leu Glu Lys Ala Pro
                165                 170                 175

Ser Tyr Phe Ala Gly Gly His Asp Val Ile Ile Gly Arg Arg His Phe
            180                 185                 190

Val Asp Asp Ala Thr Thr Ser Asp Gln Leu Ala Ser Ser Gly Thr Leu
        195                 200                 205

Thr Val Lys Glu His Glu Ala Phe Ile Arg Leu Thr Val Asp Gly Ile
    210                 215                 220

Arg Asp Leu Tyr His Arg Asn Arg Tyr Ala Pro Tyr Val Val Ala Phe
225                 230                 235                 240

Gln Asn Trp Leu Lys Pro Ala Gly Ala Ser Phe Asp His Leu His Lys
                245                 250                 255

Gln Leu Val Ala Ile Asp Glu Arg Gly Arg Leu Ile Ala Asp Glu Leu
            260                 265                 270

His His Leu Arg Gly Asn Pro Asn Met Tyr Asn Glu Leu Ala Val Asp
        275                 280                 285

Tyr Ala Gly Tyr His Asn Leu Ile Ile Ala Glu Asn Asp His Ala Val
    290                 295                 300

Ala Phe Ala Gly Phe Gly His Arg Tyr Pro Thr Ile Glu Ile Tyr Ser
305                 310                 315                 320

Lys Ser Ala Ile Pro Glu Pro Trp Leu Gln Ser Asp Glu Glu Ile Gln
                325                 330                 335
```

```
Ala Met Ser Asn Leu Ile His Ala Cys His Ala Ala Thr Gly Ala Asp
            340                 345                 350

Val Pro Cys Asn Glu Gly Trp Val His Lys Pro Ile Asp Val Asp Met
        355                 360                 365

Pro Met Pro Trp His Val Met Ile Lys Trp Arg Val Ser Thr Leu Ala
    370                 375                 380

Gly Phe
385
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<210> 2579
<211> 519
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(496)
<223> RXA02103

<400> 2579

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gaatctgttt gatcgtgccg tcagccatgg tgcgaatggg ggtgacagaa aaagaatggg 60

ggctagtcat aacaccaagg ctattgtcta ctgtggtgtt atg ccg aag att cag   115
                                              Met Pro Lys Ile Gln
                                                1               5

ttt gat gtt tta gtc ccc gac aca gat tcc atc gca cta gcg gga cgt   163
Phe Asp Val Leu Val Pro Asp Thr Asp Ser Ile Ala Leu Ala Gly Arg
                10                  15                  20

ttt acc gta gtc gcc aac ctt ttg atc gaa aaa ggc ctc atg gat cat   211
Phe Thr Val Val Ala Asn Leu Leu Ile Glu Lys Gly Leu Met Asp His
            25                  30                  35

ggc gtt gtt gtc cat gat cca gca gcg aaa atc gca gaa gct gtg gaa   259
Gly Val Val Val His Asp Pro Ala Ala Lys Ile Ala Glu Ala Val Glu
        40                  45                  50

gag cag ctt cgc cag act tac cgc gac gag cat gaa gat gca gac ttg   307
Glu Gln Leu Arg Gln Thr Tyr Arg Asp Glu His Glu Asp Ala Asp Leu
    55                  60                  65

gaa gaa tcc tcg gtc aac cgt tac ctc att gaa gtt gat gga gtt aaa   355
Glu Glu Ser Ser Val Asn Arg Tyr Leu Ile Glu Val Asp Gly Val Lys
70                  75                  80                  85

ggc tcc gtt aac caa gtg acc atg att ttt gcc cgt ttg ctc acc ccg   403
Gly Ser Val Asn Gln Val Thr Met Ile Phe Ala Arg Leu Leu Thr Pro
                90                  95                  100

cca gca gag ttg cca aag gac gct ttc ctc ctg gag cag gaa ctt gcc   451
Pro Ala Glu Leu Pro Lys Asp Ala Phe Leu Leu Glu Gln Glu Leu Ala
            105                 110                 115

tat gaa gtt cct gca gtc tac cca tgg act gtg gag atc ctt cgc       496
Tyr Glu Val Pro Ala Val Tyr Pro Trp Thr Val Glu Ile Leu Arg
        120                 125                 130
```

tagttttgag ctacgtattc ttg 519

<210> 2580
<211> 132
<212> PRT
<213> Corynebacterium glutamicum

<400> 2580
Met Pro Lys Ile Gln Phe Asp Val Leu Val Pro Asp Thr Asp Ser Ile
1 5 10 15

Ala Leu Ala Gly Arg Phe Thr Val Val Ala Asn Leu Leu Ile Glu Lys
20 25 30

Gly Leu Met Asp His Gly Val Val Val His Asp Pro Ala Ala Lys Ile
35 40 45

Ala Glu Ala Val Glu Glu Gln Leu Arg Gln Thr Tyr Arg Asp Glu His
50 55 60

Glu Asp Ala Asp Leu Glu Glu Ser Ser Val Asn Arg Tyr Leu Ile Glu
65 70 75 80

Val Asp Gly Val Lys Gly Ser Val Asn Gln Val Thr Met Ile Phe Ala
85 90 95

Arg Leu Leu Thr Pro Pro Ala Glu Leu Pro Lys Asp Ala Phe Leu Leu
100 105 110

Glu Gln Glu Leu Ala Tyr Glu Val Pro Ala Val Tyr Pro Trp Thr Val
115 120 125

Glu Ile Leu Arg
130

<210> 2581
<211> 1044
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1021)
<223> RXA02109

<400> 2581
gactctaagg gaagtgtttc gcttcaaccc gtacaggtct aatatgtcgg gagtcttgtt 60

ttaagctctt atataacctg tataggaaag cgaaaacctc atg ctt gca gtg cta 115
Met Leu Ala Val Leu
1 5

ttc ggg gtg gtg gcc ggt gcc atc atg cct ttc caa act tcg gtg aat 163
Phe Gly Val Val Ala Gly Ala Ile Met Pro Phe Gln Thr Ser Val Asn
10 15 20

aat aga ttg cgt cag tcc gtg gga gca cca ctg ctg gcg tct ttt att 211
Asn Arg Leu Arg Gln Ser Val Gly Ala Pro Leu Leu Ala Ser Phe Ile

```
                25                  30                  35

tcc ttt ttg gta gga act ttt tca ctc ctg gtt gca acg tgg atc acc   259
Ser Phe Leu Val Gly Thr Phe Ser Leu Leu Val Ala Thr Trp Ile Thr
          40                  45                  50

agt ggg cac ccg tat cct gct cta gga aat aca act ggc caa ccg tgg   307
Ser Gly His Pro Tyr Pro Ala Leu Gly Asn Thr Thr Gly Gln Pro Trp
     55                  60                  65

tgg att ttc acc ggt ggc atg ttg ggt gtt gtg ctg ctg acg gga aac   355
Trp Ile Phe Thr Gly Gly Met Leu Gly Val Val Leu Leu Thr Gly Asn
 70                  75                  80                  85

att ttg ctg ttt ccc cga gtc ggc agc gtg cag acc gtt att ttg ccc   403
Ile Leu Leu Phe Pro Arg Val Gly Ser Val Gln Thr Val Ile Leu Pro
                 90                  95                 100

atc tcc gga cag atc atc atg ggc cta att atc gat aca act ggc ctg   451
Ile Ser Gly Gln Ile Ile Met Gly Leu Ile Ile Asp Thr Thr Gly Leu
            105                 110                 115

gca cat tcg cct caa gca ccg tta acc ctg ttc aga gta ttg ggt gct   499
Ala His Ser Pro Gln Ala Pro Leu Thr Leu Phe Arg Val Leu Gly Ala
        120                 125                 130

gct gcg gta ctt gtt gga tcg ctg gcc gca gtg gga gtg ttc tct aag   547
Ala Ala Val Leu Val Gly Ser Leu Ala Ala Val Gly Val Phe Ser Lys
    135                 140                 145

aaa aac atc gga cag acc caa tcc caa ggt gcc tcc att tgg ttg tgg   595
Lys Asn Ile Gly Gln Thr Gln Ser Gln Gly Ala Ser Ile Trp Leu Trp
150                 155                 160                 165

cgc ctc ttc gga gtg gtg atg ggc atg tgc caa gca acc cag gtt gca   643
Arg Leu Phe Gly Val Val Met Gly Met Cys Gln Ala Thr Gln Val Ala
                170                 175                 180

gtc aat ggt tac ttg gga act gtc cta gga tcc ccc att gag tca gca   691
Val Asn Gly Tyr Leu Gly Thr Val Leu Gly Ser Pro Ile Glu Ser Ala
            185                 190                 195

ctg gtg tct ttc gct gtt ggc acc acc gcg ctg ttt att ctg ctg ttg   739
Leu Val Ser Phe Ala Val Gly Thr Thr Ala Leu Phe Ile Leu Leu Leu
        200                 205                 210

gtc acc cga acc aag tgg cgt gga atc aac ggc gct ggg aag aaa aac   787
Val Thr Arg Thr Lys Trp Arg Gly Ile Asn Gly Ala Gly Lys Lys Asn
    215                 220                 225

cca tgg tgg atg tgg atc ggt ggc gtc atc ggc gcg act gtt att ttc   835
Pro Trp Trp Met Trp Ile Gly Gly Val Ile Gly Ala Thr Val Ile Phe
230                 235                 240                 245

agt act gct tac ctg gga ccg atc att ggc act ggt gtt acc gtg gtg   883
Ser Thr Ala Tyr Leu Gly Pro Ile Ile Gly Thr Gly Val Thr Val Val
                250                 255                 260

gtt atg ttg ctg ggc atg atg ttg gcc agc ctg atg atc gac gct ttt   931
Val Met Leu Leu Gly Met Met Leu Ala Ser Leu Met Ile Asp Ala Phe
            265                 270                 275
```

```
gga atc ctt ggc agc ccg cgc cgc cac att cac atc gcg cag ctt ctc   979
Gly Ile Leu Gly Ser Pro Arg Arg His Ile His Ile Ala Gln Leu Leu
        280                 285                 290

ggg ctc gtg gtg atc atc ctc ggc gta aca atg atc aga atc           1021
Gly Leu Val Val Ile Ile Leu Gly Val Thr Met Ile Arg Ile
    295                 300                 305

taaaccaaga atctaaacca aga                                        1044
```

<210> 2582
<211> 307
<212> PRT
<213> Corynebacterium glutamicum

<400> 2582

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Met Leu Ala Val Leu Phe Gly Val Val Ala Gly Ala Ile Met Pro Phe
  1               5                  10                  15

Gln Thr Ser Val Asn Asn Arg Leu Arg Gln Ser Val Gly Ala Pro Leu
             20                  25                  30

Leu Ala Ser Phe Ile Ser Phe Leu Val Gly Thr Phe Ser Leu Leu Val
         35                  40                  45

Ala Thr Trp Ile Thr Ser Gly His Pro Tyr Pro Ala Leu Gly Asn Thr
     50                  55                  60

Thr Gly Gln Pro Trp Trp Ile Phe Thr Gly Gly Met Leu Gly Val Val
 65                  70                  75                  80

Leu Leu Thr Gly Asn Ile Leu Leu Phe Pro Arg Val Gly Ser Val Gln
                 85                  90                  95

Thr Val Ile Leu Pro Ile Ser Gly Gln Ile Ile Met Gly Leu Ile Ile
            100                 105                 110

Asp Thr Thr Gly Leu Ala His Ser Pro Gln Ala Pro Leu Thr Leu Phe
        115                 120                 125

Arg Val Leu Gly Ala Ala Ala Val Leu Val Gly Ser Leu Ala Ala Val
    130                 135                 140

Gly Val Phe Ser Lys Lys Asn Ile Gly Gln Thr Gln Ser Gln Gly Ala
145                 150                 155                 160

Ser Ile Trp Leu Trp Arg Leu Phe Gly Val Val Met Gly Met Cys Gln
                165                 170                 175

Ala Thr Gln Val Ala Val Asn Gly Tyr Leu Gly Thr Val Leu Gly Ser
            180                 185                 190

Pro Ile Glu Ser Ala Leu Val Ser Phe Ala Val Gly Thr Thr Ala Leu
        195                 200                 205

Phe Ile Leu Leu Leu Val Thr Arg Thr Lys Trp Arg Gly Ile Asn Gly
    210                 215                 220

Ala Gly Lys Lys Asn Pro Trp Trp Met Trp Ile Gly Gly Val Ile Gly
```

```
225                 230                 235                 240

Ala Thr Val Ile Phe Ser Thr Ala Tyr Leu Gly Pro Ile Ile Gly Thr
                245                 250                 255

Gly Val Thr Val Val Val Met Leu Leu Gly Met Met Leu Ala Ser Leu
            260                 265                 270

Met Ile Asp Ala Phe Gly Ile Leu Gly Ser Pro Arg Arg His Ile His
        275                 280                 285

Ile Ala Gln Leu Leu Gly Leu Val Val Ile Ile Leu Gly Val Thr Met
    290                 295                 300

Ile Arg Ile
305
```

<210> 2583
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> RXA02117

<400> 2583

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tgaacacaaa ctaccacgtt tattgcatca tgcaacaccc ttgctaggat ataaaatact 60

ctatgagtcc agacgttttt aaagggagcg aattaccata gtg tct aca gat cca   115
                                            Val Ser Thr Asp Pro
                                              1               5

gaa gag ttc gac caa gct gaa acc ctc gat caa ctc gcg tat gag atc   163
Glu Glu Phe Asp Gln Ala Glu Thr Leu Asp Gln Leu Ala Tyr Glu Ile
                10                  15                  20

atc ctg ctc acc cgg tat ggt gtc caa aac aca ccg acc aac aag cgc   211
Ile Leu Leu Thr Arg Tyr Gly Val Gln Asn Thr Pro Thr Asn Lys Arg
            25                  30                  35

gaa gcc atc atg gat cgc agc gcc ctc atc ttg ctc acc cgc ctt gac   259
Glu Ala Ile Met Asp Arg Ser Ala Leu Ile Leu Leu Thr Arg Leu Asp
        40                  45                  50

gct caa gga cct atg aca gtt aat gag cta gct gaa agc ttt gga ctt   307
Ala Gln Gly Pro Met Thr Val Asn Glu Leu Ala Glu Ser Phe Gly Leu
    55                  60                  65

aac gtt tct acc gtg cac cgc caa ctc aaa gca gcc att gcc aat ggc   355
Asn Val Ser Thr Val His Arg Gln Leu Lys Ala Ala Ile Ala Asn Gly
70                  75                  80                  85

tta att gaa gtc gtc gat gat caa gca tgc ccc gct aaa ctt cat cgt   403
Leu Ile Glu Val Val Asp Asp Gln Ala Cys Pro Ala Lys Leu His Arg
                90                  95                  100

cca act gag ttg ggt aaa gaa aaa ctg cag cag gag ctt ctt gcc cgc   451
Pro Thr Glu Leu Gly Lys Glu Lys Leu Gln Gln Glu Leu Leu Ala Arg
```

```
            105                 110                 115

cag cag gat ctc acc cgc att ctt cat gat tgg gat gag gaa gac att   499
Gln Gln Asp Leu Thr Arg Ile Leu His Asp Trp Asp Glu Glu Asp Ile
        120                 125                 130

aaa acg cat gcc aag cta ttg cgg aag cac aat gaa agc ttg gaa gaa   547
Lys Thr His Ala Lys Leu Leu Arg Lys His Asn Glu Ser Leu Glu Glu
    135                 140                 145

tac ctc gat atg aag tgg ccc cgc ccc taagtgccca taaacgcacc        594
Tyr Leu Asp Met Lys Trp Pro Arg Pro
150                 155

tct                                                              597


<210> 2584
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 2584
Val Ser Thr Asp Pro Glu Glu Phe Asp Gln Ala Glu Thr Leu Asp Gln
  1               5                  10                  15

Leu Ala Tyr Glu Ile Ile Leu Leu Thr Arg Tyr Gly Val Gln Asn Thr
             20                  25                  30

Pro Thr Asn Lys Arg Glu Ala Ile Met Asp Arg Ser Ala Leu Ile Leu
         35                  40                  45

Leu Thr Arg Leu Asp Ala Gln Gly Pro Met Thr Val Asn Glu Leu Ala
     50                  55                  60

Glu Ser Phe Gly Leu Asn Val Ser Thr Val His Arg Gln Leu Lys Ala
 65                  70                  75                  80

Ala Ile Ala Asn Gly Leu Ile Glu Val Val Asp Asp Gln Ala Cys Pro
                 85                  90                  95

Ala Lys Leu His Arg Pro Thr Glu Leu Gly Lys Glu Lys Leu Gln Gln
            100                 105                 110

Glu Leu Leu Ala Arg Gln Gln Asp Leu Thr Arg Ile Leu His Asp Trp
        115                 120                 125

Asp Glu Glu Asp Ile Lys Thr His Ala Lys Leu Leu Arg Lys His Asn
    130                 135                 140

Glu Ser Leu Glu Glu Tyr Leu Asp Met Lys Trp Pro Arg Pro
145                 150                 155


<210> 2585
<211> 1494
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
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<222> (101)..(1471)
<223> RXA02123

<400> 2585
ggattgagtc ttttcggcag ctgcgtgtga acccggcttc atgacatgca gcatacctgt 60

gcgaaaaatt cctgaccgcc cacttaaaaa aaggtctagg gtg tgg ggt gtg agt 115
Val Trp Gly Val Ser
1 5

ctt cca cca aat gta caa act gtc ggt gag ctg aag gcc gcc ggc cac 163
Leu Pro Pro Asn Val Gln Thr Val Gly Glu Leu Lys Ala Ala Gly His
10 15 20

atc tac cga cct ttg cgc gta gaa atc cgc gac aac ctc cta gcc aaa 211
Ile Tyr Arg Pro Leu Arg Val Glu Ile Arg Asp Asn Leu Leu Ala Lys
25 30 35

ctt cgc agc ggc gaa gat ccg tgg cca ggc ctg cac ggc ctg aac tac 259
Leu Arg Ser Gly Glu Asp Pro Trp Pro Gly Leu His Gly Leu Asn Tyr
40 45 50

acg gtc atc cgg cag ctt gaa cgc gcg ctc atc gcc ggc cac gac atc 307
Thr Val Ile Arg Gln Leu Glu Arg Ala Leu Ile Ala Gly His Asp Ile
55 60 65

gtg ctg ctc ggc gaa cgc ggc cag ggt aaa acc cgc ctg ctc cgc acg 355
Val Leu Leu Gly Glu Arg Gly Gln Gly Lys Thr Arg Leu Leu Arg Thr
70 75 80 85

tta ata acg ctt ctc gac gag tgg tcc ccg atc att ccc ggg cgc gac 403
Leu Ile Thr Leu Leu Asp Glu Trp Ser Pro Ile Ile Pro Gly Arg Asp
90 95 100

gtt cca gaa cac cct ctt gcg cca aac gta gag atc tcc gat gat cag 451
Val Pro Glu His Pro Leu Ala Pro Asn Val Glu Ile Ser Asp Asp Gln
105 110 115

ccc att gaa tgg gta cac cgc gat gcg cgc tat acc gag aaa ctt gcc 499
Pro Ile Glu Trp Val His Arg Asp Ala Arg Tyr Thr Glu Lys Leu Ala
120 125 130

acc cca gat act tcc gtg gct gat ctt atc ggt gat gtt gac cca atg 547
Thr Pro Asp Thr Ser Val Ala Asp Leu Ile Gly Asp Val Asp Pro Met
135 140 145

cgt gtt gct gaa ggc cgc agc ctc ggt gat cta gaa acc att cac tac 595
Arg Val Ala Glu Gly Arg Ser Leu Gly Asp Leu Glu Thr Ile His Tyr
150 155 160 165

ggt ctg att cct cgc gcc aac cgt ggc atc gtg gcg atc aac gag ctt 643
Gly Leu Ile Pro Arg Ala Asn Arg Gly Ile Val Ala Ile Asn Glu Leu
170 175 180

cct gac ctc gct gaa cgc atc cag gtt gcc atg ctc aac gtc atg gag 691
Pro Asp Leu Ala Glu Arg Ile Gln Val Ala Met Leu Asn Val Met Glu
185 190 195

gaa cgt gat gtg cag att cgt ggc tac aac att cgt ttg gac ttg gat 739
Glu Arg Asp Val Gln Ile Arg Gly Tyr Asn Ile Arg Leu Asp Leu Asp
200 205 210

```
gtg ctg gtt gtt gcc tca gcc aac cct gag gat tac acc aac cgt ggc   787
Val Leu Val Val Ala Ser Ala Asn Pro Glu Asp Tyr Thr Asn Arg Gly
    215                 220                 225

cga att atc act ccg ctc aaa gac cgc ttc ggt gca gaa atc cgc acc   835
Arg Ile Ile Thr Pro Leu Lys Asp Arg Phe Gly Ala Glu Ile Arg Thr
230                 235                 240                 245

cac tac cca ctt gag ttg gac gat gaa gtg gca att atc cgc cag gaa   883
His Tyr Pro Leu Glu Leu Asp Asp Glu Val Ala Ile Ile Arg Gln Glu
                250                 255                 260

gca gag ctt gtt gcg caa gtc cct gat atc ttg gtt gaa att ctt gcc   931
Ala Glu Leu Val Ala Gln Val Pro Asp Ile Leu Val Glu Ile Leu Ala
            265                 270                 275

cgc tac acc cga gcg ctt cgt gaa tcc tca tcg gtg aat cag cgt tct   979
Arg Tyr Thr Arg Ala Leu Arg Glu Ser Ser Ser Val Asn Gln Arg Ser
        280                 285                 290

ggt gtg tct gct cgt ttc tcc att gca ggt gca gaa act gtg gcc gca   1027
Gly Val Ser Ala Arg Phe Ser Ile Ala Gly Ala Glu Thr Val Ala Ala
    295                 300                 305

gca gct ctt cga cgc gca gca gtg ttc ggc gaa gat gag gcc gtt gcc   1075
Ala Ala Leu Arg Arg Ala Ala Val Phe Gly Glu Asp Glu Ala Val Ala
310                 315                 320                 325

cgc ctg gtt gat ttg gaa gca gcc gtg gaa gtc ctc ggc ggc aag att   1123
Arg Leu Val Asp Leu Glu Ala Ala Val Glu Val Leu Gly Gly Lys Ile
                330                 335                 340

gaa ttt gaa tcc ggc gaa gaa gga cgc gaa tgg gaa atc ctt gat tat   1171
Glu Phe Glu Ser Gly Glu Glu Gly Arg Glu Trp Glu Ile Leu Asp Tyr
            345                 350                 355

ctc ctg cgc acc gca acc gca gaa gcg ctg cgt tcc act ctg cgc tcg   1219
Leu Leu Arg Thr Ala Thr Ala Glu Ala Leu Arg Ser Thr Leu Arg Ser
        360                 365                 370

ctg gat ctc acc ccg ctc atc gca gca tta gac ggc agc atc acc gtt   1267
Leu Asp Leu Thr Pro Leu Ile Ala Ala Leu Asp Gly Ser Ile Thr Val
    375                 380                 385

tcc act ggc acg aac atc acc gcg tca gaa ttt ttg gct tcg ctc ccc   1315
Ser Thr Gly Thr Asn Ile Thr Ala Ser Glu Phe Leu Ala Ser Leu Pro
390                 395                 400                 405

gaa ctc ggc gaa agc acg cta tat gac gac atc gct caa gct ttt ggt   1363
Glu Leu Gly Glu Ser Thr Leu Tyr Asp Asp Ile Ala Gln Ala Phe Gly
                410                 415                 420

gcc acc aca cca agt act cgc gcg atg gcc att gag ctt gct ttg gaa   1411
Ala Thr Thr Pro Ser Thr Arg Ala Met Ala Ile Glu Leu Ala Leu Glu
            425                 430                 435

ggt ctt tac ctt tcc cga aaa att gcc aag gat tct ggc gaa ggt gaa   1459
Gly Leu Tyr Leu Ser Arg Lys Ile Ala Lys Asp Ser Gly Glu Gly Glu
        440                 445                 450
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acc att tac ggt taactggttt taaggagcac cac 1494
Thr Ile Tyr Gly
455

<210> 2586
<211> 457
<212> PRT
<213> Corynebacterium glutamicum

<400> 2586
Val Trp Gly Val Ser Leu Pro Pro Asn Val Gln Thr Val Gly Glu Leu
1 5 10 15

Lys Ala Ala Gly His Ile Tyr Arg Pro Leu Arg Val Glu Ile Arg Asp
20 25 30

Asn Leu Leu Ala Lys Leu Arg Ser Gly Glu Asp Pro Trp Pro Gly Leu
35 40 45

His Gly Leu Asn Tyr Thr Val Ile Arg Gln Leu Glu Arg Ala Leu Ile
50 55 60

Ala Gly His Asp Ile Val Leu Leu Gly Glu Arg Gly Gln Gly Lys Thr
65 70 75 80

Arg Leu Leu Arg Thr Leu Ile Thr Leu Leu Asp Glu Trp Ser Pro Ile
85 90 95

Ile Pro Gly Arg Asp Val Pro Glu His Pro Leu Ala Pro Asn Val Glu
100 105 110

Ile Ser Asp Asp Gln Pro Ile Glu Trp Val His Arg Asp Ala Arg Tyr
115 120 125

Thr Glu Lys Leu Ala Thr Pro Asp Thr Ser Val Ala Asp Leu Ile Gly
130 135 140

Asp Val Asp Pro Met Arg Val Ala Glu Gly Arg Ser Leu Gly Asp Leu
145 150 155 160

Glu Thr Ile His Tyr Gly Leu Ile Pro Arg Ala Asn Arg Gly Ile Val
165 170 175

Ala Ile Asn Glu Leu Pro Asp Leu Ala Glu Arg Ile Gln Val Ala Met
180 185 190

Leu Asn Val Met Glu Glu Arg Asp Val Gln Ile Arg Gly Tyr Asn Ile
195 200 205

Arg Leu Asp Leu Asp Val Leu Val Val Ala Ser Ala Asn Pro Glu Asp
210 215 220

Tyr Thr Asn Arg Gly Arg Ile Ile Thr Pro Leu Lys Asp Arg Phe Gly
225 230 235 240

Ala Glu Ile Arg Thr His Tyr Pro Leu Glu Leu Asp Asp Glu Val Ala
245 250 255

Ile Ile Arg Gln Glu Ala Glu Leu Val Ala Gln Val Pro Asp Ile Leu
260 265 270

```
Val Glu Ile Leu Ala Arg Tyr Thr Arg Ala Leu Arg Glu Ser Ser Ser
        275                 280                 285

Val Asn Gln Arg Ser Gly Val Ser Ala Arg Phe Ser Ile Ala Gly Ala
    290                 295                 300

Glu Thr Val Ala Ala Ala Ala Leu Arg Arg Ala Ala Val Phe Gly Glu
305                 310                 315                 320

Asp Glu Ala Val Ala Arg Leu Val Asp Leu Glu Ala Ala Val Glu Val
                325                 330                 335

Leu Gly Gly Lys Ile Glu Phe Glu Ser Gly Glu Glu Gly Arg Glu Trp
            340                 345                 350

Glu Ile Leu Asp Tyr Leu Leu Arg Thr Ala Thr Ala Glu Ala Leu Arg
        355                 360                 365

Ser Thr Leu Arg Ser Leu Asp Leu Thr Pro Leu Ile Ala Ala Leu Asp
    370                 375                 380

Gly Ser Ile Thr Val Ser Thr Gly Thr Asn Ile Thr Ala Ser Glu Phe
385                 390                 395                 400

Leu Ala Ser Leu Pro Glu Leu Gly Glu Ser Thr Leu Tyr Asp Asp Ile
                405                 410                 415

Ala Gln Ala Phe Gly Ala Thr Thr Pro Ser Thr Arg Ala Met Ala Ile
            420                 425                 430

Glu Leu Ala Leu Glu Gly Leu Tyr Leu Ser Arg Lys Ile Ala Lys Asp
        435                 440                 445

Ser Gly Glu Gly Glu Thr Ile Tyr Gly
    450                 455


<210> 2587
<211> 2079
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2056)
<223> RXA02124

<400> 2587
gcttgctttg gaaggtcttt acctttcccg aaaaattgcc aaggattctg gcgaaggtga 60

aaccatttac ggttaactgg ttttaaggag caccacagcc atg gcc act tca cat   115
                                              Met Ala Thr Ser His
                                                1               5

tca cga ccc cgc cgc agc cgt tac gga cgc tac acc gga ggc cca gat   163
Ser Arg Pro Arg Arg Ser Arg Tyr Gly Arg Tyr Thr Gly Gly Pro Asp
                10                  15                  20

ccg ctg gca cct cca gtg gat ctc agc gat gcc ctg cgc gat att gct   211
Pro Leu Ala Pro Pro Val Asp Leu Ser Asp Ala Leu Arg Asp Ile Ala
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                25                  30                  35

gat gat gtc atg gct ggt tat tcc cct gag cag gca cta cgt gaa tac   259
Asp Asp Val Met Ala Gly Tyr Ser Pro Glu Gln Ala Leu Arg Glu Tyr
         40                  45                  50

ctg cgc aga ggc gcc cga gga cag gaa ggc ctc gat gat cta gcc tgg   307
Leu Arg Arg Gly Ala Arg Gly Gln Glu Gly Leu Asp Asp Leu Ala Trp
     55                  60                  65

cgt gca gcc gaa cgc cgc cga gaa tta ctt agc cga aac aac ctc ggt   355
Arg Ala Ala Glu Arg Arg Arg Glu Leu Leu Ser Arg Asn Asn Leu Gly
 70                  75                  80                  85

ggc aca ctc gct gag gtt cgc aag ctt ctc gat gaa ggc ctc aag ctg   403
Gly Thr Leu Ala Glu Val Arg Lys Leu Leu Asp Glu Gly Leu Lys Leu
                 90                  95                 100

gaa cgc gct caa ctg gcc cgc gat atc gat atg gat gac acc gat cga   451
Glu Arg Ala Gln Leu Ala Arg Asp Ile Asp Met Asp Asp Thr Asp Arg
            105                 110                 115

gca ttc cgc gaa atg cag atc agc aac ctc cct gaa tcc acc gcc gct   499
Ala Phe Arg Glu Met Gln Ile Ser Asn Leu Pro Glu Ser Thr Ala Ala
        120                 125                 130

gcc gtt tcc gag cta aat tcc tac gat tgg caa tcc caa gaa gca cgc   547
Ala Val Ser Glu Leu Asn Ser Tyr Asp Trp Gln Ser Gln Glu Ala Arg
    135                 140                 145

caa aag ttt gaa caa atc cgt gac ctg ctt ggc cgt gaa atg tta gat   595
Gln Lys Phe Glu Gln Ile Arg Asp Leu Leu Gly Arg Glu Met Leu Asp
150                 155                 160                 165

cag caa ttc tcc ggc atg aaa caa gcc atg gaa ggt gcc tcc gac gag   643
Gln Gln Phe Ser Gly Met Lys Gln Ala Met Glu Gly Ala Ser Asp Glu
                170                 175                 180

gac aaa gca gcc atc gcc gaa atg ctg cgc gat ctc aac gac ctg ctc   691
Asp Lys Ala Ala Ile Ala Glu Met Leu Arg Asp Leu Asn Asp Leu Leu
            185                 190                 195

tcc aaa cac cgc gag gga acg gac act ccc acc gat ttc gcc aat ttt   739
Ser Lys His Arg Glu Gly Thr Asp Thr Pro Thr Asp Phe Ala Asn Phe
        200                 205                 210

atg gcc aaa cac ggc gag cac ttc ccc gag cag ccg cgc gac atc aat   787
Met Ala Lys His Gly Glu His Phe Pro Glu Gln Pro Arg Asp Ile Asn
    215                 220                 225

gag ctc atc gat gcc ctc gca gcc cgt tcc gcc gca gcc agt cgc atg   835
Glu Leu Ile Asp Ala Leu Ala Ala Arg Ser Ala Ala Ala Ser Arg Met
230                 235                 240                 245

ttc aac tcc ata tca gag gaa caa cgc cgc gaa ctc atg aaa cta tct   883
Phe Asn Ser Ile Ser Glu Glu Gln Arg Arg Glu Leu Met Lys Leu Ser
                250                 255                 260

gcc caa gct ttc gga tcc cca gag ctg cag gaa ttg ctc ggt gac ctg   931
Ala Gln Ala Phe Gly Ser Pro Glu Leu Gln Glu Leu Leu Gly Asp Leu
            265                 270                 275
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gct gga aac ctc caa ggt ctg cgc ccc gac ctc aac tgg gat ggc tcc   979
Ala Gly Asn Leu Gln Gly Leu Arg Pro Asp Leu Asn Trp Asp Gly Ser
        280                 285                 290

gaa caa ttc tcc ggc gac gaa ggc atg gga ctt ggt gat ggc acc ggc   1027
Glu Gln Phe Ser Gly Asp Glu Gly Met Gly Leu Gly Asp Gly Thr Gly
    295                 300                 305

gcc atg cag gac ctc gcc gaa ctc gac aac ctt gct gaa caa ctg agc   1075
Ala Met Gln Asp Leu Ala Glu Leu Asp Asn Leu Ala Glu Gln Leu Ser
310                 315                 320                 325

aac tcc cac acc gac ctc gac att gat gcg att cgc cgc caa ctc ggc   1123
Asn Ser His Thr Asp Leu Asp Ile Asp Ala Ile Arg Arg Gln Leu Gly
                330                 335                 340

gat gac gcc gct gtc tct gcc gaa act ttg gcc aaa ctg gag cgc gcg   1171
Asp Asp Ala Ala Val Ser Ala Glu Thr Leu Ala Lys Leu Glu Arg Ala
            345                 350                 355

ctc cgc gac agc ggc ctt ctt cgc cgc aac ccc gat ggc tca ttg aag   1219
Leu Arg Asp Ser Gly Leu Leu Arg Arg Asn Pro Asp Gly Ser Leu Lys
        360                 365                 370

ctc agc ccc cag gcc atg cgc cgt cta ggg aaa gcg ctt ctc gac gcc   1267
Leu Ser Pro Gln Ala Met Arg Arg Leu Gly Lys Ala Leu Leu Asp Ala
    375                 380                 385

gcc agc gaa caa tta tcg tcc cgc cca ggc tcg cga gac tcc cgg ttg   1315
Ala Ser Glu Gln Leu Ser Ser Arg Pro Gly Ser Arg Asp Ser Arg Leu
390                 395                 400                 405

gca gga gca aac ggt gaa gcg acg gga gca tcc cga cct tat gtt ttc   1363
Ala Gly Ala Asn Gly Glu Ala Thr Gly Ala Ser Arg Pro Tyr Val Phe
                410                 415                 420

gga gac acc caa cca tgg gat gtc acc cgc acc atc acc aat gct ctg   1411
Gly Asp Thr Gln Pro Trp Asp Val Thr Arg Thr Ile Thr Asn Ala Leu
            425                 430                 435

cag cga aca gcc gga aca gat acg gaa ggt ccg ctg cgc atc aac tta   1459
Gln Arg Thr Ala Gly Thr Asp Thr Glu Gly Pro Leu Arg Ile Asn Leu
        440                 445                 450

gat gat gtg gaa gtc att gaa act gaa gcc cgc acc ctc aac gcc gtg   1507
Asp Asp Val Glu Val Ile Glu Thr Glu Ala Arg Thr Leu Asn Ala Val
    455                 460                 465

gca ctg cta gta gac acc agt tat tcc atg gct gcc gaa ggc cgc tgg   1555
Ala Leu Leu Val Asp Thr Ser Tyr Ser Met Ala Ala Glu Gly Arg Trp
470                 475                 480                 485

gtg ccc atg aag caa aca gcg ctt gcc ctc cac cac ctg gta tcc acc   1603
Val Pro Met Lys Gln Thr Ala Leu Ala Leu His His Leu Val Ser Thr
                490                 495                 500

cgg ttt aga gga gat gaa cta gca cta atc act ttt ggt cga cat gcc   1651
Arg Phe Arg Gly Asp Glu Leu Ala Leu Ile Thr Phe Gly Arg His Ala
            505                 510                 515
```

```
caa aac atg gac atc gag gaa ctg act gca ctg cca ccg gtt cac gaa   1699
Gln Asn Met Asp Ile Glu Glu Leu Thr Ala Leu Pro Pro Val His Glu
        520                 525                 530

caa gga act aat ctc cac cac gca tta ctg ctg gca gaa cgg ttc ttt   1747
Gln Gly Thr Asn Leu His His Ala Leu Leu Leu Ala Glu Arg Phe Phe
    535                 540                 545

gct cgc cat ccc tcc atg aaa gca agc ctg ctc att gtc aca gat ggc   1795
Ala Arg His Pro Ser Met Lys Ala Ser Leu Leu Ile Val Thr Asp Gly
550                 555                 560                 565

gaa ccc aca gct cac ctc gaa gcc gat gga cac gcc tgg ttc aac tgg   1843
Glu Pro Thr Ala His Leu Glu Ala Asp Gly His Ala Trp Phe Asn Trp
                570                 575                 580

ccc act gac cca gaa acc atg ttc aag acc gtc acc caa cta gat aaa   1891
Pro Thr Asp Pro Glu Thr Met Phe Lys Thr Val Thr Gln Leu Asp Lys
            585                 590                 595

gta acc aag cga gga acc cac acc aca ctc ttc cga ctg gga cat gat   1939
Val Thr Lys Arg Gly Thr His Thr Thr Leu Phe Arg Leu Gly His Asp
        600                 605                 610

caa gga tta gag cac ttt ctc aac caa cta gcc gac cgt gtt ggc ggc   1987
Gln Gly Leu Glu His Phe Leu Asn Gln Leu Ala Asp Arg Val Gly Gly
    615                 620                 625

acc gtg gtg gct ccc gat ctg gac gga ctc ggc gcc gca gtc gtg ggc   2035
Thr Val Val Ala Pro Asp Leu Asp Gly Leu Gly Ala Ala Val Val Gly
630                 635                 640                 645

gag tat tta cga cac cgc tac tgagcattgg acgttttcgc ctt             2079
Glu Tyr Leu Arg His Arg Tyr
                650
```

<210> 2588
<211> 652
<212> PRT
<213> Corynebacterium glutamicum

<400> 2588

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Met Ala Thr Ser His Ser Arg Pro Arg Arg Ser Arg Tyr Gly Arg Tyr
  1               5                  10                  15

Thr Gly Gly Pro Asp Pro Leu Ala Pro Pro Val Asp Leu Ser Asp Ala
            20                  25                  30

Leu Arg Asp Ile Ala Asp Asp Val Met Ala Gly Tyr Ser Pro Glu Gln
        35                  40                  45

Ala Leu Arg Glu Tyr Leu Arg Arg Gly Ala Arg Gly Gln Glu Gly Leu
    50                  55                  60

Asp Asp Leu Ala Trp Arg Ala Ala Glu Arg Arg Arg Glu Leu Leu Ser
65                  70                  75                  80

Arg Asn Asn Leu Gly Gly Thr Leu Ala Glu Val Arg Lys Leu Leu Asp
                85                  90                  95
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Glu Gly Leu Lys Leu Glu Arg Ala Gln Leu Ala Arg Asp Ile Asp Met
            100                 105                 110

Asp Asp Thr Asp Arg Ala Phe Arg Glu Met Gln Ile Ser Asn Leu Pro
        115                 120                 125

Glu Ser Thr Ala Ala Ala Val Ser Glu Leu Asn Ser Tyr Asp Trp Gln
    130                 135                 140

Ser Gln Glu Ala Arg Gln Lys Phe Glu Gln Ile Arg Asp Leu Leu Gly
145                 150                 155                 160

Arg Glu Met Leu Asp Gln Gln Phe Ser Gly Met Lys Gln Ala Met Glu
                165                 170                 175

Gly Ala Ser Asp Glu Asp Lys Ala Ala Ile Ala Glu Met Leu Arg Asp
            180                 185                 190

Leu Asn Asp Leu Leu Ser Lys His Arg Glu Gly Thr Asp Thr Pro Thr
        195                 200                 205

Asp Phe Ala Asn Phe Met Ala Lys His Gly Glu His Phe Pro Glu Gln
    210                 215                 220

Pro Arg Asp Ile Asn Glu Leu Ile Asp Ala Leu Ala Ala Arg Ser Ala
225                 230                 235                 240

Ala Ala Ser Arg Met Phe Asn Ser Ile Ser Glu Glu Gln Arg Arg Glu
                245                 250                 255

Leu Met Lys Leu Ser Ala Gln Ala Phe Gly Ser Pro Glu Leu Gln Glu
            260                 265                 270

Leu Leu Gly Asp Leu Ala Gly Asn Leu Gln Gly Leu Arg Pro Asp Leu
        275                 280                 285

Asn Trp Asp Gly Ser Glu Gln Phe Ser Gly Asp Glu Gly Met Gly Leu
    290                 295                 300

Gly Asp Gly Thr Gly Ala Met Gln Asp Leu Ala Glu Leu Asp Asn Leu
305                 310                 315                 320

Ala Glu Gln Leu Ser Asn Ser His Thr Asp Leu Asp Ile Asp Ala Ile
                325                 330                 335

Arg Arg Gln Leu Gly Asp Asp Ala Ala Val Ser Ala Glu Thr Leu Ala
            340                 345                 350

Lys Leu Glu Arg Ala Leu Arg Asp Ser Gly Leu Leu Arg Arg Asn Pro
        355                 360                 365

Asp Gly Ser Leu Lys Leu Ser Pro Gln Ala Met Arg Arg Leu Gly Lys
    370                 375                 380

Ala Leu Leu Asp Ala Ala Ser Glu Gln Leu Ser Ser Arg Pro Gly Ser
385                 390                 395                 400

Arg Asp Ser Arg Leu Ala Gly Ala Asn Gly Glu Ala Thr Gly Ala Ser
                405                 410                 415

Arg Pro Tyr Val Phe Gly Asp Thr Gln Pro Trp Asp Val Thr Arg Thr
```

```
            420                 425                 430

Ile Thr Asn Ala Leu Gln Arg Thr Ala Gly Thr Asp Thr Glu Gly Pro
        435                 440                 445

Leu Arg Ile Asn Leu Asp Asp Val Glu Val Ile Glu Thr Glu Ala Arg
    450                 455                 460

Thr Leu Asn Ala Val Ala Leu Leu Val Asp Thr Ser Tyr Ser Met Ala
465                 470                 475                 480

Ala Glu Gly Arg Trp Val Pro Met Lys Gln Thr Ala Leu Ala Leu His
                485                 490                 495

His Leu Val Ser Thr Arg Phe Arg Gly Asp Glu Leu Ala Leu Ile Thr
            500                 505                 510

Phe Gly Arg His Ala Gln Asn Met Asp Ile Glu Glu Leu Thr Ala Leu
        515                 520                 525

Pro Pro Val His Glu Gln Gly Thr Asn Leu His His Ala Leu Leu Leu
    530                 535                 540

Ala Glu Arg Phe Phe Ala Arg His Pro Ser Met Lys Ala Ser Leu Leu
545                 550                 555                 560

Ile Val Thr Asp Gly Glu Pro Thr Ala His Leu Glu Ala Asp Gly His
                565                 570                 575

Ala Trp Phe Asn Trp Pro Thr Asp Pro Glu Thr Met Phe Lys Thr Val
            580                 585                 590

Thr Gln Leu Asp Lys Val Thr Lys Arg Gly Thr His Thr Thr Leu Phe
        595                 600                 605

Arg Leu Gly His Asp Gln Gly Leu Glu His Phe Leu Asn Gln Leu Ala
    610                 615                 620

Asp Arg Val Gly Gly Thr Val Val Ala Pro Asp Leu Asp Gly Leu Gly
625                 630                 635                 640

Ala Ala Val Val Gly Glu Tyr Leu Arg His Arg Tyr
                645                 650
```

<210> 2589
<211> 924
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(901)
<223> RXA02125

<400> 2589

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gacctaaaat tcatcacctc accgttttta aggcttagaa aaatagcagt gttgggatgt 60

gaatatccat ttatgctgct gtagtcggct atgtggacgc atg gtg gca acc tct   115
                                              Met Val Ala Thr Ser
                                                1               5
```

```
cag ttt atc gat gac agc gag gct gcc cag gcg gta cgc gca gct att   163
Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala Val Arg Ala Ala Ile
                 10                  15                  20

gtt gca gga tac cga aac att gat act gcc cta gcg tat gga aac gag   211
Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu Ala Tyr Gly Asn Glu
             25                  30                  35

cgc ggc gtt ggc gaa ggc att cgc acc gct gga gtg ccc cgc gag gag   259
Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly Val Pro Arg Glu Glu
         40                  45                  50

ctc ttt att tcc acc aag cta gct gca gaa atc aaa gat tac gat gga   307
Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile Lys Asp Tyr Asp Gly
     55                  60                  65

gca gtc gcc gcg att gat gag tct ttg gcg aaa att ggc ttg gat tat   355
Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys Ile Gly Leu Asp Tyr
 70                  75                  80                  85

gtc gat ctg atg ctc att cac tcc cca caa cca tgg agt gat ttc cgt   403
Val Asp Leu Met Leu Ile His Ser Pro Gln Pro Trp Ser Asp Phe Arg
                 90                  95                 100

ggt ggg gac tat tca gag gga aac cgt gaa gcg tgg cgc gcg ctg gaa   451
Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala Trp Arg Ala Leu Glu
             105                 110                 115

gat gcc tac aaa gcc gga aag att cga tcc att ggt gtc tcg aac ttc   499
Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile Gly Val Ser Asn Phe
         120                 125                 130

ctg gag gcc gat ctg gag aat atc tta gac tcc gcg acg gtt gct cct   547
Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser Ala Thr Val Ala Pro
     135                 140                 145

cac gtt aat cag ctt ctt gtg cat gtt gga aac acc cca agc gag tta   595
His Val Asn Gln Leu Leu Val His Val Gly Asn Thr Pro Ser Glu Leu
150                 155                 160                 165

atc agt ttc tgc gat tcc aag ggc att ctg gtc gaa gca tat tca ccc   643
Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val Glu Ala Tyr Ser Pro
                 170                 175                 180

atc gcc cac gga gag atg ctg aag aac cag cag gtc aag gcg att gct   691
Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln Val Lys Ala Ile Ala
             185                 190                 195

gac aag tac aac gtg agc att ccg cag cta tgc att cgg tac aca att   739
Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys Ile Arg Tyr Thr Ile
         200                 205                 210

caa ctg gga acg gtg tct ttg cca aag act gcc aac cca gat cat atg   787
Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala Asn Pro Asp His Met
     215                 220                 225

agc tcc aat gcg cag atc gac ttt gaa att tcc gag gaa gac atg gcg   835
Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser Glu Glu Asp Met Ala
230                 235                 240                 245
```

```
gca ctt caa gaa gtg acc gcc cgc gat tat ggc gag cac agc ggt ttt   883
Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly Glu His Ser Gly Phe
                250                 255                 260

cct gtg tat tcc ggc aag tagaaagatt tttatcatgg gac                924
Pro Val Tyr Ser Gly Lys
            265
```

<210> 2590
<211> 267
<212> PRT
<213> Corynebacterium glutamicum

<400> 2590

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Met Val Ala Thr Ser Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala
  1               5                  10                  15

Val Arg Ala Ala Ile Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu
             20                  25                  30

Ala Tyr Gly Asn Glu Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly
         35                  40                  45

Val Pro Arg Glu Glu Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile
     50                  55                  60

Lys Asp Tyr Asp Gly Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys
 65                  70                  75                  80

Ile Gly Leu Asp Tyr Val Asp Leu Met Leu Ile His Ser Pro Gln Pro
                 85                  90                  95

Trp Ser Asp Phe Arg Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala
            100                 105                 110

Trp Arg Ala Leu Glu Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile
        115                 120                 125

Gly Val Ser Asn Phe Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser
    130                 135                 140

Ala Thr Val Ala Pro His Val Asn Gln Leu Leu Val His Val Gly Asn
145                 150                 155                 160

Thr Pro Ser Glu Leu Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val
                165                 170                 175

Glu Ala Tyr Ser Pro Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln
            180                 185                 190

Val Lys Ala Ile Ala Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys
        195                 200                 205

Ile Arg Tyr Thr Ile Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala
    210                 215                 220

Asn Pro Asp His Met Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser
225                 230                 235                 240

Glu Glu Asp Met Ala Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly
```

```
                245                 250                 255

Glu His Ser Gly Phe Pro Val Tyr Ser Gly Lys
            260                 265


<210> 2591
<211> 357
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(334)
<223> RXA02129

<400> 2591
tgttctgccg atccagcacc agctctggtg gcaggagctg agagttttgc caattaactt 60

ggcgaacaga cttgttggaa atgaatttgt caagaatggc atg aag atc atc ttc   115
                                            Met Lys Ile Ile Phe
                                              1               5

aaa atg gct agt aac aag ttc atc gac aac aaa aag ggg ctg gct atg   163
Lys Met Ala Ser Asn Lys Phe Ile Asp Asn Lys Lys Gly Leu Ala Met
                 10                  15                  20

cta gtt ttt gcc gaa ctt gtg atg gaa atg ctt gat cag cct gaa gaa   211
Leu Val Phe Ala Glu Leu Val Met Glu Met Leu Asp Gln Pro Glu Glu
             25                  30                  35

caa ctt cat aat gtg cgt gga gtg gct att gag aag cgg gag ttc ctc   259
Gln Leu His Asn Val Arg Gly Val Ala Ile Glu Lys Arg Glu Phe Leu
         40                  45                  50

aaa gct ctc acc gct gat ttc acc agc aga ctt aaa caa gct caa acc   307
Lys Ala Leu Thr Ala Asp Phe Thr Ser Arg Leu Lys Gln Ala Gln Thr
     55                  60                  65

gat aag att ctt gtt tgg gat ttc gca tgactattat gtgggcgacc         354
Asp Lys Ile Leu Val Trp Asp Phe Ala
 70                  75

cgt                                                              357


<210> 2592
<211> 78
<212> PRT
<213> Corynebacterium glutamicum

<400> 2592
Met Lys Ile Ile Phe Lys Met Ala Ser Asn Lys Phe Ile Asp Asn Lys
  1               5                  10                  15

Lys Gly Leu Ala Met Leu Val Phe Ala Glu Leu Val Met Glu Met Leu
             20                  25                  30

Asp Gln Pro Glu Glu Gln Leu His Asn Val Arg Gly Val Ala Ile Glu
         35                  40                  45
```

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Lys Arg Glu Phe Leu Lys Ala Leu Thr Ala Asp Phe Thr Ser Arg Leu
     50                  55                  60

Lys Gln Ala Gln Thr Asp Lys Ile Leu Val Trp Asp Phe Ala
 65                  70                  75


<210> 2593
<211> 739
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(739)
<223> RXA02132

<400> 2593
gcagcccacc gccagcgatt cctcgccgaa caaggctacg cataccgcat cctcgacgcc 60

gacgacatcc tcttcccact acccaagaaa gagctataac gtg cac aac ttc tcc   115
                                              Val His Asn Phe Ser
                                                1               5

ttc gac gtg gac gaa tcc tac gcc aag aag aac aac gaa atc ctc cgc   163
Phe Asp Val Asp Glu Ser Tyr Ala Lys Lys Asn Asn Glu Ile Leu Arg
                10                  15                  20

gac gca aag cga ctc cag atc tca gca ctg tgc ctt gga ctc atc ctc   211
Asp Ala Lys Arg Leu Gln Ile Ser Ala Leu Cys Leu Gly Leu Ile Leu
            25                  30                  35

ggc ggc gga gcc gta gcc gtc tac ctg ttt tct aac gga gca gtg tgg   259
Gly Gly Gly Ala Val Ala Val Tyr Leu Phe Ser Asn Gly Ala Val Trp
        40                  45                  50

atg tgg atg atc gcc atc gtc atg gtc ttc ctc gcc ctg ttg agc ttc   307
Met Trp Met Ile Ala Ile Val Met Val Phe Leu Ala Leu Leu Ser Phe
    55                  60                  65

atc atg att cct gtg atc ccc cgc caa atg ggc aac gca caa acg ctc   355
Ile Met Ile Pro Val Ile Pro Arg Gln Met Gly Asn Ala Gln Thr Leu
70                  75                  80                  85

tac gat gac tac gaa cta gcc ccc gcc atc atc gca gaa gta aac ccc   403
Tyr Asp Asp Tyr Glu Leu Ala Pro Ala Ile Ile Ala Glu Val Asn Pro
                90                  95                 100

cgc gat gtg gtc ctc ctg gca ctc gtc aac cgc aat gtg aac ccc gaa   451
Arg Asp Val Val Leu Leu Ala Leu Val Asn Arg Asn Val Asn Pro Glu
            105                 110                 115

gcc aaa cca gag tgg gca ttg gcc acc cgc acg atc gtt cgc gtc gga   499
Ala Lys Pro Glu Trp Ala Leu Ala Thr Arg Thr Ile Val Arg Val Gly
        120                 125                 130

gca cac gaa cgt cgc ctc ggc gaa cgt atc cca tcc gtc gca atc acc   547
Ala His Glu Arg Arg Leu Gly Glu Arg Ile Pro Ser Val Ala Ile Thr
    135                 140                 145

ggc cga cgc acc gtc aaa gac caa gac cac tgg gat gaa atc agc ccc   595
```

```
Gly Arg Arg Thr Val Lys Asp Gln Asp His Trp Asp Glu Ile Ser Pro
150                 155                 160                 165

atg cca att acc tgg ggc acc acg gac aaa gac atc atc cgt gaa gcc   643
Met Pro Ile Thr Trp Gly Thr Thr Asp Lys Asp Ile Ile Arg Glu Ala
                170                 175                 180

gag aaa act atc ccc cac gaa ctc tgg gcc aaa cta gaa aag aac cgc   691
Glu Lys Thr Ile Pro His Glu Leu Trp Ala Lys Leu Glu Lys Asn Arg
            185                 190                 195

ggc aag ttg gag gac gtt aaa aag acc ccc aac aac ctg ttc aaa cta   739
Gly Lys Leu Glu Asp Val Lys Lys Thr Pro Asn Asn Leu Phe Lys Leu
        200                 205                 210


<210> 2594
<211> 213
<212> PRT
<213> Corynebacterium glutamicum

<400> 2594
Val His Asn Phe Ser Phe Asp Val Asp Glu Ser Tyr Ala Lys Lys Asn
  1               5                  10                  15

Asn Glu Ile Leu Arg Asp Ala Lys Arg Leu Gln Ile Ser Ala Leu Cys
             20                  25                  30

Leu Gly Leu Ile Leu Gly Gly Gly Ala Val Ala Val Tyr Leu Phe Ser
         35                  40                  45

Asn Gly Ala Val Trp Met Trp Met Ile Ala Ile Val Met Val Phe Leu
     50                  55                  60

Ala Leu Leu Ser Phe Ile Met Ile Pro Val Ile Pro Arg Gln Met Gly
 65                  70                  75                  80

Asn Ala Gln Thr Leu Tyr Asp Asp Tyr Glu Leu Ala Pro Ala Ile Ile
                 85                  90                  95

Ala Glu Val Asn Pro Arg Asp Val Val Leu Leu Ala Leu Val Asn Arg
            100                 105                 110

Asn Val Asn Pro Glu Ala Lys Pro Glu Trp Ala Leu Ala Thr Arg Thr
        115                 120                 125

Ile Val Arg Val Gly Ala His Glu Arg Arg Leu Gly Glu Arg Ile Pro
    130                 135                 140

Ser Val Ala Ile Thr Gly Arg Arg Thr Val Lys Asp Gln Asp His Trp
145                 150                 155                 160

Asp Glu Ile Ser Pro Met Pro Ile Thr Trp Gly Thr Thr Asp Lys Asp
                165                 170                 175

Ile Ile Arg Glu Ala Glu Lys Thr Ile Pro His Glu Leu Trp Ala Lys
            180                 185                 190

Leu Glu Lys Asn Arg Gly Lys Leu Glu Asp Val Lys Lys Thr Pro Asn
        195                 200                 205
```

```
Asn Leu Phe Lys Leu
    210


<210> 2595
<211> 921
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(898)
<223> RXA02137

<400> 2595
gcctactcac cgtccacaga tgagtaaacc cggaaaaacc cgtatttagt tattggtttt 60

acctgcgtgg gctgaaagtc ttcactttta atccttacag atg gtc gtt ctg att   115
                                            Met Val Val Leu Ile
                                              1               5

cct ttc aac gat gaa gtg tgc acc cct att ccc gat ttg gga ggt ttt   163
Pro Phe Asn Asp Glu Val Cys Thr Pro Ile Pro Asp Leu Gly Gly Phe
                 10                  15                  20

cct tgt agc cta ttg agt gtg aaa ctt cct tgg gat aaa aat aag aac   211
Pro Cys Ser Leu Leu Ser Val Lys Leu Pro Trp Asp Lys Asn Lys Asn
             25                  30                  35

aac gaa ggg gct gac gct gca ggc caa gac gcc agc tcc acc cct gag   259
Asn Glu Gly Ala Asp Ala Ala Gly Gln Asp Ala Ser Ser Thr Pro Glu
         40                  45                  50

acc gct acg cct gac gct act gag cag aaa ttg cca aag ggg cac acg   307
Thr Ala Thr Pro Asp Ala Thr Glu Gln Lys Leu Pro Lys Gly His Thr
     55                  60                  65

gca ccg aag ggc cgt ccc act ccg aag cgt cgt gaa gtt gag tta gag   355
Ala Pro Lys Gly Arg Pro Thr Pro Lys Arg Arg Glu Val Glu Leu Glu
 70                  75                  80                  85

cga ggt gtc gtt ggc ggc cag tct ttg gcg cct act gat act tat gcg   403
Arg Gly Val Val Gly Gly Gln Ser Leu Ala Pro Thr Asp Thr Tyr Ala
                 90                  95                 100

cag cag cgc cag aag cgt aaa gaa ttt aaa gct tct atg acc aag gaa   451
Gln Gln Arg Gln Lys Arg Lys Glu Phe Lys Ala Ser Met Thr Lys Glu
            105                 110                 115

gaa ttc aag gca tac aag cag aaa gag cgc gat gcc cga gtt aag cgt   499
Glu Phe Lys Ala Tyr Lys Gln Lys Glu Arg Asp Ala Arg Val Lys Arg
        120                 125                 130

cag cgc gaa acc caa gct gca atg gat cgc ggc gaa gat gct tat ttg   547
Gln Arg Glu Thr Gln Ala Ala Met Asp Arg Gly Glu Asp Ala Tyr Leu
    135                 140                 145

atg gat cgc gat aag ggc gag gtt cgc cgt ttt gcg cgt gac tgg gtg   595
Met Asp Arg Asp Lys Gly Glu Val Arg Arg Phe Ala Arg Asp Trp Val
150                 155                 160                 165
```

```
gat tcc cgc agg ttc ttg tct aac ttt gtg atg cca gta gct att gct   643
Asp Ser Arg Arg Phe Leu Ser Asn Phe Val Met Pro Val Ala Ile Ala
                170                 175                 180

ttg ctg gtt gtc atg ctg atc ggt aac ttc aac cca tca ttc gct gcg   691
Leu Leu Val Val Met Leu Ile Gly Asn Phe Asn Pro Ser Phe Ala Ala
            185                 190                 195

act tct tcc atg gtt gcc atg gtt ttg atg ttg ggc ttc ctg att gag   739
Thr Ser Ser Met Val Ala Met Val Leu Met Leu Gly Phe Leu Ile Glu
        200                 205                 210

ggc atc acc act ggt cgt cgt gtg aac aag gct gct cgc acg agg ttc   787
Gly Ile Thr Thr Gly Arg Arg Val Asn Lys Ala Ala Arg Thr Arg Phe
    215                 220                 225

cct ggt acc acc gag act ggt ttt ggt ctg ggt tac tac gcg tat tcc   835
Pro Gly Thr Thr Glu Thr Gly Phe Gly Leu Gly Tyr Tyr Ala Tyr Ser
230                 235                 240                 245

cgc acc att cag cct cgt aag tgg cgt acc cct cgt gca cgc gtt gaa   883
Arg Thr Ile Gln Pro Arg Lys Trp Arg Thr Pro Arg Ala Arg Val Glu
                250                 255                 260

att ggt gct gaa gtc tagcgcatgc gcacgttagt tct                    921
Ile Gly Ala Glu Val
            265
```

<210> 2596
<211> 266
<212> PRT
<213> Corynebacterium glutamicum

<400> 2596

```
Met Val Val Leu Ile Pro Phe Asn Asp Glu Val Cys Thr Pro Ile Pro
  1               5                  10                  15

Asp Leu Gly Gly Phe Pro Cys Ser Leu Leu Ser Val Lys Leu Pro Trp
             20                  25                  30

Asp Lys Asn Lys Asn Asn Glu Gly Ala Asp Ala Ala Gly Gln Asp Ala
         35                  40                  45

Ser Ser Thr Pro Glu Thr Ala Thr Pro Asp Ala Thr Glu Gln Lys Leu
     50                  55                  60

Pro Lys Gly His Thr Ala Pro Lys Gly Arg Pro Thr Pro Lys Arg Arg
 65                  70                  75                  80

Glu Val Glu Leu Glu Arg Gly Val Val Gly Gly Gln Ser Leu Ala Pro
                 85                  90                  95

Thr Asp Thr Tyr Ala Gln Gln Arg Gln Lys Arg Lys Glu Phe Lys Ala
            100                 105                 110

Ser Met Thr Lys Glu Glu Phe Lys Ala Tyr Lys Gln Lys Glu Arg Asp
        115                 120                 125

Ala Arg Val Lys Arg Gln Arg Glu Thr Gln Ala Ala Met Asp Arg Gly
    130                 135                 140
```

```
Glu Asp Ala Tyr Leu Met Asp Arg Asp Lys Gly Glu Val Arg Arg Phe
145                 150                 155                 160

Ala Arg Asp Trp Val Asp Ser Arg Arg Phe Leu Ser Asn Phe Val Met
                165                 170                 175

Pro Val Ala Ile Ala Leu Leu Val Val Met Leu Ile Gly Asn Phe Asn
            180                 185                 190

Pro Ser Phe Ala Ala Thr Ser Ser Met Val Ala Met Val Leu Met Leu
        195                 200                 205

Gly Phe Leu Ile Glu Gly Ile Thr Thr Gly Arg Arg Val Asn Lys Ala
    210                 215                 220

Ala Arg Thr Arg Phe Pro Gly Thr Thr Glu Thr Gly Phe Gly Leu Gly
225                 230                 235                 240

Tyr Tyr Ala Tyr Ser Arg Thr Ile Gln Pro Arg Lys Trp Arg Thr Pro
                245                 250                 255

Arg Ala Arg Val Glu Ile Gly Ala Glu Val
            260                 265


<210> 2597
<211> 531
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> RXA02141

<400> 2597
gcccattcgt ttccgatcgc accgcaaccc gcgacggcga aaacactcag agcaacgctt 60

aagaaggagt ggcgaaaaaa tgaagtcttc agcaaaactc atg tac ggc ccg acc   115
                                              Met Tyr Gly Pro Thr
                                                1               5

gta ttc atg gcc gca atg gct gtc atc tac atc ttc gca aca atg cac   163
Val Phe Met Ala Ala Met Ala Val Ile Tyr Ile Phe Ala Thr Met His
            10                  15                  20

gtt agt gat ggc ggc agc gtt aaa ggt gtt gag tgg gtc ggt tct gtg   211
Val Ser Asp Gly Gly Ser Val Lys Gly Val Glu Trp Val Gly Ser Val
        25                  30                  35

gcc ctg gtc ctg tca gca ggt ctg acg ctt atg ctc ggt gtc tac ctt   259
Ala Leu Val Leu Ser Ala Gly Leu Thr Leu Met Leu Gly Val Tyr Leu
    40                  45                  50

cac ttc act gaa gtc cgc gta gat gtt ctt cca gag gac tgg gaa gag   307
His Phe Thr Glu Val Arg Val Asp Val Leu Pro Glu Asp Trp Glu Glu
55                  60                  65

gct gag gtt gcc gac aag gca gga acc ctc ggg ttc ttc agc cca agc   355
Ala Glu Val Ala Asp Lys Ala Gly Thr Leu Gly Phe Phe Ser Pro Ser
```

```
 70                  75                  80                  85

tcc att tgg ccg gca gct atg tcc ggt gcg gtt gga ttc ctt gca ttc   403
Ser Ile Trp Pro Ala Ala Met Ser Gly Ala Val Gly Phe Leu Ala Phe
                 90                  95                 100

ggc gtt gtg tac ttc cac tac tgg atg atc gca gtt ggt ctg atg ctc   451
Gly Val Val Tyr Phe His Tyr Trp Met Ile Ala Val Gly Leu Met Leu
            105                 110                 115

ctg atc ttc acg atc acc aag ctc aac ctt cag tac ggc gtg cca aaa   499
Leu Ile Phe Thr Ile Thr Lys Leu Asn Leu Gln Tyr Gly Val Pro Lys
        120                 125                 130

gaa aag cac tagtactaaa accacatatg ctc                            531
Glu Lys His
    135
```

<210> 2598
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 2598

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Met Tyr Gly Pro Thr Val Phe Met Ala Ala Met Ala Val Ile Tyr Ile
  1               5                  10                  15

Phe Ala Thr Met His Val Ser Asp Gly Gly Ser Val Lys Gly Val Glu
             20                  25                  30

Trp Val Gly Ser Val Ala Leu Val Leu Ser Ala Gly Leu Thr Leu Met
         35                  40                  45

Leu Gly Val Tyr Leu His Phe Thr Glu Val Arg Val Asp Val Leu Pro
     50                  55                  60

Glu Asp Trp Glu Glu Ala Glu Val Ala Asp Lys Ala Gly Thr Leu Gly
 65                  70                  75                  80

Phe Phe Ser Pro Ser Ser Ile Trp Pro Ala Ala Met Ser Gly Ala Val
                 85                  90                  95

Gly Phe Leu Ala Phe Gly Val Val Tyr Phe His Tyr Trp Met Ile Ala
            100                 105                 110

Val Gly Leu Met Leu Leu Ile Phe Thr Ile Thr Lys Leu Asn Leu Gln
        115                 120                 125

Tyr Gly Val Pro Lys Glu Lys His
    130                 135
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<210> 2599
<211> 750
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(727)

<223> RXA02146

<400> 2599

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ggttctctcg cagagagaga aggagtgggg ataggggcct tccgctccga acccgacagc 60

taactcggtc agcaaacagg aagaatttgg agtttcatca gtg ggt aag cac cgt   115
                                              Val Gly Lys His Arg
                                                1               5

cgc aac aat tca aac gca act cgc aag gct gta gca gca tct gca gtt   163
Arg Asn Asn Ser Asn Ala Thr Arg Lys Ala Val Ala Ala Ser Ala Val
                  10                  15                  20

gcg ctt gga gca acc gca gct atc gcc tcc cca gca cag gca gct gag   211
Ala Leu Gly Ala Thr Ala Ala Ile Ala Ser Pro Ala Gln Ala Ala Glu
             25                  30                  35

gtt gtt gtt cct ggc acc gga atc agc gtt gac atc gct ggc atc gag   259
Val Val Val Pro Gly Thr Gly Ile Ser Val Asp Ile Ala Gly Ile Glu
         40                  45                  50

acc act cca ggt ctt aac aac gtt cca gga atc gat cag tgg atc cct   307
Thr Thr Pro Gly Leu Asn Asn Val Pro Gly Ile Asp Gln Trp Ile Pro
     55                  60                  65

tcc ctt agc agc cag gca gct cct act gct tac gca gcc gtc att gat   355
Ser Leu Ser Ser Gln Ala Ala Pro Thr Ala Tyr Ala Ala Val Ile Asp
 70                  75                  80                  85

gca cct gca gca cag gct gca cct gca gca agc acc ggt cag gca atc   403
Ala Pro Ala Ala Gln Ala Ala Pro Ala Ala Ser Thr Gly Gln Ala Ile
                  90                  95                 100

gtt gat gca gcg cgc acc aag att ggt tcc cca tac ggt tgg ggt gct   451
Val Asp Ala Ala Arg Thr Lys Ile Gly Ser Pro Tyr Gly Trp Gly Ala
             105                 110                 115

acc ggt cct aac gct ttc gac tgc tcc ggc ctt acc tca tgg gca tac   499
Thr Gly Pro Asn Ala Phe Asp Cys Ser Gly Leu Thr Ser Trp Ala Tyr
         120                 125                 130

agc cag gtt ggc aag tcc atc cca cgt acc tcc cag gct cag gct gca   547
Ser Gln Val Gly Lys Ser Ile Pro Arg Thr Ser Gln Ala Gln Ala Ala
     135                 140                 145

cag ggc acc cct gtt gct tac tct gac ctt cag gct ggc gac atc gtt   595
Gln Gly Thr Pro Val Ala Tyr Ser Asp Leu Gln Ala Gly Asp Ile Val
150                 155                 160                 165

gcg ttc tac tcc ggc gct acc cac gtt ggt atc tac tcc ggc cac ggc   643
Ala Phe Tyr Ser Gly Ala Thr His Val Gly Ile Tyr Ser Gly His Gly
                 170                 175                 180

acc gtt atc cac gca ctg aac agc agc acc cct ctg tct gag cac tcc   691
Thr Val Ile His Ala Leu Asn Ser Ser Thr Pro Leu Ser Glu His Ser
             185                 190                 195

ttg gat tac atg cca ttc cac tct gca gtt cgt ttc taatctgcat        737
Leu Asp Tyr Met Pro Phe His Ser Ala Val Arg Phe
         200                 205
```

aaagtcttaa gct 750

<210> 2600
<211> 209
<212> PRT
<213> Corynebacterium glutamicum

<400> 2600

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Val Gly Lys His Arg Arg Asn Asn Ser Asn Ala Thr Arg Lys Ala Val
  1               5                  10                  15

Ala Ala Ser Ala Val Ala Leu Gly Ala Thr Ala Ala Ile Ala Ser Pro
             20                  25                  30

Ala Gln Ala Ala Glu Val Val Val Pro Gly Thr Gly Ile Ser Val Asp
         35                  40                  45

Ile Ala Gly Ile Glu Thr Thr Pro Gly Leu Asn Asn Val Pro Gly Ile
     50                  55                  60

Asp Gln Trp Ile Pro Ser Leu Ser Ser Gln Ala Ala Pro Thr Ala Tyr
 65                  70                  75                  80

Ala Ala Val Ile Asp Ala Pro Ala Ala Gln Ala Ala Pro Ala Ala Ser
                 85                  90                  95

Thr Gly Gln Ala Ile Val Asp Ala Ala Arg Thr Lys Ile Gly Ser Pro
            100                 105                 110

Tyr Gly Trp Gly Ala Thr Gly Pro Asn Ala Phe Asp Cys Ser Gly Leu
        115                 120                 125

Thr Ser Trp Ala Tyr Ser Gln Val Gly Lys Ser Ile Pro Arg Thr Ser
    130                 135                 140

Gln Ala Gln Ala Ala Gln Gly Thr Pro Val Ala Tyr Ser Asp Leu Gln
145                 150                 155                 160

Ala Gly Asp Ile Val Ala Phe Tyr Ser Gly Ala Thr His Val Gly Ile
                165                 170                 175

Tyr Ser Gly His Gly Thr Val Ile His Ala Leu Asn Ser Ser Thr Pro
            180                 185                 190

Leu Ser Glu His Ser Leu Asp Tyr Met Pro Phe His Ser Ala Val Arg
        195                 200                 205

Phe
```

<210> 2601
<211> 525
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(502)
<223> RXA02152

<400> 2601
aagccgttaa aagttgagac tcgcgctgag aatctcacag aaaactccga agctcccgct 60

aaggtagcta ccggaatcaa atcttaggga aggaaaacat atg gct att tac cgt 115
Met Ala Ile Tyr Arg
1 5

aag ctt gcg gct tcc gct gca gca ctg gcc ctg tcc gca tca ctg gtc 163
Lys Leu Ala Ala Ser Ala Ala Ala Leu Ala Leu Ser Ala Ser Leu Val
10 15 20

gct tgt ggc gac tct gag gac acc acc gaa gaa acc tca acc acc tct 211
Ala Cys Gly Asp Ser Glu Asp Thr Thr Glu Glu Thr Ser Thr Thr Ser
25 30 35

tct tcg acc act tcc agc tcc tcc agc agc tct agc tcc agc acc gcg 259
Ser Ser Thr Thr Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Ala
40 45 50

gct act tcc gag gaa tct tcc gca gtt gaa gag cca gca gtg gaa gct 307
Ala Thr Ser Glu Glu Ser Ser Ala Val Glu Glu Pro Ala Val Glu Ala
55 60 65

cct gtg gaa gag gct cca gtc gag gca cct gtt gag cag gca cct gtc 355
Pro Val Glu Glu Ala Pro Val Glu Ala Pro Val Glu Gln Ala Pro Val
70 75 80 85

gtg gag caa gct cca gtt gag cag gct ccg gca ccg gtt cag gaa gca 403
Val Glu Gln Ala Pro Val Glu Gln Ala Pro Ala Pro Val Gln Glu Ala
90 95 100

cct gca cca gtc gag cag gct cca gct cca gtt cag gaa gca cct gca 451
Pro Ala Pro Val Glu Gln Ala Pro Ala Pro Val Gln Glu Ala Pro Ala
105 110 115

gct gac gcg cca cct gca ctt cca ggt ggt ggc ggc gga cac gct ggc 499
Ala Asp Ala Pro Pro Ala Leu Pro Gly Gly Gly Gly Gly His Ala Gly
120 125 130

tac taaaaattca tgcttttacc cac 525
Tyr

<210> 2602
<211> 134
<212> PRT
<213> Corynebacterium glutamicum

<400> 2602
Met Ala Ile Tyr Arg Lys Leu Ala Ala Ser Ala Ala Ala Leu Ala Leu
1 5 10 15

Ser Ala Ser Leu Val Ala Cys Gly Asp Ser Glu Asp Thr Thr Glu Glu
20 25 30

Thr Ser Thr Thr Ser Ser Ser Thr Thr Ser Ser Ser Ser Ser Ser Ser
35 40 45

Ser Ser Ser Thr Ala Ala Thr Ser Glu Glu Ser Ser Ala Val Glu Glu

```
     50                  55                  60

Pro Ala Val Glu Ala Pro Val Glu Glu Ala Pro Val Glu Ala Pro Val
 65                  70                  75                  80

Glu Gln Ala Pro Val Val Glu Gln Ala Pro Val Glu Gln Ala Pro Ala
                 85                  90                  95

Pro Val Gln Glu Ala Pro Ala Pro Val Glu Gln Ala Pro Ala Pro Val
            100                 105                 110

Gln Glu Ala Pro Ala Ala Asp Ala Pro Pro Ala Leu Pro Gly Gly Gly
        115                 120                 125

Gly Gly His Ala Gly Tyr
    130
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<210> 2603
<211> 876
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(853)
<223> RXA02163

<400> 2603

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agcccgtacg atttctgcgt tcccatcctc tgcaccagct gcgcagaaga tctccgaagc 60

caacaccacg acgggccgat tcacccccatt ctattcgcct atg gcg gtg gca aca   115
                                            Met Ala Val Ala Thr
                                              1               5

ttc gga acc atc acc gac atg ttg gaa acc aag ggg atc gtg agc aat   163
Phe Gly Thr Ile Thr Asp Met Leu Glu Thr Lys Gly Ile Val Ser Asn
                 10                  15                  20

gta ggc ggc acc gac acc atc gat ttg ggc gcg ttg ttg aat gaa acc   211
Val Gly Gly Thr Asp Thr Ile Asp Leu Gly Ala Leu Leu Asn Glu Thr
             25                  30                  35

caa gcc gga acc cgc tgg agc gaa ctt agc ccc aac tat cag tcc aac   259
Gln Ala Gly Thr Arg Trp Ser Glu Leu Ser Pro Asn Tyr Gln Ser Asn
         40                  45                  50

cgc gtc gtg cag att tct acc acc gat gtg cgc acc tct aac tcg gcg   307
Arg Val Val Gln Ile Ser Thr Thr Asp Val Arg Thr Ser Asn Ser Ala
     55                  60                  65

gcc atg tac cta tca atg atg tcc tgg gtg aaa aat ggc gga aaa acg   355
Ala Met Tyr Leu Ser Met Met Ser Trp Val Lys Asn Gly Gly Lys Thr
 70                  75                  80                  85

gtg agc agc act gcg gaa gcc gat gcc atc atc cca gag ctt agc caa   403
Val Ser Ser Thr Ala Glu Ala Asp Ala Ile Ile Pro Glu Leu Ser Gln
                 90                  95                 100

ctg ttc gtg ggc cag ggc tat acc gaa agc acc tcc gcc ggc ccg ttt   451
Leu Phe Val Gly Gln Gly Tyr Thr Glu Ser Thr Ser Ala Gly Pro Phe
```

```
            105                 110                 115

gat gaa tac ctc tcc caa gga atg ggt tct aaa cca atg gtg atg atc   499
Asp Glu Tyr Leu Ser Gln Gly Met Gly Ser Lys Pro Met Val Met Ile
        120                 125                 130

tac gaa gcc cag ttc ctc gcg gaa caa aac aag gaa aac tca cgg att   547
Tyr Glu Ala Gln Phe Leu Ala Glu Gln Asn Lys Glu Asn Ser Arg Ile
    135                 140                 145

tcc ggc gat atg gaa cta gtg tat cca agc ccc acc gtg tac agc acg   595
Ser Gly Asp Met Glu Leu Val Tyr Pro Ser Pro Thr Val Tyr Ser Thr
150                 155                 160                 165

cat acg gtg gtt agc ttg agt gac gtc ggc gcg gag atc ggc gaa ctc   643
His Thr Val Val Ser Leu Ser Asp Val Gly Ala Glu Ile Gly Glu Leu
                170                 175                 180

cta gaa acc gac gaa acc ctg cag cag ttg gca gtc aaa cac ggt ttt   691
Leu Glu Thr Asp Glu Thr Leu Gln Gln Leu Ala Val Lys His Gly Phe
            185                 190                 195

agg cca aag aac tcc gca atg atc gcc gat gct ggc atg acc gac cgc   739
Arg Pro Lys Asn Ser Ala Met Ile Ala Asp Ala Gly Met Thr Asp Arg
        200                 205                 210

atg ccc aac aac ctc aat gtc att gat ccg ccg gac tat gac ttc cta   787
Met Pro Asn Asn Leu Asn Val Ile Asp Pro Pro Asp Tyr Asp Phe Leu
    215                 220                 225

gaa cga ctc att gat ggc gtg ggc gca tcg tac agt gcc acc cca gca   835
Glu Arg Leu Ile Asp Gly Val Gly Ala Ser Tyr Ser Ala Thr Pro Ala
230                 235                 240                 245

gaa gag gac aca gat cta tgaaaaatct tgtaaaaggt aca                 876
Glu Glu Asp Thr Asp Leu
                250
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09600760.090705

<210> 2604
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

<400> 2604

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Met Ala Val Ala Thr Phe Gly Thr Ile Thr Asp Met Leu Glu Thr Lys
  1               5                  10                  15

Gly Ile Val Ser Asn Val Gly Gly Thr Asp Thr Ile Asp Leu Gly Ala
             20                  25                  30

Leu Leu Asn Glu Thr Gln Ala Gly Thr Arg Trp Ser Glu Leu Ser Pro
         35                  40                  45

Asn Tyr Gln Ser Asn Arg Val Val Gln Ile Ser Thr Thr Asp Val Arg
     50                  55                  60

Thr Ser Asn Ser Ala Ala Met Tyr Leu Ser Met Met Ser Trp Val Lys
 65                  70                  75                  80

Asn Gly Gly Lys Thr Val Ser Ser Thr Ala Glu Ala Asp Ala Ile Ile
```

```
                 85                  90                  95

Pro Glu Leu Ser Gln Leu Phe Val Gly Gln Gly Tyr Thr Glu Ser Thr
            100                 105                 110

Ser Ala Gly Pro Phe Asp Glu Tyr Leu Ser Gln Gly Met Gly Ser Lys
        115                 120                 125

Pro Met Val Met Ile Tyr Glu Ala Gln Phe Leu Ala Glu Gln Asn Lys
    130                 135                 140

Glu Asn Ser Arg Ile Ser Gly Asp Met Glu Leu Val Tyr Pro Ser Pro
145                 150                 155                 160

Thr Val Tyr Ser Thr His Thr Val Val Ser Leu Ser Asp Val Gly Ala
                165                 170                 175

Glu Ile Gly Glu Leu Leu Glu Thr Asp Glu Thr Leu Gln Gln Leu Ala
            180                 185                 190

Val Lys His Gly Phe Arg Pro Lys Asn Ser Ala Met Ile Ala Asp Ala
        195                 200                 205

Gly Met Thr Asp Arg Met Pro Asn Asn Leu Asn Val Ile Asp Pro Pro
    210                 215                 220

Asp Tyr Asp Phe Leu Glu Arg Leu Ile Asp Gly Val Gly Ala Ser Tyr
225                 230                 235                 240

Ser Ala Thr Pro Ala Glu Glu Asp Thr Asp Leu
                245                 250


<210> 2605
<211> 1698
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1675)
<223> RXA02164

<400> 2605
tcaatgtcat tgatccgccg gactatgact tcctagaacg actcattgat ggcgtgggcg 60

catcgtacag tgccacccca gcagaagagg acacagatct atg aaa aat ctt gta   115
                                            Met Lys Asn Leu Val
                                              1               5

aaa ggt aca gcg ctg ggc ttg agc ttg gtg ctt ctg gca ggt tgt tca   163
Lys Gly Thr Ala Leu Gly Leu Ser Leu Val Leu Leu Ala Gly Cys Ser
                  10                  15                  20

act gtt tcg gat tct atc gat agc ctc ggc ggg ggc ctg ggt ggt tcc   211
Thr Val Ser Asp Ser Ile Asp Ser Leu Gly Gly Gly Leu Gly Gly Ser
              25                  30                  35

tct gag act ttg aag att gtg gcc gcc aca gag ctg gaa gat ctg cag   259
Ser Glu Thr Leu Lys Ile Val Ala Ala Thr Glu Leu Glu Asp Leu Gln
          40                  45                  50
```

```
ccc gcg atc gag caa gcc tcc gac gac ttg ggt ttt gat att gaa ctg   307
Pro Ala Ile Glu Gln Ala Ser Asp Asp Leu Gly Phe Asp Ile Glu Leu
     55                  60                  65

agc ttt cca ggc ggc aca ctc agc aac agc caa gcc ctc atg gat ggc   355
Ser Phe Pro Gly Gly Thr Leu Ser Asn Ser Gln Ala Leu Met Asp Gly
 70                  75                  80                  85

gct ttt gac cag gac tat gat gcc acc tgg ttt gcc acc aac cgt tac   403
Ala Phe Asp Gln Asp Tyr Asp Ala Thr Trp Phe Ala Thr Asn Arg Tyr
                 90                  95                 100

gtc gat ctg atc ggc gct tcc aac aag ctg ggg gag acc acc aaa atc   451
Val Asp Leu Ile Gly Ala Ser Asn Lys Leu Gly Glu Thr Thr Lys Ile
            105                 110                 115

gcg acc tct ccc gtg gcg ttc ggt gtg aaa act tcc atg gcc cag gag   499
Ala Thr Ser Pro Val Ala Phe Gly Val Lys Thr Ser Met Ala Gln Glu
        120                 125                 130

ctc ggc tgg gat cag cgc cag cca acc tgg gaa gag ctg ggc cag gcc   547
Leu Gly Trp Asp Gln Arg Gln Pro Thr Trp Glu Glu Leu Gly Gln Ala
    135                 140                 145

tcg cag acc caa gat ttc acc ttc ggt atg acc gat ccg gcc act tcc   595
Ser Gln Thr Gln Asp Phe Thr Phe Gly Met Thr Asp Pro Ala Thr Ser
150                 155                 160                 165

aac tcc gga ttt tcc gcg ctc gtt gcc atg gcc acg gca tat gct gat   643
Asn Ser Gly Phe Ser Ala Leu Val Ala Met Ala Thr Ala Tyr Ala Asp
                170                 175                 180

acc ggc cag gcc tta aca acc aac gac atc ccc gcg atc gcc gag ccg   691
Thr Gly Gln Ala Leu Thr Thr Asn Asp Ile Pro Ala Ile Ala Glu Pro
            185                 190                 195

atg tcc aca tcc ctt tcc ggc caa acc atc acc tcc ggt tcc tct ggc   739
Met Ser Thr Ser Leu Ser Gly Gln Thr Ile Thr Ser Gly Ser Ser Gly
        200                 205                 210

tgg ctc aaa gac act ttc ctg gaa cag cct gac cgc gcg aat gcg atc   787
Trp Leu Lys Asp Thr Phe Leu Glu Gln Pro Asp Arg Ala Asn Ala Ile
    215                 220                 225

atc aac tac gag tcc gtc ctg cac acc atg atc agc gaa gac ggc gcc   835
Ile Asn Tyr Glu Ser Val Leu His Thr Met Ile Ser Glu Asp Gly Ala
230                 235                 240                 245

gat atc acc gtc gtg gtg ccc gcc gat ggc gtg gtc agc gcc gat tac   883
Asp Ile Thr Val Val Val Pro Ala Asp Gly Val Val Ser Ala Asp Tyr
                250                 255                 260

ccg ctc tct acg atc acg ggc tcc gac cag ggc gag cat gta gca gag   931
Pro Leu Ser Thr Ile Thr Gly Ser Asp Gln Gly Glu His Val Ala Glu
            265                 270                 275

ctg gcc ggc tgg ttc gct gag cac ccc gac gct tta aca gat act tat   979
Leu Ala Gly Trp Phe Ala Glu His Pro Asp Ala Leu Thr Asp Thr Tyr
        280                 285                 290
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cga cgt ccg acc acc gcg aac gca acg ctc cca gcg gag ctt agc tcg   1027
Arg Arg Pro Thr Thr Ala Asn Ala Thr Leu Pro Ala Glu Leu Ser Ser
    295                 300                 305

cag acc atc atc gaa gct ccc ttc cca ggg agc aag acg gtc acc gac   1075
Gln Thr Ile Ile Glu Ala Pro Phe Pro Gly Ser Lys Thr Val Thr Asp
310                 315                 320                 325

gcg ctt atc gac gcc tac acc aat caa ttc cgc gtc cca ggc gaa acc   1123
Ala Leu Ile Asp Ala Tyr Thr Asn Gln Phe Arg Val Pro Gly Glu Thr
                330                 335                 340

acc ttt gtg ctc gac gtt tcc gga tcc atg ctg ggc cag cgc atc acc   1171
Thr Phe Val Leu Asp Val Ser Gly Ser Met Leu Gly Gln Arg Ile Thr
            345                 350                 355

ttg ctc aaa gac acc atg tca gac ctg atc agc ggc ggc gcg acc act   1219
Leu Leu Lys Asp Thr Met Ser Asp Leu Ile Ser Gly Gly Ala Thr Thr
        360                 365                 370

gac ctt gcc aac gtg tcc ctg cgc gac cgc gaa aaa gta tcg atc att   1267
Asp Leu Ala Asn Val Ser Leu Arg Asp Arg Glu Lys Val Ser Ile Ile
    375                 380                 385

cct ttc agc ttc ggg cca cac gaa gta atc agc gaa acc ctc ggt gcg   1315
Pro Phe Ser Phe Gly Pro His Glu Val Ile Ser Glu Thr Leu Gly Ala
390                 395                 400                 405

gtg ggc agc cca agc cgc acc gat ctg cag cag cgc gtt gaa gcc ttg   1363
Val Gly Ser Pro Ser Arg Thr Asp Leu Gln Gln Arg Val Glu Ala Leu
                410                 415                 420

caa gca gac ggc gga acc gga att tac gac gca gtg ctc gcc gcc tac   1411
Gln Ala Asp Gly Gly Thr Gly Ile Tyr Asp Ala Val Leu Ala Ala Tyr
            425                 430                 435

gca gag tcc gct ggt ggc gac tac atc cca tcc atc gtg ctc atg acc   1459
Ala Glu Ser Ala Gly Gly Asp Tyr Ile Pro Ser Ile Val Leu Met Thr
        440                 445                 450

gac ggc gaa ctc acc gca gga cga acc tac gat caa ttc ctc acc gaa   1507
Asp Gly Glu Leu Thr Ala Gly Arg Thr Tyr Asp Gln Phe Leu Thr Glu
    455                 460                 465

tgg aac gcg ctt cct agc aat atc cga tca att cca gtg ttt gtc atc   1555
Trp Asn Ala Leu Pro Ser Asn Ile Arg Ser Ile Pro Val Phe Val Ile
470                 475                 480                 485

ctt tac ggt gaa gcc aat gtt gcg gat atg gaa caa ttg gca gca aca   1603
Leu Tyr Gly Glu Ala Asn Val Ala Asp Met Glu Gln Leu Ala Ala Thr
                490                 495                 500

acc ggc ggt gag acc ttt gac gcc atc aac ggt gac cta gac gaa gca   1651
Thr Gly Gly Glu Thr Phe Asp Ala Ile Asn Gly Asp Leu Asp Glu Ala
            505                 510                 515

ttt aag gag att cgt gcc tac caa taatggagga tccttctttt tct        1698
Phe Lys Glu Ile Arg Ala Tyr Gln
        520                 525
```

<210> 2606
<211> 525
<212> PRT
<213> Corynebacterium glutamicum

<400> 2606
Met Lys Asn Leu Val Lys Gly Thr Ala Leu Gly Leu Ser Leu Val Leu
1 5 10 15

Leu Ala Gly Cys Ser Thr Val Ser Asp Ser Ile Asp Ser Leu Gly Gly
20 25 30

Gly Leu Gly Gly Ser Ser Glu Thr Leu Lys Ile Val Ala Ala Thr Glu
35 40 45

Leu Glu Asp Leu Gln Pro Ala Ile Glu Gln Ala Ser Asp Asp Leu Gly
50 55 60

Phe Asp Ile Glu Leu Ser Phe Pro Gly Gly Thr Leu Ser Asn Ser Gln
65 70 75 80

Ala Leu Met Asp Gly Ala Phe Asp Gln Asp Tyr Asp Ala Thr Trp Phe
85 90 95

Ala Thr Asn Arg Tyr Val Asp Leu Ile Gly Ala Ser Asn Lys Leu Gly
100 105 110

Glu Thr Thr Lys Ile Ala Thr Ser Pro Val Ala Phe Gly Val Lys Thr
115 120 125

Ser Met Ala Gln Glu Leu Gly Trp Asp Gln Arg Gln Pro Thr Trp Glu
130 135 140

Glu Leu Gly Gln Ala Ser Gln Thr Gln Asp Phe Thr Phe Gly Met Thr
145 150 155 160

Asp Pro Ala Thr Ser Asn Ser Gly Phe Ser Ala Leu Val Ala Met Ala
165 170 175

Thr Ala Tyr Ala Asp Thr Gly Gln Ala Leu Thr Thr Asn Asp Ile Pro
180 185 190

Ala Ile Ala Glu Pro Met Ser Thr Ser Leu Ser Gly Gln Thr Ile Thr
195 200 205

Ser Gly Ser Ser Gly Trp Leu Lys Asp Thr Phe Leu Glu Gln Pro Asp
210 215 220

Arg Ala Asn Ala Ile Ile Asn Tyr Glu Ser Val Leu His Thr Met Ile
225 230 235 240

Ser Glu Asp Gly Ala Asp Ile Thr Val Val Val Pro Ala Asp Gly Val
245 250 255

Val Ser Ala Asp Tyr Pro Leu Ser Thr Ile Thr Gly Ser Asp Gln Gly
260 265 270

Glu His Val Ala Glu Leu Ala Gly Trp Phe Ala Glu His Pro Asp Ala
275 280 285

Leu Thr Asp Thr Tyr Arg Arg Pro Thr Thr Ala Asn Ala Thr Leu Pro

```
    290                 295                 300

Ala Glu Leu Ser Ser Gln Thr Ile Ile Glu Ala Pro Phe Pro Gly Ser
305                 310                 315                 320

Lys Thr Val Thr Asp Ala Leu Ile Asp Ala Tyr Thr Asn Gln Phe Arg
                325                 330                 335

Val Pro Gly Glu Thr Thr Phe Val Leu Asp Val Ser Gly Ser Met Leu
            340                 345                 350

Gly Gln Arg Ile Thr Leu Leu Lys Asp Thr Met Ser Asp Leu Ile Ser
        355                 360                 365

Gly Gly Ala Thr Thr Asp Leu Ala Asn Val Ser Leu Arg Asp Arg Glu
    370                 375                 380

Lys Val Ser Ile Ile Pro Phe Ser Phe Gly Pro His Glu Val Ile Ser
385                 390                 395                 400

Glu Thr Leu Gly Ala Val Gly Ser Pro Ser Arg Thr Asp Leu Gln Gln
                405                 410                 415

Arg Val Glu Ala Leu Gln Ala Asp Gly Gly Thr Gly Ile Tyr Asp Ala
            420                 425                 430

Val Leu Ala Ala Tyr Ala Glu Ser Ala Gly Gly Asp Tyr Ile Pro Ser
        435                 440                 445

Ile Val Leu Met Thr Asp Gly Glu Leu Thr Ala Gly Arg Thr Tyr Asp
    450                 455                 460

Gln Phe Leu Thr Glu Trp Asn Ala Leu Pro Ser Asn Ile Arg Ser Ile
465                 470                 475                 480

Pro Val Phe Val Ile Leu Tyr Gly Glu Ala Asn Val Ala Asp Met Glu
                485                 490                 495

Gln Leu Ala Ala Thr Thr Gly Gly Glu Thr Phe Asp Ala Ile Asn Gly
            500                 505                 510

Asp Leu Asp Glu Ala Phe Lys Glu Ile Arg Ala Tyr Gln
        515                 520                 525


<210> 2607
<211> 735
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(712)
<223> RXA02165

<400> 2607
gaagccaatg ttgcggatat ggaacaattg gcagcaacaa ccggcggtga gacctttgac 60

gccatcaacg gtgacctaga cgaagcattt aaggagattc gtg cct acc aat aat   115
                                              Val Pro Thr Asn Asn
                                                1               5
```

```
gga gga tcc ttc ttt ttc tcc cgc aag aat ctc gcg ggt atc gct att   163
Gly Gly Ser Phe Phe Phe Ser Arg Lys Asn Leu Ala Gly Ile Ala Ile
                 10                  15                  20

gca acg ctg att atc gcg ctg cac tta gtg atc gga ctc gga gca ttt   211
Ala Thr Leu Ile Ile Ala Leu His Leu Val Ile Gly Leu Gly Ala Phe
             25                  30                  35

tgg cct gtt gtc gcc atc gcc gga tac ggc gct gcg gtg gca ctt aca   259
Trp Pro Val Val Ala Ile Ala Gly Tyr Gly Ala Ala Val Ala Leu Thr
         40                  45                  50

cct aaa aac cct ccg aag aag gaa ctc cct ccg gtt cag gca act ccc   307
Pro Lys Asn Pro Pro Lys Lys Glu Leu Pro Pro Val Gln Ala Thr Pro
     55                  60                  65

gaa tta gat agc ccg ggt ctg ctt gca gcc agg tct caa gaa ctc gtg   355
Glu Leu Asp Ser Pro Gly Leu Leu Ala Ala Arg Ser Gln Glu Leu Val
 70                  75                  80                  85

aga act atg tat agc cac ggt gct gca gca cca gtg atc gaa gcg att   403
Arg Thr Met Tyr Ser His Gly Ala Ala Ala Pro Val Ile Glu Ala Ile
                 90                  95                 100

aag agg cta gac agc tca ctg caa ttg gtc att ggt aac tgg aca agc   451
Lys Arg Leu Asp Ser Ser Leu Gln Leu Val Ile Gly Asn Trp Thr Ser
             105                 110                 115

ctg acc aat ttt ccc gag cac caa gtc acc att cgc tca att atc aac   499
Leu Thr Asn Phe Pro Glu His Gln Val Thr Ile Arg Ser Ile Ile Asn
         120                 125                 130

cag tac atc cca ggc att atc gac gct tac ctg aag atc ccc acc cgc   547
Gln Tyr Ile Pro Gly Ile Ile Asp Ala Tyr Leu Lys Ile Pro Thr Arg
     135                 140                 145

aac gat cct cgg gca gtc gaa gac ctc att gaa tcc ttc gac ctc ctg   595
Asn Asp Pro Arg Ala Val Glu Asp Leu Ile Glu Ser Phe Asp Leu Leu
150                 155                 160                 165

aac tcc gag acg atg aag atc ttc aat gcg atc caa gaa caa ggc ctt   643
Asn Ser Glu Thr Met Lys Ile Phe Asn Ala Ile Gln Glu Gln Gly Leu
                 170                 175                 180

aat aac ctt gaa gat cac ggt cgc gca ctg cgc atg caa ttt ggt caa   691
Asn Asn Leu Glu Asp His Gly Arg Ala Leu Arg Met Gln Phe Gly Gln
             185                 190                 195

ctg cca gaa gaa ttc cgg gaa tagccactca atgcagttaa gtt             735
Leu Pro Glu Glu Phe Arg Glu
         200
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<210> 2608
<211> 204
<212> PRT
<213> Corynebacterium glutamicum

<400> 2608
Val Pro Thr Asn Asn Gly Gly Ser Phe Phe Phe Ser Arg Lys Asn Leu

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  1               5                  10                  15

Ala Gly Ile Ala Ile Ala Thr Leu Ile Ile Ala Leu His Leu Val Ile
             20                  25                  30

Gly Leu Gly Ala Phe Trp Pro Val Val Ala Ile Ala Gly Tyr Gly Ala
         35                  40                  45

Ala Val Ala Leu Thr Pro Lys Asn Pro Pro Lys Lys Glu Leu Pro Pro
     50                  55                  60

Val Gln Ala Thr Pro Glu Leu Asp Ser Pro Gly Leu Leu Ala Ala Arg
 65                  70                  75                  80

Ser Gln Glu Leu Val Arg Thr Met Tyr Ser His Gly Ala Ala Ala Pro
                 85                  90                  95

Val Ile Glu Ala Ile Lys Arg Leu Asp Ser Ser Leu Gln Leu Val Ile
            100                 105                 110

Gly Asn Trp Thr Ser Leu Thr Asn Phe Pro Glu His Gln Val Thr Ile
        115                 120                 125

Arg Ser Ile Ile Asn Gln Tyr Ile Pro Gly Ile Ile Asp Ala Tyr Leu
    130                 135                 140

Lys Ile Pro Thr Arg Asn Asp Pro Arg Ala Val Glu Asp Leu Ile Glu
145                 150                 155                 160

Ser Phe Asp Leu Leu Asn Ser Glu Thr Met Lys Ile Phe Asn Ala Ile
                165                 170                 175

Gln Glu Gln Gly Leu Asn Asn Leu Glu Asp His Gly Arg Ala Leu Arg
            180                 185                 190

Met Gln Phe Gly Gln Leu Pro Glu Glu Phe Arg Glu
        195                 200
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US20150307907A1

<210> 2609
<211> 300
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(277)
<223> RXA02166

<400> 2609
cggtcgcgca ctgcgcatgc aatttggtca actgccagaa gaattccggg aatagccact 60

caatgcagtt aagtttttcc tgcccggtag gatggtccgt atg agt ctt gat cca 115
                                        Met Ser Leu Asp Pro
                                          1   5

cag ctt ctt gaa gtc ctg gcc tgc cca aag gac aag ggc cca ctt cga 163
Gln Leu Leu Glu Val Leu Ala Cys Pro Lys Asp Lys Gly Pro Leu Arg
                10   15   20

tat ctg gag agc gaa cag ctc ttg gtc aac gaa cgc ctc aac ctg gcc 211

```
Tyr Leu Glu Ser Glu Gln Leu Leu Val Asn Glu Arg Leu Asn Leu Ala
             25                  30                  35

tat cgc att gac gac gga att ccg gtg ctt ctc atc gac gaa gcc acc   259
Tyr Arg Ile Asp Asp Gly Ile Pro Val Leu Leu Ile Asp Glu Ala Thr
         40                  45                  50

gag tgg acc ccc aac aac tagaagtaca tcaaggacat ttt                 300
Glu Trp Thr Pro Asn Asn
     55


<210> 2610
<211> 59
<212> PRT
<213> Corynebacterium glutamicum

<400> 2610
Met Ser Leu Asp Pro Gln Leu Leu Glu Val Leu Ala Cys Pro Lys Asp
  1               5                  10                  15

Lys Gly Pro Leu Arg Tyr Leu Glu Ser Glu Gln Leu Leu Val Asn Glu
             20                  25                  30

Arg Leu Asn Leu Ala Tyr Arg Ile Asp Asp Gly Ile Pro Val Leu Leu
         35                  40                  45

Ile Asp Glu Ala Thr Glu Trp Thr Pro Asn Asn
     50                  55


<210> 2611
<211> 2937
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2914)
<223> RXA02168

<400> 2611
agggtttagt catctatttc ggctacgctc acgtaaccta cgcattcgta agtggtcatg 60

ggtccaagaa gcccattcca agacttagga gctttatttc gtg agt att tct tca   115
                                        Val Ser Ile Ser Ser
                                          1               5

ctg aca ccg ctg cac tct ttc aaa gag cca gca att ctg tac gcc ggt   163
Leu Thr Pro Leu His Ser Phe Lys Glu Pro Ala Ile Leu Tyr Ala Gly
                 10                  15                  20

cag gct tct gcc tgg cag cag gtg atc gct gat tcc agc gaa gac cac   211
Gln Ala Ser Ala Trp Gln Gln Val Ile Ala Asp Ser Ser Glu Asp His
             25                  30                  35

atc acc gca acg cac ctg cgc gag ctc ctg tct cgc tcc cgt gca aag   259
Ile Thr Ala Thr His Leu Arg Glu Leu Leu Ser Arg Ser Arg Ala Lys
         40                  45                  50

act gca cct ttc gct cgc caa atc acc gcc atc gtg cct ggc tca ctt   307
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Thr Ala Pro Phe Ala Arg Gln Ile Thr Ala Ile Val Pro Gly Ser Leu
     55                  60                  65

gct cgt ctt gag gaa ctg acc cgc gaa gac gca caa atc ggt gca gac   355
Ala Arg Leu Glu Glu Leu Thr Arg Glu Asp Ala Gln Ile Gly Ala Asp
 70                  75                  80                  85

atc gac gca cag cct gcc gtt tcc att cca ggc att ctg ctg gga cag   403
Ile Asp Ala Gln Pro Ala Val Ser Ile Pro Gly Ile Leu Leu Gly Gln
                 90                  95                 100

atc gct gca acc cgt cag ctg cgt gac ctc gga ctc gat gtc gca gca   451
Ile Ala Ala Thr Arg Gln Leu Arg Asp Leu Gly Leu Asp Val Ala Ala
            105                 110                 115

gct tcc cgc ctt gga cac tcc cag ggc att ttg ggc gtt gaa gca gta   499
Ala Ser Arg Leu Gly His Ser Gln Gly Ile Leu Gly Val Glu Ala Val
        120                 125                 130

gac aat gaa gaa gac gtt tta gct ttc gcc atc ctg ctg ggc gca gca   547
Asp Asn Glu Glu Asp Val Leu Ala Phe Ala Ile Leu Leu Gly Ala Ala
    135                 140                 145

gct tcc cag ttc gct ggc aag ggc gca cat atg ctc tct gtt cgc ggc   595
Ala Ser Gln Phe Ala Gly Lys Gly Ala His Met Leu Ser Val Arg Gly
150                 155                 160                 165

ctg tcc cgt gag atc atc cag gac acc atc gct ggt gtc gat ggg gta   643
Leu Ser Arg Glu Ile Ile Gln Asp Thr Ile Ala Gly Val Asp Gly Val
                170                 175                 180

gag gtc tcc ctg cgc aac gct cgt gca cac ttt gtt gtc tct ggt aag   691
Glu Val Ser Leu Arg Asn Ala Arg Ala His Phe Val Val Ser Gly Lys
            185                 190                 195

cca gag gca ctg aag aag gct gct gct gct cta cag cgc gca gct gat   739
Pro Glu Ala Leu Lys Lys Ala Ala Ala Ala Leu Gln Arg Ala Ala Asp
        200                 205                 210

gtt tac aac gaa gac atc aac gaa aag cgc aag ggt gga tcc ctg gca   787
Val Tyr Asn Glu Asp Ile Asn Glu Lys Arg Lys Gly Gly Ser Leu Ala
    215                 220                 225

gag cct aag ttt gac tac ttg gat gtg gcc att cct ttc cac cac tcc   835
Glu Pro Lys Phe Asp Tyr Leu Asp Val Ala Ile Pro Phe His His Ser
230                 235                 240                 245

tcc atg cag gac gca gcc gac ttg gct gtc gag tgg gca acc acc tgt   883
Ser Met Gln Asp Ala Ala Asp Leu Ala Val Glu Trp Ala Thr Thr Cys
                250                 255                 260

ggc cta aac gtc aac gcg cgc gcg ttg gca gaa gca att cta gtt aac   931
Gly Leu Asn Val Asn Ala Arg Ala Leu Ala Glu Ala Ile Leu Val Asn
            265                 270                 275

cca gct gac tgg gtt gag cag atc gca aac ctc aag gct gat tac gtt   979
Pro Ala Asp Trp Val Glu Gln Ile Ala Asn Leu Lys Ala Asp Tyr Val
        280                 285                 290

ctt tcc ctc gat gca ggc gtc agc cgt ttc acc gct cca ttg cta gac   1027
Leu Ser Leu Asp Ala Gly Val Ser Arg Phe Thr Ala Pro Leu Leu Asp
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    295                 300                 305

ggt cgc gga atc tct ttg gtt cct gcg ttc tcc gct gca gag cgc gac   1075
Gly Arg Gly Ile Ser Leu Val Pro Ala Phe Ser Ala Ala Glu Arg Asp
310                 315                 320                 325

aac ttg gct cgc cct ggc ttc cac gtt cct acc gct gag gat tgg tcc   1123
Asn Leu Ala Arg Pro Gly Phe His Val Pro Thr Ala Glu Asp Trp Ser
                330                 335                 340

gag ttc gct cca aag ctg gtt aag ctt cca aac ggt gag cac aag gtt   1171
Glu Phe Ala Pro Lys Leu Val Lys Leu Pro Asn Gly Glu His Lys Val
            345                 350                 355

ctc acc ggg ttc tcc cgc ctg act ggt tat tcc cca atc gtc ctg gct   1219
Leu Thr Gly Phe Ser Arg Leu Thr Gly Tyr Ser Pro Ile Val Leu Ala
        360                 365                 370

ggc atg acc cca acc acc gtt gat cct gag atc gtt gca gct gca gcg   1267
Gly Met Thr Pro Thr Thr Val Asp Pro Glu Ile Val Ala Ala Ala Ala
    375                 380                 385

aac gct gga cac tgg gcc gaa atg gcc ggt ggc gga cag tac tct gaa   1315
Asn Ala Gly His Trp Ala Glu Met Ala Gly Gly Gly Gln Tyr Ser Glu
390                 395                 400                 405

gaa gtc ttc acc aag aac aag gaa aag ctc gtt tcc ctg ctc aag gtt   1363
Glu Val Phe Thr Lys Asn Lys Glu Lys Leu Val Ser Leu Leu Lys Val
                410                 415                 420

gga cgc tcc gca cag ttc aac tcc atg ttc ttc gac cgc tac atg tgg   1411
Gly Arg Ser Ala Gln Phe Asn Ser Met Phe Phe Asp Arg Tyr Met Trp
            425                 430                 435

aac ctg cag ttc ggt gca cag cgc atc gtt tcc aag gca cgt gca acc   1459
Asn Leu Gln Phe Gly Ala Gln Arg Ile Val Ser Lys Ala Arg Ala Thr
        440                 445                 450

ggt acc tcc atc aac ggt gtt gtt gtc tcc gct ggt atc cca gag gtt   1507
Gly Thr Ser Ile Asn Gly Val Val Val Ser Ala Gly Ile Pro Glu Val
    455                 460                 465

gag gaa gca act gag ctg atc aac gat ctg aac gct gat ggc ttc cca   1555
Glu Glu Ala Thr Glu Leu Ile Asn Asp Leu Asn Ala Asp Gly Phe Pro
470                 475                 480                 485

tac gtt gca ttc aag cca ggc acc gtg gat cag atc cgc gca acc ctg   1603
Tyr Val Ala Phe Lys Pro Gly Thr Val Asp Gln Ile Arg Ala Thr Leu
                490                 495                 500

aag att gct gat gca aac cca gag acc aag atc atc atc cag atc gag   1651
Lys Ile Ala Asp Ala Asn Pro Glu Thr Lys Ile Ile Ile Gln Ile Glu
            505                 510                 515

gac gga cac gct ggt ggc cac cac tcc tgg gtc aac ttg gac gat ctg   1699
Asp Gly His Ala Gly Gly His His Ser Trp Val Asn Leu Asp Asp Leu
        520                 525                 530

ctc ctg acc acc tac gca gag ctg cgt tcc cgc aag aac gtt gtc gtc   1747
Leu Leu Thr Thr Tyr Ala Glu Leu Arg Ser Arg Lys Asn Val Val Val
    535                 540                 545
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atg atc ggt ggc ggc atc gga acc cct gca aag gct gct tac tac ctg   1795
Met Ile Gly Gly Gly Ile Gly Thr Pro Ala Lys Ala Ala Tyr Tyr Leu
550                 555                 560                 565

acc ggt gaa tgg tcc acc gat ttg ggc ttc cca gca atg cca gtg gac   1843
Thr Gly Glu Trp Ser Thr Asp Leu Gly Phe Pro Ala Met Pro Val Asp
                570                 575                 580

ggc atc ctc gtg ggt acc gct gcc atg gca acc aag gaa gca acc act   1891
Gly Ile Leu Val Gly Thr Ala Ala Met Ala Thr Lys Glu Ala Thr Thr
            585                 590                 595

tct cct cag gtc aag cag gca ctg gtc gac acc cca ggt gtt gat cca   1939
Ser Pro Gln Val Lys Gln Ala Leu Val Asp Thr Pro Gly Val Asp Pro
        600                 605                 610

cac gac gct ggc ggc tgg gtt ggc cgt ggc gat gct cgt ggt ggc gtg   1987
His Asp Ala Gly Gly Trp Val Gly Arg Gly Asp Ala Arg Gly Gly Val
    615                 620                 625

acc tct ggt ctg tca cac ctg cac gct gac atg tac gag ctg gac aac   2035
Thr Ser Gly Leu Ser His Leu His Ala Asp Met Tyr Glu Leu Asp Asn
630                 635                 640                 645

gat tct gct gca gct tcc cgc ctg atc tct tcc atc gat tct gat gat   2083
Asp Ser Ala Ala Ala Ser Arg Leu Ile Ser Ser Ile Asp Ser Asp Asp
                650                 655                 660

tac gca gat cac cgc gaa gag ctc atc gag gct atc aac aag acc gct   2131
Tyr Ala Asp His Arg Glu Glu Leu Ile Glu Ala Ile Asn Lys Thr Ala
            665                 670                 675

aag cct ttc ttc ggc gag gtc gaa gag atg act tac gca gag tgg atc   2179
Lys Pro Phe Phe Gly Glu Val Glu Glu Met Thr Tyr Ala Glu Trp Ile
        680                 685                 690

cag cgt tgg gtt gag ctt gct tac cca act cag gac cca acc tgg gat   2227
Gln Arg Trp Val Glu Leu Ala Tyr Pro Thr Gln Asp Pro Thr Trp Asp
    695                 700                 705

gat cgt ttc ctc gat ttg gtt cac cgc att gaa gct cgt ctc aac gag   2275
Asp Arg Phe Leu Asp Leu Val His Arg Ile Glu Ala Arg Leu Asn Glu
710                 715                 720                 725

gca gag cac ggc gcc atc acc aca ctg ttc cca gac cat gcg tct gtg   2323
Ala Glu His Gly Ala Ile Thr Thr Leu Phe Pro Asp His Ala Ser Val
                730                 735                 740

gaa aat gag gaa gag gcc gtc gaa aag ctt ctt gct gct tac ccg cag   2371
Glu Asn Glu Glu Glu Ala Val Glu Lys Leu Leu Ala Ala Tyr Pro Gln
            745                 750                 755

gcc cgc gag atc cag gtc tct gcg cgc gac gcc gcg tgg ttt att ggt   2419
Ala Arg Glu Ile Gln Val Ser Ala Arg Asp Ala Ala Trp Phe Ile Gly
        760                 765                 770

ctg tgc cgc aag cac cac aag cct atg cct tgg gtt cca gca atc gat   2467
Leu Cys Arg Lys His His Lys Pro Met Pro Trp Val Pro Ala Ile Asp
    775                 780                 785
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```
gct gac cta gca cgc tgg tgg ggc ctt gac acc ctg tgg cag tcc cag   2515
Ala Asp Leu Ala Arg Trp Trp Gly Leu Asp Thr Leu Trp Gln Ser Gln
790                 795                 800                 805

aac gag cgc tac ggc gcg aac tca gtc cgc gtt atc cca gga cca gtc   2563
Asn Glu Arg Tyr Gly Ala Asn Ser Val Arg Val Ile Pro Gly Pro Val
                810                 815                 820

tcc gtc gcc ggc atc gac cgt gtt gac gag cca gtt gca gag ctg ctc   2611
Ser Val Ala Gly Ile Asp Arg Val Asp Glu Pro Val Ala Glu Leu Leu
            825                 830                 835

ggc cgc ttc gaa gct gcc tgc gtt gac gct ctc gac ggc gag cca gaa   2659
Gly Arg Phe Glu Ala Ala Cys Val Asp Ala Leu Asp Gly Glu Pro Glu
        840                 845                 850

gag atc ttc gct cgc ctc aat gag tcc aag aac gag cgc gaa ttc ctg   2707
Glu Ile Phe Ala Arg Leu Asn Glu Ser Lys Asn Glu Arg Glu Phe Leu
    855                 860                 865

ctg gct acc cca cac atc gtg tgg cac ggc aac ctg atc gac aac cca   2755
Leu Ala Thr Pro His Ile Val Trp His Gly Asn Leu Ile Asp Asn Pro
870                 875                 880                 885

gct cac gtc ctc aac gag ggt gct ttc gag ctc atc gag gag gat ggc   2803
Ala His Val Leu Asn Glu Gly Ala Phe Glu Leu Ile Glu Glu Asp Gly
                890                 895                 900

tac tgg gtc atc cgt atc ctg gct gat tcc tac ttc gac gat ctg cca   2851
Tyr Trp Val Ile Arg Ile Leu Ala Asp Ser Tyr Phe Asp Asp Leu Pro
            905                 910                 915

gtt gag cag cgc cca tac ctg gtt cag cat gtt gac atc cca gtt gag   2899
Val Glu Gln Arg Pro Tyr Leu Val Gln His Val Asp Ile Pro Val Glu
        920                 925                 930

ctg ggt gac gct ggt tgaaccggtg gtttcccaat tgg                    2937
Leu Gly Asp Ala Gly
    935
```

CONFIDENTIAL

<210> 2612
<211> 938
<212> PRT
<213> Corynebacterium glutamicum

<400> 2612

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Val Ser Ile Ser Ser Leu Thr Pro Leu His Ser Phe Lys Glu Pro Ala
  1               5                  10                  15

Ile Leu Tyr Ala Gly Gln Ala Ser Ala Trp Gln Gln Val Ile Ala Asp
             20                  25                  30

Ser Ser Glu Asp His Ile Thr Ala Thr His Leu Arg Glu Leu Leu Ser
         35                  40                  45

Arg Ser Arg Ala Lys Thr Ala Pro Phe Ala Arg Gln Ile Thr Ala Ile
     50                  55                  60

Val Pro Gly Ser Leu Ala Arg Leu Glu Glu Leu Thr Arg Glu Asp Ala
 65                  70                  75                  80
```

```
Gln Ile Gly Ala Asp Ile Asp Ala Gln Pro Ala Val Ser Ile Pro Gly
                 85                  90                  95

Ile Leu Leu Gly Gln Ile Ala Ala Thr Arg Gln Leu Arg Asp Leu Gly
            100                 105                 110

Leu Asp Val Ala Ala Ala Ser Arg Leu Gly His Ser Gln Gly Ile Leu
        115                 120                 125

Gly Val Glu Ala Val Asp Asn Glu Glu Asp Val Leu Ala Phe Ala Ile
    130                 135                 140

Leu Leu Gly Ala Ala Ala Ser Gln Phe Ala Gly Lys Gly Ala His Met
145                 150                 155                 160

Leu Ser Val Arg Gly Leu Ser Arg Glu Ile Ile Gln Asp Thr Ile Ala
                165                 170                 175

Gly Val Asp Gly Val Glu Val Ser Leu Arg Asn Ala Arg Ala His Phe
            180                 185                 190

Val Val Ser Gly Lys Pro Glu Ala Leu Lys Lys Ala Ala Ala Ala Leu
        195                 200                 205

Gln Arg Ala Ala Asp Val Tyr Asn Glu Asp Ile Asn Glu Lys Arg Lys
    210                 215                 220

Gly Gly Ser Leu Ala Glu Pro Lys Phe Asp Tyr Leu Asp Val Ala Ile
225                 230                 235                 240

Pro Phe His His Ser Ser Met Gln Asp Ala Ala Asp Leu Ala Val Glu
                245                 250                 255

Trp Ala Thr Thr Cys Gly Leu Asn Val Asn Ala Arg Ala Leu Ala Glu
            260                 265                 270

Ala Ile Leu Val Asn Pro Ala Asp Trp Val Glu Gln Ile Ala Asn Leu
        275                 280                 285

Lys Ala Asp Tyr Val Leu Ser Leu Asp Ala Gly Val Ser Arg Phe Thr
    290                 295                 300

Ala Pro Leu Leu Asp Gly Arg Gly Ile Ser Leu Val Pro Ala Phe Ser
305                 310                 315                 320

Ala Ala Glu Arg Asp Asn Leu Ala Arg Pro Gly Phe His Val Pro Thr
                325                 330                 335

Ala Glu Asp Trp Ser Glu Phe Ala Pro Lys Leu Val Lys Leu Pro Asn
            340                 345                 350

Gly Glu His Lys Val Leu Thr Gly Phe Ser Arg Leu Thr Gly Tyr Ser
        355                 360                 365

Pro Ile Val Leu Ala Gly Met Thr Pro Thr Thr Val Asp Pro Glu Ile
    370                 375                 380

Val Ala Ala Ala Ala Asn Ala Gly His Trp Ala Glu Met Ala Gly Gly
385                 390                 395                 400
```

```
Gly Gln Tyr Ser Glu Glu Val Phe Thr Lys Asn Lys Glu Lys Leu Val
                405                 410                 415

Ser Leu Leu Lys Val Gly Arg Ser Ala Gln Phe Asn Ser Met Phe Phe
            420                 425                 430

Asp Arg Tyr Met Trp Asn Leu Gln Phe Gly Ala Gln Arg Ile Val Ser
        435                 440                 445

Lys Ala Arg Ala Thr Gly Thr Ser Ile Asn Gly Val Val Val Ser Ala
    450                 455                 460

Gly Ile Pro Glu Val Glu Glu Ala Thr Glu Leu Ile Asn Asp Leu Asn
465                 470                 475                 480

Ala Asp Gly Phe Pro Tyr Val Ala Phe Lys Pro Gly Thr Val Asp Gln
                485                 490                 495

Ile Arg Ala Thr Leu Lys Ile Ala Asp Ala Asn Pro Glu Thr Lys Ile
            500                 505                 510

Ile Ile Gln Ile Glu Asp Gly His Ala Gly Gly His His Ser Trp Val
        515                 520                 525

Asn Leu Asp Asp Leu Leu Leu Thr Thr Tyr Ala Glu Leu Arg Ser Arg
    530                 535                 540

Lys Asn Val Val Val Met Ile Gly Gly Gly Ile Gly Thr Pro Ala Lys
545                 550                 555                 560

Ala Ala Tyr Tyr Leu Thr Gly Glu Trp Ser Thr Asp Leu Gly Phe Pro
                565                 570                 575

Ala Met Pro Val Asp Gly Ile Leu Val Gly Thr Ala Ala Met Ala Thr
            580                 585                 590

Lys Glu Ala Thr Thr Ser Pro Gln Val Lys Gln Ala Leu Val Asp Thr
        595                 600                 605

Pro Gly Val Asp Pro His Asp Ala Gly Gly Trp Val Gly Arg Gly Asp
    610                 615                 620

Ala Arg Gly Gly Val Thr Ser Gly Leu Ser His Leu His Ala Asp Met
625                 630                 635                 640

Tyr Glu Leu Asp Asn Asp Ser Ala Ala Ala Ser Arg Leu Ile Ser Ser
                645                 650                 655

Ile Asp Ser Asp Asp Tyr Ala Asp His Arg Glu Glu Leu Ile Glu Ala
            660                 665                 670

Ile Asn Lys Thr Ala Lys Pro Phe Phe Gly Glu Val Glu Glu Met Thr
        675                 680                 685

Tyr Ala Glu Trp Ile Gln Arg Trp Val Glu Leu Ala Tyr Pro Thr Gln
    690                 695                 700

Asp Pro Thr Trp Asp Asp Arg Phe Leu Asp Leu Val His Arg Ile Glu
705                 710                 715                 720

Ala Arg Leu Asn Glu Ala Glu His Gly Ala Ile Thr Thr Leu Phe Pro
```

```
                725                 730                 735

Asp His Ala Ser Val Glu Asn Glu Glu Glu Ala Val Glu Lys Leu Leu
            740                 745                 750

Ala Ala Tyr Pro Gln Ala Arg Glu Ile Gln Val Ser Ala Arg Asp Ala
        755                 760                 765

Ala Trp Phe Ile Gly Leu Cys Arg Lys His His Lys Pro Met Pro Trp
    770                 775                 780

Val Pro Ala Ile Asp Ala Asp Leu Ala Arg Trp Trp Gly Leu Asp Thr
785                 790                 795                 800

Leu Trp Gln Ser Gln Asn Glu Arg Tyr Gly Ala Asn Ser Val Arg Val
                805                 810                 815

Ile Pro Gly Pro Val Ser Val Ala Gly Ile Asp Arg Val Asp Glu Pro
            820                 825                 830

Val Ala Glu Leu Leu Gly Arg Phe Glu Ala Ala Cys Val Asp Ala Leu
        835                 840                 845

Asp Gly Glu Pro Glu Glu Ile Phe Ala Arg Leu Asn Glu Ser Lys Asn
    850                 855                 860

Glu Arg Glu Phe Leu Leu Ala Thr Pro His Ile Val Trp His Gly Asn
865                 870                 875                 880

Leu Ile Asp Asn Pro Ala His Val Leu Asn Glu Gly Ala Phe Glu Leu
                885                 890                 895

Ile Glu Glu Asp Gly Tyr Trp Val Ile Arg Ile Leu Ala Asp Ser Tyr
            900                 905                 910

Phe Asp Asp Leu Pro Val Glu Gln Arg Pro Tyr Leu Val Gln His Val
        915                 920                 925

Asp Ile Pro Val Glu Leu Gly Asp Ala Gly
    930                 935
```

<210> 2613
<211> 897
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> RXA02170

<400> 2613

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atttaaaccg cccactctcc agtcggagga tgggcggttt tcgcatgcag tactattagt 60

ggacgtgtca agaacttcta aggttcaccc gggatggcgg gtg tct act gtc ctt   115
                                            Val Ser Thr Val Leu
                                              1               5

tta gca gga gta gtt att att ggc gga att ttt act ctc cct cag aag   163
Leu Ala Gly Val Val Ile Ile Gly Gly Ile Phe Thr Leu Pro Gln Lys
```

```
                    10                  15                  20

gag gaa gta aag gtt tcc gaa ttg cag cca cag gcc agc gct gca tcc   211
Glu Glu Val Lys Val Ser Glu Leu Gln Pro Gln Ala Ser Ala Ala Ser
            25                  30                  35

atc ccg tct tca tct tcc aca gct ggg aaa gca gtg gaa gaa agc cct   259
Ile Pro Ser Ser Ser Ser Thr Ala Gly Lys Ala Val Glu Glu Ser Pro
        40                  45                  50

cta acg cag ttt gtg gaa aac tcg aca ggc tcc caa att acg tac atg   307
Leu Thr Gln Phe Val Glu Asn Ser Thr Gly Ser Gln Ile Thr Tyr Met
    55                  60                  65

agc ctg aaa gac gat ttc cat act ggc acg tct acg gaa cgt ttt gcg   355
Ser Leu Lys Asp Asp Phe His Thr Gly Thr Ser Thr Glu Arg Phe Ala
70                  75                  80                  85

cgc cca gcg tta agt ttg tct aag ctc tac atc gct gaa tat gtg ctc   403
Arg Pro Ala Leu Ser Leu Ser Lys Leu Tyr Ile Ala Glu Tyr Val Leu
                90                  95                  100

gag cac ggc acg aat aat gag aag tct ttg gcg atg gaa atg atc aaa   451
Glu His Gly Thr Asn Asn Glu Lys Ser Leu Ala Met Glu Met Ile Lys
            105                 110                 115

gat tcc tcc gac gta tcc gcc gaa atc ttg tat gag gcg tac cca gaa   499
Asp Ser Ser Asp Val Ser Ala Glu Ile Leu Tyr Glu Ala Tyr Pro Glu
        120                 125                 130

tca att gag gag att gcg gat caa tac gga ttg ctc tcc aca agg gga   547
Ser Ile Glu Glu Ile Ala Asp Gln Tyr Gly Leu Leu Ser Thr Arg Gly
    135                 140                 145

gac gcg cac tgg gga tac tcg gtg aca tcc act tac gat ttg gtg aaa   595
Asp Ala His Trp Gly Tyr Ser Val Thr Ser Thr Tyr Asp Leu Val Lys
150                 155                 160                 165

ttt gtc agc gct ctc att atc gat gat cca gat tca ccg atc ctt gaa   643
Phe Val Ser Ala Leu Ile Ile Asp Asp Pro Asp Ser Pro Ile Leu Glu
                170                 175                 180

gcg atg cgt aat gcc agc gca gtc gcg gct gac ggt tat ccg caa gac   691
Ala Met Arg Asn Ala Ser Ala Val Ala Ala Asp Gly Tyr Pro Gln Asp
            185                 190                 195

tgg ggg aca gcg gtg ctt gat gag gca gaa gga tcc aaa tgg gga tgg   739
Trp Gly Thr Ala Val Leu Asp Glu Ala Glu Gly Ser Lys Trp Gly Trp
        200                 205                 210

tct gat gat ctc atg ctg cac tcc tct gtg acc ttt ggc gaa gac tat   787
Ser Asp Asp Leu Met Leu His Ser Ser Val Thr Phe Gly Glu Asp Tyr
    215                 220                 225

gtt gtg gca gct gct gtg act gga tca aaa gaa gac ctc acc caa ttg   835
Val Val Ala Ala Ala Val Thr Gly Ser Lys Glu Asp Leu Thr Gln Leu
230                 235                 240                 245

gtg gaa aac caa ttg ggt gag gtt gtg agt cag cac ggc tagtttagct    884
Val Glu Asn Gln Leu Gly Glu Val Val Ser Gln His Gly
                250                 255
```

agatagggtg cca 897

<210> 2614
<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 2614

```
Val Ser Thr Val Leu Leu Ala Gly Val Val Ile Ile Gly Gly Ile Phe
  1               5                  10                  15

Thr Leu Pro Gln Lys Glu Glu Val Lys Val Ser Glu Leu Gln Pro Gln
             20                  25                  30

Ala Ser Ala Ala Ser Ile Pro Ser Ser Ser Ser Thr Ala Gly Lys Ala
         35                  40                  45

Val Glu Glu Ser Pro Leu Thr Gln Phe Val Glu Asn Ser Thr Gly Ser
     50                  55                  60

Gln Ile Thr Tyr Met Ser Leu Lys Asp Asp Phe His Thr Gly Thr Ser
 65                  70                  75                  80

Thr Glu Arg Phe Ala Arg Pro Ala Leu Ser Leu Ser Lys Leu Tyr Ile
                 85                  90                  95

Ala Glu Tyr Val Leu Glu His Gly Thr Asn Asn Glu Lys Ser Leu Ala
            100                 105                 110

Met Glu Met Ile Lys Asp Ser Ser Asp Val Ser Ala Glu Ile Leu Tyr
        115                 120                 125

Glu Ala Tyr Pro Glu Ser Ile Glu Glu Ile Ala Asp Gln Tyr Gly Leu
    130                 135                 140

Leu Ser Thr Arg Gly Asp Ala His Trp Gly Tyr Ser Val Thr Ser Thr
145                 150                 155                 160

Tyr Asp Leu Val Lys Phe Val Ser Ala Leu Ile Ile Asp Asp Pro Asp
                165                 170                 175

Ser Pro Ile Leu Glu Ala Met Arg Asn Ala Ser Ala Val Ala Ala Asp
            180                 185                 190

Gly Tyr Pro Gln Asp Trp Gly Thr Ala Val Leu Asp Glu Ala Glu Gly
        195                 200                 205

Ser Lys Trp Gly Trp Ser Asp Asp Leu Met Leu His Ser Ser Val Thr
    210                 215                 220

Phe Gly Glu Asp Tyr Val Val Ala Ala Ala Val Thr Gly Ser Lys Glu
225                 230                 235                 240

Asp Leu Thr Gln Leu Val Glu Asn Gln Leu Gly Glu Val Val Ser Gln
                245                 250                 255

His Gly
```

<210> 2615
<211> 462
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(439)
<223> RXA02172

<400> 2615
gagaaacata taagttgctt tattttaaag ccggcattgc ttagagagtg gccgatcacc 60

gactcccgct cgagggatat gaaagcgaga taagtttcca gtg aat gca gaa caa 115
Val Asn Ala Glu Gln
1 5

atc acc cag ggg cgt cgc cag ccg acg gct caa gag ttt cgg gac atg 163
Ile Thr Gln Gly Arg Arg Gln Pro Thr Ala Gln Glu Phe Arg Asp Met
10 15 20

cag gcg agc cca gaa ttt gga gag ctc cgc agc aag ttc cgt tcc ttt 211
Gln Ala Ser Pro Glu Phe Gly Glu Leu Arg Ser Lys Phe Arg Ser Phe
25 30 35

gct ttc cca atg acc gtt gcc ttc ttc ttg tgg tac gtc gtc tac gtt 259
Ala Phe Pro Met Thr Val Ala Phe Phe Leu Trp Tyr Val Val Tyr Val
40 45 50

ctg gtt gca tcc ttt gca tca gag tgg atg gca acc cca gtt ttc ggc 307
Leu Val Ala Ser Phe Ala Ser Glu Trp Met Ala Thr Pro Val Phe Gly
55 60 65

gca atc aac att ggc cta atc ttc ggc ttc ctt cag ttc gta acc aca 355
Ala Ile Asn Ile Gly Leu Ile Phe Gly Phe Leu Gln Phe Val Thr Thr
70 75 80 85

ttc gtc att act tac atc tat gtc atg ttt gcg aac aag aac ttg gag 403
Phe Val Ile Thr Tyr Ile Tyr Val Met Phe Ala Asn Lys Asn Leu Glu
90 95 100

cct cgt cag gct gct att cgc cag aag atg gaa ggt taatcagata 449
Pro Arg Gln Ala Ala Ile Arg Gln Lys Met Glu Gly
105 110

tgaattccac tat 462

<210> 2616
<211> 113
<212> PRT
<213> Corynebacterium glutamicum

<400> 2616
Val Asn Ala Glu Gln Ile Thr Gln Gly Arg Arg Gln Pro Thr Ala Gln
1 5 10 15

Glu Phe Arg Asp Met Gln Ala Ser Pro Glu Phe Gly Glu Leu Arg Ser
20 25 30

```
Lys Phe Arg Ser Phe Ala Phe Pro Met Thr Val Ala Phe Phe Leu Trp
         35                  40                  45

Tyr Val Val Tyr Val Leu Val Ala Ser Phe Ala Ser Glu Trp Met Ala
     50                  55                  60

Thr Pro Val Phe Gly Ala Ile Asn Ile Gly Leu Ile Phe Gly Phe Leu
 65                  70                  75                  80

Gln Phe Val Thr Thr Phe Val Ile Thr Tyr Ile Tyr Val Met Phe Ala
                 85                  90                  95

Asn Lys Asn Leu Glu Pro Arg Gln Ala Ala Ile Arg Gln Lys Met Glu
            100                 105                 110

Gly
```

<210> 2617
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1033)
<223> RXA02177

<400> 2617

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aatacccccа ctttgaaaaa caccccgtac agttacacca gtacggggtg ttttttagtt 60

aagcttgggt gatcacttaa cccagctaga aggagtcaac atg cgg gaa ata ttc   115
                                            Met Arg Glu Ile Phe
                                              1               5

ctg atc agc ggt gat tcc acc gaa tca tcc ttg gtt ttc aag acc tcc   163
Leu Ile Ser Gly Asp Ser Thr Glu Ser Ser Leu Val Phe Lys Thr Ser
                 10                  15                  20

gaa gag gac ggc gct gag gaa ttt ttc att gct gta aca gat gaa ctc   211
Glu Glu Asp Gly Ala Glu Glu Phe Phe Ile Ala Val Thr Asp Glu Leu
             25                  30                  35

cac gcc att ctt gca ggt cat agc gag att aag agc gcc cca gaa ccc   259
His Ala Ile Leu Ala Gly His Ser Glu Ile Lys Ser Ala Pro Glu Pro
         40                  45                  50

gaa gaa cac aaa gag gtc cca cct cct gtt cta gag ccg gtc gct gcg   307
Glu Glu His Lys Glu Val Pro Pro Pro Val Leu Glu Pro Val Ala Ala
     55                  60                  65

gta gaa gag ccc cgt gag gaa aaa gaa att gac cct cgt atc agc gct   355
Val Glu Glu Pro Arg Glu Glu Lys Glu Ile Asp Pro Arg Ile Ser Ala
 70                  75                  80                  85

ccc ctg acg atg tca ccc cgc gaa att cag att cgg gtt cgc tca ggc   403
Pro Leu Thr Met Ser Pro Arg Glu Ile Gln Ile Arg Val Arg Ser Gly
                 90                  95                 100

gcc acc atc gaa gaa tta gcc gaa gaa atc ggc gtc acc gaa gcc cgc   451
```

```
Ala Thr Ile Glu Glu Leu Ala Glu Glu Ile Gly Val Thr Glu Ala Arg
            105                 110                 115

gtt gag ccc tat gcc cac ccc gtt ttg ctg gaa cgt gcc cgc att gcc   499
Val Glu Pro Tyr Ala His Pro Val Leu Leu Glu Arg Ala Arg Ile Ala
        120                 125                 130

gac ttg gct aag caa tca cac ccc atc agg gaa aat ggt cct gca aaa   547
Asp Leu Ala Lys Gln Ser His Pro Ile Arg Glu Asn Gly Pro Ala Lys
    135                 140                 145

ctg act ctc tgg gaa att ctt gca acg gcg ttt gcc act cgc ggc cac   595
Leu Thr Leu Trp Glu Ile Leu Ala Thr Ala Phe Ala Thr Arg Gly His
150                 155                 160                 165

gat ctc acc aca gca cgc tgg gac gcc tac aaa gac gcc acc aac cag   643
Asp Leu Thr Thr Ala Arg Trp Asp Ala Tyr Lys Asp Ala Thr Asn Gln
                170                 175                 180

tgg atc gtg cga gtt gat tgg aaa gca gga ctc agc gac aac tac gcg   691
Trp Ile Val Arg Val Asp Trp Lys Ala Gly Leu Ser Asp Asn Tyr Ala
            185                 190                 195

gag tgg acg tta aac ctg cac aac acc agc aat ccc acc gct gat ccg   739
Glu Trp Thr Leu Asn Leu His Asn Thr Ser Asn Pro Thr Ala Asp Pro
        200                 205                 210

cgg acc cca gtc gca gcc gat ttg atc gat cct gaa ttc att cag ccg   787
Arg Thr Pro Val Ala Ala Asp Leu Ile Asp Pro Glu Phe Ile Gln Pro
    215                 220                 225

gta cgt acc ttg acg tcc gta aac tcc acc cag gaa cag tac gac gac   835
Val Arg Thr Leu Thr Ser Val Asn Ser Thr Gln Glu Gln Tyr Asp Asp
230                 235                 240                 245

gaa acc gat gtt ttc gac acc gta cca agc cct gac gac gca cca gac   883
Glu Thr Asp Val Phe Asp Thr Val Pro Ser Pro Asp Asp Ala Pro Asp
                250                 255                 260

tca gaa tcc gat gcc gtt gct gaa atc acc aac gac aac gaa cct gaa   931
Ser Glu Ser Asp Ala Val Ala Glu Ile Thr Asn Asp Asn Glu Pro Glu
            265                 270                 275

gtc gat gcg gaa ggc cca cgc aac agg cgt cga aaa gca gta acc cca   979
Val Asp Ala Glu Gly Pro Arg Asn Arg Arg Arg Lys Ala Val Thr Pro
        280                 285                 290

cac tgg gaa gat gtt ctt tta gga gtt cgc gca aac aca aag cgc ccg   1027
His Trp Glu Asp Val Leu Leu Gly Val Arg Ala Asn Thr Lys Arg Pro
    295                 300                 305

aag aaa taggatgtgc tgatgccaag tca                                1056
Lys Lys
310
```

<210> 2618
<211> 311
<212> PRT
<213> Corynebacterium glutamicum

<400> 2618

```
Met Arg Glu Ile Phe Leu Ile Ser Gly Asp Ser Thr Glu Ser Ser Leu
  1               5                  10                  15

Val Phe Lys Thr Ser Glu Glu Asp Gly Ala Glu Glu Phe Phe Ile Ala
             20                  25                  30

Val Thr Asp Glu Leu His Ala Ile Leu Ala Gly His Ser Glu Ile Lys
         35                  40                  45

Ser Ala Pro Glu Pro Glu Glu His Lys Glu Val Pro Pro Pro Val Leu
     50                  55                  60

Glu Pro Val Ala Ala Val Glu Glu Pro Arg Glu Glu Lys Glu Ile Asp
 65                  70                  75                  80

Pro Arg Ile Ser Ala Pro Leu Thr Met Ser Pro Arg Glu Ile Gln Ile
                 85                  90                  95

Arg Val Arg Ser Gly Ala Thr Ile Glu Glu Leu Ala Glu Glu Ile Gly
            100                 105                 110

Val Thr Glu Ala Arg Val Glu Pro Tyr Ala His Pro Val Leu Leu Glu
        115                 120                 125

Arg Ala Arg Ile Ala Asp Leu Ala Lys Gln Ser His Pro Ile Arg Glu
    130                 135                 140

Asn Gly Pro Ala Lys Leu Thr Leu Trp Glu Ile Leu Ala Thr Ala Phe
145                 150                 155                 160

Ala Thr Arg Gly His Asp Leu Thr Thr Ala Arg Trp Asp Ala Tyr Lys
                165                 170                 175

Asp Ala Thr Asn Gln Trp Ile Val Arg Val Asp Trp Lys Ala Gly Leu
            180                 185                 190

Ser Asp Asn Tyr Ala Glu Trp Thr Leu Asn Leu His Asn Thr Ser Asn
        195                 200                 205

Pro Thr Ala Asp Pro Arg Thr Pro Val Ala Ala Asp Leu Ile Asp Pro
    210                 215                 220

Glu Phe Ile Gln Pro Val Arg Thr Leu Thr Ser Val Asn Ser Thr Gln
225                 230                 235                 240

Glu Gln Tyr Asp Asp Glu Thr Asp Val Phe Asp Thr Val Pro Ser Pro
                245                 250                 255

Asp Asp Ala Pro Asp Ser Glu Ser Asp Ala Val Ala Glu Ile Thr Asn
            260                 265                 270

Asp Asn Glu Pro Glu Val Asp Ala Glu Gly Pro Arg Asn Arg Arg Arg
        275                 280                 285

Lys Ala Val Thr Pro His Trp Glu Asp Val Leu Leu Gly Val Arg Ala
    290                 295                 300

Asn Thr Lys Arg Pro Lys Lys
305                 310
```

<210> 2619
<211> 993
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(970)
<223> RXA02178

<400> 2619
cccacgcaac aggcgtcgaa aagcagtaac cccacactgg gaagatgttc ttttaggagt 60

tcgcgcaaac acaaagcgcc cgaagaaata ggatgtgctg atg cca agt caa ttg 115
Met Pro Ser Gln Leu
1 5

gga gaa aac gcg gcg atc gtc acc ctc tgg ttt gtt agc gca tcc gat 163
Gly Glu Asn Ala Ala Ile Val Thr Leu Trp Phe Val Ser Ala Ser Asp
10 15 20

ccc caa tcc atc atc cgc tcg gaa cct cgg gcg gat cgt gga tat ggc 211
Pro Gln Ser Ile Ile Arg Ser Glu Pro Arg Ala Asp Arg Gly Tyr Gly
25 30 35

cga aaa ctg ttg gca cag ctc aac cca acg tgg cca att acc ccc atc 259
Arg Lys Leu Leu Ala Gln Leu Asn Pro Thr Trp Pro Ile Thr Pro Ile
40 45 50

ggg cag ttc gcc ctc aac aga tcc gtt cct gct agt gcc aac gag ttc 307
Gly Gln Phe Ala Leu Asn Arg Ser Val Pro Ala Ser Ala Asn Glu Phe
55 60 65

tac atc gct ggt ttt ccc ggc atc acc atc att caa acc gtg ttg gaa 355
Tyr Ile Ala Gly Phe Pro Gly Ile Thr Ile Ile Gln Thr Val Leu Glu
70 75 80 85

gat gtc acc tct tta tcc aag ctg aat cct cgg tta ctg cgc agc gtc 403
Asp Val Thr Ser Leu Ser Lys Leu Asn Pro Arg Leu Leu Arg Ser Val
90 95 100

ccg gca aca gat gtc tac att ttc gcc gtc aat gaa gaa acc acc ctt 451
Pro Ala Thr Asp Val Tyr Ile Phe Ala Val Asn Glu Glu Thr Thr Leu
105 110 115

ggt ggc ttc gca cac atc tac aac ggt gag atc aaa cga tcc ttc atc 499
Gly Gly Phe Ala His Ile Tyr Asn Gly Glu Ile Lys Arg Ser Phe Ile
120 125 130

gcc tat gaa gag cgc gtc ttc gaa gac aac ggc atc ccc ggc ggc ttt 547
Ala Tyr Glu Glu Arg Val Phe Glu Asp Asn Gly Ile Pro Gly Gly Phe
135 140 145

gaa acc ccc tac tgg gca ggc aaa aaa ggc acc cgg aaa act gcg ctg 595
Glu Thr Pro Tyr Trp Ala Gly Lys Lys Gly Thr Arg Lys Thr Ala Leu
150 155 160 165

tcg ttg ccc ttc aac ccc atc gaa cta gtc cac gaa gca caa cgt gca 643
Ser Leu Pro Phe Asn Pro Ile Glu Leu Val His Glu Ala Gln Arg Ala
170 175 180

```
tgg ctc gga ttc gac gcc acc acc tcc cct gac atc aac gtc gtt gcc   691
Trp Leu Gly Phe Asp Ala Thr Thr Ser Pro Asp Ile Asn Val Val Ala
            185                 190                 195

tat gcc acc gat ggt cgc ccc gag ccg cgc atc gct gca ccc cgc ata   739
Tyr Ala Thr Asp Gly Arg Pro Glu Pro Arg Ile Ala Ala Pro Arg Ile
        200                 205                 210

att aac agc gag gaa gtg aca agg tcc gcc gtc gaa aag cta gga ctg   787
Ile Asn Ser Glu Glu Val Thr Arg Ser Ala Val Glu Lys Leu Gly Leu
    215                 220                 225

cgc gaa tcc gcc ttc tac gac gac tac gaa gaa tac gag gca ccc gat   835
Arg Glu Ser Ala Phe Tyr Asp Asp Tyr Glu Glu Tyr Glu Ala Pro Asp
230                 235                 240                 245

cga gtg gtg tcc aag cgc att acc tca aac gcg aaa aaa gcg gcc agc   883
Arg Val Val Ser Lys Arg Ile Thr Ser Asn Ala Lys Lys Ala Ala Ser
                250                 255                 260

tca gca cag aaa ttt ggt aaa tct ctg tgg cga gcc agc cgc gaa ttc   931
Ser Ala Gln Lys Phe Gly Lys Ser Leu Trp Arg Ala Ser Arg Glu Phe
            265                 270                 275

ggg tca aac atg gcg gaa aga ctc cgc cac act gac cgc tagcgctact   980
Gly Ser Asn Met Ala Glu Arg Leu Arg His Thr Asp Arg
        280                 285                 290

acttagcgct gtt                                                  993
```

<210> 2620
<211> 290
<212> PRT
<213> Corynebacterium glutamicum

<400> 2620

```
Met Pro Ser Gln Leu Gly Glu Asn Ala Ala Ile Val Thr Leu Trp Phe
  1               5                  10                  15

Val Ser Ala Ser Asp Pro Gln Ser Ile Ile Arg Ser Glu Pro Arg Ala
             20                  25                  30

Asp Arg Gly Tyr Gly Arg Lys Leu Leu Ala Gln Leu Asn Pro Thr Trp
         35                  40                  45

Pro Ile Thr Pro Ile Gly Gln Phe Ala Leu Asn Arg Ser Val Pro Ala
     50                  55                  60

Ser Ala Asn Glu Phe Tyr Ile Ala Gly Phe Pro Gly Ile Thr Ile Ile
 65                  70                  75                  80

Gln Thr Val Leu Glu Asp Val Thr Ser Leu Ser Lys Leu Asn Pro Arg
                 85                  90                  95

Leu Leu Arg Ser Val Pro Ala Thr Asp Val Tyr Ile Phe Ala Val Asn
            100                 105                 110

Glu Glu Thr Thr Leu Gly Gly Phe Ala His Ile Tyr Asn Gly Glu Ile
        115                 120                 125
```

```
Lys Arg Ser Phe Ile Ala Tyr Glu Glu Arg Val Phe Glu Asp Asn Gly
    130                 135                 140

Ile Pro Gly Gly Phe Glu Thr Pro Tyr Trp Ala Gly Lys Lys Gly Thr
145                 150                 155                 160

Arg Lys Thr Ala Leu Ser Leu Pro Phe Asn Pro Ile Glu Leu Val His
                165                 170                 175

Glu Ala Gln Arg Ala Trp Leu Gly Phe Asp Ala Thr Thr Ser Pro Asp
            180                 185                 190

Ile Asn Val Val Ala Tyr Ala Thr Asp Gly Arg Pro Glu Pro Arg Ile
        195                 200                 205

Ala Ala Pro Arg Ile Ile Asn Ser Glu Glu Val Thr Arg Ser Ala Val
    210                 215                 220

Glu Lys Leu Gly Leu Arg Glu Ser Ala Phe Tyr Asp Asp Tyr Glu Glu
225                 230                 235                 240

Tyr Glu Ala Pro Asp Arg Val Val Ser Lys Arg Ile Thr Ser Asn Ala
                245                 250                 255

Lys Lys Ala Ala Ser Ser Ala Gln Lys Phe Gly Lys Ser Leu Trp Arg
            260                 265                 270

Ala Ser Arg Glu Phe Gly Ser Asn Met Ala Glu Arg Leu Arg His Thr
        275                 280                 285

Asp Arg
    290
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US20050176120A1

<210> 2621
<211> 801
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(778)
<223> RXA02181

<400> 2621

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tttggctagt agggtgataa tctcaaataa aatgcacttt caccagcttt ttcgattccg 60

gaaggtctaa ctacacgtcg tggtgaccac aagttttctc atg gtt gac gga cac   115
                                            Met Val Asp Gly His
                                              1               5

atc cgc aat ctt cag ggc cac atc gat cgc ctc gag gcg gca gcc cct   163
Ile Arg Asn Leu Gln Gly His Ile Asp Arg Leu Glu Ala Ala Ala Pro
                 10                  15                  20

act gct tca cag ttc cat gat cgc atc atc act caa ttg cgt gaa gct   211
Thr Ala Ser Gln Phe His Asp Arg Ile Ile Thr Gln Leu Arg Glu Ala
             25                  30                  35

ccg ggc agt gtt cag gca gct gtc acg att gaa aat aac cac tat aac   259
```

```
Pro Gly Ser Val Gln Ala Ala Val Thr Ile Glu Asn Asn His Tyr Asn
         40                  45                  50

gtc gag ctg cgc ccg ccc cgc aag tta aat tca ctg gtc acc ctt gat   307
Val Glu Leu Arg Pro Pro Arg Lys Leu Asn Ser Leu Val Thr Leu Asp
     55                  60                  65

acc cac ggc cac cgc gat gag cgc cta cat cca aag att aaa ggc cac   355
Thr His Gly His Arg Asp Glu Arg Leu His Pro Lys Ile Lys Gly His
 70                  75                  80                  85

gat atc gcg tgg cag aac acg gcc acc gca aac agc cgc cgc cag ggc   403
Asp Ile Ala Trp Gln Asn Thr Ala Thr Ala Asn Ser Arg Arg Gln Gly
                 90                  95                 100

gcc gat gat gga ttg ctt gtc gac gag tcc ggc cag gtg atc atg gct   451
Ala Asp Asp Gly Leu Leu Val Asp Glu Ser Gly Gln Val Ile Met Ala
            105                 110                 115

atc aat gcc tct ctc ttg gcg att aag ggc gac acc gtg ttt cat tcc   499
Ile Asn Ala Ser Leu Leu Ala Ile Lys Gly Asp Thr Val Phe His Ser
        120                 125                 130

acg cac ccc agg tcg ctg ccg tct gtt ctg gaa tca acg gtc att gcc   547
Thr His Pro Arg Ser Leu Pro Ser Val Leu Glu Ser Thr Val Ile Ala
    135                 140                 145

tac ctg cag gaa caa ggc tgt aat gca aag cct cga gag caa ggc ttc   595
Tyr Leu Gln Glu Gln Gly Cys Asn Ala Lys Pro Arg Glu Gln Gly Phe
150                 155                 160                 165

aac atc aat gat ttg cgc tct tcg gaa gtg tgg ctg gtg gat tct ttg   643
Asn Ile Asn Asp Leu Arg Ser Ser Glu Val Trp Leu Val Asp Ser Leu
                170                 175                 180

tcc ggc atc cgt cgc gtc gct gca tgg ctc gaa tac ggt tcc aaa ttc   691
Ser Gly Ile Arg Arg Val Ala Ala Trp Leu Glu Tyr Gly Ser Lys Phe
            185                 190                 195

cca gtc tca gaa acg cga cct gtg gca gct ttc gtg ccg acg ttt tct   739
Pro Val Ser Glu Thr Arg Pro Val Ala Ala Phe Val Pro Thr Phe Ser
        200                 205                 210

gaa gtc aat gac tac cta tgg agc act gca cag caa gtg taggtcgctc    788
Glu Val Asn Asp Tyr Leu Trp Ser Thr Ala Gln Gln Val
    215                 220                 225

gactgttatt ctc                                                   801


<210> 2622
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 2622
Met Val Asp Gly His Ile Arg Asn Leu Gln Gly His Ile Asp Arg Leu
  1               5                  10                  15

Glu Ala Ala Ala Pro Thr Ala Ser Gln Phe His Asp Arg Ile Ile Thr
             20                  25                  30
```

```
Gln Leu Arg Glu Ala Pro Gly Ser Val Gln Ala Ala Val Thr Ile Glu
         35                  40                  45

Asn Asn His Tyr Asn Val Glu Leu Arg Pro Pro Arg Lys Leu Asn Ser
     50                  55                  60

Leu Val Thr Leu Asp Thr His Gly His Arg Asp Glu Arg Leu His Pro
 65                  70                  75                  80

Lys Ile Lys Gly His Asp Ile Ala Trp Gln Asn Thr Ala Thr Ala Asn
                 85                  90                  95

Ser Arg Arg Gln Gly Ala Asp Asp Gly Leu Leu Val Asp Glu Ser Gly
            100                 105                 110

Gln Val Ile Met Ala Ile Asn Ala Ser Leu Leu Ala Ile Lys Gly Asp
        115                 120                 125

Thr Val Phe His Ser Thr His Pro Arg Ser Leu Pro Ser Val Leu Glu
    130                 135                 140

Ser Thr Val Ile Ala Tyr Leu Gln Glu Gln Gly Cys Asn Ala Lys Pro
145                 150                 155                 160

Arg Glu Gln Gly Phe Asn Ile Asn Asp Leu Arg Ser Ser Glu Val Trp
                165                 170                 175

Leu Val Asp Ser Leu Ser Gly Ile Arg Arg Val Ala Ala Trp Leu Glu
            180                 185                 190

Tyr Gly Ser Lys Phe Pro Val Ser Glu Thr Arg Pro Val Ala Ala Phe
        195                 200                 205

Val Pro Thr Phe Ser Glu Val Asn Asp Tyr Leu Trp Ser Thr Ala Gln
    210                 215                 220

Gln Val
225
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09605705.1

<210> 2623
<211> 648
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(625)
<223> RXA02183

<400> 2623
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atgaggttag attcgtccct gctgactaga atcaagactc atg gca agc cgg aag 115
                                                Met Ala Ser Arg Lys
                                                  1   5

acc aag cgt aaa aac ctc att cag att ctc agc ctt atc gtt gct gtg 163
Thr Lys Arg Lys Asn Leu Ile Gln Ile Leu Ser Leu Ile Val Ala Val
                10   15   20

```
tta ttg gtg gtg att ttg tct gtg gtg ttc cag caa tgg tgg aac aat   211
Leu Leu Val Val Ile Leu Ser Val Val Phe Gln Gln Trp Trp Asn Asn
             25                  30                  35

cgc cca gag cca ctc ccc caa gag atc tct atc tca gca tct tct ccc   259
Arg Pro Glu Pro Leu Pro Gln Glu Ile Ser Ile Ser Ala Ser Ser Pro
         40                  45                  50

gct ggt gaa atc gag gta ttc cca ttc agc atg tgt gaa cca ggt gtt   307
Ala Gly Glu Ile Glu Val Phe Pro Phe Ser Met Cys Glu Pro Gly Val
     55                  60                  65

gaa tgc gaa gag aac gag gtg cca acg ctg gaa gtt ggt gct gat gaa   355
Glu Cys Glu Glu Asn Glu Val Pro Thr Leu Glu Val Gly Ala Asp Glu
 70                  75                  80                  85

gag ttg cac ctg acg att cca gag gca att cat gat cat gac tgg tac   403
Glu Leu His Leu Thr Ile Pro Glu Ala Ile His Asp His Asp Trp Tyr
                 90                  95                 100

ttg ttg acc att tat gat gat ccg gct gca aat gac gag ttc tac cac   451
Leu Leu Thr Ile Tyr Asp Asp Pro Ala Ala Asn Asp Glu Phe Tyr His
            105                 110                 115

acc agt tac gac gcc acc gag gca acc gtt cct ggt tct gtg gat cca   499
Thr Ser Tyr Asp Ala Thr Glu Ala Thr Val Pro Gly Ser Val Asp Pro
        120                 125                 130

acc gaa gag ggt gcg gag cgc cca cgt ctg gtc gta gtg gaa gtg tcc   547
Thr Glu Glu Gly Ala Glu Arg Pro Arg Leu Val Val Val Glu Val Ser
    135                 140                 145

gct gtg atg atc ggt gag gat gaa aat ggt gag gaa agc cct tac acc   595
Ala Val Met Ile Gly Glu Asp Glu Asn Gly Glu Glu Ser Pro Tyr Thr
150                 155                 160                 165

gtc acg tgg tcg cta tcc acg atg aac gag taactcactc acaaacaata     645
Val Thr Trp Ser Leu Ser Thr Met Asn Glu
                170                 175

agg                                                               648
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<210> 2624
<211> 175
<212> PRT
<213> Corynebacterium glutamicum

<400> 2624

```
Met Ala Ser Arg Lys Thr Lys Arg Lys Asn Leu Ile Gln Ile Leu Ser
  1               5                  10                  15

Leu Ile Val Ala Val Leu Leu Val Val Ile Leu Ser Val Val Phe Gln
             20                  25                  30

Gln Trp Trp Asn Asn Arg Pro Glu Pro Leu Pro Gln Glu Ile Ser Ile
         35                  40                  45

Ser Ala Ser Ser Pro Ala Gly Glu Ile Glu Val Phe Pro Phe Ser Met
     50                  55                  60
```

```
Cys Glu Pro Gly Val Glu Cys Glu Glu Asn Glu Val Pro Thr Leu Glu
 65                  70                  75                  80

Val Gly Ala Asp Glu Glu Leu His Leu Thr Ile Pro Glu Ala Ile His
                 85                  90                  95

Asp His Asp Trp Tyr Leu Leu Thr Ile Tyr Asp Asp Pro Ala Ala Asn
            100                 105                 110

Asp Glu Phe Tyr His Thr Ser Tyr Asp Ala Thr Glu Ala Thr Val Pro
        115                 120                 125

Gly Ser Val Asp Pro Thr Glu Glu Gly Ala Glu Arg Pro Arg Leu Val
    130                 135                 140

Val Val Glu Val Ser Ala Val Met Ile Gly Glu Asp Glu Asn Gly Glu
145                 150                 155                 160

Glu Ser Pro Tyr Thr Val Thr Trp Ser Leu Ser Thr Met Asn Glu
                165                 170                 175
```

<210> 2625
<211> 2322
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2299)
<223> RXA02187

<400> 2625

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ggatcgacga agtgcttctt ctctacgttt gccatgtcat acattctttc aaactctggg 60

aacaaaagtc acctcaacaa ggcttaaact taacaacatc atg aaa aaa gac tcc   115
                                            Met Lys Lys Asp Ser
                                              1               5

ccc atc ccc acc ctc aag ggg tgg ttg gat act caa agt gat gat cag   163
Pro Ile Pro Thr Leu Lys Gly Trp Leu Asp Thr Gln Ser Asp Asp Gln
                 10                  15                  20

ctc tcc aca atc ctt aga aat cga ccc gat acg gtt ctc cct tta cca   211
Leu Ser Thr Ile Leu Arg Asn Arg Pro Asp Thr Val Leu Pro Leu Pro
             25                  30                  35

cct aat ttg gcc tct ctt gct gcg cgt tta cag ctg agg gcg tct gcg   259
Pro Asn Leu Ala Ser Leu Ala Ala Arg Leu Gln Leu Arg Ala Ser Ala
         40                  45                  50

att cgc gcg gtg ttg aaa ctc aat gcg ttg gaa ctt ggt gtg ttg gag   307
Ile Arg Ala Val Leu Lys Leu Asn Ala Leu Glu Leu Gly Val Leu Glu
     55                  60                  65

gcc gtg gcc aac ctt ggt ggt gaa ctc cac ccg gtt act gcc ccc gaa   355
Ala Val Ala Asn Leu Gly Gly Glu Leu His Pro Val Thr Ala Pro Glu
 70                  75                  80                  85

gtg gtg gaa tat ttg cat gtg gcg ttg gca gag gat ctt cca gcg caa   403
```

```
Val Val Glu Tyr Leu His Val Ala Leu Ala Glu Asp Leu Pro Ala Gln
                 90                  95                 100

gac acg att ggt gcg gct ctt gcc acg ctg aaa aat ttc gcg ttg gtt   451
Asp Thr Ile Gly Ala Ala Leu Ala Thr Leu Lys Asn Phe Ala Leu Val
            105                 110                 115

tat ggc gat gac cag ttg atg att gct cag gag acg atg gct gcg ttg   499
Tyr Gly Asp Asp Gln Leu Met Ile Ala Gln Glu Thr Met Ala Ala Leu
        120                 125                 130

cct gtt cat tgg cgg ttg ctt ccg gag gta agt gat cgc ggg cag agt   547
Pro Val His Trp Arg Leu Leu Pro Glu Val Ser Asp Arg Gly Gln Ser
    135                 140                 145

gag gaa cag gtg agg gaa agc gtc gat aag ctt tct gat agg cac cgc   595
Glu Glu Gln Val Arg Glu Ser Val Asp Lys Leu Ser Asp Arg His Arg
150                 155                 160                 165

aaa ctt ttg cac acg ctt gcg gcc tcg ggt ggc ttc ggt ctg acg cgc   643
Lys Leu Leu His Thr Leu Ala Ala Ser Gly Gly Phe Gly Leu Thr Arg
                170                 175                 180

gat gcg gcg cct gat gcg gat ccg tcg cgg ccg att ccg cag ttg ctg   691
Asp Ala Ala Pro Asp Ala Asp Pro Ser Arg Pro Ile Pro Gln Leu Leu
            185                 190                 195

gcg tcg ggg ttg ttg gcg cgc gtg gat gag cag acc gtg cgc ctg ccg   739
Ala Ser Gly Leu Leu Ala Arg Val Asp Glu Gln Thr Val Arg Leu Pro
        200                 205                 210

gcg atg gtg cgg cgt gtg att gag ggc cgc gag cag ctg ccc gct cag   787
Ala Met Val Arg Arg Val Ile Glu Gly Arg Glu Gln Leu Pro Ala Gln
    215                 220                 225

gtg cgc cca att ccg cgc acg gcg gcg cca ggt tcg aat gat ggc ggc   835
Val Arg Pro Ile Pro Arg Thr Ala Ala Pro Gly Ser Asn Asp Gly Gly
230                 235                 240                 245

att gca gcc ggc ctt gag gtg gtg cgg cac atg cga ttg ctt atc gac   883
Ile Ala Ala Gly Leu Glu Val Val Arg His Met Arg Leu Leu Ile Asp
                250                 255                 260

gcc ctc agc cac gtt ccc gcc ccc acg ctg aaa gtc gga gcc ctc ggt   931
Ala Leu Ser His Val Pro Ala Pro Thr Leu Lys Val Gly Ala Leu Gly
            265                 270                 275

gtg cgc gtg gtg act cgc ctg agc aag gaa tta gac ctt gat gag acc   979
Val Arg Val Val Thr Arg Leu Ser Lys Glu Leu Asp Leu Asp Glu Thr
        280                 285                 290

gag ctg gca cgt cta ctg agt ttg ggt atg gcc agc ggt cta atc cgt   1027
Glu Leu Ala Arg Leu Leu Ser Leu Gly Met Ala Ser Gly Leu Ile Arg
    295                 300                 305

aaa ggc gtg ccc gat cca ttg ccc atg gat gat gat ggc ggc gat tac   1075
Lys Gly Val Pro Asp Pro Leu Pro Met Asp Asp Asp Gly Gly Asp Tyr
310                 315                 320                 325

gtc gct ccc acc ccg ctg gct gac gaa tgg atg gaa tat gat ctg gcg   1123
Val Ala Pro Thr Pro Leu Ala Asp Glu Trp Met Glu Tyr Asp Leu Ala
```

```
                  330                 335                 340

cac caa ttg ggc acg ttg atg tct ggt tgg tgg aag caa act tac gcg   1171
His Gln Leu Gly Thr Leu Met Ser Gly Trp Trp Lys Gln Thr Tyr Ala
            345                 350                 355

ccg tgg ttg gtg ggt cgg gct gat gat aag gac aag ccg atc cat gtt   1219
Pro Trp Leu Val Gly Arg Ala Asp Asp Lys Asp Lys Pro Ile His Val
        360                 365                 370

ctc agt aaa aca agc atc att gat tcg ctt cct gat gct cgt gcg aag   1267
Leu Ser Lys Thr Ser Ile Ile Asp Ser Leu Pro Asp Ala Arg Ala Lys
    375                 380                 385

atc ctg tcc tct tta tct agg gtt tta gtg gac aat ctg cac gcg gat   1315
Ile Leu Ser Ser Leu Ser Arg Val Leu Val Asp Asn Leu His Ala Asp
390                 395                 400                 405

tta gca ttc cat tat ccc ctt gcg gcg agt cgg atg aat cct gac acc   1363
Leu Ala Phe His Tyr Pro Leu Ala Ala Ser Arg Met Asn Pro Asp Thr
                410                 415                 420

atc aca cag ctg gta cag gaa gcc cag tgg atc gga gca tat tct caa   1411
Ile Thr Gln Leu Val Gln Glu Ala Gln Trp Ile Gly Ala Tyr Ser Gln
            425                 430                 435

ggc gtg acc gca gcg ggt cag gcc tta att gat ggc gaa aac cct acg   1459
Gly Val Thr Ala Ala Gly Gln Ala Leu Ile Asp Gly Glu Asn Pro Thr
        440                 445                 450

gag gta atc aag gct cct gcg ccg gtg gag aat ttc atc gtg caa ggc   1507
Glu Val Ile Lys Ala Pro Ala Pro Val Glu Asn Phe Ile Val Gln Gly
    455                 460                 465

gat ttc acc atc atg gtt cca gga cca cta acc cct gcg atg caa aaa   1555
Asp Phe Thr Ile Met Val Pro Gly Pro Leu Thr Pro Ala Met Gln Lys
470                 475                 480                 485

acc atg gat tcg atc gca tcg ttg gaa tca cct ggt ttg gcc tcg gtg   1603
Thr Met Asp Ser Ile Ala Ser Leu Glu Ser Pro Gly Leu Ala Ser Val
                490                 495                 500

tat cga ctc agc gag aaa tcc atc agg cat gct ctg gat ctt ggg ctc   1651
Tyr Arg Leu Ser Glu Lys Ser Ile Arg His Ala Leu Asp Leu Gly Leu
            505                 510                 515

acc acc ccg gaa atc ttg gag ttt ctc aaa gaa cat tcc atg aca gat   1699
Thr Thr Pro Glu Ile Leu Glu Phe Leu Lys Glu His Ser Met Thr Asp
        520                 525                 530

ctg ccc caa tct gtg ggc tat ttg ctc agc gat atc gcc aga aag cac   1747
Leu Pro Gln Ser Val Gly Tyr Leu Leu Ser Asp Ile Ala Arg Lys His
    535                 540                 545

ggc acc ctc cga ggc ggc cct gca ctg tcc tat atc cgt agc gac gat   1795
Gly Thr Leu Arg Gly Gly Pro Ala Leu Ser Tyr Ile Arg Ser Asp Asp
550                 555                 560                 565

ccc gct ttg ctg cat tcc gca gtg gag gcg ggc gcc gat gtg gcg ctt   1843
Pro Ala Leu Leu His Ser Ala Val Glu Ala Gly Ala Asp Val Ala Leu
                570                 575                 580
```

```
cgg cag atc gct ccc acc gtt gcg att gct caa gca ccc ctg ctt cag   1891
Arg Gln Ile Ala Pro Thr Val Ala Ile Ala Gln Ala Pro Leu Leu Gln
            585                 590                 595

gtg atc act gtg ctg cgt gct gcc ggg ttc caa cct gtg gca gaa gac   1939
Val Ile Thr Val Leu Arg Ala Ala Gly Phe Gln Pro Val Ala Glu Asp
        600                 605                 610

ggc gaa ggc gca agt ctg aat atc tcg cca tcc cct gca cgt gtg ccc   1987
Gly Glu Gly Ala Ser Leu Asn Ile Ser Pro Ser Pro Ala Arg Val Pro
    615                 620                 625

gca gct tcc cca cca cca gtt gtt ccg gca ctg gat gaa agc cgg gta   2035
Ala Ala Ser Pro Pro Pro Val Val Pro Ala Leu Asp Glu Ser Arg Val
630                 635                 640                 645

cag gca gca gtc aaa gca atc cga cgg gaa aat tca gca tct caa gga   2083
Gln Ala Ala Val Lys Ala Ile Arg Arg Glu Asn Ser Ala Ser Gln Gly
                650                 655                 660

act gtt tcc aca cag cca act ctt tcg gtg ctg cag gct gca gtg cga   2131
Thr Val Ser Thr Gln Pro Thr Leu Ser Val Leu Gln Ala Ala Val Arg
            665                 670                 675

ggg cag cgc acg gtg acg ttg ggg ttc gtc gat aag caa ggc gtg gcc   2179
Gly Gln Arg Thr Val Thr Leu Gly Phe Val Asp Lys Gln Gly Val Ala
        680                 685                 690

gtg cac cgc gtc gtc aag cct tta acc gtc aac gcc ggg cag gtg gac   2227
Val His Arg Val Val Lys Pro Leu Thr Val Asn Ala Gly Gln Val Asp
    695                 700                 705

gct gtg gat gaa gcc aca ggt gcg gtg cat cgt ttc atg ttg cac agg   2275
Ala Val Asp Glu Ala Thr Gly Ala Val His Arg Phe Met Leu His Arg
710                 715                 720                 725

atc aca gaa gta ata gtg gat aac tagcctagaa gtgacataat gga         2322
Ile Thr Glu Val Ile Val Asp Asn
                730
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<210> 2626
<211> 733
<212> PRT
<213> Corynebacterium glutamicum

<400> 2626

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Met Lys Lys Asp Ser Pro Ile Pro Thr Leu Lys Gly Trp Leu Asp Thr
  1               5                  10                  15

Gln Ser Asp Asp Gln Leu Ser Thr Ile Leu Arg Asn Arg Pro Asp Thr
             20                  25                  30

Val Leu Pro Leu Pro Pro Asn Leu Ala Ser Leu Ala Ala Arg Leu Gln
         35                  40                  45

Leu Arg Ala Ser Ala Ile Arg Ala Val Leu Lys Leu Asn Ala Leu Glu
     50                  55                  60

Leu Gly Val Leu Glu Ala Val Ala Asn Leu Gly Gly Glu Leu His Pro
```

```
 65                  70                  75                  80

Val Thr Ala Pro Glu Val Val Glu Tyr Leu His Val Ala Leu Ala Glu
                 85                  90                  95

Asp Leu Pro Ala Gln Asp Thr Ile Gly Ala Ala Leu Ala Thr Leu Lys
            100                 105                 110

Asn Phe Ala Leu Val Tyr Gly Asp Asp Gln Leu Met Ile Ala Gln Glu
        115                 120                 125

Thr Met Ala Ala Leu Pro Val His Trp Arg Leu Leu Pro Glu Val Ser
    130                 135                 140

Asp Arg Gly Gln Ser Glu Glu Gln Val Arg Glu Ser Val Asp Lys Leu
145                 150                 155                 160

Ser Asp Arg His Arg Lys Leu Leu His Thr Leu Ala Ala Ser Gly Gly
                165                 170                 175

Phe Gly Leu Thr Arg Asp Ala Ala Pro Asp Ala Asp Pro Ser Arg Pro
            180                 185                 190

Ile Pro Gln Leu Leu Ala Ser Gly Leu Leu Ala Arg Val Asp Glu Gln
        195                 200                 205

Thr Val Arg Leu Pro Ala Met Val Arg Arg Val Ile Glu Gly Arg Glu
    210                 215                 220

Gln Leu Pro Ala Gln Val Arg Pro Ile Pro Arg Thr Ala Ala Pro Gly
225                 230                 235                 240

Ser Asn Asp Gly Gly Ile Ala Ala Gly Leu Glu Val Val Arg His Met
                245                 250                 255

Arg Leu Leu Ile Asp Ala Leu Ser His Val Pro Ala Pro Thr Leu Lys
            260                 265                 270

Val Gly Ala Leu Gly Val Arg Val Val Thr Arg Leu Ser Lys Glu Leu
        275                 280                 285

Asp Leu Asp Glu Thr Glu Leu Ala Arg Leu Leu Ser Leu Gly Met Ala
    290                 295                 300

Ser Gly Leu Ile Arg Lys Gly Val Pro Asp Pro Leu Pro Met Asp Asp
305                 310                 315                 320

Asp Gly Gly Asp Tyr Val Ala Pro Thr Pro Leu Ala Asp Glu Trp Met
                325                 330                 335

Glu Tyr Asp Leu Ala His Gln Leu Gly Thr Leu Met Ser Gly Trp Trp
            340                 345                 350

Lys Gln Thr Tyr Ala Pro Trp Leu Val Gly Arg Ala Asp Asp Lys Asp
        355                 360                 365

Lys Pro Ile His Val Leu Ser Lys Thr Ser Ile Ile Asp Ser Leu Pro
    370                 375                 380

Asp Ala Arg Ala Lys Ile Leu Ser Ser Leu Ser Arg Val Leu Val Asp
385                 390                 395                 400
```

```
Asn Leu His Ala Asp Leu Ala Phe His Tyr Pro Leu Ala Ala Ser Arg
                405                 410                 415

Met Asn Pro Asp Thr Ile Thr Gln Leu Val Gln Glu Ala Gln Trp Ile
            420                 425                 430

Gly Ala Tyr Ser Gln Gly Val Thr Ala Ala Gly Gln Ala Leu Ile Asp
        435                 440                 445

Gly Glu Asn Pro Thr Glu Val Ile Lys Ala Pro Ala Pro Val Glu Asn
    450                 455                 460

Phe Ile Val Gln Gly Asp Phe Thr Ile Met Val Pro Gly Pro Leu Thr
465                 470                 475                 480

Pro Ala Met Gln Lys Thr Met Asp Ser Ile Ala Ser Leu Glu Ser Pro
                485                 490                 495

Gly Leu Ala Ser Val Tyr Arg Leu Ser Glu Lys Ser Ile Arg His Ala
            500                 505                 510

Leu Asp Leu Gly Leu Thr Thr Pro Glu Ile Leu Glu Phe Leu Lys Glu
        515                 520                 525

His Ser Met Thr Asp Leu Pro Gln Ser Val Gly Tyr Leu Leu Ser Asp
    530                 535                 540

Ile Ala Arg Lys His Gly Thr Leu Arg Gly Gly Pro Ala Leu Ser Tyr
545                 550                 555                 560

Ile Arg Ser Asp Asp Pro Ala Leu Leu His Ser Ala Val Glu Ala Gly
                565                 570                 575

Ala Asp Val Ala Leu Arg Gln Ile Ala Pro Thr Val Ala Ile Ala Gln
            580                 585                 590

Ala Pro Leu Leu Gln Val Ile Thr Val Leu Arg Ala Ala Gly Phe Gln
        595                 600                 605

Pro Val Ala Glu Asp Gly Glu Gly Ala Ser Leu Asn Ile Ser Pro Ser
    610                 615                 620

Pro Ala Arg Val Pro Ala Ala Ser Pro Pro Pro Val Val Pro Ala Leu
625                 630                 635                 640

Asp Glu Ser Arg Val Gln Ala Ala Val Lys Ala Ile Arg Arg Glu Asn
                645                 650                 655

Ser Ala Ser Gln Gly Thr Val Ser Thr Gln Pro Thr Leu Ser Val Leu
            660                 665                 670

Gln Ala Ala Val Arg Gly Gln Arg Thr Val Thr Leu Gly Phe Val Asp
        675                 680                 685

Lys Gln Gly Val Ala Val His Arg Val Val Lys Pro Leu Thr Val Asn
    690                 695                 700

Ala Gly Gln Val Asp Ala Val Asp Glu Ala Thr Gly Ala Val His Arg
705                 710                 715                 720
```

```
Phe Met Leu His Arg Ile Thr Glu Val Ile Val Asp Asn
                725                 730


<210> 2627
<211> 693
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(670)
<223> RXA02199

<400> 2627
acagcttagt acggattaga caattcccga acttttcatt cgtagttcat tttcaacgcc 60

gcctaagcaa cacaggcaaa gcgccactag tctcggtcgc atg act gac tcc act   115
                                            Met Thr Asp Ser Thr
                                              1               5

ccg caa ggc tca aca cca ggc atg tcc cct gaa gct atc ctc aac ggc   163
Pro Gln Gly Ser Thr Pro Gly Met Ser Pro Glu Ala Ile Leu Asn Gly
                 10                  15                  20

acc gga aag ccg tgg gaa gag tgg cta aaa ttg ctt gac gac gta aaa   211
Thr Gly Lys Pro Trp Glu Glu Trp Leu Lys Leu Leu Asp Asp Val Lys
             25                  30                  35

gcc acc tct tgg act cac acc cac atc gca aag cac atc gtg gac aac   259
Ala Thr Ser Trp Thr His Thr His Ile Ala Lys His Ile Val Asp Asn
         40                  45                  50

ttt gat gtc agt ggc tgg tgg gct caa ggc atc gcg att ggt tat gaa   307
Phe Asp Val Ser Gly Trp Trp Ala Gln Gly Ile Ala Ile Gly Tyr Glu
     55                  60                  65

tac gaa cgt ggc atg cgc aaa ccc ggg atg acc agc gat ggg ttc gcg   355
Tyr Glu Arg Gly Met Arg Lys Pro Gly Met Thr Ser Asp Gly Phe Ala
 70                  75                  80                  85

gcc aat gcc tcc aaa acc ctt aac ctg ccg gtc gaa aaa gtg tgg aag   403
Ala Asn Ala Ser Lys Thr Leu Asn Leu Pro Val Glu Lys Val Trp Lys
                 90                  95                 100

ctc ttc gga gac gat gac ctg cgg gcg cag tgg ctc gat ccc gca cta   451
Leu Phe Gly Asp Asp Asp Leu Arg Ala Gln Trp Leu Asp Pro Ala Leu
            105                 110                 115

att gag aaa acc tcc gcc tcc gaa cct aga aca ttc aat gcc aaa tgg   499
Ile Glu Lys Thr Ser Ala Ser Glu Pro Arg Thr Phe Asn Ala Lys Trp
        120                 125                 130

ttg gcc gat gat tct cga gtg agc gtc aac ttc acc tcc aaa ggc gac   547
Leu Ala Asp Asp Ser Arg Val Ser Val Asn Phe Thr Ser Lys Gly Asp
    135                 140                 145

aat aaa tcc agc ttc ggc atc cag cac aga cgc ctg cct gat caa gac   595
Asn Lys Ser Ser Phe Gly Ile Gln His Arg Arg Leu Pro Asp Gln Asp
150                 155                 160                 165
```

```
agc atc cct gtc atg aaa gca ttc tgg aaa gaa cgc atc gct gca tta   643
Ser Ile Pro Val Met Lys Ala Phe Trp Lys Glu Arg Ile Ala Ala Leu
                170                 175                 180

gtt gag gtg tca aaa caa ttt tcg ctt taacattaag ttcttagcct        690
Val Glu Val Ser Lys Gln Phe Ser Leu
            185                 190

tca                                                              693
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<210> 2628
<211> 190
<212> PRT
<213> Corynebacterium glutamicum

<400> 2628

```
Met Thr Asp Ser Thr Pro Gln Gly Ser Thr Pro Gly Met Ser Pro Glu
  1               5                  10                  15

Ala Ile Leu Asn Gly Thr Gly Lys Pro Trp Glu Glu Trp Leu Lys Leu
             20                  25                  30

Leu Asp Asp Val Lys Ala Thr Ser Trp Thr His Thr His Ile Ala Lys
         35                  40                  45

His Ile Val Asp Asn Phe Asp Val Ser Gly Trp Trp Ala Gln Gly Ile
     50                  55                  60

Ala Ile Gly Tyr Glu Tyr Glu Arg Gly Met Arg Lys Pro Gly Met Thr
 65                  70                  75                  80

Ser Asp Gly Phe Ala Ala Asn Ala Ser Lys Thr Leu Asn Leu Pro Val
                 85                  90                  95

Glu Lys Val Trp Lys Leu Phe Gly Asp Asp Asp Leu Arg Ala Gln Trp
            100                 105                 110

Leu Asp Pro Ala Leu Ile Glu Lys Thr Ser Ala Ser Glu Pro Arg Thr
        115                 120                 125

Phe Asn Ala Lys Trp Leu Ala Asp Asp Ser Arg Val Ser Val Asn Phe
    130                 135                 140

Thr Ser Lys Gly Asp Asn Lys Ser Ser Phe Gly Ile Gln His Arg Arg
145                 150                 155                 160

Leu Pro Asp Gln Asp Ser Ile Pro Val Met Lys Ala Phe Trp Lys Glu
                165                 170                 175

Arg Ile Ala Ala Leu Val Glu Val Ser Lys Gln Phe Ser Leu
            180                 185                 190
```

<210> 2629
<211> 501
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(478)
<223> RXA02203

<400> 2629
cgattcaaaa gagttcaccg aggtaggaaa catcgtggtc gcagccattg atgccctcct 60

gggcgtgcag ctctaggaaa tttcaggaac aatacatctc atg acc att cgc gcc 115
Met Thr Ile Arg Ala
1 5

act ttc cag cct tcc gta gat gaa ttc atc tcc act ctc gaa gag ttt 163
Thr Phe Gln Pro Ser Val Asp Glu Phe Ile Ser Thr Leu Glu Glu Phe
10 15 20

gca aca ggt tca tac ctt aaa gag gac gaa aag gaa ttc tgg gac gaa 211
Ala Thr Gly Ser Tyr Leu Lys Glu Asp Glu Lys Glu Phe Trp Asp Glu
25 30 35

cct ttc gat gtc aag gca ctt cca gat ctt cgt ttc atc ttg gaa aac 259
Pro Phe Asp Val Lys Ala Leu Pro Asp Leu Arg Phe Ile Leu Glu Asn
40 45 50

tac ctt gat tcc cta gat aag ctc ggt gaa gca cca gac ctt gat gct 307
Tyr Leu Asp Ser Leu Asp Lys Leu Gly Glu Ala Pro Asp Leu Asp Ala
55 60 65

gtt aac gcc tcc gct cag tcc acc ctt gat gag ctg gag aag ttc aac 355
Val Asn Ala Ser Ala Gln Ser Thr Leu Asp Glu Leu Glu Lys Phe Asn
70 75 80 85

aca aag cac cac ggt gct gtt gtt gag cct gaa gaa aaa gaa gag atc 403
Thr Lys His His Gly Ala Val Val Glu Pro Glu Glu Lys Glu Glu Ile
90 95 100

act aaa ttg atg ttt gat gct gca aag cag act ggt gca gat gat ctt 451
Thr Lys Leu Met Phe Asp Ala Ala Lys Gln Thr Gly Ala Asp Asp Leu
105 110 115

tct gca gag gct ttc cct gag ttt gag taaatttcag tagaagtttt 498
Ser Ala Glu Ala Phe Pro Glu Phe Glu
120 125

tta 501

<210> 2630
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 2630
Met Thr Ile Arg Ala Thr Phe Gln Pro Ser Val Asp Glu Phe Ile Ser
1 5 10 15

Thr Leu Glu Glu Phe Ala Thr Gly Ser Tyr Leu Lys Glu Asp Glu Lys
20 25 30

Glu Phe Trp Asp Glu Pro Phe Asp Val Lys Ala Leu Pro Asp Leu Arg
35 40 45

Phe Ile Leu Glu Asn Tyr Leu Asp Ser Leu Asp Lys Leu Gly Glu Ala

```
     50                  55                  60

Pro Asp Leu Asp Ala Val Asn Ala Ser Ala Gln Ser Thr Leu Asp Glu
 65                  70                  75                  80

Leu Glu Lys Phe Asn Thr Lys His His Gly Ala Val Val Glu Pro Glu
                 85                  90                  95

Glu Lys Glu Glu Ile Thr Lys Leu Met Phe Asp Ala Ala Lys Gln Thr
            100                 105                 110

Gly Ala Asp Asp Leu Ser Ala Glu Ala Phe Pro Glu Phe Glu
        115                 120                 125


<210> 2631
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1036)
<223> RXA02206

<400> 2631
ggcaggatct gctgctgcgg ctaggagggt tatctcttca ttcacccgat ctaccgtact 60

accttatgac ctcagtagtg tggtgggcgt gaaacagcga atg gtc ggt tca agt   115
                                        Met Val Gly Ser Ser
                                          1               5

ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg   163
Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser
                 10                  15                  20

ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat   211
Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn
             25                  30                  35

tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc   259
Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val
         40                  45                  50

gcg gaa gaa atg ctc ggc acg atg ttg gat gcg gaa gtc tct cgt tcg   307
Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser
     55                  60                  65

gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc   355
Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu
 70                  75                  80                  85

ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat   403
Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp
                 90                  95                 100

gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg   451
Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val
            105                 110                 115

ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg   499
```

```
Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu
        120                 125                 130

gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga   547
Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly
    135                 140                 145

tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca   595
Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala
150                 155                 160                 165

gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg   643
Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu
                170                 175                 180

ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta   691
Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu
            185                 190                 195

ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act   739
Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr
        200                 205                 210

gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca   787
Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr
    215                 220                 225

gga cgc gac gca gaa gtc caa agc tac cta gat aat cga ggc cgc atc   835
Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp Asn Arg Gly Arg Ile
230                 235                 240                 245

att gtc gat gct ctt gat act gca gcc aaa gga tta ggc att agc ccc   883
Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly Leu Gly Ile Ser Pro
                250                 255                 260

gct gtc aca gcc acc acc tgg gtg cgt gat cgt ccc gga gtg aca gct   931
Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg Pro Gly Val Thr Ala
            265                 270                 275

gtc atc gtg ggc gct cgc aca cat gaa cag ctg tca cat ctt ctc aag   979
Val Ile Val Gly Ala Arg Thr His Glu Gln Leu Ser His Leu Leu Lys
        280                 285                 290

gcg gaa tcg gtg act ttg cca aca cca atc aca caa gcc ctt gat gat  1027
Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp
    295                 300                 305

gtc tcc ctg tgacttggtc caattacatt cac                           1059
Val Ser Leu
310


<210> 2632
<211> 312
<212> PRT
<213> Corynebacterium glutamicum

<400> 2632
Met Val Gly Ser Ser Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr
  1               5                  10                  15
```

```
Ser Thr Trp Gly Ser Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe
            20                  25                  30

Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn
        35                  40                  45

Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala
    50                  55                  60

Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn
65                  70                  75                  80

Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu
                85                  90                  95

Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu
            100                 105                 110

Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu
        115                 120                 125

Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr
    130                 135                 140

Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala
145                 150                 155                 160

Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln
                165                 170                 175

Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro
            180                 185                 190

Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly
        195                 200                 205

Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser
    210                 215                 220

Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp
225                 230                 235                 240

Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly
                245                 250                 255

Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg
            260                 265                 270

Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu
        275                 280                 285

Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr
    290                 295                 300

Gln Ala Leu Asp Asp Val Ser Leu
305                 310
```

<210> 2633
<211> 553
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(553)
<223> RXA02211

<400> 2633
actgtccgaa gtattggatc tggtcgaggg aactgtccgt aaacgcgact aaacgacccc 60

tgattcacac tttcagacta caagaactag actaagcggt atg gtt tca gtt ctt 115
Met Val Ser Val Leu
1 5

tta att cag ccc cgt cag gga gaa gca gtc gcc gca gct gag cga cgt 163
Leu Ile Gln Pro Arg Gln Gly Glu Ala Val Ala Ala Ala Glu Arg Arg
10 15 20

gac ttt ttg cag gcc acc ggt ctt aag cct caa gaa ctg acc tcc cga 211
Asp Phe Leu Gln Ala Thr Gly Leu Lys Pro Gln Glu Leu Thr Ser Arg
25 30 35

atg ttg gat acc acc act tct cga att ggc agt ctg gaa ggt ttc gac 259
Met Leu Asp Thr Thr Thr Ser Arg Ile Gly Ser Leu Glu Gly Phe Asp
40 45 50

ggc gtg att gtg ggc gga agc cca ctg aat gcc acc aac ttt gag tac 307
Gly Val Ile Val Gly Gly Ser Pro Leu Asn Ala Thr Asn Phe Glu Tyr
55 60 65

agc gat tgg caa cgc cac gtc cac cgc gaa ttg tcc ttg ctg atc aat 355
Ser Asp Trp Gln Arg His Val His Arg Glu Leu Ser Leu Leu Ile Asn
70 75 80 85

cac cca ctg cca aca atc ttt gtc tgc tac ggc aat acc ttt ttg acc 403
His Pro Leu Pro Thr Ile Phe Val Cys Tyr Gly Asn Thr Phe Leu Thr
90 95 100

ttc ttc tct ggc gga cag att ggt cgc aca cac ccc gaa gat tcc ggc 451
Phe Phe Ser Gly Gly Gln Ile Gly Arg Thr His Pro Glu Asp Ser Gly
105 110 115

gcc acc aca gtg ttg cta act gac gcc ggc aaa cga gac gta ctc act 499
Ala Thr Thr Val Leu Leu Thr Asp Ala Gly Lys Arg Asp Val Leu Thr
120 125 130

caa gac cta ccg gat agc ttt acg tcc ttt act ggt cac acg gaa aac 547
Gln Asp Leu Pro Asp Ser Phe Thr Ser Phe Thr Gly His Thr Glu Asn
135 140 145

tcc gta 553
Ser Val
150

<210> 2634
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 2634

```
Met Val Ser Val Leu Leu Ile Gln Pro Arg Gln Gly Glu Ala Val Ala
  1               5                  10                  15

Ala Ala Glu Arg Arg Asp Phe Leu Gln Ala Thr Gly Leu Lys Pro Gln
             20                  25                  30

Glu Leu Thr Ser Arg Met Leu Asp Thr Thr Thr Ser Arg Ile Gly Ser
         35                  40                  45

Leu Glu Gly Phe Asp Gly Val Ile Val Gly Gly Ser Pro Leu Asn Ala
     50                  55                  60

Thr Asn Phe Glu Tyr Ser Asp Trp Gln Arg His Val His Arg Glu Leu
 65                  70                  75                  80

Ser Leu Leu Ile Asn His Pro Leu Pro Thr Ile Phe Val Cys Tyr Gly
                 85                  90                  95

Asn Thr Phe Leu Thr Phe Phe Ser Gly Gly Gln Ile Gly Arg Thr His
            100                 105                 110

Pro Glu Asp Ser Gly Ala Thr Thr Val Leu Leu Thr Asp Ala Gly Lys
        115                 120                 125

Arg Asp Val Leu Thr Gln Asp Leu Pro Asp Ser Phe Thr Ser Phe Thr
    130                 135                 140

Gly His Thr Glu Asn Ser Val
145                 150


<210> 2635
<211> 621
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(598)
<223> RXA02212

<400> 2635
gtgatgtgac tttctatcac ccccttactc acccccattg cttattgagt aaagtcggtt 60

cccgctcttt cgtgagcccg acactaatga aggtttttag atg att cca gaa aat   115
                                            Met Ile Pro Glu Asn
                                              1               5

att gat ctc aag cag ctc gct tcg gag ctt ggt gat gat gcc gtg gca   163
Ile Asp Leu Lys Gln Leu Ala Ser Glu Leu Gly Asp Asp Ala Val Ala
                 10                  15                  20

atg ggg gag cac aca ggc aac cag ttt ccg act ttg gaa aaa gac ctt   211
Met Gly Glu His Thr Gly Asn Gln Phe Pro Thr Leu Glu Lys Asp Leu
             25                  30                  35

att aat gtt gtg aca gat gca aag gaa tca gat ttt gga tct tta ggg   259
Ile Asn Val Val Thr Asp Ala Lys Glu Ser Asp Phe Gly Ser Leu Gly
         40                  45                  50

gtc gtg att ctt gat gaa act cca gtg atg act tcc aac ctg agg gat   307
```

```
Val Val Ile Leu Asp Glu Thr Pro Val Met Thr Ser Asn Leu Arg Asp
     55                  60                  65

att gcg cag gag ctg ttg att caa acg gat ctg gac acc gtt gtg gtg   355
Ile Ala Gln Glu Leu Leu Ile Gln Thr Asp Leu Asp Thr Val Val Val
 70                  75                  80                  85

cgg gct cca atg tcg gct gcg gtg gtg agt gat gtt cat tcg agg gcg   403
Arg Ala Pro Met Ser Ala Ala Val Val Ser Asp Val His Ser Arg Ala
                 90                  95                 100

gcg ctt gag tca ggg cag cat gat ttg ctt ggg acc act gat tac gtg   451
Ala Leu Glu Ser Gly Gln His Asp Leu Leu Gly Thr Thr Asp Tyr Val
            105                 110                 115

ctg gga acg gag ctt ttg gta cag gat gta acg gaa tcg acg gtg ggg   499
Leu Gly Thr Glu Leu Leu Val Gln Asp Val Thr Glu Ser Thr Val Gly
        120                 125                 130

aat att gat tgg ggt caa ttg ctg att tgg ggg ttg gtt gct ttg gca   547
Asn Ile Asp Trp Gly Gln Leu Leu Ile Trp Gly Leu Val Ala Leu Ala
    135                 140                 145

atc gcc gtg gtt gtt gcg ggt gcg tct gtg cgt cga aaa gca ata tct   595
Ile Ala Val Val Val Ala Gly Ala Ser Val Arg Arg Lys Ala Ile Ser
150                 155                 160                 165

tta taagtaaagt tctaaagctt tac                                    621
Leu
```

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<210> 2636
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

<400> 2636

```
Met Ile Pro Glu Asn Ile Asp Leu Lys Gln Leu Ala Ser Glu Leu Gly
  1               5                  10                  15

Asp Asp Ala Val Ala Met Gly Glu His Thr Gly Asn Gln Phe Pro Thr
             20                  25                  30

Leu Glu Lys Asp Leu Ile Asn Val Val Thr Asp Ala Lys Glu Ser Asp
         35                  40                  45

Phe Gly Ser Leu Gly Val Val Ile Leu Asp Glu Thr Pro Val Met Thr
     50                  55                  60

Ser Asn Leu Arg Asp Ile Ala Gln Glu Leu Leu Ile Gln Thr Asp Leu
 65                  70                  75                  80

Asp Thr Val Val Val Arg Ala Pro Met Ser Ala Ala Val Val Ser Asp
                 85                  90                  95

Val His Ser Arg Ala Ala Leu Glu Ser Gly Gln His Asp Leu Leu Gly
            100                 105                 110

Thr Thr Asp Tyr Val Leu Gly Thr Glu Leu Leu Val Gln Asp Val Thr
        115                 120                 125
```

```
Glu Ser Thr Val Gly Asn Ile Asp Trp Gly Gln Leu Leu Ile Trp Gly
    130                 135                 140

Leu Val Ala Leu Ala Ile Ala Val Val Val Ala Gly Ala Ser Val Arg
145                 150                 155                 160

Arg Lys Ala Ile Ser Leu
                165
```

<210> 2637
<211> 329
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(306)
<223> RXA02216

<400> 2637

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gta gcg ccc gcc cct gga cac gtg gtg ttg gca acg gga cca acc tgc   48
Val Ala Pro Ala Pro Gly His Val Val Leu Ala Thr Gly Pro Thr Cys
  1               5                  10                  15

ccc atc cag atg ctg cgc gcc aac aag aac acc tgg tca gtt caa ttc   96
Pro Ile Gln Met Leu Arg Ala Asn Lys Asn Thr Trp Ser Val Gln Phe
             20                  25                  30

cat gcg gat atg gat gcc gta ggc atg aaa aac cgc atg gat ttt tac  144
His Ala Asp Met Asp Ala Val Gly Met Lys Asn Arg Met Asp Phe Tyr
         35                  40                  45

tcc aac tac cgg ttc ttc tcc cca gaa gat tat gac cgc atc att gca  192
Ser Asn Tyr Arg Phe Phe Ser Pro Glu Asp Tyr Asp Arg Ile Ile Ala
     50                  55                  60

gag cta ccc tct gtt gac tcc att tat gcc aac agg gtg ctc cgc aac  240
Glu Leu Pro Ser Val Asp Ser Ile Tyr Ala Asn Arg Val Leu Arg Asn
 65                  70                  75                  80

ttc gtg gag gtc tgc gaa gga att cgt gtt gct gat ggt gct gag cac  288
Phe Val Glu Val Cys Glu Gly Ile Arg Val Ala Asp Gly Ala Glu His
                 85                  90                  95

caa ctc cca aag ctt aac taatcgagga gactggtgat tcg                329
Gln Leu Pro Lys Leu Asn
            100
```

<210> 2638
<211> 102
<212> PRT
<213> Corynebacterium glutamicum

<400> 2638

```
Val Ala Pro Ala Pro Gly His Val Val Leu Ala Thr Gly Pro Thr Cys
  1               5                  10                  15

Pro Ile Gln Met Leu Arg Ala Asn Lys Asn Thr Trp Ser Val Gln Phe
```

```
            20                  25                  30

His Ala Asp Met Asp Ala Val Gly Met Lys Asn Arg Met Asp Phe Tyr
         35                  40                  45

Ser Asn Tyr Arg Phe Phe Ser Pro Glu Asp Tyr Asp Arg Ile Ile Ala
     50                  55                  60

Glu Leu Pro Ser Val Asp Ser Ile Tyr Ala Asn Arg Val Leu Arg Asn
 65                  70                  75                  80

Phe Val Glu Val Cys Glu Gly Ile Arg Val Ala Asp Gly Ala Glu His
                 85                  90                  95

Gln Leu Pro Lys Leu Asn
            100


<210> 2639
<211> 786
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(763)
<223> RXA02217

<400> 2639
ccaaatgggt atgggcgctt ttgaccatcg tcaatggtgt tggccccgct gcctactggg 60

ctttcggcag gaaaaactaa gagttgttag ggtggcgctc atg act aat aaa aca   115
                                            Met Thr Asn Lys Thr
                                              1               5

cga gct cta ctc att ggt ggc cac ggc aag gtg gcc ctc cta gca acc   163
Arg Ala Leu Leu Ile Gly Gly His Gly Lys Val Ala Leu Leu Ala Thr
                 10                  15                  20

ccc atg ctt atc gac gcc tcg gtg cag gtc act tcc atg tac cgc aat   211
Pro Met Leu Ile Asp Ala Ser Val Gln Val Thr Ser Met Tyr Arg Asn
             25                  30                  35

ccg gac cac agg tcc gaa att gag gcg ctg ggc gcc aca act tta gag   259
Pro Asp His Arg Ser Glu Ile Glu Ala Leu Gly Ala Thr Thr Leu Glu
         40                  45                  50

cgt gac gtc acc aca ctc agc gtg gag gat tgg gca gat ctg ctc aag   307
Arg Asp Val Thr Thr Leu Ser Val Glu Asp Trp Ala Asp Leu Leu Lys
     55                  60                  65

gac ttc gac gta gtg gtg tgg agc gcc gga aac ggt ggc aag aac ggc   355
Asp Phe Asp Val Val Val Trp Ser Ala Gly Asn Gly Gly Lys Asn Gly
 70                  75                  80                  85

gcg gat gca act tat gcc att gat cgt gat gcc gcg atc gca tcc att   403
Ala Asp Ala Thr Tyr Ala Ile Asp Arg Asp Ala Ala Ile Ala Ser Ile
                 90                  95                 100

gat ggt gca gct agc cta ggg gag aag gca cct cgc tac atc atg gtg   451
Asp Gly Ala Ala Ser Leu Gly Glu Lys Ala Pro Arg Tyr Ile Met Val
```

```
            105                 110                 115

agc tac att gga tcc tcc acg cac acc att gat cct tca gca tcc ttc   499
Ser Tyr Ile Gly Ser Ser Thr His Thr Ile Asp Pro Ser Ala Ser Phe
        120                 125                 130

tac cca tat gca gaa tcc aaa aag gcc gct gat gag cac cta agc tcc   547
Tyr Pro Tyr Ala Glu Ser Lys Lys Ala Ala Asp Glu His Leu Ser Ser
    135                 140                 145

acc aac ctg gat tac ctt atc ctc gca cca gca gcc tta act ctg gat   595
Thr Asn Leu Asp Tyr Leu Ile Leu Ala Pro Ala Ala Leu Thr Leu Asp
150                 155                 160                 165

gaa gtc aat ggc gtt gag gtg atc gcc gat acc aac gaa gca gcc gca   643
Glu Val Asn Gly Val Glu Val Ile Ala Asp Thr Asn Glu Ala Ala Ala
                170                 175                 180

ggc cgc acc aca tca aga gtc ctc gtt gcg gaa gtt atc acc gag ttg   691
Gly Arg Thr Thr Ser Arg Val Leu Val Ala Glu Val Ile Thr Glu Leu
            185                 190                 195

gtg gtt cgc gac ttc cca caa acc cgt gtg ctg cct ttc gtg gat ggc   739
Val Val Arg Asp Phe Pro Gln Thr Arg Val Leu Pro Phe Val Asp Gly
        200                 205                 210

gaa tca cca gtc tcc tcg att agt taagctttgg gagttggtgc tca         786
Glu Ser Pro Val Ser Ser Ile Ser
    215                 220
```

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<210> 2640
<211> 221
<212> PRT
<213> Corynebacterium glutamicum

<400> 2640

```
Met Thr Asn Lys Thr Arg Ala Leu Leu Ile Gly Gly His Gly Lys Val
  1               5                  10                  15

Ala Leu Leu Ala Thr Pro Met Leu Ile Asp Ala Ser Val Gln Val Thr
             20                  25                  30

Ser Met Tyr Arg Asn Pro Asp His Arg Ser Glu Ile Glu Ala Leu Gly
         35                  40                  45

Ala Thr Thr Leu Glu Arg Asp Val Thr Thr Leu Ser Val Glu Asp Trp
     50                  55                  60

Ala Asp Leu Leu Lys Asp Phe Asp Val Val Val Trp Ser Ala Gly Asn
 65                  70                  75                  80

Gly Gly Lys Asn Gly Ala Asp Ala Thr Tyr Ala Ile Asp Arg Asp Ala
                 85                  90                  95

Ala Ile Ala Ser Ile Asp Gly Ala Ala Ser Leu Gly Glu Lys Ala Pro
            100                 105                 110

Arg Tyr Ile Met Val Ser Tyr Ile Gly Ser Ser Thr His Thr Ile Asp
        115                 120                 125
```

```
Pro Ser Ala Ser Phe Tyr Pro Tyr Ala Glu Ser Lys Lys Ala Ala Asp
    130                 135                 140

Glu His Leu Ser Ser Thr Asn Leu Asp Tyr Leu Ile Leu Ala Pro Ala
145                 150                 155                 160

Ala Leu Thr Leu Asp Glu Val Asn Gly Val Glu Val Ile Ala Asp Thr
                165                 170                 175

Asn Glu Ala Ala Ala Gly Arg Thr Thr Ser Arg Val Leu Val Ala Glu
            180                 185                 190

Val Ile Thr Glu Leu Val Val Arg Asp Phe Pro Gln Thr Arg Val Leu
        195                 200                 205

Pro Phe Val Asp Gly Glu Ser Pro Val Ser Ser Ile Ser
    210                 215                 220


<210> 2641
<211> 390
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(367)
<223> RXA02218

<400> 2641
caatgattta tatgtcttgg acgagcgatt aaatagagtt ggcatacccc aaatgataga 60

cccaaagtgt cgtgtccacc gctcgttgta gcatgaaccc atg ttt gca atc atg   115
                                            Met Phe Ala Ile Met
                                              1               5

act gtc aca ggg cag gac cac acc gga att atc gcc gca gtt tcc acc   163
Thr Val Thr Gly Gln Asp His Thr Gly Ile Ile Ala Ala Val Ser Thr
                  10                  15                  20

gcg ttg gct gag cta gat gtc aat att cac aac gtt tcc caa acc atc   211
Ala Leu Ala Glu Leu Asp Val Asn Ile His Asn Val Ser Gln Thr Ile
             25                  30                  35

atg gat caa tgg ttc acc atg atc ttg cac gtt ggt ttc gat gaa tcg   259
Met Asp Gln Trp Phe Thr Met Ile Leu His Val Gly Phe Asp Glu Ser
         40                  45                  50

gtc ttg gat atc gcc aca gtt cag gaa cgc atg aag cca gtg gaa aag   307
Val Leu Asp Ile Ala Thr Val Gln Glu Arg Met Lys Pro Val Glu Lys
     55                  60                  65

gaa cag ggc ttg gtt att cgt atc cag tct gaa gcc ttg ttc aac gcg   355
Glu Gln Gly Leu Val Ile Arg Ile Gln Ser Glu Ala Leu Phe Asn Ala
 70                  75                  80                  85

gtt aat gag atc taggggtgc acatggatga ttt                         390
Val Asn Glu Ile
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<210> 2642
<211> 89
<212> PRT
<213> Corynebacterium glutamicum

<400> 2642
Met Phe Ala Ile Met Thr Val Thr Gly Gln Asp His Thr Gly Ile Ile
1 5 10 15

Ala Ala Val Ser Thr Ala Leu Ala Glu Leu Asp Val Asn Ile His Asn
20 25 30

Val Ser Gln Thr Ile Met Asp Gln Trp Phe Thr Met Ile Leu His Val
35 40 45

Gly Phe Asp Glu Ser Val Leu Asp Ile Ala Thr Val Gln Glu Arg Met
50 55 60

Lys Pro Val Glu Lys Glu Gln Gly Leu Val Ile Arg Ile Gln Ser Glu
65 70 75 80

Ala Leu Phe Asn Ala Val Asn Glu Ile
85

<210> 2643
<211> 1509
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1486)
<223> RXA02219

<400> 2643
tcaggaacgc atgaagccag tggaaaagga acagggcttg gttattcgta tccagtctga 60

agccttgttc aacgcggtta atgagatcta gggggtgcac atg gat gat ttt tct 115
Met Asp Asp Phe Ser
1 5

gca tcg cta ggt ttt act gac cgt tcc tcg agg gga att ctg gac acc 163
Ala Ser Leu Gly Phe Thr Asp Arg Ser Ser Arg Gly Ile Leu Asp Thr
10 15 20

atc gag atg att gag aag tat cgt ctt gat att cgc acc gtg acc atg 211
Ile Glu Met Ile Glu Lys Tyr Arg Leu Asp Ile Arg Thr Val Thr Met
25 30 35

gga atc agc ctg ttg gaa tgc gcg cgt ggc tcg atg gaa gag acc gcg 259
Gly Ile Ser Leu Leu Glu Cys Ala Arg Gly Ser Met Glu Glu Thr Ala
40 45 50

acg gct gtt tat gat cgc gtg acg tca cag gct gca cgt ctg gtt gag 307
Thr Ala Val Tyr Asp Arg Val Thr Ser Gln Ala Ala Arg Leu Val Glu
55 60 65

gtt tgt gaa ggc att gag cgt gaa ttg ggc att ccc att gtg aat aag 355
Val Cys Glu Gly Ile Glu Arg Glu Leu Gly Ile Pro Ile Val Asn Lys
70 75 80 85

```
cgc atc tcg gtg act cca att gcc ctg gtg act gct ggt tgc agt ggc   403
Arg Ile Ser Val Thr Pro Ile Ala Leu Val Thr Ala Gly Cys Ser Gly
                 90                  95                 100

gat ccc gtt gac gtt gct cga gcc tta gat aag gca gca aaa gat gtc   451
Asp Pro Val Asp Val Ala Arg Ala Leu Asp Lys Ala Ala Lys Asp Val
            105                 110                 115

gga gtg aac ttc atc ggc ggg tat tca gca ctg gtt gaa aaa ggt gga   499
Gly Val Asn Phe Ile Gly Gly Tyr Ser Ala Leu Val Glu Lys Gly Gly
        120                 125                 130

acc acc tcc gat att cgg ctg atc cgc tcc att ccc gag gca ttg agc   547
Thr Thr Ser Asp Ile Arg Leu Ile Arg Ser Ile Pro Glu Ala Leu Ser
    135                 140                 145

aca acc gat gtg gtg tgt gga tcc gtc aat gtg gcg tcg tct cgc gcg   595
Thr Thr Asp Val Val Cys Gly Ser Val Asn Val Ala Ser Ser Arg Ala
150                 155                 160                 165

ggt atc aac atg aac gca gtc aat gag atg ggc aag gtg gtc aag caa   643
Gly Ile Asn Met Asn Ala Val Asn Glu Met Gly Lys Val Val Lys Gln
                170                 175                 180

gca gct gaa ttg acc aaa gat cgc tcc gcc atc gca tgt gca aag cta   691
Ala Ala Glu Leu Thr Lys Asp Arg Ser Ala Ile Ala Cys Ala Lys Leu
            185                 190                 195

gtg gtc ttt gcc aat tct gtg ggc gat aat cca ttc atg gct ggc gct   739
Val Val Phe Ala Asn Ser Val Gly Asp Asn Pro Phe Met Ala Gly Ala
        200                 205                 210

ttc cac ggc att gag gag ccg gat tgt gtg gtc agc gtt ggt gtc tca   787
Phe His Gly Ile Glu Glu Pro Asp Cys Val Val Ser Val Gly Val Ser
    215                 220                 225

gga cca ggc gtg gtt agt cgc gcg ctg ggc aat ctt caa ggt gcc acc   835
Gly Pro Gly Val Val Ser Arg Ala Leu Gly Asn Leu Gln Gly Ala Thr
230                 235                 240                 245

ctt gat caa gtc gca gaa gag atc aag aaa gcg gcc ttc aag atc act   883
Leu Asp Gln Val Ala Glu Glu Ile Lys Lys Ala Ala Phe Lys Ile Thr
                250                 255                 260

cgt act gga caa ctg gtt ggt gcg atg gcc tca gaa cgc cta gga gtt   931
Arg Thr Gly Gln Leu Val Gly Ala Met Ala Ser Glu Arg Leu Gly Val
            265                 270                 275

cct ttc ggc atc gtt gat ctt tcg ctc gct ccc act gct gaa gtg ggc   979
Pro Phe Gly Ile Val Asp Leu Ser Leu Ala Pro Thr Ala Glu Val Gly
        280                 285                 290

gat tcc gtg gca aat atc ctt gag gtc atg ggt ctt gac cag gtg ggc  1027
Asp Ser Val Ala Asn Ile Leu Glu Val Met Gly Leu Asp Gln Val Gly
    295                 300                 305

aca cat ggc acc acc gcg gca ctc gca ctg ctc aac gac gcg gtg aaa  1075
Thr His Gly Thr Thr Ala Ala Leu Ala Leu Leu Asn Asp Ala Val Lys
310                 315                 320                 325
```

```
aag ggt ggc atg atg gcc tgc tca cgt gtc ggc ggc ttg tcc gga tcc   1123
Lys Gly Gly Met Met Ala Cys Ser Arg Val Gly Gly Leu Ser Gly Ser
                330                 335                 340

ttc att cca gtt tct gaa gat aaa ggc atg atc gat gcg gtt cgc aca   1171
Phe Ile Pro Val Ser Glu Asp Lys Gly Met Ile Asp Ala Val Arg Thr
            345                 350                 355

gga gca att tct att gac aag ctc gaa gcg atg acc gcg atc tgc tca   1219
Gly Ala Ile Ser Ile Asp Lys Leu Glu Ala Met Thr Ala Ile Cys Ser
        360                 365                 370

gtt ggt ttg gat atg att gcg atc cct ggc gac acc ccg gcg gaa act   1267
Val Gly Leu Asp Met Ile Ala Ile Pro Gly Asp Thr Pro Ala Glu Thr
    375                 380                 385

att tcg ggc atg atc gcg gac gaa gca gcc atc ggt gtg atg aat cat   1315
Ile Ser Gly Met Ile Ala Asp Glu Ala Ala Ile Gly Val Met Asn His
390                 395                 400                 405

aag act aca gct gtg cgt gtt att cct gtt cca gga act gtc cct ggc   1363
Lys Thr Thr Ala Val Arg Val Ile Pro Val Pro Gly Thr Val Pro Gly
                410                 415                 420

gat gag gta gat ttc ggt ggc ttg ctg ggt tac gcg ccg gtc att cca   1411
Asp Glu Val Asp Phe Gly Gly Leu Leu Gly Tyr Ala Pro Val Ile Pro
            425                 430                 435

gta aat acc gtg gga aat agt gag ttt att cac cgc ggc ggc ttc att   1459
Val Asn Thr Val Gly Asn Ser Glu Phe Ile His Arg Gly Gly Phe Ile
        440                 445                 450

cca gca ccc gtt cac ggg ttt aga aac taggagatcc ggggccttta         1506
Pro Ala Pro Val His Gly Phe Arg Asn
    455                 460

cct                                                               1509
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<210> 2644
<211> 462
<212> PRT
<213> Corynebacterium glutamicum

<400> 2644
Met Asp Asp Phe Ser Ala Ser Leu Gly Phe Thr Asp Arg Ser Ser Arg
  1               5                  10                  15

Gly Ile Leu Asp Thr Ile Glu Met Ile Glu Lys Tyr Arg Leu Asp Ile
             20                  25                  30

Arg Thr Val Thr Met Gly Ile Ser Leu Leu Glu Cys Ala Arg Gly Ser
         35                  40                  45

Met Glu Glu Thr Ala Thr Ala Val Tyr Asp Arg Val Thr Ser Gln Ala
     50                  55                  60

Ala Arg Leu Val Glu Val Cys Glu Gly Ile Glu Arg Glu Leu Gly Ile
 65                  70                  75                  80

Pro Ile Val Asn Lys Arg Ile Ser Val Thr Pro Ile Ala Leu Val Thr
```

```
                  85                  90                  95

Ala Gly Cys Ser Gly Asp Pro Val Asp Val Ala Arg Ala Leu Asp Lys
            100                 105                 110

Ala Ala Lys Asp Val Gly Val Asn Phe Ile Gly Gly Tyr Ser Ala Leu
        115                 120                 125

Val Glu Lys Gly Gly Thr Thr Ser Asp Ile Arg Leu Ile Arg Ser Ile
    130                 135                 140

Pro Glu Ala Leu Ser Thr Thr Asp Val Val Cys Gly Ser Val Asn Val
145                 150                 155                 160

Ala Ser Ser Arg Ala Gly Ile Asn Met Asn Ala Val Asn Glu Met Gly
                165                 170                 175

Lys Val Val Lys Gln Ala Ala Glu Leu Thr Lys Asp Arg Ser Ala Ile
            180                 185                 190

Ala Cys Ala Lys Leu Val Val Phe Ala Asn Ser Val Gly Asp Asn Pro
        195                 200                 205

Phe Met Ala Gly Ala Phe His Gly Ile Glu Glu Pro Asp Cys Val Val
    210                 215                 220

Ser Val Gly Val Ser Gly Pro Gly Val Val Ser Arg Ala Leu Gly Asn
225                 230                 235                 240

Leu Gln Gly Ala Thr Leu Asp Gln Val Ala Glu Glu Ile Lys Lys Ala
                245                 250                 255

Ala Phe Lys Ile Thr Arg Thr Gly Gln Leu Val Gly Ala Met Ala Ser
            260                 265                 270

Glu Arg Leu Gly Val Pro Phe Gly Ile Val Asp Leu Ser Leu Ala Pro
        275                 280                 285

Thr Ala Glu Val Gly Asp Ser Val Ala Asn Ile Leu Glu Val Met Gly
    290                 295                 300

Leu Asp Gln Val Gly Thr His Gly Thr Thr Ala Ala Leu Ala Leu Leu
305                 310                 315                 320

Asn Asp Ala Val Lys Lys Gly Gly Met Met Ala Cys Ser Arg Val Gly
                325                 330                 335

Gly Leu Ser Gly Ser Phe Ile Pro Val Ser Glu Asp Lys Gly Met Ile
            340                 345                 350

Asp Ala Val Arg Thr Gly Ala Ile Ser Ile Asp Lys Leu Glu Ala Met
        355                 360                 365

Thr Ala Ile Cys Ser Val Gly Leu Asp Met Ile Ala Ile Pro Gly Asp
    370                 375                 380

Thr Pro Ala Glu Thr Ile Ser Gly Met Ile Ala Asp Glu Ala Ala Ile
385                 390                 395                 400

Gly Val Met Asn His Lys Thr Thr Ala Val Arg Val Ile Pro Val Pro
                405                 410                 415
```

```
Gly Thr Val Pro Gly Asp Glu Val Asp Phe Gly Gly Leu Leu Gly Tyr
            420                 425                 430

Ala Pro Val Ile Pro Val Asn Thr Val Gly Asn Ser Glu Phe Ile His
        435                 440                 445

Arg Gly Gly Phe Ile Pro Ala Pro Val His Gly Phe Arg Asn
    450                 455                 460


<210> 2645
<211> 1485
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1462)
<223> RXA02221

<400> 2645
ttcaatgata tttgctctga tttttggttc tcgtctaatt tcattatttt gtcacgccag 60

ccatcacgac ttcataccca ccaattgaaa gtaaagtcca atg ttt acc gca tcc   115
                                          Met Phe Thr Ala Ser
                                            1               5

att cct act tat gaa tta ggg tct ttc agc aag ggc tcc tac gtt gag   163
Ile Pro Thr Tyr Glu Leu Gly Ser Phe Ser Lys Gly Ser Tyr Val Glu
                10                  15                  20

atc aaa gga act tac ttc tac cct gac acg cta aat act tta ttt aga   211
Ile Lys Gly Thr Tyr Phe Tyr Pro Asp Thr Leu Asn Thr Leu Phe Arg
            25                  30                  35

aat tct ggg gca aaa gac aac gaa gag ttc ttt gta gac gta act ctt   259
Asn Ser Gly Ala Lys Asp Asn Glu Glu Phe Phe Val Asp Val Thr Leu
        40                  45                  50

gtt cca gaa cca gat aat ccg cat agc act cga ggc cat gcc att tca   307
Val Pro Glu Pro Asp Asn Pro His Ser Thr Arg Gly His Ala Ile Ser
    55                  60                  65

gtc cgc tgg aat gat ctc gta ata gga cat att gcc tcg gat atg act   355
Val Arg Trp Asn Asp Leu Val Ile Gly His Ile Ala Ser Asp Met Thr
70                  75                  80                  85

gaa aaa ttc caa caa gtg cga cga gtt gca gct agt ggc tac gat gct   403
Glu Lys Phe Gln Gln Val Arg Arg Val Ala Ala Ser Gly Tyr Asp Ala
                90                  95                  100

cga gtc tct gct cgg att tgg acg aat aca aac tat aag aat gaa cga   451
Arg Val Ser Ala Arg Ile Trp Thr Asn Thr Asn Tyr Lys Asn Glu Arg
            105                 110                 115

gat ttt tgg gta tct gtt aag ctc ccc gat cca gat ttc ctt gtt cct   499
Asp Phe Trp Val Ser Val Lys Leu Pro Asp Pro Asp Phe Leu Val Pro
        120                 125                 130

ctt aat gat cct ccc cat gac ggg ttt acc ctc ctc cct tat gga aca   547
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```
Leu Asn Asp Pro Pro His Asp Gly Phe Thr Leu Leu Pro Tyr Gly Thr
    135                 140                 145

gca atc caa gtc acc aag gaa tct gat cac atg gac gtg ctc tca gaa   595
Ala Ile Gln Val Thr Lys Glu Ser Asp His Met Asp Val Leu Ser Glu
150                 155                 160                 165

ttc gtg cct cca tct gga caa ggt cag att ctc gta tcg cta cac atc   643
Phe Val Pro Pro Ser Gly Gln Gly Gln Ile Leu Val Ser Leu His Ile
                170                 175                 180

att aac gca ggc gtg aga aaa gaa tgg gat ggc att gaa gtt cgg ctc   691
Ile Asn Ala Gly Val Arg Lys Glu Trp Asp Gly Ile Glu Val Arg Leu
            185                 190                 195

gat aat caa cgg atc gga gag ctt aca aag gcc agt tca gaa aaa ttc   739
Asp Asn Gln Arg Ile Gly Glu Leu Thr Lys Ala Ser Ser Glu Lys Phe
        200                 205                 210

gca ccc gta gtg cga cat ttc gat gac cta gga ctt agt aca cta tgt   787
Ala Pro Val Val Arg His Phe Asp Asp Leu Gly Leu Ser Thr Leu Cys
    215                 220                 225

cgt gcg ctc atc aag ggg tca tca cta gct gct gaa gta act cta tat   835
Arg Ala Leu Ile Lys Gly Ser Ser Leu Ala Ala Glu Val Thr Leu Tyr
230                 235                 240                 245

gga gct cgt gca cat gag ctt tcc gaa gaa gac tta gaa cct aaa agc   883
Gly Ala Arg Ala His Glu Leu Ser Glu Glu Asp Leu Glu Pro Lys Ser
                250                 255                 260

tct tcc cca ttg ccc agg ttg gtt gaa tac cag tca aat ccg ttt aat   931
Ser Ser Pro Leu Pro Arg Leu Val Glu Tyr Gln Ser Asn Pro Phe Asn
            265                 270                 275

tat caa gtc ccc aac agg tgg ccc ggc gag cag aat caa cgt gct cct   979
Tyr Gln Val Pro Asn Arg Trp Pro Gly Glu Gln Asn Gln Arg Ala Pro
        280                 285                 290

aag tcg caa aag tct tct tca tca cct ttc gca gcg tat cgc ggg cca   1027
Lys Ser Gln Lys Ser Ser Ser Ser Pro Phe Ala Ala Tyr Arg Gly Pro
    295                 300                 305

tcg caa cct agt aaa tca ctc aca ccg ttt gta gcg cag aca cct gcg   1075
Ser Gln Pro Ser Lys Ser Leu Thr Pro Phe Val Ala Gln Thr Pro Ala
310                 315                 320                 325

cct cag cct agt gat cga ttt att gat tgg gat tca ttg ctt caa ccg   1123
Pro Gln Pro Ser Asp Arg Phe Ile Asp Trp Asp Ser Leu Leu Gln Pro
                330                 335                 340

gac gga act cca aga gct acg cca ttc caa aga gga gta acc cgc ggg   1171
Asp Gly Thr Pro Arg Ala Thr Pro Phe Gln Arg Gly Val Thr Arg Gly
            345                 350                 355

tta att ggc aag cat ttt tcg aat caa aaa tct cca aga att gac ttt   1219
Leu Ile Gly Lys His Phe Ser Asn Gln Lys Ser Pro Arg Ile Asp Phe
        360                 365                 370

gca acg gtg ggg caa tgt gat gca att ctc cga act ttc gga gag ccg   1267
Ala Thr Val Gly Gln Cys Asp Ala Ile Leu Arg Thr Phe Gly Glu Pro
```

```
    375                 380                 385

acc gac aag ctt tat aaa gac ggc agg act tct tgg cct ttg tgg tgg   1315
Thr Asp Lys Leu Tyr Lys Asp Gly Arg Thr Ser Trp Pro Leu Trp Trp
390                 395                 400                 405

gcg ctc atg gcg ata gtc acc ctt ctc gtc atg ttg ctg aac ttt att   1363
Ala Leu Met Ala Ile Val Thr Leu Leu Val Met Leu Leu Asn Phe Ile
                410                 415                 420

cca gga att ggt ccg atc ttc cca ctt atc gga ttg atc gta ctt ggt   1411
Pro Gly Ile Gly Pro Ile Phe Pro Leu Ile Gly Leu Ile Val Leu Gly
            425                 430                 435

cat cac ttt tgg act cgc cga aaa ctt aac cca cca ttc ggt aga tca   1459
His His Phe Trp Thr Arg Arg Lys Leu Asn Pro Pro Phe Gly Arg Ser
        440                 445                 450

aaa tagatattct catcaaatat cgc                                    1485
Lys
```

US-09-850-950-3

<210> 2646
<211> 454
<212> PRT
<213> Corynebacterium glutamicum

<400> 2646

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Met Phe Thr Ala Ser Ile Pro Thr Tyr Glu Leu Gly Ser Phe Ser Lys
  1               5                  10                  15

Gly Ser Tyr Val Glu Ile Lys Gly Thr Tyr Phe Tyr Pro Asp Thr Leu
             20                  25                  30

Asn Thr Leu Phe Arg Asn Ser Gly Ala Lys Asp Asn Glu Glu Phe Phe
         35                  40                  45

Val Asp Val Thr Leu Val Pro Glu Pro Asp Asn Pro His Ser Thr Arg
     50                  55                  60

Gly His Ala Ile Ser Val Arg Trp Asn Asp Leu Val Ile Gly His Ile
 65                  70                  75                  80

Ala Ser Asp Met Thr Glu Lys Phe Gln Gln Val Arg Arg Val Ala Ala
                 85                  90                  95

Ser Gly Tyr Asp Ala Arg Val Ser Ala Arg Ile Trp Thr Asn Thr Asn
            100                 105                 110

Tyr Lys Asn Glu Arg Asp Phe Trp Val Ser Val Lys Leu Pro Asp Pro
        115                 120                 125

Asp Phe Leu Val Pro Leu Asn Asp Pro Pro His Asp Gly Phe Thr Leu
    130                 135                 140

Leu Pro Tyr Gly Thr Ala Ile Gln Val Thr Lys Glu Ser Asp His Met
145                 150                 155                 160

Asp Val Leu Ser Glu Phe Val Pro Pro Ser Gly Gln Gly Gln Ile Leu
                165                 170                 175
```

```
Val Ser Leu His Ile Ile Asn Ala Gly Val Arg Lys Glu Trp Asp Gly
            180                 185                 190

Ile Glu Val Arg Leu Asp Asn Gln Arg Ile Gly Glu Leu Thr Lys Ala
        195                 200                 205

Ser Ser Glu Lys Phe Ala Pro Val Val Arg His Phe Asp Asp Leu Gly
    210                 215                 220

Leu Ser Thr Leu Cys Arg Ala Leu Ile Lys Gly Ser Ser Leu Ala Ala
225                 230                 235                 240

Glu Val Thr Leu Tyr Gly Ala Arg Ala His Glu Leu Ser Glu Glu Asp
                245                 250                 255

Leu Glu Pro Lys Ser Ser Ser Pro Leu Pro Arg Leu Val Glu Tyr Gln
            260                 265                 270

Ser Asn Pro Phe Asn Tyr Gln Val Pro Asn Arg Trp Pro Gly Glu Gln
        275                 280                 285

Asn Gln Arg Ala Pro Lys Ser Gln Lys Ser Ser Ser Ser Pro Phe Ala
    290                 295                 300

Ala Tyr Arg Gly Pro Ser Gln Pro Ser Lys Ser Leu Thr Pro Phe Val
305                 310                 315                 320

Ala Gln Thr Pro Ala Pro Gln Pro Ser Asp Arg Phe Ile Asp Trp Asp
                325                 330                 335

Ser Leu Leu Gln Pro Asp Gly Thr Pro Arg Ala Thr Pro Phe Gln Arg
            340                 345                 350

Gly Val Thr Arg Gly Leu Ile Gly Lys His Phe Ser Asn Gln Lys Ser
        355                 360                 365

Pro Arg Ile Asp Phe Ala Thr Val Gly Gln Cys Asp Ala Ile Leu Arg
    370                 375                 380

Thr Phe Gly Glu Pro Thr Asp Lys Leu Tyr Lys Asp Gly Arg Thr Ser
385                 390                 395                 400

Trp Pro Leu Trp Trp Ala Leu Met Ala Ile Val Thr Leu Leu Val Met
                405                 410                 415

Leu Leu Asn Phe Ile Pro Gly Ile Gly Pro Ile Phe Pro Leu Ile Gly
            420                 425                 430

Leu Ile Val Leu Gly His His Phe Trp Thr Arg Arg Lys Leu Asn Pro
        435                 440                 445

Pro Phe Gly Arg Ser Lys
    450
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<210> 2647
<211> 741
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(718)
<223> RXA02227

<400> 2647
accgcgtgcc ataggaggtg tcagccagat agggtgcact atcttgaaaa accgcgctca 60

ggagaggtgt ttgcccagca atttcggtgg gcaggatagg gtg gaa gac gtg aat 115
Val Glu Asp Val Asn
1 5

gca acg ctg att atc atg cct gga agt ccg gcg ctg gta cct gaa ctg 163
Ala Thr Leu Ile Ile Met Pro Gly Ser Pro Ala Leu Val Pro Glu Leu
10 15 20

gca cca gcg gat gct gcg ggg gcg cgc ttg ttg gcg tcg tta cgt gca 211
Ala Pro Ala Asp Ala Ala Gly Ala Arg Leu Leu Ala Ser Leu Arg Ala
25 30 35

gtt ttt gat gcg gaa ctg gct aat gat gat cgc ccg atc gag ttg gtt 259
Val Phe Asp Ala Glu Leu Ala Asn Asp Asp Arg Pro Ile Glu Leu Val
40 45 50

ggc tcc cgg gat gag gcg tgg ttt acc aag cat gcg gga aat ctg cgg 307
Gly Ser Arg Asp Glu Ala Trp Phe Thr Lys His Ala Gly Asn Leu Arg
55 60 65

gcc tgg ggt gca ccg agc gtg cag gtt tct gac gga cat tat ttg ccg 355
Ala Trp Gly Ala Pro Ser Val Gln Val Ser Asp Gly His Tyr Leu Pro
70 75 80 85

gaa att ttg cag cgt gtc gcg ctg ggt ggt ttc gaa tcg cgt gta act 403
Glu Ile Leu Gln Arg Val Ala Leu Gly Gly Phe Glu Ser Arg Val Thr
90 95 100

cat gtg cgc gat cgg ttg ggt agc gtc aac gac aac acg gtt acg gtg 451
His Val Arg Asp Arg Leu Gly Ser Val Asn Asp Asn Thr Val Thr Val
105 110 115

ctt gcc ctt gac ggc ccc acg ggc ttg acc acc cgc gcg ccg tcc gca 499
Leu Ala Leu Asp Gly Pro Thr Gly Leu Thr Thr Arg Ala Pro Ser Ala
120 125 130

ctc gtg ccc ggc gcg tcc aac atc gac gcc tgg tgc cgc tca ttg ctg 547
Leu Val Pro Gly Ala Ser Asn Ile Asp Ala Trp Cys Arg Ser Leu Leu
135 140 145

tct gga aag ccc ggg gaa gtg ccc agc acc agc acg ctt atc gac gcc 595
Ser Gly Lys Pro Gly Glu Val Pro Ser Thr Ser Thr Leu Ile Asp Ala
150 155 160 165

tcc ctc cgc gaa cca cag ctc tgg ctc gac tta tcc gcc gtg gca aca 643
Ser Leu Arg Glu Pro Gln Leu Trp Leu Asp Leu Ser Ala Val Ala Thr
170 175 180

gaa gcg tca act gct caa ctt ctc gac agc gac gac aca cac ggc gtg 691
Glu Ala Ser Thr Ala Gln Leu Leu Asp Ser Asp Asp Thr His Gly Val
185 190 195

gga cgc tac gtt gct cgc tgg act ttt taacttaagg gagatctaga 738

```
Gly Arg Tyr Val Ala Arg Trp Thr Phe
        200                 205

tcg                                                                  741


<210> 2648
<211> 206
<212> PRT
<213> Corynebacterium glutamicum

<400> 2648
Val Glu Asp Val Asn Ala Thr Leu Ile Ile Met Pro Gly Ser Pro Ala
  1               5                  10                  15

Leu Val Pro Glu Leu Ala Pro Ala Asp Ala Ala Gly Ala Arg Leu Leu
             20                  25                  30

Ala Ser Leu Arg Ala Val Phe Asp Ala Glu Leu Ala Asn Asp Asp Arg
         35                  40                  45

Pro Ile Glu Leu Val Gly Ser Arg Asp Glu Ala Trp Phe Thr Lys His
     50                  55                  60

Ala Gly Asn Leu Arg Ala Trp Gly Ala Pro Ser Val Gln Val Ser Asp
 65                  70                  75                  80

Gly His Tyr Leu Pro Glu Ile Leu Gln Arg Val Ala Leu Gly Gly Phe
                 85                  90                  95

Glu Ser Arg Val Thr His Val Arg Asp Arg Leu Gly Ser Val Asn Asp
            100                 105                 110

Asn Thr Val Thr Val Leu Ala Leu Asp Gly Pro Thr Gly Leu Thr Thr
        115                 120                 125

Arg Ala Pro Ser Ala Leu Val Pro Gly Ala Ser Asn Ile Asp Ala Trp
    130                 135                 140

Cys Arg Ser Leu Leu Ser Gly Lys Pro Gly Glu Val Pro Ser Thr Ser
145                 150                 155                 160

Thr Leu Ile Asp Ala Ser Leu Arg Glu Pro Gln Leu Trp Leu Asp Leu
                165                 170                 175

Ser Ala Val Ala Thr Glu Ala Ser Thr Ala Gln Leu Leu Asp Ser Asp
            180                 185                 190

Asp Thr His Gly Val Gly Arg Tyr Val Ala Arg Trp Thr Phe
        195                 200                 205


<210> 2649
<211> 660
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(637)
<223> RXA02230
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<400> 2649
catcgcatag aatactggtg caatcgttta cgttcgctat taatgtgaca cgtataagcc 60

gacactttta acgaagcgca gaaggagtga gagcaagaaa atg gga gaa caa ctt 115
Met Gly Glu Gln Leu
1 5

ccg ttt gct aat ggt tca cgc tcc aac aaa ctg ccg ctc atc gtc atc 163
Pro Phe Ala Asn Gly Ser Arg Ser Asn Lys Leu Pro Leu Ile Val Ile
10 15 20

ggt ttg tgc tgc ata atg ctg atc ctg tgg ctt aaa ctt ccc ggc gta 211
Gly Leu Cys Cys Ile Met Leu Ile Leu Trp Leu Lys Leu Pro Gly Val
25 30 35

ctg ctt gcc acc atc att ggg gtt gcc acg atg agt gtg atg cgg atg 259
Leu Leu Ala Thr Ile Ile Gly Val Ala Thr Met Ser Val Met Arg Met
40 45 50

cgc acc tcc acc cca gaa act gcc tcg ctg gtt act tct att cgg ctg 307
Arg Thr Ser Thr Pro Glu Thr Ala Ser Leu Val Thr Ser Ile Arg Leu
55 60 65

tct gcg gaa gat att tcc gat gtg caa cat gag tgg cag cag ttt ttg 355
Ser Ala Glu Asp Ile Ser Asp Val Gln His Glu Trp Gln Gln Phe Leu
70 75 80 85

acc tcc ccc gag gcc gat gcg ctg gct gat cgc acg ctt gtc cgt ccc 403
Thr Ser Pro Glu Ala Asp Ala Leu Ala Asp Arg Thr Leu Val Arg Pro
90 95 100

gca ctg gcg gat cca gat tgt ggc gat aag gct atc gag aaa ttt cat 451
Ala Leu Ala Asp Pro Asp Cys Gly Asp Lys Ala Ile Glu Lys Phe His
105 110 115

tat gaa atc agc aat gcc aat cgc ttc ttg ggc agg ttg gac gct cgt 499
Tyr Glu Ile Ser Asn Ala Asn Arg Phe Leu Gly Arg Leu Asp Ala Arg
120 125 130

ctg caa caa aac ctc gtg gtc agt gag cta gaa aca ctt ctc aaa gta 547
Leu Gln Gln Asn Leu Val Val Ser Glu Leu Glu Thr Leu Leu Lys Val
135 140 145

acg gac gag cgc gca cta gag ctg cgg gaa acg tgg ctg gat gcg cgt 595
Thr Asp Glu Arg Ala Leu Glu Leu Arg Glu Thr Trp Leu Asp Ala Arg
150 155 160 165

aaa gcg gcc cag aaa ctt ggg ccg aac tac aat cgc gaa tct 637
Lys Ala Ala Gln Lys Leu Gly Pro Asn Tyr Asn Arg Glu Ser
170 175

tagatctgca cctcaccgag tgc 660

<210> 2650
<211> 179
<212> PRT
<213> Corynebacterium glutamicum

<400> 2650

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Met Gly Glu Gln Leu Pro Phe Ala Asn Gly Ser Arg Ser Asn Lys Leu
  1               5                  10                  15

Pro Leu Ile Val Ile Gly Leu Cys Cys Ile Met Leu Ile Leu Trp Leu
             20                  25                  30

Lys Leu Pro Gly Val Leu Leu Ala Thr Ile Ile Gly Val Ala Thr Met
         35                  40                  45

Ser Val Met Arg Met Arg Thr Ser Thr Pro Glu Thr Ala Ser Leu Val
     50                  55                  60

Thr Ser Ile Arg Leu Ser Ala Glu Asp Ile Ser Asp Val Gln His Glu
 65                  70                  75                  80

Trp Gln Gln Phe Leu Thr Ser Pro Glu Ala Asp Ala Leu Ala Asp Arg
                 85                  90                  95

Thr Leu Val Arg Pro Ala Leu Ala Asp Pro Asp Cys Gly Asp Lys Ala
            100                 105                 110

Ile Glu Lys Phe His Tyr Glu Ile Ser Asn Ala Asn Arg Phe Leu Gly
        115                 120                 125

Arg Leu Asp Ala Arg Leu Gln Gln Asn Leu Val Val Ser Glu Leu Glu
    130                 135                 140

Thr Leu Leu Lys Val Thr Asp Glu Arg Ala Leu Glu Leu Arg Glu Thr
145                 150                 155                 160

Trp Leu Asp Ala Arg Lys Ala Ala Gln Lys Leu Gly Pro Asn Tyr Asn
                165                 170                 175

Arg Glu Ser
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<210> 2651
<211> 879
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(856)
<223> RXA02231

<400> 2651
taaacaccta aattgagcgc tctattccat caacgcgggg gcaatttctc acgtgtagga 60

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aaagtgacta ttgcctgtta agggagttag actaatcgcc atg act agc gat ctg   115
                                              Met Thr Ser Asp Leu
                                                1               5

aag aca atc ggt atg gat ttc gcc aag tgg caa gat gca gtg gaa gca   163
Lys Thr Ile Gly Met Asp Phe Ala Lys Trp Gln Asp Ala Val Glu Ala
            10                  15                  20

gca att gct tca cag cgt ctc gag gta aca ggc gag gtc cgt ggc ggc   211
Ala Ile Ala Ser Gln Arg Leu Glu Val Thr Gly Glu Val Arg Gly Gly
        25                  30                  35
```

```
cag ctc atc cag ttc tcg gat gat tcc ggc gcc caa att aac att ctg   259
Gln Leu Ile Gln Phe Ser Asp Asp Ser Gly Ala Gln Ile Asn Ile Leu
         40                  45                  50

gct gtc gag cct ttt gcc acc ttc gcc ggc ttt aac tcc gca aca gtc   307
Ala Val Glu Pro Phe Ala Thr Phe Ala Gly Phe Asn Ser Ala Thr Val
     55                  60                  65

gct tac ggc cac gtc agc atg atc aat gat gtg ctg tcc ctg gtc gat   355
Ala Tyr Gly His Val Ser Met Ile Asn Asp Val Leu Ser Leu Val Asp
 70                  75                  80                  85

atc atc gat cct ttc ggc acc cct gtt gcc acc att acc tgc aac ctt   403
Ile Ile Asp Pro Phe Gly Thr Pro Val Ala Thr Ile Thr Cys Asn Leu
                 90                  95                 100

gct caa ggc cca ctg ctt gtt gat gaa cca gtg cag cgc tgg cag cag   451
Ala Gln Gly Pro Leu Leu Val Asp Glu Pro Val Gln Arg Trp Gln Gln
            105                 110                 115

atc cgc att act gcc ctg ggc att gat gtt gag gtc cac gac aat gca   499
Ile Arg Ile Thr Ala Leu Gly Ile Asp Val Glu Val His Asp Asn Ala
        120                 125                 130

gat gct tac atc cgc aat ggt ggc gaa act gtc ggc atg ctg gtt tct   547
Asp Ala Tyr Ile Arg Asn Gly Gly Glu Thr Val Gly Met Leu Val Ser
    135                 140                 145

gaa ggt gca gag aag att gcc agc ggc agc ggc gct gtc atc ccg gac   595
Glu Gly Ala Glu Lys Ile Ala Ser Gly Ser Gly Ala Val Ile Pro Asp
150                 155                 160                 165

gca tcc gca gag ttt tcc gca cgc gtg ttg tct gcg gag tac cgc acc   643
Ala Ser Ala Glu Phe Ser Ala Arg Val Leu Ser Ala Glu Tyr Arg Thr
                170                 175                 180

aac act ctt acc ggc cag cgt ttt atc cac gca aca gtt gat ggc ctc   691
Asn Thr Leu Thr Gly Gln Arg Phe Ile His Ala Thr Val Asp Gly Leu
            185                 190                 195

ttc gct ttt gat gtg tgc ctt cct gat gca cca gaa cta cct gcc cgt   739
Phe Ala Phe Asp Val Cys Leu Pro Asp Ala Pro Glu Leu Pro Ala Arg
        200                 205                 210

gac agc gtg ttg tct ggc aaa gtc atg ctg act gct gcc gtt atc ccc   787
Asp Ser Val Leu Ser Gly Lys Val Met Leu Thr Ala Ala Val Ile Pro
    215                 220                 225

act gag gtc acc ggc tgc ggt ggc tcc ggt ggc ggc tgt ggc tca ggt   835
Thr Glu Val Thr Gly Cys Gly Gly Ser Gly Gly Gly Cys Gly Ser Gly
230                 235                 240                 245

agc tgt ggc tgc ggc gga cac taaaattctg cacaattttt taa             879
Ser Cys Gly Cys Gly Gly His
                250
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<210> 2652
<211> 252
<212> PRT

<213> Corynebacterium glutamicum

<400> 2652

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Met Thr Ser Asp Leu Lys Thr Ile Gly Met Asp Phe Ala Lys Trp Gln
  1               5                  10                  15

Asp Ala Val Glu Ala Ala Ile Ala Ser Gln Arg Leu Glu Val Thr Gly
             20                  25                  30

Glu Val Arg Gly Gly Gln Leu Ile Gln Phe Ser Asp Asp Ser Gly Ala
         35                  40                  45

Gln Ile Asn Ile Leu Ala Val Glu Pro Phe Ala Thr Phe Ala Gly Phe
     50                  55                  60

Asn Ser Ala Thr Val Ala Tyr Gly His Val Ser Met Ile Asn Asp Val
 65                  70                  75                  80

Leu Ser Leu Val Asp Ile Ile Asp Pro Phe Gly Thr Pro Val Ala Thr
                 85                  90                  95

Ile Thr Cys Asn Leu Ala Gln Gly Pro Leu Leu Val Asp Glu Pro Val
            100                 105                 110

Gln Arg Trp Gln Gln Ile Arg Ile Thr Ala Leu Gly Ile Asp Val Glu
        115                 120                 125

Val His Asp Asn Ala Asp Ala Tyr Ile Arg Asn Gly Gly Glu Thr Val
    130                 135                 140

Gly Met Leu Val Ser Glu Gly Ala Glu Lys Ile Ala Ser Gly Ser Gly
145                 150                 155                 160

Ala Val Ile Pro Asp Ala Ser Ala Glu Phe Ser Ala Arg Val Leu Ser
                165                 170                 175

Ala Glu Tyr Arg Thr Asn Thr Leu Thr Gly Gln Arg Phe Ile His Ala
            180                 185                 190

Thr Val Asp Gly Leu Phe Ala Phe Asp Val Cys Leu Pro Asp Ala Pro
        195                 200                 205

Glu Leu Pro Ala Arg Asp Ser Val Leu Ser Gly Lys Val Met Leu Thr
    210                 215                 220

Ala Ala Val Ile Pro Thr Glu Val Thr Gly Cys Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Cys Gly Ser Gly Ser Cys Gly Cys Gly Gly His
                245                 250
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<210> 2653
<211> 1656
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1633)
<223> RXA02244

<400> 2653
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gggcgcgtgg tgtccaactt gatcaggaag cgaaattcca atg agc cta gaa aaa 115
Met Ser Leu Glu Lys
1 5

tcc ggc gga ttc cgc tcc agg act cca aaa gcg cag cag gaa cct gct 163
Ser Gly Gly Phe Arg Ser Arg Thr Pro Lys Ala Gln Gln Glu Pro Ala
10 15 20

aag cag aag ccg cag gcg cgt aaa tct ccg tca aag aag gcc ccg gct 211
Lys Gln Lys Pro Gln Ala Arg Lys Ser Pro Ser Lys Lys Ala Pro Ala
25 30 35

cgg ggg cag ggg cag agt cag ggg cag cgc cag ggc caa agc agt ggc 259
Arg Gly Gln Gly Gln Ser Gln Gly Gln Arg Gln Gly Gln Ser Ser Gly
40 45 50

aaa ggc ggc gga aac cgc aag ccc cct gcg cag gcc agg gaa gtg agg 307
Lys Gly Gly Gly Asn Arg Lys Pro Pro Ala Gln Ala Arg Glu Val Arg
55 60 65

gct ctg ggc gtc gat aag ccg aga gaa att gcg ttt gag gtg ctt gat 355
Ala Leu Gly Val Asp Lys Pro Arg Glu Ile Ala Phe Glu Val Leu Asp
70 75 80 85

cgt gtg cgt acc ggt gag gcg tat gcc aac ttg gtg ttg cca cga ctg 403
Arg Val Arg Thr Gly Glu Ala Tyr Ala Asn Leu Val Leu Pro Arg Leu
90 95 100

ctg agc aag cac aat ctt tct ggc cgt gac gcg gcc ttt gct acg gaa 451
Leu Ser Lys His Asn Leu Ser Gly Arg Asp Ala Ala Phe Ala Thr Glu
105 110 115

att acc tac ggc acc ttg cgt aat gtc ggc ttg ctg gat gag gtc att 499
Ile Thr Tyr Gly Thr Leu Arg Asn Val Gly Leu Leu Asp Glu Val Ile
120 125 130

aag gct gca tct ggg cgt gaa ctg tct gat att gat cca gag gtt ttg 547
Lys Ala Ala Ser Gly Arg Glu Leu Ser Asp Ile Asp Pro Glu Val Leu
135 140 145

gac gtg ctg cgt ttg ggc gcg tac cag gtg atg ttt acc cgc gtg gag 595
Asp Val Leu Arg Leu Gly Ala Tyr Gln Val Met Phe Thr Arg Val Glu
150 155 160 165

gat cac gct gcg gtc gat act tca gta aag atg gtc ggt ggg ctg aag 643
Asp His Ala Ala Val Asp Thr Ser Val Lys Met Val Gly Gly Leu Lys
170 175 180

aaa ttc cag gcc act ggt ttt gcc aat gca att ttg cgc aac atc acg 691
Lys Phe Gln Ala Thr Gly Phe Ala Asn Ala Ile Leu Arg Asn Ile Thr
185 190 195

cgc aag gaa cca gag cag tgg ttg aag gaa ttg gag ccc gcg gaa gag 739
Arg Lys Glu Pro Glu Gln Trp Leu Lys Glu Leu Glu Pro Ala Glu Glu
200 205 210

ttg gct cgc gtt gcg ttc cgt act gcg cac cca cgc tgg att gcg cag 787

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Leu Ala Arg Val Ala Phe Arg Thr Ala His Pro Arg Trp Ile Ala Gln
    215                 220                 225

agt ttc tca cag gtg ctc ccg gca gat gag ttg gaa gca gcg ctt gct   835
Ser Phe Ser Gln Val Leu Pro Ala Asp Glu Leu Glu Ala Ala Leu Ala
230                 235                 240                 245

gcg gac tct gag cgc cca gtg gtg cac ttg gtg gct cgc cca ggt gag   883
Ala Asp Ser Glu Arg Pro Val Val His Leu Val Ala Arg Pro Gly Glu
                250                 255                 260

atc agt gca gag gaa ttg gcg ctg atc acc ggt ggt gac gag ggc aag   931
Ile Ser Ala Glu Glu Leu Ala Leu Ile Thr Gly Gly Asp Glu Gly Lys
            265                 270                 275

tat tcc cca tac gcg gtg tac ctc gag ggt ggc gac ccg ggt gat att   979
Tyr Ser Pro Tyr Ala Val Tyr Leu Glu Gly Gly Asp Pro Gly Asp Ile
        280                 285                 290

gag cca gtg aag gat ggt ctt gca gca gtg caa gat gag ggt tct cag   1027
Glu Pro Val Lys Asp Gly Leu Ala Ala Val Gln Asp Glu Gly Ser Gln
    295                 300                 305

ctg att gct cgc gcc ttg gtg gaa atc ccc gtg gag ggc acc gat gcc   1075
Leu Ile Ala Arg Ala Leu Val Glu Ile Pro Val Glu Gly Thr Asp Ala
310                 315                 320                 325

ggc cgt tgg ctg gat atg tgt gca ggt cct ggc ggt aaa gcg gcg ctc   1123
Gly Arg Trp Leu Asp Met Cys Ala Gly Pro Gly Gly Lys Ala Ala Leu
                330                 335                 340

att ggt gcg ttg gct cgc atg gat cgt gcc acc gtt gat gcc gtg gag   1171
Ile Gly Ala Leu Ala Arg Met Asp Arg Ala Thr Val Asp Ala Val Glu
            345                 350                 355

gtc tct gat cac cgt gcc cga ctg att gaa aag tcc gtg cgt ggt ttg   1219
Val Ser Asp His Arg Ala Arg Leu Ile Glu Lys Ser Val Arg Gly Leu
        360                 365                 370

ccc gtc aag gtt cat gtg ggc gat ggc cgc acc atc aac ttg acc ggt   1267
Pro Val Lys Val His Val Gly Asp Gly Arg Thr Ile Asn Leu Thr Gly
    375                 380                 385

ggt tac gat cgt gcg cta gtc gat gcg ccg tgt tct ggt ttg ggt gca   1315
Gly Tyr Asp Arg Ala Leu Val Asp Ala Pro Cys Ser Gly Leu Gly Ala
390                 395                 400                 405

ctg cgt cgt cgc cct gag gcg cgt tgg cgc aag cag gaa agc gac att   1363
Leu Arg Arg Arg Pro Glu Ala Arg Trp Arg Lys Gln Glu Ser Asp Ile
                410                 415                 420

gtt gag ctc aac acc ctg cag tac gag ctg ctt gaa tcc gct gtg aac   1411
Val Glu Leu Asn Thr Leu Gln Tyr Glu Leu Leu Glu Ser Ala Val Asn
            425                 430                 435

aag gtg cgt tcc ggt ggc gtg att gtg tac tcc aca tgt tca cct gat   1459
Lys Val Arg Ser Gly Gly Val Ile Val Tyr Ser Thr Cys Ser Pro Asp
        440                 445                 450

ctg cgt gaa acc cgc gga atc gtg gac aag gca ctg ggg gct ctg gag   1507
Leu Arg Glu Thr Arg Gly Ile Val Asp Lys Ala Leu Gly Ala Leu Glu
```

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    455                 460                 465

atc gaa gag ctt gag gct gcg gag ttc atg cca ggc atg acc gat acc   1555
Ile Glu Glu Leu Glu Ala Ala Glu Phe Met Pro Gly Met Thr Asp Thr
470                 475                 480                 485

ggc gat gag aaa tca gtg cag atg tgg cca cac cgc cac ggc acc gat   1603
Gly Asp Glu Lys Ser Val Gln Met Trp Pro His Arg His Gly Thr Asp
                490                 495                 500

gcg atg ttt gtg gca gtg ctg cga aag aag tagacctgtg agctaagtgg     1653
Ala Met Phe Val Ala Val Leu Arg Lys Lys
            505                 510

ggt                                                               1656


<210> 2654
<211> 511
<212> PRT
<213> Corynebacterium glutamicum

<400> 2654
Met Ser Leu Glu Lys Ser Gly Gly Phe Arg Ser Arg Thr Pro Lys Ala
  1               5                  10                  15

Gln Gln Glu Pro Ala Lys Gln Lys Pro Gln Ala Arg Lys Ser Pro Ser
             20                  25                  30

Lys Lys Ala Pro Ala Arg Gly Gln Gly Gln Ser Gln Gly Gln Arg Gln
         35                  40                  45

Gly Gln Ser Ser Gly Lys Gly Gly Gly Asn Arg Lys Pro Pro Ala Gln
     50                  55                  60

Ala Arg Glu Val Arg Ala Leu Gly Val Asp Lys Pro Arg Glu Ile Ala
 65                  70                  75                  80

Phe Glu Val Leu Asp Arg Val Arg Thr Gly Glu Ala Tyr Ala Asn Leu
                 85                  90                  95

Val Leu Pro Arg Leu Leu Ser Lys His Asn Leu Ser Gly Arg Asp Ala
            100                 105                 110

Ala Phe Ala Thr Glu Ile Thr Tyr Gly Thr Leu Arg Asn Val Gly Leu
        115                 120                 125

Leu Asp Glu Val Ile Lys Ala Ala Ser Gly Arg Glu Leu Ser Asp Ile
    130                 135                 140

Asp Pro Glu Val Leu Asp Val Leu Arg Leu Gly Ala Tyr Gln Val Met
145                 150                 155                 160

Phe Thr Arg Val Glu Asp His Ala Ala Val Asp Thr Ser Val Lys Met
                165                 170                 175

Val Gly Gly Leu Lys Lys Phe Gln Ala Thr Gly Phe Ala Asn Ala Ile
            180                 185                 190

Leu Arg Asn Ile Thr Arg Lys Glu Pro Glu Gln Trp Leu Lys Glu Leu
        195                 200                 205
```

```
Glu Pro Ala Glu Glu Leu Ala Arg Val Ala Phe Arg Thr Ala His Pro
    210                 215                 220

Arg Trp Ile Ala Gln Ser Phe Ser Gln Val Leu Pro Ala Asp Glu Leu
225                 230                 235                 240

Glu Ala Ala Leu Ala Ala Asp Ser Glu Arg Pro Val Val His Leu Val
                245                 250                 255

Ala Arg Pro Gly Glu Ile Ser Ala Glu Glu Leu Ala Leu Ile Thr Gly
            260                 265                 270

Gly Asp Glu Gly Lys Tyr Ser Pro Tyr Ala Val Tyr Leu Glu Gly Gly
        275                 280                 285

Asp Pro Gly Asp Ile Glu Pro Val Lys Asp Gly Leu Ala Ala Val Gln
    290                 295                 300

Asp Glu Gly Ser Gln Leu Ile Ala Arg Ala Leu Val Glu Ile Pro Val
305                 310                 315                 320

Glu Gly Thr Asp Ala Gly Arg Trp Leu Asp Met Cys Ala Gly Pro Gly
                325                 330                 335

Gly Lys Ala Ala Leu Ile Gly Ala Leu Ala Arg Met Asp Arg Ala Thr
            340                 345                 350

Val Asp Ala Val Glu Val Ser Asp His Arg Ala Arg Leu Ile Glu Lys
        355                 360                 365

Ser Val Arg Gly Leu Pro Val Lys Val His Val Gly Asp Gly Arg Thr
    370                 375                 380

Ile Asn Leu Thr Gly Gly Tyr Asp Arg Ala Leu Val Asp Ala Pro Cys
385                 390                 395                 400

Ser Gly Leu Gly Ala Leu Arg Arg Arg Pro Glu Ala Arg Trp Arg Lys
                405                 410                 415

Gln Glu Ser Asp Ile Val Glu Leu Asn Thr Leu Gln Tyr Glu Leu Leu
            420                 425                 430

Glu Ser Ala Val Asn Lys Val Arg Ser Gly Gly Val Ile Val Tyr Ser
        435                 440                 445

Thr Cys Ser Pro Asp Leu Arg Glu Thr Arg Gly Ile Val Asp Lys Ala
    450                 455                 460

Leu Gly Ala Leu Glu Ile Glu Glu Leu Glu Ala Ala Glu Phe Met Pro
465                 470                 475                 480

Gly Met Thr Asp Thr Gly Asp Glu Lys Ser Val Gln Met Trp Pro His
                485                 490                 495

Arg His Gly Thr Asp Ala Met Phe Val Ala Val Leu Arg Lys Lys
            500                 505                 510
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US 2009/0155275 A1

<210> 2655
<211> 1059

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1036)
<223> RXA02255

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actgacgagt gatatcaaac aagaattggc gcaggtccat gtg gcc aaa aac agt 115
Val Ala Lys Asn Ser
1 5

gtt cgt gct gcg gaa gtg tct gca att tta agg ttt gct ggt gag atg 163
Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg Phe Ala Gly Glu Met
10 15 20

caa gct gtc ggc ggc aag ctg gtc atc gaa gca aat ttg gac agc atg 211
Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala Asn Leu Asp Ser Met
25 30 35

caa gtc ggt atg agg ctt cag gag ttt atc caa ggt ttg tac aac tct 259
Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln Gly Leu Tyr Asn Ser
40 45 50

cga gtc gat gtg cac acc gtg aac ccg act gtg agc agg aaa acg cca 307
Arg Val Asp Val His Thr Val Asn Pro Thr Val Ser Arg Lys Thr Pro
55 60 65

cgg tat ttg gtg cgc atc att gac aat gcc gat gaa att gcg cga cgc 355
Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp Glu Ile Ala Arg Arg
70 75 80 85

acc gga ctg gtc acc agg tct gga cat gtg gtt aaa ggt cta gcg cct 403
Thr Gly Leu Val Thr Arg Ser Gly His Val Val Lys Gly Leu Ala Pro
90 95 100

tct gtg gtc agc gga aca atc agt gac gct gaa gct gca tgg cgc ggt 451
Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu Ala Ala Trp Arg Gly
105 110 115

gcg ttt cta gcc aat gga tct tta agt gat cca ggt cgt tcc tct tcg 499
Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro Gly Arg Ser Ser Ser
120 125 130

ttg gag gtg ttg tgt cct ggt caa gaa tca gca ttg gca ctg gtt gga 547
Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala Leu Ala Leu Val Gly
135 140 145

tgt gcg cga aga att ggg atc gcg gcg aaa acg aaa gat tct cga gga 595
Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr Lys Asp Ser Arg Gly
150 155 160 165

ttt gat cgc gtc aat gtt cgt gat gcg gaa gca att ggg gca ctg ctc 643
Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala Ile Gly Ala Leu Leu
170 175 180

act cga atg ggt gcc cag aaa act cgc atg ttg tgg gaa gaa aaa cgc 691
Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu Trp Glu Glu Lys Arg

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            185                 190                 195

atc aag cgg gaa agt cga act ccg caa acc ggg ttg gcc aac ttc gac   739
Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly Leu Ala Asn Phe Asp
        200                 205                 210

gat gcc aat ctg cgc agg tca gcc cga gca gca gtt gcc gct gca gcg   787
Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala Val Ala Ala Ala Ala
    215                 220                 225

agg gta gaa cgc gcc atg aag att ctt ggt gat gat gtt cct gag cat   835
Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp Asp Val Pro Glu His
230                 235                 240                 245

ttg gct gag gct gga cag ctg cgt gtg cag cac cgt cag gca tcg ttg   883
Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His Arg Gln Ala Ser Leu
                250                 255                 260

gag gag ttg ggc cgg ttg gct gat cct caa atg acc aag gat gct gtg   931
Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met Thr Lys Asp Ala Val
            265                 270                 275

gcc ggt cgt att cgt cgt ctt ttg acg atg gca gat aag cgc gcc gaa   979
Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala Asp Lys Arg Ala Glu
        280                 285                 290

gat ctg aag att cct gat aca aat tct gtt gtg acg gaa gat ttg ttg   1027
Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val Thr Glu Asp Leu Leu
    295                 300                 305

gaa gaa att tagatgattg aagcctaaaa acg                            1059
Glu Glu Ile
310
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09/05/2005 09:55:55 PM

<210> 2656
<211> 312
<212> PRT
<213> Corynebacterium glutamicum

<400> 2656

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Val Ala Lys Asn Ser Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg
  1               5                  10                  15

Phe Ala Gly Glu Met Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala
             20                  25                  30

Asn Leu Asp Ser Met Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln
         35                  40                  45

Gly Leu Tyr Asn Ser Arg Val Asp Val His Thr Val Asn Pro Thr Val
     50                  55                  60

Ser Arg Lys Thr Pro Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp
 65                  70                  75                  80

Glu Ile Ala Arg Arg Thr Gly Leu Val Thr Arg Ser Gly His Val Val
                 85                  90                  95

Lys Gly Leu Ala Pro Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu
            100                 105                 110
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```
Ala Ala Trp Arg Gly Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro
        115                 120                 125

Gly Arg Ser Ser Ser Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala
    130                 135                 140

Leu Ala Leu Val Gly Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr
145                 150                 155                 160

Lys Asp Ser Arg Gly Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala
                165                 170                 175

Ile Gly Ala Leu Leu Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu
            180                 185                 190

Trp Glu Glu Lys Arg Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly
        195                 200                 205

Leu Ala Asn Phe Asp Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala
    210                 215                 220

Val Ala Ala Ala Ala Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp
225                 230                 235                 240

Asp Val Pro Glu His Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His
                245                 250                 255

Arg Gln Ala Ser Leu Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met
            260                 265                 270

Thr Lys Asp Ala Val Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala
        275                 280                 285

Asp Lys Arg Ala Glu Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val
    290                 295                 300

Thr Glu Asp Leu Leu Glu Glu Ile
305                 310
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09/05/2006 15:50:50 FILE 'HOME' ENTERED

<210> 2657
<211> 636
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(613)
<223> RXA02266

<400> 2657
gaggaaagta gcgctacatc tgcatatcta ccccttaaa aatgaagcat aaaaccgccg 60

```
tgtaccggcc ttttattgat tttgacgtaa gcttgcaccg atg act caa gat gaa   115
                                            Met Thr Gln Asp Glu
                                              1               5

cac ccc cga cag gcc gac tcc cat ttc aac atg ctt tta ccg gat gga   163
His Pro Arg Gln Ala Asp Ser His Phe Asn Met Leu Leu Pro Asp Gly
                  10                  15                  20
```

```
aat gaa aac gca cac cag ctt tct gtc gct cta aat cag gtg gca cat   211
Asn Glu Asn Ala His Gln Leu Ser Val Ala Leu Asn Gln Val Ala His
            25                  30                  35

ctg ttg gcc tat gat gcg gac tct tca att cat cgg cct gat ggg cta   259
Leu Leu Ala Tyr Asp Ala Asp Ser Ser Ile His Arg Pro Asp Gly Leu
        40                  45                  50

agt ctg gcg tcc tat aga att ctc ttt tca ctg tgg act gat ggc ccg   307
Ser Leu Ala Ser Tyr Arg Ile Leu Phe Ser Leu Trp Thr Asp Gly Pro
    55                  60                  65

atg agt cca ctc cag gtg act gac aag act gga atg aaa aag tct gcg   355
Met Ser Pro Leu Gln Val Thr Asp Lys Thr Gly Met Lys Lys Ser Ala
70                  75                  80                  85

att tct aac ctg tta aag cca ttg ctc gct gaa tct ctg att gtg cag   403
Ile Ser Asn Leu Leu Lys Pro Leu Leu Ala Glu Ser Leu Ile Val Gln
                90                  95                  100

gtg acg gca gaa aat gat cga cgc tca aag gtt tta agc ctt agc gaa   451
Val Thr Ala Glu Asn Asp Arg Arg Ser Lys Val Leu Ser Leu Ser Glu
            105                 110                 115

aaa ggc act aca tac att cag aaa aca gcc acc cgc caa aat gct ttg   499
Lys Gly Thr Thr Tyr Ile Gln Lys Thr Ala Thr Arg Gln Asn Ala Leu
        120                 125                 130

gaa tcc gag tgg ttt ggc acc ctg acc gac atc gag cag gat tta ttg   547
Glu Ser Glu Trp Phe Gly Thr Leu Thr Asp Ile Glu Gln Asp Leu Leu
    135                 140                 145

gag tcg ttg ctc agg aaa ctg ctc gac tcc aac cgc gca tcc aag gtt   595
Glu Ser Leu Leu Arg Lys Leu Leu Asp Ser Asn Arg Ala Ser Lys Val
150                 155                 160                 165

cgt aaa aac cga tct aac tagcgtcgat ccttagggat gta                636
Arg Lys Asn Arg Ser Asn
                170
```

EV 450 150 205 US

<210> 2658
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 2658

```
Met Thr Gln Asp Glu His Pro Arg Gln Ala Asp Ser His Phe Asn Met
  1               5                  10                  15

Leu Leu Pro Asp Gly Asn Glu Asn Ala His Gln Leu Ser Val Ala Leu
            20                  25                  30

Asn Gln Val Ala His Leu Leu Ala Tyr Asp Ala Asp Ser Ser Ile His
        35                  40                  45

Arg Pro Asp Gly Leu Ser Leu Ala Ser Tyr Arg Ile Leu Phe Ser Leu
    50                  55                  60

Trp Thr Asp Gly Pro Met Ser Pro Leu Gln Val Thr Asp Lys Thr Gly
```

```
 65                  70                  75                  80

Met Lys Lys Ser Ala Ile Ser Asn Leu Leu Lys Pro Leu Leu Ala Glu
                 85                  90                  95

Ser Leu Ile Val Gln Val Thr Ala Glu Asn Asp Arg Arg Ser Lys Val
            100                 105                 110

Leu Ser Leu Ser Glu Lys Gly Thr Thr Tyr Ile Gln Lys Thr Ala Thr
        115                 120                 125

Arg Gln Asn Ala Leu Glu Ser Glu Trp Phe Gly Thr Leu Thr Asp Ile
    130                 135                 140

Glu Gln Asp Leu Leu Glu Ser Leu Leu Arg Lys Leu Leu Asp Ser Asn
145                 150                 155                 160

Arg Ala Ser Lys Val Arg Lys Asn Arg Ser Asn
                165                 170
```

<210> 2659
<211> 996
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(973)
<223> RXA02267

<400> 2659

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tgcgctcggc aagtgttttg cttatcgacg tctccccaca taacaatccc aactcgaagc 60

accaacgatt caagccttat cagttttgta caggaaaata gtg caa aaa tgg ggt   115
                                            Val Gln Lys Trp Gly
                                              1               5

tta agc ttc gtg gag agg att gtc atc gtg aac aac gtg caa cag ttt   163
Leu Ser Phe Val Glu Arg Ile Val Ile Val Asn Asn Val Gln Gln Phe
                 10                  15                  20

cat cga ttt ttt gat gat tcc gca gtc tat tat ccc tgc ttc gtc ccg   211
His Arg Phe Phe Asp Asp Ser Ala Val Tyr Tyr Pro Cys Phe Val Pro
             25                  30                  35

ctt gac cga gcc atc ggc gaa cac ttt gat cgt cag aac aaa ccg atg   259
Leu Asp Arg Ala Ile Gly Glu His Phe Asp Arg Gln Asn Lys Pro Met
         40                  45                  50

tcc aga ttc atc gga acg ctc att ctg ccg tta gcc aaa ctg gaa gaa   307
Ser Arg Phe Ile Gly Thr Leu Ile Leu Pro Leu Ala Lys Leu Glu Glu
     55                  60                  65

gcc gcc caa tac acc ggc gat gaa gtc ctt cgc gtg tcg gca gta atc   355
Ala Ala Gln Tyr Thr Gly Asp Glu Val Leu Arg Val Ser Ala Val Ile
 70                  75                  80                  85

agt act gat ggg ctc gct gat ctg cga agg gat ttt tac gaa ctc ccc   403
Ser Thr Asp Gly Leu Ala Asp Leu Arg Arg Asp Phe Tyr Glu Leu Pro
                 90                  95                 100
```

```
aac atc gac atc gcc tcg gtg gaa atc aag ctg gtc ggc gca gcc ctc   451
Asn Ile Asp Ile Ala Ser Val Glu Ile Lys Leu Val Gly Ala Ala Leu
            105                 110                 115

acc aac acc gct tgg ttg gga gat gtg gaa aaa ctc atc caa caa cat   499
Thr Asn Thr Ala Trp Leu Gly Asp Val Glu Lys Leu Ile Gln Gln His
        120                 125                 130

cgc aac act ttc gta tgg gtt gag att ccg aca gcc ctg gtc acc gca   547
Arg Asn Thr Phe Val Trp Val Glu Ile Pro Thr Ala Leu Val Thr Ala
    135                 140                 145

gat att gtc cga aaa ctc cgc cac atg gga gct ggc ctg aaa tac aga   595
Asp Ile Val Arg Lys Leu Arg His Met Gly Ala Gly Leu Lys Tyr Arg
150                 155                 160                 165

act gga ggt gat agg gaa gag ctc ttc ccc tca ccg cag gac ttg gtc   643
Thr Gly Gly Asp Arg Glu Glu Leu Phe Pro Ser Pro Gln Asp Leu Val
                170                 175                 180

act gtg ctg cgc acc gcc atc gat gct gca ttg ccg ttt aaa ctc act   691
Thr Val Leu Arg Thr Ala Ile Asp Ala Ala Leu Pro Phe Lys Leu Thr
            185                 190                 195

gca ggc ctg cat cgt gct ctc agg tat cgt gac gag aaa acc ggc cga   739
Ala Gly Leu His Arg Ala Leu Arg Tyr Arg Asp Glu Lys Thr Gly Arg
        200                 205                 210

ctt cac ttc gga ttc ctc aac att gca gcc gcc gtg gcg aca ctt cgt   787
Leu His Phe Gly Phe Leu Asn Ile Ala Ala Ala Val Ala Thr Leu Arg
    215                 220                 225

gct gga aaa ggc gag gca gag gca ctg aag atc ctt gaa ggc gat gat   835
Ala Gly Lys Gly Glu Ala Glu Ala Leu Lys Ile Leu Glu Gly Asp Asp
230                 235                 240                 245

gcc gct ccg ctt att cac gca cta caa agc ggc gaa aac tgg cgg gat   883
Ala Ala Pro Leu Ile His Ala Leu Gln Ser Gly Glu Asn Trp Arg Asp
                250                 255                 260

tcc ttc cgc agc ttc agt acc tgc aat gtt gtt gaa cca ctc aac act   931
Ser Phe Arg Ser Phe Ser Thr Cys Asn Val Val Glu Pro Leu Asn Thr
            265                 270                 275

ctg att gat ctt gat gtg ttg gcg gaa gga gac gta cat ccc           973
Leu Ile Asp Leu Asp Val Leu Ala Glu Gly Asp Val His Pro
        280                 285                 290

taaggatcga cgctagttag atc                                        996
```

<210> 2660
<211> 291
<212> PRT
<213> Corynebacterium glutamicum

<400> 2660

```
Val Gln Lys Trp Gly Leu Ser Phe Val Glu Arg Ile Val Ile Val Asn
  1               5                  10                  15
```

```
Asn Val Gln Gln Phe His Arg Phe Phe Asp Asp Ser Ala Val Tyr Tyr
            20                  25                  30

Pro Cys Phe Val Pro Leu Asp Arg Ala Ile Gly Glu His Phe Asp Arg
        35                  40                  45

Gln Asn Lys Pro Met Ser Arg Phe Ile Gly Thr Leu Ile Leu Pro Leu
    50                  55                  60

Ala Lys Leu Glu Glu Ala Ala Gln Tyr Thr Gly Asp Glu Val Leu Arg
65                  70                  75                  80

Val Ser Ala Val Ile Ser Thr Asp Gly Leu Ala Asp Leu Arg Arg Asp
                85                  90                  95

Phe Tyr Glu Leu Pro Asn Ile Asp Ile Ala Ser Val Glu Ile Lys Leu
            100                 105                 110

Val Gly Ala Ala Leu Thr Asn Thr Ala Trp Leu Gly Asp Val Glu Lys
        115                 120                 125

Leu Ile Gln Gln His Arg Asn Thr Phe Val Trp Val Glu Ile Pro Thr
    130                 135                 140

Ala Leu Val Thr Ala Asp Ile Val Arg Lys Leu Arg His Met Gly Ala
145                 150                 155                 160

Gly Leu Lys Tyr Arg Thr Gly Gly Asp Arg Glu Glu Leu Phe Pro Ser
                165                 170                 175

Pro Gln Asp Leu Val Thr Val Leu Arg Thr Ala Ile Asp Ala Ala Leu
            180                 185                 190

Pro Phe Lys Leu Thr Ala Gly Leu His Arg Ala Leu Arg Tyr Arg Asp
        195                 200                 205

Glu Lys Thr Gly Arg Leu His Phe Gly Phe Leu Asn Ile Ala Ala Ala
    210                 215                 220

Val Ala Thr Leu Arg Ala Gly Lys Gly Glu Ala Glu Ala Leu Lys Ile
225                 230                 235                 240

Leu Glu Gly Asp Asp Ala Ala Pro Leu Ile His Ala Leu Gln Ser Gly
                245                 250                 255

Glu Asn Trp Arg Asp Ser Phe Arg Ser Phe Ser Thr Cys Asn Val Val
            260                 265                 270

Glu Pro Leu Asn Thr Leu Ile Asp Leu Asp Val Leu Ala Glu Gly Asp
        275                 280                 285

Val His Pro
    290
```

<210> 2661
<211> 776
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (1)..(753)
<223> RXA02280

<400> 2661

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gcg gac ctg gct gaa acc atg ttg ggt ctt ctc acc ttg gag acc tcc   48
Ala Asp Leu Ala Glu Thr Met Leu Gly Leu Leu Thr Leu Glu Thr Ser
  1               5                  10                  15

cgt ggt cgc atc tcg atc ggt gag atc acc acg ttg tcc atc acc gag   96
Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr Leu Ser Ile Thr Glu
             20                  25                  30

gat gtg tcg ctg cag ctg gct acc acg ttg gat gat ttc agg cag ctc   144
Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp Asp Phe Arg Gln Leu
         35                  40                  45

aac acc att gcg cgc ccg gac acc ttg att att aat ggc ggc tac att   192
Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile Asn Gly Gly Tyr Ile
     50                  55                  60

cac gac agc gat ctg gct cgg ctc att ccc gtt cac tac cca ccg ctt   240
His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val His Tyr Pro Pro Leu
 65                  70                  75                  80

acg gta tct act gct gac ctg cgc gaa tcc atg gat ctg atg gag ctt   288
Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met Asp Leu Met Glu Leu
                 85                  90                  95

ccg ccg ctg cag gac att gag aaa gcc aag gca ctg gat gcg cag gtc   336
Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala Leu Asp Ala Gln Val
            100                 105                 110

acg gaa tca ttg aag gat ttt cag atc aag ggc gca acg agg gtt ttt   384
Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly Ala Thr Arg Val Phe
        115                 120                 125

gaa ccc gca gat gtt cct gcc gtg gtg atc att gat tcc aag gcg cag   432
Glu Pro Ala Asp Val Pro Ala Val Val Ile Ile Asp Ser Lys Ala Gln
    130                 135                 140

gcc tca cgg gat cgc aat gaa aca caa agc gca acc act gat cgt tgg   480
Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala Thr Thr Asp Arg Trp
145                 150                 155                 160

gct gac att ttg gca acg gtg gat aac acg ttg agc cgt caa aca gcc   528
Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu Ser Arg Gln Thr Ala
                165                 170                 175

aac att cca cag gat cag gga ctg tcg gcg ttg tgc ttg aat tgg aac   576
Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu Cys Leu Asn Trp Asn
            180                 185                 190

aat tcg ctg gtc agg aaa ttg gcg tcc act gat gac acc gcc gtg gtg   624
Asn Ser Leu Val Arg Lys Leu Ala Ser Thr Asp Asp Thr Ala Val Val
        195                 200                 205

tcg cgc acg gtg cgt ttg ctc tac gtt cag gca ttg ttg tcc agc aag   672
Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala Leu Leu Ser Ser Lys
    210                 215                 220
```

```
agg cca ctg cgg gtg aag gaa cgc gcg ctg ctt aat gat tcg ctg gca   720
Arg Pro Leu Arg Val Lys Glu Arg Ala Leu Leu Asn Asp Ser Leu Ala
225                 230                 235                 240

gat ctg gtt tct ttg tct ttg tca tcc gat atc taagacaatc ctccgctaat 773
Asp Leu Val Ser Leu Ser Leu Ser Ser Asp Ile
                245                 250

ctt                                                               776
```

<210> 2662
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

<400> 2662

```
Ala Asp Leu Ala Glu Thr Met Leu Gly Leu Leu Thr Leu Glu Thr Ser
  1               5                  10                  15

Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr Leu Ser Ile Thr Glu
             20                  25                  30

Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp Asp Phe Arg Gln Leu
         35                  40                  45

Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile Asn Gly Gly Tyr Ile
     50                  55                  60

His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val His Tyr Pro Pro Leu
 65                  70                  75                  80

Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met Asp Leu Met Glu Leu
                 85                  90                  95

Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala Leu Asp Ala Gln Val
            100                 105                 110

Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly Ala Thr Arg Val Phe
        115                 120                 125

Glu Pro Ala Asp Val Pro Ala Val Val Ile Ile Asp Ser Lys Ala Gln
    130                 135                 140

Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala Thr Thr Asp Arg Trp
145                 150                 155                 160

Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu Ser Arg Gln Thr Ala
                165                 170                 175

Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu Cys Leu Asn Trp Asn
            180                 185                 190

Asn Ser Leu Val Arg Lys Leu Ala Ser Thr Asp Asp Thr Ala Val Val
        195                 200                 205

Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala Leu Leu Ser Ser Lys
    210                 215                 220

Arg Pro Leu Arg Val Lys Glu Arg Ala Leu Leu Asn Asp Ser Leu Ala
225                 230                 235                 240
```

```
Asp Leu Val Ser Leu Ser Leu Ser Ser Asp Ile
                245                 250


<210> 2663
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
<223> RXA02286

<400> 2663
gcagcgcaca cgctttcccc tcagcctgct gataccccg ttttgccacc taaaacaacc 60

tctcatcttc atttcatatt cacttcatag ggttgaatac atg aag aac gca aaa   115
                                          Met Lys Asn Ala Lys
                                            1               5

ctt ttc ctc gcg ctc ata tcc gct cct ctt atc ctc gct ggc tgc agc   163
Leu Phe Leu Ala Leu Ile Ser Ala Pro Leu Ile Leu Ala Gly Cys Ser
                  10                  15                  20

tcc acc gat act gga aca gca gaa tcc acc att tcc agc gaa act gct   211
Ser Thr Asp Thr Gly Thr Ala Glu Ser Thr Ile Ser Ser Glu Thr Ala
              25                  30                  35

tct gca gta gat gcc acc act tct acc tcc tca agt acc gcc acc tct   259
Ser Ala Val Asp Ala Thr Thr Ser Thr Ser Ser Ser Thr Ala Thr Ser
          40                  45                  50

gcc gtg att gat gac gat ccg gta ttc gac atc atc gac atc gtc ctt   307
Ala Val Ile Asp Asp Asp Pro Val Phe Asp Ile Ile Asp Ile Val Leu
      55                  60                  65

gcc caa tac ccc gac agg atc atc acc gac att gac cgc gaa gac tcc   355
Ala Gln Tyr Pro Asp Arg Ile Ile Thr Asp Ile Asp Arg Glu Asp Ser
  70                  75                  80                  85

tcc gat caa tac gaa gtc gat gtt gtg gtt ggc caa gaa gtc ctt gaa   403
Ser Asp Gln Tyr Glu Val Asp Val Val Val Gly Gln Glu Val Leu Glu
                  90                  95                 100

ctt gat gtc acc acc agt ggc cag atc cat acc gac gac cgc gac aac   451
Leu Asp Val Thr Thr Ser Gly Gln Ile His Thr Asp Asp Arg Asp Asn
              105                 110                 115

gat gat gat gac gac atc cgc gaa gct cac gca gcc aca gtc acc gca   499
Asp Asp Asp Asp Asp Ile Arg Glu Ala His Ala Ala Thr Val Thr Ala
          120                 125                 130

gct caa gcc att ggc cta gcg ctg gat caa tac cca gac gga att att   547
Ala Gln Ala Ile Gly Leu Ala Leu Asp Gln Tyr Pro Asp Gly Ile Ile
      135                 140                 145

gat tct gtt gaa tta gac gaa gac gac ggc cag ctg aaa tgg aaa ata   595
Asp Ser Val Glu Leu Asp Glu Asp Asp Gly Gln Leu Lys Trp Lys Ile
150                 155                 160                 165
```

```
gac ctc gat gac act tcc ggc aat gat ctt gct gac gtt gaa atc gca   643
Asp Leu Asp Asp Thr Ser Gly Asn Asp Leu Ala Asp Val Glu Ile Ala
                170                 175                 180

gca gtt taagcacgcg cacggaaagc cac                                 672
Ala Val
```

<210> 2664
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 2664

```
Met Lys Asn Ala Lys Leu Phe Leu Ala Leu Ile Ser Ala Pro Leu Ile
  1               5                  10                  15

Leu Ala Gly Cys Ser Ser Thr Asp Thr Gly Thr Ala Glu Ser Thr Ile
             20                  25                  30

Ser Ser Glu Thr Ala Ser Ala Val Asp Ala Thr Thr Ser Thr Ser Ser
         35                  40                  45

Ser Thr Ala Thr Ser Ala Val Ile Asp Asp Asp Pro Val Phe Asp Ile
     50                  55                  60

Ile Asp Ile Val Leu Ala Gln Tyr Pro Asp Arg Ile Ile Thr Asp Ile
 65                  70                  75                  80

Asp Arg Glu Asp Ser Ser Asp Gln Tyr Glu Val Asp Val Val Val Gly
                 85                  90                  95

Gln Glu Val Leu Glu Leu Asp Val Thr Thr Ser Gly Gln Ile His Thr
            100                 105                 110

Asp Asp Arg Asp Asn Asp Asp Asp Asp Asp Ile Arg Glu Ala His Ala
        115                 120                 125

Ala Thr Val Thr Ala Ala Gln Ala Ile Gly Leu Ala Leu Asp Gln Tyr
    130                 135                 140

Pro Asp Gly Ile Ile Asp Ser Val Glu Leu Asp Glu Asp Asp Gly Gln
145                 150                 155                 160

Leu Lys Trp Lys Ile Asp Leu Asp Asp Thr Ser Gly Asn Asp Leu Ala
                165                 170                 175

Asp Val Glu Ile Ala Ala Val
            180
```

<210> 2665
<211> 675
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(652)

<223> RXA02287

<400> 2665

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ttgaaaaagg aacattagtg ccagtaacaa gagcccagtt gaattcaagc gggcagagac 60

acatctggcc ctcaaaattt tccttttact ggagaccact gtg tac tca att tca   115
                                              Val Tyr Ser Ile Ser
                                                1               5

gaa act atc gcc cga act ctt atg ccc cgc acc gat cac gtt ttc gac   163
Glu Thr Ile Ala Arg Thr Leu Met Pro Arg Thr Asp His Val Phe Asp
                10                  15                  20

ctg atg ggc aac gga aac gcc tgg ttc gtc gat gcc cta gaa cgc ctc   211
Leu Met Gly Asn Gly Asn Ala Trp Phe Val Asp Ala Leu Glu Arg Leu
            25                  30                  35

ggg cga ggc atc atc acc gtc cgc ccc aca gtt gaa acc gtg gcc gcc   259
Gly Arg Gly Ile Ile Thr Val Arg Pro Thr Val Glu Thr Val Ala Ala
        40                  45                  50

gcg gac acc tac cac cgc gtc acc cgc cgc ccg gcg gtc gct acc acc   307
Ala Asp Thr Tyr His Arg Val Thr Arg Arg Pro Ala Val Ala Thr Thr
    55                  60                  65

acc tat ggt gct ggt ttc acc aac acc atg acc acg ctt gcc gac gtc   355
Thr Tyr Gly Ala Gly Phe Thr Asn Thr Met Thr Thr Leu Ala Asp Val
70                  75                  80                  85

gcc ctc tcc cgt atc cca ctt ctt tta gtt gtg ggc act gcc ccg agc   403
Ala Leu Ser Arg Ile Pro Leu Leu Leu Val Val Gly Thr Ala Pro Ser
                90                  95                  100

gcc ggg cct cgc tgt ttc gac att gac cgg caa gga ctc gca cgt gcc   451
Ala Gly Pro Arg Cys Phe Asp Ile Asp Arg Gln Gly Leu Ala Arg Ala
            105                 110                 115

gta ggt gtg gaa acc ttc acc gtg cat gca gat gac gtt gct gcg gta   499
Val Gly Val Glu Thr Phe Thr Val His Ala Asp Asp Val Ala Ala Val
        120                 125                 130

act ctt cag gct tgg aat aat acg ccg gaa aac aca cac gtg atc ctg   547
Thr Leu Gln Ala Trp Asn Asn Thr Pro Glu Asn Thr His Val Ile Leu
    135                 140                 145

gaa atc ccc tat gac cta gca gct gcc aca gcc acc gat cca aca gtg   595
Glu Ile Pro Tyr Asp Leu Ala Ala Ala Thr Ala Thr Asp Pro Thr Val
150                 155                 160                 165

act aca tac ctg ctg cgc ccc gga ttt cag aaa ctc ccg atg tca ccg   643
Thr Thr Tyr Leu Leu Arg Pro Gly Phe Gln Lys Leu Pro Met Ser Pro
                170                 175                 180

acc ttg tcc tagctctacg caatgcccaa aat                            675
Thr Leu Ser
```

<210> 2666
<211> 184
<212> PRT

<213> Corynebacterium glutamicum

<400> 2666

```
Val Tyr Ser Ile Ser Glu Thr Ile Ala Arg Thr Leu Met Pro Arg Thr
  1               5                  10                  15

Asp His Val Phe Asp Leu Met Gly Asn Gly Asn Ala Trp Phe Val Asp
             20                  25                  30

Ala Leu Glu Arg Leu Gly Arg Gly Ile Ile Thr Val Arg Pro Thr Val
         35                  40                  45

Glu Thr Val Ala Ala Ala Asp Thr Tyr His Arg Val Thr Arg Arg Pro
     50                  55                  60

Ala Val Ala Thr Thr Thr Tyr Gly Ala Gly Phe Thr Asn Thr Met Thr
 65                  70                  75                  80

Thr Leu Ala Asp Val Ala Leu Ser Arg Ile Pro Leu Leu Leu Val Val
                 85                  90                  95

Gly Thr Ala Pro Ser Ala Gly Pro Arg Cys Phe Asp Ile Asp Arg Gln
            100                 105                 110

Gly Leu Ala Arg Ala Val Gly Val Glu Thr Phe Thr Val His Ala Asp
        115                 120                 125

Asp Val Ala Ala Val Thr Leu Gln Ala Trp Asn Asn Thr Pro Glu Asn
    130                 135                 140

Thr His Val Ile Leu Glu Ile Pro Tyr Asp Leu Ala Ala Ala Thr Ala
145                 150                 155                 160

Thr Asp Pro Thr Val Thr Thr Tyr Leu Leu Arg Pro Gly Phe Gln Lys
                165                 170                 175

Leu Pro Met Ser Pro Thr Leu Ser
            180
```

<210> 2667
<211> 498
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(475)
<223> RXA02294

<400> 2667

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tacctcacct ggcaacaaat ccaaggaatg tagataagtc ggggcaaact ctaagaaatc 60

atcctggttt gtggcaggga acattcctag gatgggaggc atg gca aag aca aaa   115
                                              Met Ala Lys Thr Lys
                                                1               5

cta gaa agc atc tcc gag cgc aac tcg gat gat ccg ctt agt tac ccc   163
Leu Glu Ser Ile Ser Glu Arg Asn Ser Asp Asp Pro Leu Ser Tyr Pro
                10                  15                  20
```

```
gac ctg act ctt gca cca ata tcc aca aca gtc aca gtc gtg gtc gcc   211
Asp Leu Thr Leu Ala Pro Ile Ser Thr Thr Val Thr Val Val Val Ala
             25                  30                  35

gaa gac acc cca aac gat aac ttc tca gaa ctt ctc ctc ggc gca gca   259
Glu Asp Thr Pro Asn Asp Asn Phe Ser Glu Leu Leu Leu Gly Ala Ala
         40                  45                  50

gaa tca acc cgt ctt tta gga ctc gac gag ctc cac atc atc gct cca   307
Glu Ser Thr Arg Leu Leu Gly Leu Asp Glu Leu His Ile Ile Ala Pro
     55                  60                  65

tca gtc cac cta ccc gct ctc gca gta gca gcc gcc gac atc gca cac   355
Ser Val His Leu Pro Ala Leu Ala Val Ala Ala Ala Asp Ile Ala His
 70                  75                  80                  85

cat ctg cca gag aaa ttc caa ttc tgt gaa gcc gaa acc tgc act cat   403
His Leu Pro Glu Lys Phe Gln Phe Cys Glu Ala Glu Thr Cys Thr His
                 90                  95                 100

ctc cac ccc gac gat gac acc tat ctc acg gct gaa tcc gtt gct caa   451
Leu His Pro Asp Asp Asp Thr Tyr Leu Thr Ala Glu Ser Val Ala Gln
            105                 110                 115

ttg ggt acg aag ctg aag tct gcg tagttgttag gagccaccac aga         498
Leu Gly Thr Lys Leu Lys Ser Ala
        120                 125
```

09500750.090501

<210> 2668
<211> 125
<212> PRT
<213> Corynebacterium glutamicum

<400> 2668

```
Met Ala Lys Thr Lys Leu Glu Ser Ile Ser Glu Arg Asn Ser Asp Asp
  1               5                  10                  15

Pro Leu Ser Tyr Pro Asp Leu Thr Leu Ala Pro Ile Ser Thr Thr Val
             20                  25                  30

Thr Val Val Val Ala Glu Asp Thr Pro Asn Asp Asn Phe Ser Glu Leu
         35                  40                  45

Leu Leu Gly Ala Ala Glu Ser Thr Arg Leu Leu Gly Leu Asp Glu Leu
     50                  55                  60

His Ile Ile Ala Pro Ser Val His Leu Pro Ala Leu Ala Val Ala Ala
 65                  70                  75                  80

Ala Asp Ile Ala His His Leu Pro Glu Lys Phe Gln Phe Cys Glu Ala
                 85                  90                  95

Glu Thr Cys Thr His Leu His Pro Asp Asp Asp Thr Tyr Leu Thr Ala
            100                 105                 110

Glu Ser Val Ala Gln Leu Gly Thr Lys Leu Lys Ser Ala
        115                 120                 125
```

<210> 2669

<211> 903
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(880)
<223> RXA02295

<400> 2669
ttcccatgct aatccgcgaa aatggcactt caacagccat atactttaaa caacacaaat 60

gatgcaagac tgataccggg atgtgatagg agcgcaccac atg ggg ttg gaa tta 115
Met Gly Leu Glu Leu
1 5

gca gct agc ggg tgg ggc atc ctc atc gca ggc gcc gcc gta gcc gga 163
Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly Ala Ala Val Ala Gly
10 15 20

tgg atc gac gca gta atc ggc ggt ggc gga ctc gtc ctc atc ccg ctg 211
Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu Val Leu Ile Pro Leu
25 30 35

atc ctc gcg gtc atg ccg caa ctc gca cct gtg aca gcg ctg gcc tcc 259
Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val Thr Ala Leu Ala Ser
40 45 50

aac aaa ctg gca gcc gtc acc ggc acg gca tcg gcg gca ttc acc ctg 307
Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser Ala Ala Phe Thr Leu
55 60 65

gtc agg cgc gtc aaa ccc gac aaa aaa ctg ctt gcg ctc tac gtt ctg 355
Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu Ala Leu Tyr Val Leu
70 75 80 85

gtg gca gct gtg tgc tcc ggt gca ggc gcc ctg gct gcg agt ctc att 403
Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu Ala Ala Ser Leu Ile
90 95 100

gac aaa caa atc atg cga ccg ctg atc atc gtg ttg atg ctg gtc gtt 451
Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val Leu Met Leu Val Val
105 110 115

ggc ctg atc gtg gtg ttc aaa cca aac ttc gga acc ggc gaa agc aaa 499
Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly Thr Gly Glu Ser Lys
120 125 130

gcc ctg ccc acc gga tgg aaa cgc tgg gcc gcc atc gtt gca gtc gga 547
Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala Ile Val Ala Val Gly
135 140 145

ctc atc gca gcc tac gac ggc atc ttc gga ccc gga acc ggc atg ttc 595
Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro Gly Thr Gly Met Phe
150 155 160 165

ctc atc atg gcg ttc acc gca ctg ctc tcc caa aat ttc ctg tcc tcc 643
Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln Asn Phe Leu Ser Ser
170 175 180

gca gcc atg gcg aag gtc gta aac acc gca aca aac ctg ggt gcg cta 691

```
Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu
            185                 190                 195

att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg   739
Ile Val Phe Ile Ile Gly Gly His Met Trp Trp Thr Leu Gly Leu Val
        200                 205                 210

ctg gca gtc gcc aat gtc gca ggc gca caa ctc ggt gcc cga acg gtg   787
Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu Gly Ala Arg Thr Val
    215                 220                 225

ctt ggt ggc ggt acc agg cta att aga tac gca cta cta acc ctg gtt   835
Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val
230                 235                 240                 245

gtc gtc atg agc gtc tac ctc acc tgg caa caa atc caa gga atg       880
Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln Ile Gln Gly Met
                250                 255                 260

tagataagtc ggggcaaact cta                                       903
```

<210> 2670
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

<400> 2670

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Met Gly Leu Glu Leu Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly
  1               5                  10                  15

Ala Ala Val Ala Gly Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu
            20                  25                  30

Val Leu Ile Pro Leu Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val
        35                  40                  45

Thr Ala Leu Ala Ser Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser
    50                  55                  60

Ala Ala Phe Thr Leu Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu
65                  70                  75                  80

Ala Leu Tyr Val Leu Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu
                85                  90                  95

Ala Ala Ser Leu Ile Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val
            100                 105                 110

Leu Met Leu Val Val Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly
        115                 120                 125

Thr Gly Glu Ser Lys Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala
    130                 135                 140

Ile Val Ala Val Gly Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro
145                 150                 155                 160

Gly Thr Gly Met Phe Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln
                165                 170                 175
```

```
Asn Phe Leu Ser Ser Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr
            180                 185                 190

Asn Leu Gly Ala Leu Ile Val Phe Ile Ile Gly Gly His Met Trp Trp
        195                 200                 205

Thr Leu Gly Leu Val Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu
    210                 215                 220

Gly Ala Arg Thr Val Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala
225                 230                 235                 240

Leu Leu Thr Leu Val Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln
                245                 250                 255

Ile Gln Gly Met
            260
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<210> 2671
<211> 1260
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1237)
<223> RXA02297

<400> 2671

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tgctgatcac gcctgactcc tatgaagtgt tgaccgattc cgctgctaaa gtgaaagcga 60

cattatgaaa taaacgtgga tcaaggagtc cggtgcccaa ttg agc gat aaa gaa   115
                                            Leu Ser Asp Lys Glu
                                              1               5

cca gac ccc cac gaa caa att cca gag aag cca tcc cgc aag gtt att   163
Pro Asp Pro His Glu Gln Ile Pro Glu Lys Pro Ser Arg Lys Val Ile
                  10                  15                  20

gca ctt cgt tgg tgc atc gta gcg ccg ctg tcg cta gcc gtg ggg tgg   211
Ala Leu Arg Trp Cys Ile Val Ala Pro Leu Ser Leu Ala Val Gly Trp
              25                  30                  35

ctt ttt act atg tgg ggt gtg cca gcc gca tgg atc ctc ggg gcg atc   259
Leu Phe Thr Met Trp Gly Val Pro Ala Ala Trp Ile Leu Gly Ala Ile
          40                  45                  50

ctt gtt gcc ggt gta tgt gcg ctg acc aca ggg caa gat ctt ccg atg   307
Leu Val Ala Gly Val Cys Ala Leu Thr Thr Gly Gln Asp Leu Pro Met
      55                  60                  65

gcc aag ggg gtg cat gtt ttt ggt cgc tca atc gtg gcg atg ctg gcg   355
Ala Lys Gly Val His Val Phe Gly Arg Ser Ile Val Ala Met Leu Ala
  70                  75                  80                  85

gcg ctg cct ttg att agt tct tct ggt tcg gaa ctt gtt cgt ttc ctc   403
Ala Leu Pro Leu Ile Ser Ser Ser Gly Ser Glu Leu Val Arg Phe Leu
                  90                  95                  100

atc ccg ggt ctt gtg att tcc ttt ttc acc atc gcg gta ggc atc gtt   451
```

```
Ile Pro Gly Leu Val Ile Ser Phe Phe Thr Ile Ala Val Gly Ile Val
            105                 110                 115

ggt ggt ttg ttg ctg gca aga tcc agg ccg gag att ttg ccg gaa act   499
Gly Gly Leu Leu Leu Ala Arg Ser Arg Pro Glu Ile Leu Pro Glu Thr
        120                 125                 130

ggt gtg ctg tcc atg ctg gcg ggt ggc gcg tcg gtg atg ccg att ctg   547
Gly Val Leu Ser Met Leu Ala Gly Gly Ala Ser Val Met Pro Ile Leu
    135                 140                 145

gcc cga gag ttg ggc gct gat ttc cgc tat gtg gcg ctg acg cag tac   595
Ala Arg Glu Leu Gly Ala Asp Phe Arg Tyr Val Ala Leu Thr Gln Tyr
150                 155                 160                 165

ctc agg ttg ttg gtt gtg tcc atg acg ttg ccg ctg gtg acg cac ttt   643
Leu Arg Leu Leu Val Val Ser Met Thr Leu Pro Leu Val Thr His Phe
                170                 175                 180

ttc gtc cct ggc ggg gcg gat ttg gga tcg ccg cct gag aaa tgg ttg   691
Phe Val Pro Gly Gly Ala Asp Leu Gly Ser Pro Pro Glu Lys Trp Leu
            185                 190                 195

gac gtg ttg agt ttg gga gag ttc ggg acg tcg ata agc gtt tta tcg   739
Asp Val Leu Ser Leu Gly Glu Phe Gly Thr Ser Ile Ser Val Leu Ser
        200                 205                 210

ctg ctg gtg ctc ttc ggt att gtg ctg gcc ggc gaa cct ctc ggc agg   787
Leu Leu Val Leu Phe Gly Ile Val Leu Ala Gly Glu Pro Leu Gly Arg
    215                 220                 225

ttg ctg cgc ttg cct gcc cct gcg gtg atg ggg ccg ctg atc ctg acc   835
Leu Leu Arg Leu Pro Ala Pro Ala Val Met Gly Pro Leu Ile Leu Thr
230                 235                 240                 245

gtg ctg gtg agt ttt gtg att cca gat gat ctc agc ctg caa ccg cca   883
Val Leu Val Ser Phe Val Ile Pro Asp Asp Leu Ser Leu Gln Pro Pro
                250                 255                 260

acc gtg ttt aag att atc gcg ttc atg gcg atc ggt tgg atg tgt ggc   931
Thr Val Phe Lys Ile Ile Ala Phe Met Ala Ile Gly Trp Met Cys Gly
            265                 270                 275

ggt ccc ttg aat atg acc gcg ctg aag gtg ttt tct aag cag ctt ccg   979
Gly Pro Leu Asn Met Thr Ala Leu Lys Val Phe Ser Lys Gln Leu Pro
        280                 285                 290

gcc acg ttc ttg ttt att ttc gcg ctg ctt gcg gtg tgc gca ggt gcg   1027
Ala Thr Phe Leu Phe Ile Phe Ala Leu Leu Ala Val Cys Ala Gly Ala
    295                 300                 305

gcg ggg ctg ctc acc tgg tgg ttg gat atc agc ttc ttc gag gct tac   1075
Ala Gly Leu Leu Thr Trp Trp Leu Asp Ile Ser Phe Phe Glu Ala Tyr
310                 315                 320                 325

cta gca acc agc cct gga gct ctg gag acg gtg ttg gcg ctg tcc tcg   1123
Leu Ala Thr Ser Pro Gly Ala Leu Glu Thr Val Leu Ala Leu Ser Ser
                330                 335                 340

gaa gga tct gca ggc ccg gtg gtg gtc acg atc cag atc att cga cta   1171
Glu Gly Ser Ala Gly Pro Val Val Val Thr Ile Gln Ile Ile Arg Leu
```

```
            345                 350                 355

ctg gca atc ttg acc atc gcc ggt ttg atc ccc acg cta ctg cga cgc   1219
Leu Ala Ile Leu Thr Ile Ala Gly Leu Ile Pro Thr Leu Leu Arg Arg
        360                 365                 370

att ttg cgt agg gat cgt taaaggcctt ctagttcagc acc                1260
Ile Leu Arg Arg Asp Arg
    375
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<210> 2672
<211> 379
<212> PRT
<213> Corynebacterium glutamicum

<400> 2672

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Leu Ser Asp Lys Glu Pro Asp Pro His Glu Gln Ile Pro Glu Lys Pro
  1               5                  10                  15

Ser Arg Lys Val Ile Ala Leu Arg Trp Cys Ile Val Ala Pro Leu Ser
             20                  25                  30

Leu Ala Val Gly Trp Leu Phe Thr Met Trp Gly Val Pro Ala Ala Trp
         35                  40                  45

Ile Leu Gly Ala Ile Leu Val Ala Gly Val Cys Ala Leu Thr Thr Gly
     50                  55                  60

Gln Asp Leu Pro Met Ala Lys Gly Val His Val Phe Gly Arg Ser Ile
 65                  70                  75                  80

Val Ala Met Leu Ala Ala Leu Pro Leu Ile Ser Ser Ser Gly Ser Glu
                 85                  90                  95

Leu Val Arg Phe Leu Ile Pro Gly Leu Val Ile Ser Phe Phe Thr Ile
            100                 105                 110

Ala Val Gly Ile Val Gly Gly Leu Leu Leu Ala Arg Ser Arg Pro Glu
        115                 120                 125

Ile Leu Pro Glu Thr Gly Val Leu Ser Met Leu Ala Gly Gly Ala Ser
    130                 135                 140

Val Met Pro Ile Leu Ala Arg Glu Leu Gly Ala Asp Phe Arg Tyr Val
145                 150                 155                 160

Ala Leu Thr Gln Tyr Leu Arg Leu Leu Val Val Ser Met Thr Leu Pro
                165                 170                 175

Leu Val Thr His Phe Phe Val Pro Gly Gly Ala Asp Leu Gly Ser Pro
            180                 185                 190

Pro Glu Lys Trp Leu Asp Val Leu Ser Leu Gly Glu Phe Gly Thr Ser
        195                 200                 205

Ile Ser Val Leu Ser Leu Leu Val Leu Phe Gly Ile Val Leu Ala Gly
    210                 215                 220

Glu Pro Leu Gly Arg Leu Leu Arg Leu Pro Ala Pro Ala Val Met Gly
225                 230                 235                 240
```

```
Pro Leu Ile Leu Thr Val Leu Val Ser Phe Val Ile Pro Asp Asp Leu
               245                 250                 255

Ser Leu Gln Pro Pro Thr Val Phe Lys Ile Ile Ala Phe Met Ala Ile
            260                 265                 270

Gly Trp Met Cys Gly Gly Pro Leu Asn Met Thr Ala Leu Lys Val Phe
        275                 280                 285

Ser Lys Gln Leu Pro Ala Thr Phe Leu Phe Ile Phe Ala Leu Leu Ala
    290                 295                 300

Val Cys Ala Gly Ala Ala Gly Leu Leu Thr Trp Trp Leu Asp Ile Ser
305                 310                 315                 320

Phe Phe Glu Ala Tyr Leu Ala Thr Ser Pro Gly Ala Leu Glu Thr Val
                325                 330                 335

Leu Ala Leu Ser Ser Glu Gly Ser Ala Gly Pro Val Val Val Thr Ile
            340                 345                 350

Gln Ile Ile Arg Leu Leu Ala Ile Leu Thr Ile Ala Gly Leu Ile Pro
        355                 360                 365

Thr Leu Leu Arg Arg Ile Leu Arg Arg Asp Arg
    370                 375
```

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<210> 2673
<211> 1782
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1759)
<223> RXA02298

<400> 2673

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aaatcatagc gtgagatgac aaggaaagga atatttcgat ccggcaacaa cccccgcgtc 60

aggtgggatt atgccgaaaa aatcgctacg atagccactt atg act ctt cag agt   115
                                              Met Thr Leu Gln Ser
                                                1               5

tct gat aaa cgt tct cct tca ctg tta gac gcc tcc tcc gag gtc ttt   163
Ser Asp Lys Arg Ser Pro Ser Leu Leu Asp Ala Ser Ser Glu Val Phe
                  10                  15                  20

gtc cat gat ttg gca gct ttg tct ccc act gat gcc act gca tgg ggt   211
Val His Asp Leu Ala Ala Leu Ser Pro Thr Asp Ala Thr Ala Trp Gly
              25                  30                  35

atc tca ggc ttc gaa ggt gat ctt cag gat ttc tct cct gac tat tgg   259
Ile Ser Gly Phe Glu Gly Asp Leu Gln Asp Phe Ser Pro Asp Tyr Trp
          40                  45                  50

aat gcc atc gcc gaa cgc aac cgc gac atg gtt gcc gat gtt gat gct   307
Asn Ala Ile Ala Glu Arg Asn Arg Asp Met Val Ala Asp Val Asp Ala
      55                  60                  65
```

```
ttt gat gac ggc act gat gac aac gat gac gaa gaa gat ttc gat gac   355
Phe Asp Asp Gly Thr Asp Asp Asn Asp Asp Glu Glu Asp Phe Asp Asp
 70                  75                  80                  85

gtt gac cgc gtc acc gct gat gtt ctc cgt gat cgc gta tgc ctg gat   403
Val Asp Arg Val Thr Ala Asp Val Leu Arg Asp Arg Val Cys Leu Asp
                 90                  95                 100

ctg gcc ctg cac cac cag ggc gaa acc tta gcg aat ctc aac aac att   451
Leu Ala Leu His His Gln Gly Glu Thr Leu Ala Asn Leu Asn Asn Ile
            105                 110                 115

gat tcc cca gtc cag acc atc cgc gat acc ttc ctc atc atg ccc cgc   499
Asp Ser Pro Val Gln Thr Ile Arg Asp Thr Phe Leu Ile Met Pro Arg
        120                 125                 130

gag acg gac gat gat gtg gaa aat ctc cgc gaa cgt ctc tcc cgc gtc   547
Glu Thr Asp Asp Asp Val Glu Asn Leu Arg Glu Arg Leu Ser Arg Val
    135                 140                 145

ccc gac gct ctc cac gga tac tgt gaa tca ctc gct gag gct gcc agc   595
Pro Asp Ala Leu His Gly Tyr Cys Glu Ser Leu Ala Glu Ala Ala Ser
150                 155                 160                 165

caa ggc cat gtt gca gcg gtc cgc cag gtg gaa gaa gtg gtg tcg caa   643
Gln Gly His Val Ala Ala Val Arg Gln Val Glu Glu Val Val Ser Gln
                170                 175                 180

tgt gag gac ctc gct gat gag gac tcc gtt ttg cag cac ctt ggc ttg   691
Cys Glu Asp Leu Ala Asp Glu Asp Ser Val Leu Gln His Leu Gly Leu
            185                 190                 195

gat gaa aat gat cca gta gtt gta gag gcc cag gaa gct ttt gca cga   739
Asp Glu Asn Asp Pro Val Val Val Glu Ala Gln Glu Ala Phe Ala Arg
        200                 205                 210

gtt gcc ggt tgg tta gca gag caa ctg gct ccg cat gct cct cat gtg   787
Val Ala Gly Trp Leu Ala Glu Gln Leu Ala Pro His Ala Pro His Val
    215                 220                 225

gat gcg gtt ggc cgg gat cgc tat gaa atg ttc tcc cac ctg cac gtc   835
Asp Ala Val Gly Arg Asp Arg Tyr Glu Met Phe Ser His Leu His Val
230                 235                 240                 245

ggc gag ttt gta gat ctg gat gag gct tac caa tgg tcc ctg gaa cag   883
Gly Glu Phe Val Asp Leu Asp Glu Ala Tyr Gln Trp Ser Leu Glu Gln
                250                 255                 260

ctg cgt gac att gat gct cag cag ctt cag gta gcc cag cag ctg tac   931
Leu Arg Asp Ile Asp Ala Gln Gln Leu Gln Val Ala Gln Gln Leu Tyr
            265                 270                 275

ggc cct ggc acc acg atc cgt gag gcc atg aag aag ctc aat gct gat   979
Gly Pro Gly Thr Thr Ile Arg Glu Ala Met Lys Lys Leu Asn Ala Asp
        280                 285                 290

gag cgc tac ctc atc cga ggc act gat gct ctg cag gag tgg atg caa   1027
Glu Arg Tyr Leu Ile Arg Gly Thr Asp Ala Leu Gln Glu Trp Met Gln
    295                 300                 305
```

```
aag acc gct gat cag gca atc gct gat cta gat ggc gtt tcc ttc aac   1075
Lys Thr Ala Asp Gln Ala Ile Ala Asp Leu Asp Gly Val Ser Phe Asn
310                 315                 320                 325

att cca gag cag gct cga cag gtt gag tgc ctc atc gat cct gct gga   1123
Ile Pro Glu Gln Ala Arg Gln Val Glu Cys Leu Ile Asp Pro Ala Gly
                330                 335                 340

act ggc ggc att ttc tac acc cca cca agc gat gat ttc tcc agg cct   1171
Thr Gly Gly Ile Phe Tyr Thr Pro Pro Ser Asp Asp Phe Ser Arg Pro
            345                 350                 355

ggc cgc atg tgg tgg tct gtg cct aaa acc cag gaa gtc ttc cac acc   1219
Gly Arg Met Trp Trp Ser Val Pro Lys Thr Gln Glu Val Phe His Thr
        360                 365                 370

tgg caa gag ctc acc acc gtg ttc cac gag ggt gtt cct ggc cac cac   1267
Trp Gln Glu Leu Thr Thr Val Phe His Glu Gly Val Pro Gly His His
    375                 380                 385

ctg cag atc tcc caa act ttg gtg gaa aag gat ctg aac ctg tgg cgt   1315
Leu Gln Ile Ser Gln Thr Leu Val Glu Lys Asp Leu Asn Leu Trp Arg
390                 395                 400                 405

cga gtc gct tgc tgg aac tct ggc cac ggt gaa ggt tgg gcg ctg tac   1363
Arg Val Ala Cys Trp Asn Ser Gly His Gly Glu Gly Trp Ala Leu Tyr
                410                 415                 420

gca gaa tct ctc atg aag gaa ttg gga tac cac gaa gat cca ggc aac   1411
Ala Glu Ser Leu Met Lys Glu Leu Gly Tyr His Glu Asp Pro Gly Asn
            425                 430                 435

ctc atg ggc tac ctt gat gct cag cga ctc cgt gca gcc cgc gtg gcc   1459
Leu Met Gly Tyr Leu Asp Ala Gln Arg Leu Arg Ala Ala Arg Val Ala
        440                 445                 450

att gac atc gga att cac ctg aac aag agg aac cca gag tgc acc ggc   1507
Ile Asp Ile Gly Ile His Leu Asn Lys Arg Asn Pro Glu Cys Thr Gly
    455                 460                 465

ctg tgg gat gcg tct tat gcg cgc agc ttc ctg cgt gaa aat acg tcc   1555
Leu Trp Asp Ala Ser Tyr Ala Arg Ser Phe Leu Arg Glu Asn Thr Ser
470                 475                 480                 485

atg aat gaa gat gcg ctg tac ttt gag ctc aac cgt tac ctt ggt tgg   1603
Met Asn Glu Asp Ala Leu Tyr Phe Glu Leu Asn Arg Tyr Leu Gly Trp
                490                 495                 500

cca ggt cag gcc gca tcg tat gcc att ggt cag cga ctc tgg ttg aac   1651
Pro Gly Gln Ala Ala Ser Tyr Ala Ile Gly Gln Arg Leu Trp Leu Asn
            505                 510                 515

ctg cgc gat gag gcc att agc cag ggg caa acc ttg gcg caa ttc cac   1699
Leu Arg Asp Glu Ala Ile Ser Gln Gly Gln Thr Leu Ala Gln Phe His
        520                 525                 530

agc aag gca ttg tcc tat ggc agc atc ccg atg ggc att ttg cgc gat   1747
Ser Lys Ala Leu Ser Tyr Gly Ser Ile Pro Met Gly Ile Leu Arg Asp
    535                 540                 545

cag gtg ctg aac tagaaggcct ttaacgatcc cta                         1782
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Gln Val Leu Asn
550

<210> 2674
<211> 553
<212> PRT
<213> Corynebacterium glutamicum

<400> 2674
Met Thr Leu Gln Ser Ser Asp Lys Arg Ser Pro Ser Leu Leu Asp Ala
1 5 10 15

Ser Ser Glu Val Phe Val His Asp Leu Ala Ala Leu Ser Pro Thr Asp
20 25 30

Ala Thr Ala Trp Gly Ile Ser Gly Phe Glu Gly Asp Leu Gln Asp Phe
35 40 45

Ser Pro Asp Tyr Trp Asn Ala Ile Ala Glu Arg Asn Arg Asp Met Val
50 55 60

Ala Asp Val Asp Ala Phe Asp Asp Gly Thr Asp Asp Asn Asp Asp Glu
65 70 75 80

Glu Asp Phe Asp Asp Val Asp Arg Val Thr Ala Asp Val Leu Arg Asp
85 90 95

Arg Val Cys Leu Asp Leu Ala Leu His His Gln Gly Glu Thr Leu Ala
100 105 110

Asn Leu Asn Asn Ile Asp Ser Pro Val Gln Thr Ile Arg Asp Thr Phe
115 120 125

Leu Ile Met Pro Arg Glu Thr Asp Asp Asp Val Glu Asn Leu Arg Glu
130 135 140

Arg Leu Ser Arg Val Pro Asp Ala Leu His Gly Tyr Cys Glu Ser Leu
145 150 155 160

Ala Glu Ala Ala Ser Gln Gly His Val Ala Ala Val Arg Gln Val Glu
165 170 175

Glu Val Val Ser Gln Cys Glu Asp Leu Ala Asp Glu Asp Ser Val Leu
180 185 190

Gln His Leu Gly Leu Asp Glu Asn Asp Pro Val Val Val Glu Ala Gln
195 200 205

Glu Ala Phe Ala Arg Val Ala Gly Trp Leu Ala Glu Gln Leu Ala Pro
210 215 220

His Ala Pro His Val Asp Ala Val Gly Arg Asp Arg Tyr Glu Met Phe
225 230 235 240

Ser His Leu His Val Gly Glu Phe Val Asp Leu Asp Glu Ala Tyr Gln
245 250 255

Trp Ser Leu Glu Gln Leu Arg Asp Ile Asp Ala Gln Gln Leu Gln Val
260 265 270

Ala Gln Gln Leu Tyr Gly Pro Gly Thr Thr Ile Arg Glu Ala Met Lys
275 280 285

Lys Leu Asn Ala Asp Glu Arg Tyr Leu Ile Arg Gly Thr Asp Ala Leu
290 295 300

Gln Glu Trp Met Gln Lys Thr Ala Asp Gln Ala Ile Ala Asp Leu Asp
305 310 315 320

Gly Val Ser Phe Asn Ile Pro Glu Gln Ala Arg Gln Val Glu Cys Leu
325 330 335

Ile Asp Pro Ala Gly Thr Gly Gly Ile Phe Tyr Thr Pro Pro Ser Asp
340 345 350

Asp Phe Ser Arg Pro Gly Arg Met Trp Trp Ser Val Pro Lys Thr Gln
355 360 365

Glu Val Phe His Thr Trp Gln Glu Leu Thr Thr Val Phe His Glu Gly
370 375 380

Val Pro Gly His His Leu Gln Ile Ser Gln Thr Leu Val Glu Lys Asp
385 390 395 400

Leu Asn Leu Trp Arg Arg Val Ala Cys Trp Asn Ser Gly His Gly Glu
405 410 415

Gly Trp Ala Leu Tyr Ala Glu Ser Leu Met Lys Glu Leu Gly Tyr His
420 425 430

Glu Asp Pro Gly Asn Leu Met Gly Tyr Leu Asp Ala Gln Arg Leu Arg
435 440 445

Ala Ala Arg Val Ala Ile Asp Ile Gly Ile His Leu Asn Lys Arg Asn
450 455 460

Pro Glu Cys Thr Gly Leu Trp Asp Ala Ser Tyr Ala Arg Ser Phe Leu
465 470 475 480

Arg Glu Asn Thr Ser Met Asn Glu Asp Ala Leu Tyr Phe Glu Leu Asn
485 490 495

Arg Tyr Leu Gly Trp Pro Gly Gln Ala Ala Ser Tyr Ala Ile Gly Gln
500 505 510

Arg Leu Trp Leu Asn Leu Arg Asp Glu Ala Ile Ser Gln Gly Gln Thr
515 520 525

Leu Ala Gln Phe His Ser Lys Ala Leu Ser Tyr Gly Ser Ile Pro Met
530 535 540

Gly Ile Leu Arg Asp Gln Val Leu Asn
545 550

<210> 2675
<211> 1014
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(991)
<223> RXA02304

<400> 2675
ctagccatca ttggtagttc ctaattgttt ccgtacagta tagctccagc acaacttctg 60

agtgcaagtt ttttataaca gggcagtaac gtttactggt atg aaa act ccc cgt 115
Met Lys Thr Pro Arg
1 5

ctg ctg aag atc ctc agc gcg atg gtg gct gtc act gga ctt ctc att 163
Leu Leu Lys Ile Leu Ser Ala Met Val Ala Val Thr Gly Leu Leu Ile
10 15 20

cca acg gtg gtc ccc atg gcc gcc gct gat gct gct gaa ctg tcc gac 211
Pro Thr Val Val Pro Met Ala Ala Ala Asp Ala Ala Glu Leu Ser Asp
25 30 35

aac gtt ccc gat cgc acc caa att gcc atc atc aac cct gat ggc agc 259
Asn Val Pro Asp Arg Thr Gln Ile Ala Ile Ile Asn Pro Asp Gly Ser
40 45 50

gtg caa gaa tct gac aac gcc gaa gaa tcc cgc ccg gca tta tcc ctg 307
Val Gln Glu Ser Asp Asn Ala Glu Glu Ser Arg Pro Ala Leu Ser Leu
55 60 65

gcc aag ctg tat ttg ggt tat tat gtg ttg gct caa ggc gcg gaa gaa 355
Ala Lys Leu Tyr Leu Gly Tyr Tyr Val Leu Ala Gln Gly Ala Glu Glu
70 75 80 85

gat att gaa cta gtc cca gat atg atc cgc tac tct gat gat ttc acc 403
Asp Ile Glu Leu Val Pro Asp Met Ile Arg Tyr Ser Asp Asp Phe Thr
90 95 100

gcg gat tat ttg gag agc gaa tac ccg gaa gca att cct gag gtt att 451
Ala Asp Tyr Leu Glu Ser Glu Tyr Pro Glu Ala Ile Pro Glu Val Ile
105 110 115

gat gcc ttc gat ttg gaa gac acc gaa tgg gct ggt ttc tgg ggc aat 499
Asp Ala Phe Asp Leu Glu Asp Thr Glu Trp Ala Gly Phe Trp Gly Asn
120 125 130

gca act acc agt gcg gtg gat att gcg acg ttt gta gca gca ctc atc 547
Ala Thr Thr Ser Ala Val Asp Ile Ala Thr Phe Val Ala Ala Leu Ile
135 140 145

gac gat ccc acg gcg cag ccc ttg ctt gac gca atg tct gac acc gct 595
Asp Asp Pro Thr Ala Gln Pro Leu Leu Asp Ala Met Ser Asp Thr Ala
150 155 160 165

gag tat gcg gcg gat ggc tac gcc cag aac ttt ggc act ttt aca ttg 643
Glu Tyr Ala Ala Asp Gly Tyr Ala Gln Asn Phe Gly Thr Phe Thr Leu
170 175 180

tcc gat gtc acc ggt act aaa ttt ggt tgg tct gat tcc ctc gat gtg 691
Ser Asp Val Thr Gly Thr Lys Phe Gly Trp Ser Asp Ser Leu Asp Val
185 190 195

cat tca tcg gtc agc ttt ggc cct ggt ttt gtg atc gct gcc aac acc 739
His Ser Ser Val Ser Phe Gly Pro Gly Phe Val Ile Ala Ala Asn Thr

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        200                 205                 210

tac ggt gac gcc gaa acg ctc acc gaa gat gtc caa gat tcc gtg tct   787
Tyr Gly Asp Ala Glu Thr Leu Thr Glu Asp Val Gln Asp Ser Val Ser
    215                 220                 225

tcg ctg tat ccg gag gaa gta acc acc gcg atc gag gag cag gtg gat   835
Ser Leu Tyr Pro Glu Glu Val Thr Thr Ala Ile Glu Glu Gln Val Asp
230                 235                 240                 245

cag ctg tgt gag tgc gct gca gag act acg cat ttg gga atg cac act   883
Gln Leu Cys Glu Cys Ala Ala Glu Thr Thr His Leu Gly Met His Thr
                250                 255                 260

ggc gcg gag ctg aaa gca cag ctt gag ggc act att tat gga aaa acc   931
Gly Ala Glu Leu Lys Ala Gln Leu Glu Gly Thr Ile Tyr Gly Lys Thr
            265                 270                 275

ctc agc ttt tta cct aat tca gcc cca gcg cca gcg ttt att tac aac   979
Leu Ser Phe Leu Pro Asn Ser Ala Pro Ala Pro Ala Phe Ile Tyr Asn
        280                 285                 290

ctg ctg gca cat tagcaaacag ttttaaggaa ctc                        1014
Leu Leu Ala His
    295


<210> 2676
<211> 297
<212> PRT
<213> Corynebacterium glutamicum

<400> 2676
Met Lys Thr Pro Arg Leu Leu Lys Ile Leu Ser Ala Met Val Ala Val
  1               5                  10                  15

Thr Gly Leu Leu Ile Pro Thr Val Val Pro Met Ala Ala Ala Asp Ala
             20                  25                  30

Ala Glu Leu Ser Asp Asn Val Pro Asp Arg Thr Gln Ile Ala Ile Ile
         35                  40                  45

Asn Pro Asp Gly Ser Val Gln Glu Ser Asp Asn Ala Glu Glu Ser Arg
     50                  55                  60

Pro Ala Leu Ser Leu Ala Lys Leu Tyr Leu Gly Tyr Tyr Val Leu Ala
 65                  70                  75                  80

Gln Gly Ala Glu Glu Asp Ile Glu Leu Val Pro Asp Met Ile Arg Tyr
                 85                  90                  95

Ser Asp Asp Phe Thr Ala Asp Tyr Leu Glu Ser Glu Tyr Pro Glu Ala
            100                 105                 110

Ile Pro Glu Val Ile Asp Ala Phe Asp Leu Glu Asp Thr Glu Trp Ala
        115                 120                 125

Gly Phe Trp Gly Asn Ala Thr Thr Ser Ala Val Asp Ile Ala Thr Phe
    130                 135                 140

Val Ala Ala Leu Ile Asp Asp Pro Thr Ala Gln Pro Leu Leu Asp Ala
```

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145                 150                 155                 160

Met Ser Asp Thr Ala Glu Tyr Ala Ala Asp Gly Tyr Ala Gln Asn Phe
                165                 170                 175

Gly Thr Phe Thr Leu Ser Asp Val Thr Gly Thr Lys Phe Gly Trp Ser
            180                 185                 190

Asp Ser Leu Asp Val His Ser Ser Val Ser Phe Gly Pro Gly Phe Val
        195                 200                 205

Ile Ala Ala Asn Thr Tyr Gly Asp Ala Glu Thr Leu Thr Glu Asp Val
    210                 215                 220

Gln Asp Ser Val Ser Ser Leu Tyr Pro Glu Glu Val Thr Thr Ala Ile
225                 230                 235                 240

Glu Glu Gln Val Asp Gln Leu Cys Glu Cys Ala Ala Glu Thr Thr His
                245                 250                 255

Leu Gly Met His Thr Gly Ala Glu Leu Lys Ala Gln Leu Glu Gly Thr
            260                 265                 270

Ile Tyr Gly Lys Thr Leu Ser Phe Leu Pro Asn Ser Ala Pro Ala Pro
        275                 280                 285

Ala Phe Ile Tyr Asn Leu Leu Ala His
    290                 295


<210> 2677
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> RXA02308

<400> 2677
gggtgagatt ggaatgattt cggcccgggc gctcgaaaac cgtgatagac acaatgaacc 60

gagcaaatcc gccaggaaat aaattaagta aggaatatcc atg agt gaa acc cag   115
                                              Met Ser Glu Thr Gln
                                                1               5

tcg aat tca gtg tca gcg gta atg cct gcg cag ctc cct cca ggg cct   163
Ser Asn Ser Val Ser Ala Val Met Pro Ala Gln Leu Pro Pro Gly Pro
                10                  15                  20

gcc gag cgt act gtg tac tcc tac ggt gtt cgc gca ggg gat cag gtg   211
Ala Glu Arg Thr Val Tyr Ser Tyr Gly Val Arg Ala Gly Asp Gln Val
            25                  30                  35

cac att tta aga atg gag gct ttt gat tct gac gcg aat att gtc ggc   259
His Ile Leu Arg Met Glu Ala Phe Asp Ser Asp Ala Asn Ile Val Gly
        40                  45                  50

gaa agg gac att gag gcg cat gct gaa caa gtc ttt aag aac ctg caa   307
Glu Arg Asp Ile Glu Ala His Ala Glu Gln Val Phe Lys Asn Leu Gln
```

```
     55                  60                  65

gca gta atc cac gag gca gga gga acg atc aac aac att gtt tcc acc   355
Ala Val Ile His Glu Ala Gly Gly Thr Ile Asn Asn Ile Val Ser Thr
 70                  75                  80                  85

act act tat ctt gcc gat gtc acc gat gct ccc gtt gtt aac gct gct   403
Thr Thr Tyr Leu Ala Asp Val Thr Asp Ala Pro Val Val Asn Ala Ala
                 90                  95                 100

cgc tcc cgc tat ttc acc gga gaa gta ttg ccc acc cac acc gta att   451
Arg Ser Arg Tyr Phe Thr Gly Glu Val Leu Pro Thr His Thr Val Ile
            105                 110                 115

gga gtt gct gct ctt gct cgg cca cag ttt cta gtc gag atc tca gcg   499
Gly Val Ala Ala Leu Ala Arg Pro Gln Phe Leu Val Glu Ile Ser Ala
        120                 125                 130

gtg gcc tat ttg ggg gac ctt tca aaa gac tagatacatg attatttttg     549
Val Ala Tyr Leu Gly Asp Leu Ser Lys Asp
    135                 140

cat                                                               552


<210> 2678
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 2678
Met Ser Glu Thr Gln Ser Asn Ser Val Ser Ala Val Met Pro Ala Gln
  1               5                  10                  15

Leu Pro Pro Gly Pro Ala Glu Arg Thr Val Tyr Ser Tyr Gly Val Arg
             20                  25                  30

Ala Gly Asp Gln Val His Ile Leu Arg Met Glu Ala Phe Asp Ser Asp
         35                  40                  45

Ala Asn Ile Val Gly Glu Arg Asp Ile Glu Ala His Ala Glu Gln Val
     50                  55                  60

Phe Lys Asn Leu Gln Ala Val Ile His Glu Ala Gly Gly Thr Ile Asn
 65                  70                  75                  80

Asn Ile Val Ser Thr Thr Thr Tyr Leu Ala Asp Val Thr Asp Ala Pro
                 85                  90                  95

Val Val Asn Ala Ala Arg Ser Arg Tyr Phe Thr Gly Glu Val Leu Pro
            100                 105                 110

Thr His Thr Val Ile Gly Val Ala Ala Leu Ala Arg Pro Gln Phe Leu
        115                 120                 125

Val Glu Ile Ser Ala Val Ala Tyr Leu Gly Asp Leu Ser Lys Asp
    130                 135                 140


<210> 2679
<211> 1209
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1186)
<223> RXA02324

<400> 2679
gaaggtcaaa aaacttgact ttattgaaaa caatttccat taagaagtgt acacttgcgt 60

cgactctatt gaaaatgatt cccaaaagga gggctttcac atg gcc aca acg acc 115
Met Ala Thr Thr Thr
1 5

cca gtc acc gtg cta tca gga ttt ctc ggc tcc gga aaa acc aca ttg 163
Pro Val Thr Val Leu Ser Gly Phe Leu Gly Ser Gly Lys Thr Thr Leu
10 15 20

ctc aac cag atc ctc cac cac cga gga tcc cgg aaa atc gca gtc att 211
Leu Asn Gln Ile Leu His His Arg Gly Ser Arg Lys Ile Ala Val Ile
25 30 35

gtc aac gat ttt tca gaa atc aac atc gac gca gcc ctc atc gca tcc 259
Val Asn Asp Phe Ser Glu Ile Asn Ile Asp Ala Ala Leu Ile Ala Ser
40 45 50

gaa ggc cac ctc acc cgc ggc gaa gac cgc ttc gtg gaa ctg acc aac 307
Glu Gly His Leu Thr Arg Gly Glu Asp Arg Phe Val Glu Leu Thr Asn
55 60 65

gga tgc atc tgc tgc acc ctg cgc gaa gac ctc gtg gat tcc gtc ggc 355
Gly Cys Ile Cys Cys Thr Leu Arg Glu Asp Leu Val Asp Ser Val Gly
70 75 80 85

gaa ctc gcc agc agc gac cgc ttc gac cac atc gtc atc gaa tcc acg 403
Glu Leu Ala Ser Ser Asp Arg Phe Asp His Ile Val Ile Glu Ser Thr
90 95 100

ggt atc tcc gaa cca atg ccg gta gcc gcc aca ttt gaa tgg cag tgg 451
Gly Ile Ser Glu Pro Met Pro Val Ala Ala Thr Phe Glu Trp Gln Trp
105 110 115

gat gac ggc acc cgc ctg gct gac aaa gca ccg atc gac acc atg gtc 499
Asp Asp Gly Thr Arg Leu Ala Asp Lys Ala Pro Ile Asp Thr Met Val
120 125 130

acc ctg gtc gat gcc acc caa ttc atc gac ctc atc cgc aaa aac acc 547
Thr Leu Val Asp Ala Thr Gln Phe Ile Asp Leu Ile Arg Lys Asn Thr
135 140 145

tcc ctc acc gag gct gac atg ggc gca acc gag gac gat gaa cgc acc 595
Ser Leu Thr Glu Ala Asp Met Gly Ala Thr Glu Asp Asp Glu Arg Thr
150 155 160 165

atc gcc gac cta ctc acc gat caa atc gag ttc gcc gac cgc atc tac 643
Ile Ala Asp Leu Leu Thr Asp Gln Ile Glu Phe Ala Asp Arg Ile Tyr
170 175 180

atc acc aaa tcc gac ctg gtg gac cgc act gtc ctc gag caa acc cgc 691
Ile Thr Lys Ser Asp Leu Val Asp Arg Thr Val Leu Glu Gln Thr Arg

```
            185                 190                 195

gca cta atc gcc agc atg agt cca cgc gcc cgc att gac tta ctc atc   739
Ala Leu Ile Ala Ser Met Ser Pro Arg Ala Arg Ile Asp Leu Leu Ile
        200                 205                 210

gat ggc ctc aat gac ggc tcc ccc atc acc gac gac atc ctc gga gct   787
Asp Gly Leu Asn Asp Gly Ser Pro Ile Thr Asp Asp Ile Leu Gly Ala
    215                 220                 225

ttc ctc tac gac gaa gcc acc gcc cgc gcc tac gag ggc tac acg gaa   835
Phe Leu Tyr Asp Glu Ala Thr Ala Arg Ala Tyr Glu Gly Tyr Thr Glu
230                 235                 240                 245

gaa ctc gaa aac ccg cac act ccc gaa acc gag gaa tac ggc atc agt   883
Glu Leu Glu Asn Pro His Thr Pro Glu Thr Glu Glu Tyr Gly Ile Ser
                250                 255                 260

tcc gtg gta ttc cgc tct gac cgg ccg ttc aac aag gat cgc cta ctt   931
Ser Val Val Phe Arg Ser Asp Arg Pro Phe Asn Lys Asp Arg Leu Leu
            265                 270                 275

cag gta ctg cgt tcc acc act gga ctc gtt cgc tcc aaa ggc tat tgc   979
Gln Val Leu Arg Ser Thr Thr Gly Leu Val Arg Ser Lys Gly Tyr Cys
        280                 285                 290

tgg atc gct gat cac ctc aac atc gtc cag gtc tgg cac caa gcc ggc   1027
Trp Ile Ala Asp His Leu Asn Ile Val Gln Val Trp His Gln Ala Gly
    295                 300                 305

ccc aat ttg agc att cgc ccg gcc gcc tat tgg gcc aat tca gag atc   1075
Pro Asn Leu Ser Ile Arg Pro Ala Ala Tyr Trp Ala Asn Ser Glu Ile
310                 315                 320                 325

acc ccc ggc act gaa ttg gtc ctg atc ggc atc cac atc gac ggc ccc   1123
Thr Pro Gly Thr Glu Leu Val Leu Ile Gly Ile His Ile Asp Gly Pro
                330                 335                 340

acc ttg ctc gca ctg cta caa ggc gcg acg ctt acc gat gcg gaa gtg   1171
Thr Leu Leu Ala Leu Leu Gln Gly Ala Thr Leu Thr Asp Ala Glu Val
            345                 350                 355

gcg gca ctg gtt ttg tgagttcctc aagtccgtga att                    1209
Ala Ala Leu Val Leu
        360


<210> 2680
<211> 362
<212> PRT
<213> Corynebacterium glutamicum

<400> 2680
Met Ala Thr Thr Thr Pro Val Thr Val Leu Ser Gly Phe Leu Gly Ser
  1               5                  10                  15

Gly Lys Thr Thr Leu Leu Asn Gln Ile Leu His His Arg Gly Ser Arg
             20                  25                  30

Lys Ile Ala Val Ile Val Asn Asp Phe Ser Glu Ile Asn Ile Asp Ala
         35                  40                  45
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Ala Leu Ile Ala Ser Glu Gly His Leu Thr Arg Gly Glu Asp Arg Phe
     50                  55                  60

Val Glu Leu Thr Asn Gly Cys Ile Cys Cys Thr Leu Arg Glu Asp Leu
 65                  70                  75                  80

Val Asp Ser Val Gly Glu Leu Ala Ser Ser Asp Arg Phe Asp His Ile
                 85                  90                  95

Val Ile Glu Ser Thr Gly Ile Ser Glu Pro Met Pro Val Ala Ala Thr
            100                 105                 110

Phe Glu Trp Gln Trp Asp Asp Gly Thr Arg Leu Ala Asp Lys Ala Pro
        115                 120                 125

Ile Asp Thr Met Val Thr Leu Val Asp Ala Thr Gln Phe Ile Asp Leu
    130                 135                 140

Ile Arg Lys Asn Thr Ser Leu Thr Glu Ala Asp Met Gly Ala Thr Glu
145                 150                 155                 160

Asp Asp Glu Arg Thr Ile Ala Asp Leu Leu Thr Asp Gln Ile Glu Phe
                165                 170                 175

Ala Asp Arg Ile Tyr Ile Thr Lys Ser Asp Leu Val Asp Arg Thr Val
            180                 185                 190

Leu Glu Gln Thr Arg Ala Leu Ile Ala Ser Met Ser Pro Arg Ala Arg
        195                 200                 205

Ile Asp Leu Leu Ile Asp Gly Leu Asn Asp Gly Ser Pro Ile Thr Asp
    210                 215                 220

Asp Ile Leu Gly Ala Phe Leu Tyr Asp Glu Ala Thr Ala Arg Ala Tyr
225                 230                 235                 240

Glu Gly Tyr Thr Glu Glu Leu Glu Asn Pro His Thr Pro Glu Thr Glu
                245                 250                 255

Glu Tyr Gly Ile Ser Ser Val Val Phe Arg Ser Asp Arg Pro Phe Asn
            260                 265                 270

Lys Asp Arg Leu Leu Gln Val Leu Arg Ser Thr Thr Gly Leu Val Arg
        275                 280                 285

Ser Lys Gly Tyr Cys Trp Ile Ala Asp His Leu Asn Ile Val Gln Val
    290                 295                 300

Trp His Gln Ala Gly Pro Asn Leu Ser Ile Arg Pro Ala Ala Tyr Trp
305                 310                 315                 320

Ala Asn Ser Glu Ile Thr Pro Gly Thr Glu Leu Val Leu Ile Gly Ile
                325                 330                 335

His Ile Asp Gly Pro Thr Leu Leu Ala Leu Leu Gln Gly Ala Thr Leu
            340                 345                 350

Thr Asp Ala Glu Val Ala Ala Leu Val Leu
        355                 360
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<210> 2681
<211> 993
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(970)
<223> RXA02325

<400> 2681
gggcagagat ttgaagatgg agaccaaggc tcaaagggaa tccatgccgt cttggtttaa 60

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tactgcaccc gtctaatgaa aatcattact attaggtgtc atg atg gac cat gca   115
                                              Met Met Asp His Ala
                                                1               5

cac gat tcc tgc tca cca act ctg cgc cgt gat ttg gag gtc act ggc   163
His Asp Ser Cys Ser Pro Thr Leu Arg Arg Asp Leu Glu Val Thr Gly
                 10                  15                  20

cag ctc caa cct gag aaa gct gtc gat tta gca gcg ccg cac gaa ggg   211
Gln Leu Gln Pro Glu Lys Ala Val Asp Leu Ala Ala Pro His Glu Gly
             25                  30                  35

aag gtt gcc aat ata acg aag gtg acc tcc tca aat atg gag cac acc   259
Lys Val Ala Asn Ile Thr Lys Val Thr Ser Ser Asn Met Glu His Thr
         40                  45                  50

atc acg cag gcc tca aaa gct aag gag gtg gtg gtg ctc att ggt cac   307
Ile Thr Gln Ala Ser Lys Ala Lys Glu Val Val Val Leu Ile Gly His
     55                  60                  65

tcc ctg ctg ccc aca ttt cag gat ttg gaa aaa gac att ctg cac ttt   355
Ser Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys Asp Ile Leu His Phe
 70                  75                  80                  85

cag gca ggt aat aaa ggg cga ttt tct gta gcg att gtt gat cct gat   403
Gln Ala Gly Asn Lys Gly Arg Phe Ser Val Ala Ile Val Asp Pro Asp
                 90                  95                 100

cgc agt gca gat gtg gtt gcc aga ttt agg cca aaa cag att ccg gtg   451
Arg Ser Ala Asp Val Val Ala Arg Phe Arg Pro Lys Gln Ile Pro Val
             105                 110                 115

gca tac gtg gtg aaa gat ggc gcc agc att gcg gag ttc aac tcg ctc   499
Ala Tyr Val Val Lys Asp Gly Ala Ser Ile Ala Glu Phe Asn Ser Leu
         120                 125                 130

aac aag gag ccg gtt gca caa tgg ctt gat cat ttt gtg tcg cgg gaa   547
Asn Lys Glu Pro Val Ala Gln Trp Leu Asp His Phe Val Ser Arg Glu
     135                 140                 145

acg atc ccc aat gaa aaa gag ggg gac gtc gat aag caa ata gac ccg   595
Thr Ile Pro Asn Glu Lys Glu Gly Asp Val Asp Lys Gln Ile Asp Pro
150                 155                 160                 165

cgc ctg tgg cgg gca gcg gaa ttg gtg aac gcc ggt gat ttt cgc gcg   643
Arg Leu Trp Arg Ala Ala Glu Leu Val Asn Ala Gly Asp Phe Arg Ala
                170                 175                 180
```

```
gcg ttg gcg ttg tat gag cag ttg ccg cag gat gcg acg gtg aag cgg   691
Ala Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp Ala Thr Val Lys Arg
            185                 190                 195

gcg cac gcg gcg gtg tcg gta ttg gcg cgg atg tct gtg gcg gat cgg   739
Ala His Ala Ala Val Ser Val Leu Ala Arg Met Ser Val Ala Asp Arg
        200                 205                 210

gga gag gat ccg atc gag aag tcg cgc cgg gat cca gac gat gtg aac   787
Gly Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp Pro Asp Asp Val Asn
    215                 220                 225

aag gcg ctg gcg gcg gcg gat atg tat gtg ttg atg aat cag ccg gac   835
Lys Ala Leu Ala Ala Ala Asp Met Tyr Val Leu Met Asn Gln Pro Asp
230                 235                 240                 245

aca gcg ctc gcg cac ctt gca gca cta ttg cca aaa ccg gag gct gcc   883
Thr Ala Leu Ala His Leu Ala Ala Leu Leu Pro Lys Pro Glu Ala Ala
                250                 255                 260

cgg cgg atc gtg gag ttg ctg aac ttg ttt gat ccg ctg gac ctg gtc   931
Arg Arg Ile Val Glu Leu Leu Asn Leu Phe Asp Pro Leu Asp Leu Val
            265                 270                 275

gca ttg gaa atc agg gcg cag gtg ggg aat gca atg agc taagaaaaca    980
Ala Leu Glu Ile Arg Ala Gln Val Gly Asn Ala Met Ser
        280                 285                 290

ctttaaatat tct                                                   993


<210> 2682
<211> 290
<212> PRT
<213> Corynebacterium glutamicum

<400> 2682
Met Met Asp His Ala His Asp Ser Cys Ser Pro Thr Leu Arg Arg Asp
  1               5                  10                  15

Leu Glu Val Thr Gly Gln Leu Gln Pro Glu Lys Ala Val Asp Leu Ala
             20                  25                  30

Ala Pro His Glu Gly Lys Val Ala Asn Ile Thr Lys Val Thr Ser Ser
         35                  40                  45

Asn Met Glu His Thr Ile Thr Gln Ala Ser Lys Ala Lys Glu Val Val
     50                  55                  60

Val Leu Ile Gly His Ser Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys
 65                  70                  75                  80

Asp Ile Leu His Phe Gln Ala Gly Asn Lys Gly Arg Phe Ser Val Ala
                 85                  90                  95

Ile Val Asp Pro Asp Arg Ser Ala Asp Val Val Ala Arg Phe Arg Pro
            100                 105                 110

Lys Gln Ile Pro Val Ala Tyr Val Val Lys Asp Gly Ala Ser Ile Ala
        115                 120                 125
```

```
Glu Phe Asn Ser Leu Asn Lys Glu Pro Val Ala Gln Trp Leu Asp His
    130                 135                 140

Phe Val Ser Arg Glu Thr Ile Pro Asn Glu Lys Glu Gly Asp Val Asp
145                 150                 155                 160

Lys Gln Ile Asp Pro Arg Leu Trp Arg Ala Ala Glu Leu Val Asn Ala
                165                 170                 175

Gly Asp Phe Arg Ala Ala Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp
            180                 185                 190

Ala Thr Val Lys Arg Ala His Ala Ala Val Ser Val Leu Ala Arg Met
        195                 200                 205

Ser Val Ala Asp Arg Gly Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp
    210                 215                 220

Pro Asp Asp Val Asn Lys Ala Leu Ala Ala Ala Asp Met Tyr Val Leu
225                 230                 235                 240

Met Asn Gln Pro Asp Thr Ala Leu Ala His Leu Ala Ala Leu Leu Pro
                245                 250                 255

Lys Pro Glu Ala Ala Arg Arg Ile Val Glu Leu Leu Asn Leu Phe Asp
            260                 265                 270

Pro Leu Asp Leu Val Ala Leu Glu Ile Arg Ala Gln Val Gly Asn Ala
        275                 280                 285

Met Ser
    290
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<210> 2683
<211> 489
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(466)
<223> RXA02331

<400> 2683
tgcagcgtgc attcccacca tcgggtcaag aatctatccg cccagcccct gtccaactcc 60

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tcaactaaaa aggcagcact taaaaaacac tatggaaccc atg gaa cta aac ggc   115
                                            Met Glu Leu Asn Gly
                                              1               5

ggt cgt ttc tac gcc cgc aag ctc acc tca gat aat cgg att gat gat   163
Gly Arg Phe Tyr Ala Arg Lys Leu Thr Ser Asp Asn Arg Ile Asp Asp
                  10                  15                  20

gtc ccg gcg ctc tca ctg atc ctt gcc gat gca gca cag ttc atc gcg   211
Val Pro Ala Leu Ser Leu Ile Leu Ala Asp Ala Ala Gln Phe Ile Ala
              25                  30                  35

gac gcc acc aca gcc tgg cac gag gac acc gaa tac acc tgg gct atc   259
```

```
Asp Ala Thr Thr Ala Trp His Glu Asp Thr Glu Tyr Thr Trp Ala Ile
         40                  45                  50

tgc gag cag acc agt gtt gaa cta ctg gca ctg gca cgc ctt gat ccc   307
Cys Glu Gln Thr Ser Val Glu Leu Leu Ala Leu Ala Arg Leu Asp Pro
     55                  60                  65

aag cag cgc aca ctc gag gtc gtg ccc gca ggt gat ccc gcc acc caa   355
Lys Gln Arg Thr Leu Glu Val Val Pro Ala Gly Asp Pro Ala Thr Gln
 70                  75                  80                  85

ttg ccc aat gat cca gtg ctc gct ccg aaa acc atc ggc gat gct gtg   403
Leu Pro Asn Asp Pro Val Leu Ala Pro Lys Thr Ile Gly Asp Ala Val
                 90                  95                 100

gcg gag ggc cgc gac acc atc acc aga tgg gca caa ggc tat tta gaa   451
Ala Glu Gly Arg Asp Thr Ile Thr Arg Trp Ala Gln Gly Tyr Leu Glu
            105                 110                 115

atc agc ctc act gat taggttctct ccgaaatggg cac                    489
Ile Ser Leu Thr Asp
        120
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09/05/2005 15:00:00

<210> 2684
<211> 122
<212> PRT
<213> Corynebacterium glutamicum

<400> 2684

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Met Glu Leu Asn Gly Gly Arg Phe Tyr Ala Arg Lys Leu Thr Ser Asp
  1               5                  10                  15

Asn Arg Ile Asp Asp Val Pro Ala Leu Ser Leu Ile Leu Ala Asp Ala
            20                  25                  30

Ala Gln Phe Ile Ala Asp Ala Thr Thr Ala Trp His Glu Asp Thr Glu
        35                  40                  45

Tyr Thr Trp Ala Ile Cys Glu Gln Thr Ser Val Glu Leu Leu Ala Leu
    50                  55                  60

Ala Arg Leu Asp Pro Lys Gln Arg Thr Leu Glu Val Val Pro Ala Gly
65                  70                  75                  80

Asp Pro Ala Thr Gln Leu Pro Asn Asp Pro Val Leu Ala Pro Lys Thr
                85                  90                  95

Ile Gly Asp Ala Val Ala Glu Gly Arg Asp Thr Ile Thr Arg Trp Ala
            100                 105                 110

Gln Gly Tyr Leu Glu Ile Ser Leu Thr Asp
        115                 120
```

<210> 2685
<211> 303
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(280)
<223> RXA02336

<400> 2685
caaatccaca cgacacaatt acacaaattt taccttgtgc attgaaagcc gtcagccgat 60

tagcgttaaa gaaaataaaa aaccacaagg ggagcacacc atg aaa gac acc acc 115
Met Lys Asp Thr Thr
1 5

gag atc aac tgg caa ggc tac gcc gat gga acc gca atc cgc gaa gca 163
Glu Ile Asn Trp Gln Gly Tyr Ala Asp Gly Thr Ala Ile Arg Glu Ala
10 15 20

gtc atc cac tcc att gaa cga gaa gta tca gcg ggc gag cag cca acc 211
Val Ile His Ser Ile Glu Arg Glu Val Ser Ala Gly Glu Gln Pro Thr
25 30 35

cca aac gat ctt aaa ttt ctc ggg ctg ttc cag cac cgc gcc ggg tat 259
Pro Asn Asp Leu Lys Phe Leu Gly Leu Phe Gln His Arg Ala Gly Tyr
40 45 50

gtg ggc tcg ttg atc acc ggt taagtgtggg gagcaggctg gct 303
Val Gly Ser Leu Ile Thr Gly
55 60

<210> 2686
<211> 60
<212> PRT
<213> Corynebacterium glutamicum

<400> 2686
Met Lys Asp Thr Thr Glu Ile Asn Trp Gln Gly Tyr Ala Asp Gly Thr
1 5 10 15

Ala Ile Arg Glu Ala Val Ile His Ser Ile Glu Arg Glu Val Ser Ala
20 25 30

Gly Glu Gln Pro Thr Pro Asn Asp Leu Lys Phe Leu Gly Leu Phe Gln
35 40 45

His Arg Ala Gly Tyr Val Gly Ser Leu Ile Thr Gly
50 55 60

<210> 2687
<211> 444
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(421)
<223> RXA02347

<400> 2687
acggttggaa cagagctgca cctttaatca ggcagttgct ggccaactga gttagcctaa 60

aacgatgaag aaaaatcctt tggttgaatg ggtctgggtt atg gat gaa ctc ggg 115

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                                                    Met Asp Glu Leu Gly
                                                      1               5

gtt ggc tgg tgc caa tgc gag aaa gat tcc atc acc gga aaa gca cca   163
Val Gly Trp Cys Gln Cys Glu Lys Asp Ser Ile Thr Gly Lys Ala Pro
                 10                  15                  20

cat ccc gtg aac aag cca ctg gtc acc aaa tcc att atc agg gct cta   211
His Pro Val Asn Lys Pro Leu Val Thr Lys Ser Ile Ile Arg Ala Leu
             25                  30                  35

ggc gat gtc ccc gat gtc atg agc aac cag gac atc agc ctt gtg gtg   259
Gly Asp Val Pro Asp Val Met Ser Asn Gln Asp Ile Ser Leu Val Val
         40                  45                  50

gtg gat ttg tgg aaa ttc gat acc att act cct cca atc gca gaa tcc   307
Val Asp Leu Trp Lys Phe Asp Thr Ile Thr Pro Pro Ile Ala Glu Ser
     55                  60                  65

ctc atg cgt tcc gtc aaa gct gtt aac ggt gag atg cac ccg cag tat   355
Leu Met Arg Ser Val Lys Ala Val Asn Gly Glu Met His Pro Gln Tyr
 70                  75                  80                  85

ccc acc gcg aca gca atg gct gcg atc aag cat ttc tcc aac act ttt   403
Pro Thr Ala Thr Ala Met Ala Ala Ile Lys His Phe Ser Asn Thr Phe
                 90                  95                 100

gat gga cag att aac gct taaaaggcct gttatagact gat                444
Asp Gly Gln Ile Asn Ala
             105
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<210> 2688
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

<400> 2688

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Met Asp Glu Leu Gly Val Gly Trp Cys Gln Cys Glu Lys Asp Ser Ile
  1               5                  10                  15

Thr Gly Lys Ala Pro His Pro Val Asn Lys Pro Leu Val Thr Lys Ser
             20                  25                  30

Ile Ile Arg Ala Leu Gly Asp Val Pro Asp Val Met Ser Asn Gln Asp
         35                  40                  45

Ile Ser Leu Val Val Val Asp Leu Trp Lys Phe Asp Thr Ile Thr Pro
     50                  55                  60

Pro Ile Ala Glu Ser Leu Met Arg Ser Val Lys Ala Val Asn Gly Glu
 65                  70                  75                  80

Met His Pro Gln Tyr Pro Thr Ala Thr Ala Met Ala Ala Ile Lys His
                 85                  90                  95

Phe Ser Asn Thr Phe Asp Gly Gln Ile Asn Ala
             100                 105
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<210> 2689

<211> 490
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(490)
<223> RXA02349

<400> 2689
cttcgagtgc tgtggcgaaa aatccgaact ccaaagaact agcctaagaa ctagccccat 60

gagctatccc tcaaaaaatt actgatagtg aggttttcgc atg tca act gca tat 115
Met Ser Thr Ala Tyr
1 5

ttt att gcg cac gga aac gat acg tac cgc cca acg gag cat tcc agc 163
Phe Ile Ala His Gly Asn Asp Thr Tyr Arg Pro Thr Glu His Ser Ser
10 15 20

ggt gcg tgg cgc gat gat gaa ctc cac ctt gca ccg gtt gcc ggt ttg 211
Gly Ala Trp Arg Asp Asp Glu Leu His Leu Ala Pro Val Ala Gly Leu
25 30 35

gtg att cac cat atg gaa cgt tgg cgc agg gaa gtg gtt ggc gat gct 259
Val Ile His His Met Glu Arg Trp Arg Arg Glu Val Val Gly Asp Ala
40 45 50

ttg gtg ttc agc cgt ttt agt ttg gag gtc ttg ggc cag atc gct cgg 307
Leu Val Phe Ser Arg Phe Ser Leu Glu Val Leu Gly Gln Ile Ala Arg
55 60 65

gat gat gtc acc ttg aga aca gag atc gtt cgt ccc ggg cgc acc att 355
Asp Asp Val Thr Leu Arg Thr Glu Ile Val Arg Pro Gly Arg Thr Ile
70 75 80 85

gaa ctt att gaa acc gtg gct gaa atc aac ggc aga gtg acg att cgt 403
Glu Leu Ile Glu Thr Val Ala Glu Ile Asn Gly Arg Val Thr Ile Arg
90 95 100

gca cgc gcc tgg ttg ctg aag acc tct gat ctt gcc cat att tct ggc 451
Ala Arg Ala Trp Leu Leu Lys Thr Ser Asp Leu Ala His Ile Ser Gly
105 110 115

gat act ttt gaa gcg ttg ccg tca atg act gaa ctg gca 490
Asp Thr Phe Glu Ala Leu Pro Ser Met Thr Glu Leu Ala
120 125 130

<210> 2690
<211> 130
<212> PRT
<213> Corynebacterium glutamicum

<400> 2690
Met Ser Thr Ala Tyr Phe Ile Ala His Gly Asn Asp Thr Tyr Arg Pro
1 5 10 15

Thr Glu His Ser Ser Gly Ala Trp Arg Asp Asp Glu Leu His Leu Ala
20 25 30

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Pro Val Ala Gly Leu Val Ile His His Met Glu Arg Trp Arg Arg Glu
         35                  40                  45

Val Val Gly Asp Ala Leu Val Phe Ser Arg Phe Ser Leu Glu Val Leu
     50                  55                  60

Gly Gln Ile Ala Arg Asp Asp Val Thr Leu Arg Thr Glu Ile Val Arg
 65                  70                  75                  80

Pro Gly Arg Thr Ile Glu Leu Ile Glu Thr Val Ala Glu Ile Asn Gly
                 85                  90                  95

Arg Val Thr Ile Arg Ala Arg Ala Trp Leu Leu Lys Thr Ser Asp Leu
            100                 105                 110

Ala His Ile Ser Gly Asp Thr Phe Glu Ala Leu Pro Ser Met Thr Glu
        115                 120                 125

Leu Ala
    130
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US20070269857A1

<210> 2691
<211> 578
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(555)
<223> RXA02352

<400> 2691

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atc tac aac aca tcg agc acg ctc aac ggc ttc atc gca gac aaa gac   48
Ile Tyr Asn Thr Ser Ser Thr Leu Asn Gly Phe Ile Ala Asp Lys Asp
  1               5                  10                  15

aac tcc ctg caa tgg ctt ttc gac gtc ccc ggc agc gac ggt gcc tct   96
Asn Ser Leu Gln Trp Leu Phe Asp Val Pro Gly Ser Asp Gly Ala Ser
             20                  25                  30

gaa gac ttc ggt aat ttc ctt tca aaa gcc ggc acc atc gta atg gga   144
Glu Asp Phe Gly Asn Phe Leu Ser Lys Ala Gly Thr Ile Val Met Gly
         35                  40                  45

tcc acc acc tat gaa tgg ctg ctc aag gac cta gat ttc atc agc gat   192
Ser Thr Thr Tyr Glu Trp Leu Leu Lys Asp Leu Asp Phe Ile Ser Asp
     50                  55                  60

ccc cac aag tgg acc gat gtg tat ggc gat cgc ccc acg tgg gtg ttc   240
Pro His Lys Trp Thr Asp Val Tyr Gly Asp Arg Pro Thr Trp Val Phe
 65                  70                  75                  80

agc agc agg aac ttg gaa acc ccg gaa gga aaa cct gtc aag gta gta   288
Ser Ser Arg Asn Leu Glu Thr Pro Glu Gly Lys Pro Val Lys Val Val
                 85                  90                  95

aat gga gat gtc gcc gat gtt ctc ccc gcc ata ctg gaa gag agt cca   336
Asn Gly Asp Val Ala Asp Val Leu Pro Ala Ile Leu Glu Glu Ser Pro
            100                 105                 110
```

```
gag aac act gat att tgg atc gtc ggt ggt ggc gat ctg gcg ggt caa   384
Glu Asn Thr Asp Ile Trp Ile Val Gly Gly Gly Asp Leu Ala Gly Gln
        115                 120                 125

ttc ttt gat gcg ggt gca ctc gat cgg atc atc ttg acc atg gcg cca   432
Phe Phe Asp Ala Gly Ala Leu Asp Arg Ile Ile Leu Thr Met Ala Pro
    130                 135                 140

gtg ttt ctc gat gaa ggg cag cca gcg atg ccc cgc cgg atc gaa agt   480
Val Phe Leu Asp Glu Gly Gln Pro Ala Met Pro Arg Arg Ile Glu Ser
145                 150                 155                 160

aat cgt ctc cgc acc gta aat gtc cgc gag gtt gga caa ttc acc gag   528
Asn Arg Leu Arg Thr Val Asn Val Arg Glu Val Gly Gln Phe Thr Glu
                165                 170                 175

atc acc ctg gag acg att aaa ggg gct taatttgtag agttttgggc         575
Ile Thr Leu Glu Thr Ile Lys Gly Ala
            180                 185

aga                                                               578
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<210> 2692
<211> 185
<212> PRT
<213> Corynebacterium glutamicum

<400> 2692

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Ile Tyr Asn Thr Ser Ser Thr Leu Asn Gly Phe Ile Ala Asp Lys Asp
  1               5                  10                  15

Asn Ser Leu Gln Trp Leu Phe Asp Val Pro Gly Ser Asp Gly Ala Ser
             20                  25                  30

Glu Asp Phe Gly Asn Phe Leu Ser Lys Ala Gly Thr Ile Val Met Gly
         35                  40                  45

Ser Thr Thr Tyr Glu Trp Leu Leu Lys Asp Leu Asp Phe Ile Ser Asp
     50                  55                  60

Pro His Lys Trp Thr Asp Val Tyr Gly Asp Arg Pro Thr Trp Val Phe
 65                  70                  75                  80

Ser Ser Arg Asn Leu Glu Thr Pro Glu Gly Lys Pro Val Lys Val Val
                 85                  90                  95

Asn Gly Asp Val Ala Asp Val Leu Pro Ala Ile Leu Glu Glu Ser Pro
            100                 105                 110

Glu Asn Thr Asp Ile Trp Ile Val Gly Gly Gly Asp Leu Ala Gly Gln
        115                 120                 125

Phe Phe Asp Ala Gly Ala Leu Asp Arg Ile Ile Leu Thr Met Ala Pro
    130                 135                 140

Val Phe Leu Asp Glu Gly Gln Pro Ala Met Pro Arg Arg Ile Glu Ser
145                 150                 155                 160

Asn Arg Leu Arg Thr Val Asn Val Arg Glu Val Gly Gln Phe Thr Glu
                165                 170                 175
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```
Ile Thr Leu Glu Thr Ile Lys Gly Ala
            180                 185


<210> 2693
<211> 1119
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1096)
<223> RXA02356

<400> 2693
ttggcagtag ccatgcgttc tgctcctgac cttgaacagc ggtcccaatt tagacccgct 60

aaacccacaa tgtgtactgg tgctggtaat ttagtagaac atg gca acg gtc aca   115
                                            Met Ala Thr Val Thr
                                              1               5

ttc gac aag gtc aca atc cgg tac ccc ggc gcg gag cgc gca aca gtt   163
Phe Asp Lys Val Thr Ile Arg Tyr Pro Gly Ala Glu Arg Ala Thr Val
                  10                  15                  20

cat gag ctt gat tta gat atc gct gat ggc gag ttt ttg gtg ctc gtc   211
His Glu Leu Asp Leu Asp Ile Ala Asp Gly Glu Phe Leu Val Leu Val
              25                  30                  35

ggc cct tcg ggt tgt ggt aaa tcc act acg ctg cgt gct ttg gcg ggg   259
Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu Arg Ala Leu Ala Gly
          40                  45                  50

ctt gag ggc gtg gag tcg ggt gtg atc aaa att gat ggc aag gat gtc   307
Leu Glu Gly Val Glu Ser Gly Val Ile Lys Ile Asp Gly Lys Asp Val
      55                  60                  65

act ggt cag gag ccg gcg gat cgc gat atc gcg atg gtg ttc cag aat   355
Thr Gly Gln Glu Pro Ala Asp Arg Asp Ile Ala Met Val Phe Gln Asn
  70                  75                  80                  85

tat gct ctg tac cct cac atg acg gtg gcg aag aat atg ggt ttt gcg   403
Tyr Ala Leu Tyr Pro His Met Thr Val Ala Lys Asn Met Gly Phe Ala
                  90                  95                 100

ctg aag ttg gct aag ctg ccg cag gcg cag atc gat gcg aag gtc aat   451
Leu Lys Leu Ala Lys Leu Pro Gln Ala Gln Ile Asp Ala Lys Val Asn
              105                 110                 115

gag gct gcg gaa att ctt ggg ttg acg gag ttt ttg gat cgc aag cct   499
Glu Ala Ala Glu Ile Leu Gly Leu Thr Glu Phe Leu Asp Arg Lys Pro
          120                 125                 130

aag gat tta tcg ggt ggt cag cgt cag cgt gtg gcg atg ggt cgc gcg   547
Lys Asp Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala
      135                 140                 145

ttg gtg cgt gat ccg aag gtg ttc ctc atg gat gag ccg ctg tcc aac   595
Leu Val Arg Asp Pro Lys Val Phe Leu Met Asp Glu Pro Leu Ser Asn
150                 155                 160                 165
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```
ctg gat gcg aaa ttg cgc gtg caa acc cgc gcg gag gtc gct gct ttg   643
Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Ala Glu Val Ala Ala Leu
                170                 175                 180

cag cgt cgc ctg ggc acc acc acg gtg tat gtc acc cac gat cag gtt   691
Gln Arg Arg Leu Gly Thr Thr Thr Val Tyr Val Thr His Asp Gln Val
            185                 190                 195

gag gca atg acg atg ggc gat cgg gtt gcg gtg ctc aag gac ggg ttg   739
Glu Ala Met Thr Met Gly Asp Arg Val Ala Val Leu Lys Asp Gly Leu
        200                 205                 210

ctg cag cag gtc gca ccg ccc agg gag ctt tac gac gcc ccg gtc aac   787
Leu Gln Gln Val Ala Pro Pro Arg Glu Leu Tyr Asp Ala Pro Val Asn
    215                 220                 225

gaa ttc gtt gcg ggc ttc atc ggc tcg ccg tcc atg aac ctc ttc cct   835
Glu Phe Val Ala Gly Phe Ile Gly Ser Pro Ser Met Asn Leu Phe Pro
230                 235                 240                 245

gcc aac ggg cac aag atg ggt gtg cgc ccg gag aag atg ctg gtc aat   883
Ala Asn Gly His Lys Met Gly Val Arg Pro Glu Lys Met Leu Val Asn
                250                 255                 260

gag acc cct gag ggt ttc aca agc att gat gct gtg gtg gat atc gtc   931
Glu Thr Pro Glu Gly Phe Thr Ser Ile Asp Ala Val Val Asp Ile Val
            265                 270                 275

gag gag ctt ggc tcc gaa tcg tat gtt tat gcc act tgg gag ggc cac   979
Glu Glu Leu Gly Ser Glu Ser Tyr Val Tyr Ala Thr Trp Glu Gly His
        280                 285                 290

cgc ctg gtg gcc cgt tgg gtg gaa ggc ccc gtg cca gcc cct ggc acg   1027
Arg Leu Val Ala Arg Trp Val Glu Gly Pro Val Pro Ala Pro Gly Thr
    295                 300                 305

cct gtg act ttt tcc tat gat gcg gcg cag gcg cat cat ttc gat ctg   1075
Pro Val Thr Phe Ser Tyr Asp Ala Ala Gln Ala His His Phe Asp Leu
310                 315                 320                 325

gag tcg ggc gag cgt atc gct tagtttcgga cgtggggagg cgt             1119
Glu Ser Gly Glu Arg Ile Ala
                330
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<210> 2694
<211> 332
<212> PRT
<213> Corynebacterium glutamicum

<400> 2694

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Met Ala Thr Val Thr Phe Asp Lys Val Thr Ile Arg Tyr Pro Gly Ala
  1               5                  10                  15

Glu Arg Ala Thr Val His Glu Leu Asp Leu Asp Ile Ala Asp Gly Glu
             20                  25                  30

Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu
         35                  40                  45
```

```
Arg Ala Leu Ala Gly Leu Glu Gly Val Glu Ser Gly Val Ile Lys Ile
     50                  55                  60

Asp Gly Lys Asp Val Thr Gly Gln Glu Pro Ala Asp Arg Asp Ile Ala
 65                  70                  75                  80

Met Val Phe Gln Asn Tyr Ala Leu Tyr Pro His Met Thr Val Ala Lys
                 85                  90                  95

Asn Met Gly Phe Ala Leu Lys Leu Ala Lys Leu Pro Gln Ala Gln Ile
            100                 105                 110

Asp Ala Lys Val Asn Glu Ala Ala Glu Ile Leu Gly Leu Thr Glu Phe
        115                 120                 125

Leu Asp Arg Lys Pro Lys Asp Leu Ser Gly Gly Gln Arg Gln Arg Val
    130                 135                 140

Ala Met Gly Arg Ala Leu Val Arg Asp Pro Lys Val Phe Leu Met Asp
145                 150                 155                 160

Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Ala
                165                 170                 175

Glu Val Ala Ala Leu Gln Arg Arg Leu Gly Thr Thr Thr Val Tyr Val
            180                 185                 190

Thr His Asp Gln Val Glu Ala Met Thr Met Gly Asp Arg Val Ala Val
        195                 200                 205

Leu Lys Asp Gly Leu Leu Gln Gln Val Ala Pro Pro Arg Glu Leu Tyr
    210                 215                 220

Asp Ala Pro Val Asn Glu Phe Val Ala Gly Phe Ile Gly Ser Pro Ser
225                 230                 235                 240

Met Asn Leu Phe Pro Ala Asn Gly His Lys Met Gly Val Arg Pro Glu
                245                 250                 255

Lys Met Leu Val Asn Glu Thr Pro Glu Gly Phe Thr Ser Ile Asp Ala
            260                 265                 270

Val Val Asp Ile Val Glu Glu Leu Gly Ser Glu Ser Tyr Val Tyr Ala
        275                 280                 285

Thr Trp Glu Gly His Arg Leu Val Ala Arg Trp Val Glu Gly Pro Val
    290                 295                 300

Pro Ala Pro Gly Thr Pro Val Thr Phe Ser Tyr Asp Ala Ala Gln Ala
305                 310                 315                 320

His His Phe Asp Leu Glu Ser Gly Glu Arg Ile Ala
                325                 330
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<210> 2695
<211> 414
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(391)
<223> RXA02358

<400> 2695
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tcgtccctag tacacccaaa gtttatgaaa gataaaaatc atg gtt tct tat agc 115
Met Val Ser Tyr Ser
1 5

gtg cac ggc gca cta gat atc gac ggc agc ctc aaa aaa ctc acc ctc 163
Val His Gly Ala Leu Asp Ile Asp Gly Ser Leu Lys Lys Leu Thr Leu
10 15 20

gat ttc ctc aat aaa cta gcc acc aat cca gct tcc ccg ggg ctt cat 211
Asp Phe Leu Asn Lys Leu Ala Thr Asn Pro Ala Ser Pro Gly Leu His
25 30 35

att gag ccc atc aaa aac agc atc gac tcc cgc gtc cgc aca ggt cgg 259
Ile Glu Pro Ile Lys Asn Ser Ile Asp Ser Arg Val Arg Thr Gly Arg
40 45 50

gtc aat gat caa ttc cgc gca gtg ctt ttt gag ctt cac gac gaa ttt 307
Val Asn Asp Gln Phe Arg Ala Val Leu Phe Glu Leu His Asp Glu Phe
55 60 65

gat cat cac ttt gta gtg ggt ggg ttt atc ccc atg atg atg cca tca 355
Asp His His Phe Val Val Gly Gly Phe Ile Pro Met Met Met Pro Ser
70 75 80 85

cca agg cag gaa aaa tcc gcc ttg aag tca act ctg taacggcatt 401
Pro Arg Gln Glu Lys Ser Ala Leu Lys Ser Thr Leu
90 95

actcgactca tcg 414

<210> 2696
<211> 97
<212> PRT
<213> Corynebacterium glutamicum

<400> 2696
Met Val Ser Tyr Ser Val His Gly Ala Leu Asp Ile Asp Gly Ser Leu
1 5 10 15

Lys Lys Leu Thr Leu Asp Phe Leu Asn Lys Leu Ala Thr Asn Pro Ala
20 25 30

Ser Pro Gly Leu His Ile Glu Pro Ile Lys Asn Ser Ile Asp Ser Arg
35 40 45

Val Arg Thr Gly Arg Val Asn Asp Gln Phe Arg Ala Val Leu Phe Glu
50 55 60

Leu His Asp Glu Phe Asp His His Phe Val Val Gly Gly Phe Ile Pro
65 70 75 80

Met Met Met Pro Ser Pro Arg Gln Glu Lys Ser Ala Leu Lys Ser Thr
85 90 95

Leu

<210> 2697
<211> 3822
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(3799)
<223> RXA02362

<400> 2697
acaattgttc ccattcgcat atctcgtgtc caccagagtc gctacagtaa cgagaaactt 60

aattatttga tccgattctt ccgttcaaag gcctcattcc gtg act atc tct cgc 115
Val Thr Ile Ser Arg
1 5

cga ctc aaa caa gag cgc agt ttc gct gac gat ctt caa gat ctc aaa 163
Arg Leu Lys Gln Glu Arg Ser Phe Ala Asp Asp Leu Gln Asp Leu Lys
10 15 20

act ctc aat gat caa ctg cgg ttt aca aac gcc aaa ttg caa gct cgc 211
Thr Leu Asn Asp Gln Leu Arg Phe Thr Asn Ala Lys Leu Gln Ala Arg
25 30 35

atc agt ggt att ggc aat gat gga aag aaa atc acg cgc cct acc cca 259
Ile Ser Gly Ile Gly Asn Asp Gly Lys Lys Ile Thr Arg Pro Thr Pro
40 45 50

ctc ctt gcg ctg gat ttt cag ctg acc gtt gaa gaa tac gaa acg atc 307
Leu Leu Ala Leu Asp Phe Gln Leu Thr Val Glu Glu Tyr Glu Thr Ile
55 60 65

att gca atc ttg gtg gaa gca gtt ggc gga aat caa tcc aag cca gcg 355
Ile Ala Ile Leu Val Glu Ala Val Gly Gly Asn Gln Ser Lys Pro Ala
70 75 80 85

att ctt aaa gat ctg ttt ata gaa tat cca ctc gtc ttc ctg gca gcg 403
Ile Leu Lys Asp Leu Phe Ile Glu Tyr Pro Leu Val Phe Leu Ala Ala
90 95 100

ctt tct gga acc gcc atg ctc gat gct caa gaa ggt ttc tgg cct gcg 451
Leu Ser Gly Thr Ala Met Leu Asp Ala Gln Glu Gly Phe Trp Pro Ala
105 110 115

ttc tgg aaa cgc act cag gtg tca gtt cca gag cat gta tac gac gcg 499
Phe Trp Lys Arg Thr Gln Val Ser Val Pro Glu His Val Tyr Asp Ala
120 125 130

atc cgt aaa gaa cta gtt aat agc atc cgc aaa aat ggc cta gaa act 547
Ile Arg Lys Glu Leu Val Asn Ser Ile Arg Lys Asn Gly Leu Glu Thr
135 140 145

ttt tct ctc gct gac ctc aat cga cgc gaa tat gtc gga ctc atc caa 595
Phe Ser Leu Ala Asp Leu Asn Arg Arg Glu Tyr Val Gly Leu Ile Gln
150 155 160 165

```
ctt cac agt ggc ctt tct gca aaa gac atg ctc gcc ttg gtc aaa ttt   643
Leu His Ser Gly Leu Ser Ala Lys Asp Met Leu Ala Leu Val Lys Phe
                170                 175                 180

atc gat cac act cga gca gaa aac caa gga tgg gat tct ggt gag gac   691
Ile Asp His Thr Arg Ala Glu Asn Gln Gly Trp Asp Ser Gly Glu Asp
            185                 190                 195

ttt gca tca tat gcg aag agt gtc ttc tcc tcc ggg gac aac cta tta   739
Phe Ala Ser Tyr Ala Lys Ser Val Phe Ser Ser Gly Asp Asn Leu Leu
        200                 205                 210

acc acg gag tcg ctc aag caa tta gtc acc cac atc cct gcg cgt tcc   787
Thr Thr Glu Ser Leu Lys Gln Leu Val Thr His Ile Pro Ala Arg Ser
    215                 220                 225

gtc gac ttc atc gcc aga gtc tat gaa cta acc aat tgg tac cgc gac   835
Val Asp Phe Ile Ala Arg Val Tyr Glu Leu Thr Asn Trp Tyr Arg Asp
230                 235                 240                 245

ctc aaa gac ctc aat gaa gta gaa gcc ttc gta ggt act cat ggg ctg   883
Leu Lys Asp Leu Asn Glu Val Glu Ala Phe Val Gly Thr His Gly Leu
                250                 255                 260

ccg gaa ttg tct ttc aaa ttt ctt ctg gag tgt ctg agc ggc gaa gct   931
Pro Glu Leu Ser Phe Lys Phe Leu Leu Glu Cys Leu Ser Gly Glu Ala
            265                 270                 275

gaa caa att gcc gaa aag acg aaa gca gca cca gca agc ctg gaa aac   979
Glu Gln Ile Ala Glu Lys Thr Lys Ala Ala Pro Ala Ser Leu Glu Asn
        280                 285                 290

ctg gaa cct ccg cat ctc tat ctg gat cca cag agt ttt gaa ctc agt   1027
Leu Glu Pro Pro His Leu Tyr Leu Asp Pro Gln Ser Phe Glu Leu Ser
    295                 300                 305

ctt gtt ttc cca gcg atc tct aaa act gca gca ctt cag att cca gca   1075
Leu Val Phe Pro Ala Ile Ser Lys Thr Ala Ala Leu Gln Ile Pro Ala
310                 315                 320                 325

cca gaa tgg aca gtg att tat gac gga aac tcc att aaa gtt cgt ccc   1123
Pro Glu Trp Thr Val Ile Tyr Asp Gly Asn Ser Ile Lys Val Arg Pro
                330                 335                 340

gaa cag gac tgg tcc tac gga ggt ttc gcc gaa tac cgt ttg cct tta   1171
Glu Gln Asp Trp Ser Tyr Gly Gly Phe Ala Glu Tyr Arg Leu Pro Leu
            345                 350                 355

gac aaa ccg ctc tcc agc ttg aga gtc atc act cca aca gag aaa tcc   1219
Asp Lys Pro Leu Ser Ser Leu Arg Val Ile Thr Pro Thr Glu Lys Ser
        360                 365                 370

cta att ctg att gaa gga ttt ggc cac aag aat ccc att atg ttc ttt   1267
Leu Ile Leu Ile Glu Gly Phe Gly His Lys Asn Pro Ile Met Phe Phe
    375                 380                 385

aag aac aac ggt cag cca tat gca aac caa gaa atg ctc agt ggc aac   1315
Lys Asn Asn Gly Gln Pro Tyr Ala Asn Gln Glu Met Leu Ser Gly Asn
390                 395                 400                 405
```

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gct gtc aca gct ata gtc cca gct gca gca atc att cgt gca cgt atg   1363
Ala Val Thr Ala Ile Val Pro Ala Ala Ala Ile Ile Arg Ala Arg Met
                410                 415                 420

cga gct tcc aag act ttc aac tat caa gac ttg ggt ccc ttg tcc gga   1411
Arg Ala Ser Lys Thr Phe Asn Tyr Gln Asp Leu Gly Pro Leu Ser Gly
            425                 430                 435

tgg aac aag tgg gtc att cgt tcg atc cca ctc aaa cga gct gaa tcg   1459
Trp Asn Lys Trp Val Ile Arg Ser Ile Pro Leu Lys Arg Ala Glu Ser
        440                 445                 450

atc aca gtc tcc cac ggt ggc ttc aga aaa gaa ctc cca gtt cga cgc   1507
Ile Thr Val Ser His Gly Gly Phe Arg Lys Glu Leu Pro Val Arg Arg
    455                 460                 465

aaa gtt gat gtt caa tgg att act gag gat ctc acg atc gag aat ctt   1555
Lys Val Asp Val Gln Trp Ile Thr Glu Asp Leu Thr Ile Glu Asn Leu
470                 475                 480                 485

caa ggt ctc gat cat gag ccc gtt ttc cac acg agt ccc cgc atc gaa   1603
Gln Gly Leu Asp His Glu Pro Val Phe His Thr Ser Pro Arg Ile Glu
                490                 495                 500

ttc ccc acc tct gga tca aac tgg gta att cag tat tca cag att ctt   1651
Phe Pro Thr Ser Gly Ser Asn Trp Val Ile Gln Tyr Ser Gln Ile Leu
            505                 510                 515

cca gat ggc agc ctc atc gaa atg gaa gat tac cca gtc gaa cct gaa   1699
Pro Asp Gly Ser Leu Ile Glu Met Glu Asp Tyr Pro Val Glu Pro Glu
        520                 525                 530

aac ttc gga tac gaa cta gac ctc ttc gaa gaa tcc gac gac cct tgg   1747
Asn Phe Gly Tyr Glu Leu Asp Leu Phe Glu Glu Ser Asp Asp Pro Trp
    535                 540                 545

gtc ggg caa ttt tta gta act ctg ctc aag gat gaa aaa gtc tat gaa   1795
Val Gly Gln Phe Leu Val Thr Leu Leu Lys Asp Glu Lys Val Tyr Glu
550                 555                 560                 565

acc cgc aaa ttc aat ctc gcg gaa ggc ctc gat ctt tcc cta aca ttc   1843
Thr Arg Lys Phe Asn Leu Ala Glu Gly Leu Asp Leu Ser Leu Thr Phe
                570                 575                 580

agc gga ggc gga cct gaa aat cga ttt agg tac ccc agc atc aat cag   1891
Ser Gly Gly Gly Pro Glu Asn Arg Phe Arg Tyr Pro Ser Ile Asn Gln
            585                 590                 595

gga caa act ggc tta aca aag act ttc gcc cgt ttt agt tcc aat tct   1939
Gly Gln Thr Gly Leu Thr Lys Thr Phe Ala Arg Phe Ser Ser Asn Ser
        600                 605                 610

gaa aag cac atc agg ttc cca gat gag atc atc ggg ctt gat gca ttc   1987
Glu Lys His Ile Arg Phe Pro Asp Glu Ile Ile Gly Leu Asp Ala Phe
    615                 620                 625

acc tct caa aaa gcg ttt aac atc gca agc ggt gat ttc cct gag gac   2035
Thr Ser Gln Lys Ala Phe Asn Ile Ala Ser Gly Asp Phe Pro Glu Asp
630                 635                 640                 645

tac aac ctc gac gtt ttc atc acg cct ccg caa ctt cac tac caa gta   2083
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Tyr Asn Leu Asp Val Phe Ile Thr Pro Pro Gln Leu His Tyr Gln Val
                650                 655                 660

cct gtc aca cac agc caa aca aag tgg gaa agc aca aag acg aca cta   2131
Pro Val Thr His Ser Gln Thr Lys Trp Glu Ser Thr Lys Thr Thr Leu
            665                 670                 675

gat ttc aat gac ttt gcc gat gga aac ctc cag atc aga ttc cct aat   2179
Asp Phe Asn Asp Phe Ala Asp Gly Asn Leu Gln Ile Arg Phe Pro Asn
        680                 685                 690

gaa gtc tat gat cca aac ttg aaa atc att aaa atg gtg gca tac aag   2227
Glu Val Tyr Asp Pro Asn Leu Lys Ile Ile Lys Met Val Ala Tyr Lys
    695                 700                 705

aaa cct gag tcc agt gag cct aaa tac tta agc aaa att ggt tca agc   2275
Lys Pro Glu Ser Ser Glu Pro Lys Tyr Leu Ser Lys Ile Gly Ser Ser
710                 715                 720                 725

aaa gtg tgg tct atc cct atg gat cgc atc aag gaa ctc atg gat gat   2323
Lys Val Trp Ser Ile Pro Met Asp Arg Ile Lys Glu Leu Met Asp Asp
                730                 735                 740

gat gcc caa ttc ctt ttg atc gcg gag tgg ttc gct gaa agt aaa gac   2371
Asp Ala Gln Phe Leu Leu Ile Ala Glu Trp Phe Ala Glu Ser Lys Asp
            745                 750                 755

cag cac cga gag aag atc att agc gaa gct aag cga act gga aaa atc   2419
Gln His Arg Glu Lys Ile Ile Ser Glu Ala Lys Arg Thr Gly Lys Ile
        760                 765                 770

tcc aat gca gcg ctt aag agt gct cgt cct caa cct caa gca agt tcc   2467
Ser Asn Ala Ala Leu Lys Ser Ala Arg Pro Gln Pro Gln Ala Ser Ser
    775                 780                 785

cac att gca aca att gag aaa aag ccc cta cta gct gcg gct gaa att   2515
His Ile Ala Thr Ile Glu Lys Lys Pro Leu Leu Ala Ala Ala Glu Ile
790                 795                 800                 805

aag ctt tct acc gtg gag ttg gaa ctt ggt cgg cac act tct aag aga   2563
Lys Leu Ser Thr Val Glu Leu Glu Leu Gly Arg His Thr Ser Lys Arg
                810                 815                 820

ctg gaa ggc tgg gca tgg tct gcg ctc aac ccg ctt gat cca cca atc   2611
Leu Glu Gly Trp Ala Trp Ser Ala Leu Asn Pro Leu Asp Pro Pro Ile
            825                 830                 835

aaa gtc gat ttc caa gga acc tca ggc tca ctt cca gac acc cac ttc   2659
Lys Val Asp Phe Gln Gly Thr Ser Gly Ser Leu Pro Asp Thr His Phe
        840                 845                 850

gtc gtt ggc cct tta atc gtg gaa gtg aga gaa aaa gag ttt ctc tcc   2707
Val Val Gly Pro Leu Ile Val Glu Val Arg Glu Lys Glu Phe Leu Ser
    855                 860                 865

caa tgg cag cca aaa gtt ccc tca gtt aaa gcc gtg gtt gca aat gat   2755
Gln Trp Gln Pro Lys Val Pro Ser Val Lys Ala Val Val Ala Asn Asp
870                 875                 880                 885

ccc tca ttt gaa ttg gac cct caa ttt gat cct ttc ctc aca cac cga   2803
Pro Ser Phe Glu Leu Asp Pro Gln Phe Asp Pro Phe Leu Thr His Arg
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                890                 895                 900

tgg atg ttc gct cca cga agt ggg aag gtc tta ctc cca caa gaa atc   2851
Trp Met Phe Ala Pro Arg Ser Gly Lys Val Leu Leu Pro Gln Glu Ile
            905                 910                 915

cgc aca gtg tgg gac gcc cga ttc aat atg cgc cat gtc tta gcg cag   2899
Arg Thr Val Trp Asp Ala Arg Phe Asn Met Arg His Val Leu Ala Gln
        920                 925                 930

cgt gaa aac ctt cat gtg aaa tcg att caa gat ttt gac gat gcc acc   2947
Arg Glu Asn Leu His Val Lys Ser Ile Gln Asp Phe Asp Asp Ala Thr
    935                 940                 945

agt acc tat ctc acc agt gat cct cgg gtg gca tta gat gaa ttg gat   2995
Ser Thr Tyr Leu Thr Ser Asp Pro Arg Val Ala Leu Asp Glu Leu Asp
950                 955                 960                 965

aag agc tca att ccg tct aat tcc cac ttt gaa tca ttc atc cga tcc   3043
Lys Ser Ser Ile Pro Ser Asn Ser His Phe Glu Ser Phe Ile Arg Ser
                970                 975                 980

gga tta gct gag ctt tct ttc gaa gtt gac gac aca gcc gga gat atc   3091
Gly Leu Ala Glu Leu Ser Phe Glu Val Asp Asp Thr Ala Gly Asp Ile
            985                 990                 995

cat cgc gtt ccc tgg atc ggc ctg atc cag gaa atg aac gac ctc aga   3139
His Arg Val Pro Trp Ile Gly Leu Ile Gln Glu Met Asn Asp Leu Arg
        1000                1005                1010

att ctg cag ata caa ggc tat gaa aca gaa gaa cga gcc atc gaa cgc   3187
Ile Leu Gln Ile Gln Gly Tyr Glu Thr Glu Glu Arg Ala Ile Glu Arg
    1015                1020                1025

cga aat tcg cag agc tac atc cgt gag ata gga ggc agt gaa ttg tgg   3235
Arg Asn Ser Gln Ser Tyr Ile Arg Glu Ile Gly Gly Ser Glu Leu Trp
1030                1035                1040                1045

aat atc cta aaa gga aat tca gag gga ttg tct ctt gct caa aaa tgc   3283
Asn Ile Leu Lys Gly Asn Ser Glu Gly Leu Ser Leu Ala Gln Lys Cys
                1050                1055                1060

gca cca caa gcc act gag att aat gtg att cgt aat tca ggc ttg gaa   3331
Ala Pro Gln Ala Thr Glu Ile Asn Val Ile Arg Asn Ser Gly Leu Glu
            1065                1070                1075

gct atg cgc aat ggg ctg ggc gcc gat cag ttc agc gcc gag ttt att   3379
Ala Met Arg Asn Gly Leu Gly Ala Asp Gln Phe Ser Ala Glu Phe Ile
        1080                1085                1090

tca gca gac tca cgc cta cga gct cag ctt gaa tgg ttg gaa aac cgc   3427
Ser Ala Asp Ser Arg Leu Arg Ala Gln Leu Glu Trp Leu Glu Asn Arg
    1095                1100                1105

cga gag ctc aat gat ctc ggc cag ctc cca acg ctc ttc gat ttc gcc   3475
Arg Glu Leu Asn Asp Leu Gly Gln Leu Pro Thr Leu Phe Asp Phe Ala
1110                1115                1120                1125

gag aaa tac gag tac ctc atc gat cac tta ggt gat gat cgc atc aag   3523
Glu Lys Tyr Glu Tyr Leu Ile Asp His Leu Gly Asp Asp Arg Ile Lys
                1130                1135                1140
```

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gtc act gca cgt gag ctg tct act ctt gcg tcg gaa cac cgt cgc ggc   3571
Val Thr Ala Arg Glu Leu Ser Thr Leu Ala Ser Glu His Arg Arg Gly
            1145                1150                1155

aac gct gaa aac tgg ctt tat gca cca tat gtg tca ttc att tac agc   3619
Asn Ala Glu Asn Trp Leu Tyr Ala Pro Tyr Val Ser Phe Ile Tyr Ser
        1160                1165                1170

ttg ctt aac cga atg atc gct cat gaa gta ata cgt ccg atc gct cag   3667
Leu Leu Asn Arg Met Ile Ala His Glu Val Ile Arg Pro Ile Ala Gln
    1175                1180                1185

atc aat tac tca cgg cac gat tgg gca aac gct gct cgg ctg att cct   3715
Ile Asn Tyr Ser Arg His Asp Trp Ala Asn Ala Ala Arg Leu Ile Pro
1190                1195                1200                1205

cgt ctc aca gga ttt gac ctg gtg agt gcc gaa gcg aaa gtg ctc agc   3763
Arg Leu Thr Gly Phe Asp Leu Val Ser Ala Glu Ala Lys Val Leu Ser
                1210                1215                1220

gca ata aac aac aac aat ata atc cca act gca att taaggatcac        3809
Ala Ile Asn Asn Asn Asn Ile Ile Pro Thr Ala Ile
            1225                1230

tatgtccaac gca                                                   3822


<210> 2698
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<213> Corynebacterium glutamicum

<400> 2698
Val Thr Ile Ser Arg Arg Leu Lys Gln Glu Arg Ser Phe Ala Asp Asp
  1               5                  10                  15

Leu Gln Asp Leu Lys Thr Leu Asn Asp Gln Leu Arg Phe Thr Asn Ala
             20                  25                  30

Lys Leu Gln Ala Arg Ile Ser Gly Ile Gly Asn Asp Gly Lys Lys Ile
         35                  40                  45

Thr Arg Pro Thr Pro Leu Leu Ala Leu Asp Phe Gln Leu Thr Val Glu
     50                  55                  60

Glu Tyr Glu Thr Ile Ile Ala Ile Leu Val Glu Ala Val Gly Gly Asn
 65                  70                  75                  80

Gln Ser Lys Pro Ala Ile Leu Lys Asp Leu Phe Ile Glu Tyr Pro Leu
                 85                  90                  95

Val Phe Leu Ala Ala Leu Ser Gly Thr Ala Met Leu Asp Ala Gln Glu
            100                 105                 110

Gly Phe Trp Pro Ala Phe Trp Lys Arg Thr Gln Val Ser Val Pro Glu
        115                 120                 125

His Val Tyr Asp Ala Ile Arg Lys Glu Leu Val Asn Ser Ile Arg Lys
    130                 135                 140
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Asn Gly Leu Glu Thr Phe Ser Leu Ala Asp Leu Asn Arg Arg Glu Tyr
145                 150                 155                 160

Val Gly Leu Ile Gln Leu His Ser Gly Leu Ser Ala Lys Asp Met Leu
                165                 170                 175

Ala Leu Val Lys Phe Ile Asp His Thr Arg Ala Glu Asn Gln Gly Trp
            180                 185                 190

Asp Ser Gly Glu Asp Phe Ala Ser Tyr Ala Lys Ser Val Phe Ser Ser
        195                 200                 205

Gly Asp Asn Leu Leu Thr Thr Glu Ser Leu Lys Gln Leu Val Thr His
    210                 215                 220

Ile Pro Ala Arg Ser Val Asp Phe Ile Ala Arg Val Tyr Glu Leu Thr
225                 230                 235                 240

Asn Trp Tyr Arg Asp Leu Lys Asp Leu Asn Glu Val Glu Ala Phe Val
                245                 250                 255

Gly Thr His Gly Leu Pro Glu Leu Ser Phe Lys Phe Leu Leu Glu Cys
            260                 265                 270

Leu Ser Gly Glu Ala Glu Gln Ile Ala Glu Lys Thr Lys Ala Ala Pro
        275                 280                 285

Ala Ser Leu Glu Asn Leu Glu Pro Pro His Leu Tyr Leu Asp Pro Gln
    290                 295                 300

Ser Phe Glu Leu Ser Leu Val Phe Pro Ala Ile Ser Lys Thr Ala Ala
305                 310                 315                 320

Leu Gln Ile Pro Ala Pro Glu Trp Thr Val Ile Tyr Asp Gly Asn Ser
                325                 330                 335

Ile Lys Val Arg Pro Glu Gln Asp Trp Ser Tyr Gly Gly Phe Ala Glu
            340                 345                 350

Tyr Arg Leu Pro Leu Asp Lys Pro Leu Ser Ser Leu Arg Val Ile Thr
        355                 360                 365

Pro Thr Glu Lys Ser Leu Ile Leu Ile Glu Gly Phe Gly His Lys Asn
    370                 375                 380

Pro Ile Met Phe Phe Lys Asn Asn Gly Gln Pro Tyr Ala Asn Gln Glu
385                 390                 395                 400

Met Leu Ser Gly Asn Ala Val Thr Ala Ile Val Pro Ala Ala Ala Ile
                405                 410                 415

Ile Arg Ala Arg Met Arg Ala Ser Lys Thr Phe Asn Tyr Gln Asp Leu
            420                 425                 430

Gly Pro Leu Ser Gly Trp Asn Lys Trp Val Ile Arg Ser Ile Pro Leu
        435                 440                 445

Lys Arg Ala Glu Ser Ile Thr Val Ser His Gly Gly Phe Arg Lys Glu
    450                 455                 460

Leu Pro Val Arg Arg Lys Val Asp Val Gln Trp Ile Thr Glu Asp Leu
```

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465                 470                 475                 480

Thr Ile Glu Asn Leu Gln Gly Leu Asp His Glu Pro Val Phe His Thr
                485                 490                 495

Ser Pro Arg Ile Glu Phe Pro Thr Ser Gly Ser Asn Trp Val Ile Gln
            500                 505                 510

Tyr Ser Gln Ile Leu Pro Asp Gly Ser Leu Ile Glu Met Glu Asp Tyr
        515                 520                 525

Pro Val Glu Pro Glu Asn Phe Gly Tyr Glu Leu Asp Leu Phe Glu Glu
    530                 535                 540

Ser Asp Asp Pro Trp Val Gly Gln Phe Leu Val Thr Leu Leu Lys Asp
545                 550                 555                 560

Glu Lys Val Tyr Glu Thr Arg Lys Phe Asn Leu Ala Glu Gly Leu Asp
                565                 570                 575

Leu Ser Leu Thr Phe Ser Gly Gly Gly Pro Glu Asn Arg Phe Arg Tyr
            580                 585                 590

Pro Ser Ile Asn Gln Gly Gln Thr Gly Leu Thr Lys Thr Phe Ala Arg
        595                 600                 605

Phe Ser Ser Asn Ser Glu Lys His Ile Arg Phe Pro Asp Glu Ile Ile
    610                 615                 620

Gly Leu Asp Ala Phe Thr Ser Gln Lys Ala Phe Asn Ile Ala Ser Gly
625                 630                 635                 640

Asp Phe Pro Glu Asp Tyr Asn Leu Asp Val Phe Ile Thr Pro Pro Gln
                645                 650                 655

Leu His Tyr Gln Val Pro Val Thr His Ser Gln Thr Lys Trp Glu Ser
            660                 665                 670

Thr Lys Thr Thr Leu Asp Phe Asn Asp Phe Ala Asp Gly Asn Leu Gln
        675                 680                 685

Ile Arg Phe Pro Asn Glu Val Tyr Asp Pro Asn Leu Lys Ile Ile Lys
    690                 695                 700

Met Val Ala Tyr Lys Lys Pro Glu Ser Ser Glu Pro Lys Tyr Leu Ser
705                 710                 715                 720

Lys Ile Gly Ser Ser Lys Val Trp Ser Ile Pro Met Asp Arg Ile Lys
                725                 730                 735

Glu Leu Met Asp Asp Asp Ala Gln Phe Leu Leu Ile Ala Glu Trp Phe
            740                 745                 750

Ala Glu Ser Lys Asp Gln His Arg Glu Lys Ile Ile Ser Glu Ala Lys
        755                 760                 765

Arg Thr Gly Lys Ile Ser Asn Ala Ala Leu Lys Ser Ala Arg Pro Gln
    770                 775                 780

Pro Gln Ala Ser Ser His Ile Ala Thr Ile Glu Lys Lys Pro Leu Leu
785                 790                 795                 800
```

```
Ala Ala Ala Glu Ile Lys Leu Ser Thr Val Glu Leu Glu Leu Gly Arg
                805                 810                 815

His Thr Ser Lys Arg Leu Glu Gly Trp Ala Trp Ser Ala Leu Asn Pro
            820                 825                 830

Leu Asp Pro Pro Ile Lys Val Asp Phe Gln Gly Thr Ser Gly Ser Leu
        835                 840                 845

Pro Asp Thr His Phe Val Val Gly Pro Leu Ile Val Glu Val Arg Glu
    850                 855                 860

Lys Glu Phe Leu Ser Gln Trp Gln Pro Lys Val Pro Ser Val Lys Ala
865                 870                 875                 880

Val Val Ala Asn Asp Pro Ser Phe Glu Leu Asp Pro Gln Phe Asp Pro
                885                 890                 895

Phe Leu Thr His Arg Trp Met Phe Ala Pro Arg Ser Gly Lys Val Leu
            900                 905                 910

Leu Pro Gln Glu Ile Arg Thr Val Trp Asp Ala Arg Phe Asn Met Arg
        915                 920                 925

His Val Leu Ala Gln Arg Glu Asn Leu His Val Lys Ser Ile Gln Asp
    930                 935                 940

Phe Asp Asp Ala Thr Ser Thr Tyr Leu Thr Ser Asp Pro Arg Val Ala
945                 950                 955                 960

Leu Asp Glu Leu Asp Lys Ser Ser Ile Pro Ser Asn Ser His Phe Glu
                965                 970                 975

Ser Phe Ile Arg Ser Gly Leu Ala Glu Leu Ser Phe Glu Val Asp Asp
            980                 985                 990

Thr Ala Gly Asp Ile His Arg Val Pro Trp Ile Gly Leu Ile Gln Glu
        995                1000                1005

Met Asn Asp Leu Arg Ile Leu Gln Ile Gln Gly Tyr Glu Thr Glu Glu
    1010                1015                1020

Arg Ala Ile Glu Arg Arg Asn Ser Gln Ser Tyr Ile Arg Glu Ile Gly
1025                1030                1035                1040

Gly Ser Glu Leu Trp Asn Ile Leu Lys Gly Asn Ser Glu Gly Leu Ser
                1045                1050                1055

Leu Ala Gln Lys Cys Ala Pro Gln Ala Thr Glu Ile Asn Val Ile Arg
            1060                1065                1070

Asn Ser Gly Leu Glu Ala Met Arg Asn Gly Leu Gly Ala Asp Gln Phe
        1075                1080                1085

Ser Ala Glu Phe Ile Ser Ala Asp Ser Arg Leu Arg Ala Gln Leu Glu
    1090                1095                1100

Trp Leu Glu Asn Arg Arg Glu Leu Asn Asp Leu Gly Gln Leu Pro Thr
1105                1110                1115                1120
```

```
Leu Phe Asp Phe Ala Glu Lys Tyr Glu Tyr Leu Ile Asp His Leu Gly
                1125                1130                1135

Asp Asp Arg Ile Lys Val Thr Ala Arg Glu Leu Ser Thr Leu Ala Ser
            1140                1145                1150

Glu His Arg Arg Gly Asn Ala Glu Asn Trp Leu Tyr Ala Pro Tyr Val
        1155                1160                1165

Ser Phe Ile Tyr Ser Leu Leu Asn Arg Met Ile Ala His Glu Val Ile
    1170                1175                1180

Arg Pro Ile Ala Gln Ile Asn Tyr Ser Arg His Asp Trp Ala Asn Ala
1185                1190                1195                1200

Ala Arg Leu Ile Pro Arg Leu Thr Gly Phe Asp Leu Val Ser Ala Glu
                1205                1210                1215

Ala Lys Val Leu Ser Ala Ile Asn Asn Asn Asn Ile Ile Pro Thr Ala
            1220                1225                1230

Ile
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CONFIDENTIAL

<210> 2699
<211> 744
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(721)
<223> RXA02374

<400> 2699

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attggatagc ccaccgtacg cctatctaca ctgaattacc atg agc tat gac ttt   115
                                            Met Ser Tyr Asp Phe
                                              1               5

gtc ctc ttt gaa acc gat ggc gac cca ggt agc gcc cgt att tcc aaa   163
Val Leu Phe Glu Thr Asp Gly Asp Pro Gly Ser Ala Arg Ile Ser Lys
                 10                  15                  20

acc cca ctg acc gaa cgc atc gat ttc gcc acg cca tct aca acc cct   211
Thr Pro Leu Thr Glu Arg Ile Asp Phe Ala Thr Pro Ser Thr Thr Pro
             25                  30                  35

gtg ttg gaa tct ctt tcg gca ggg ctt gcc gaa acg gtg cca gac acc   259
Val Leu Glu Ser Leu Ser Ala Gly Leu Ala Glu Thr Val Pro Asp Thr
         40                  45                  50

gtc aag ctt gaa gaa gac gcc atc cac tta tcc ggt gat cgt tgc ctt   307
Val Lys Leu Glu Glu Asp Ala Ile His Leu Ser Gly Asp Arg Cys Leu
     55                  60                  65

tac gtt gtg acc aac tac aac tcc gcc gaa gaa gca gcc gaa tgg ctc   355
Tyr Val Val Thr Asn Tyr Asn Ser Ala Glu Glu Ala Ala Glu Trp Leu
 70                  75                  80                  85
```

```
acc gcc atc gct ttc gat tac gga ctg ggc ctt gcc gac atg aac gcg   403
Thr Ala Ile Ala Phe Asp Tyr Gly Leu Gly Leu Ala Asp Met Asn Ala
                 90                  95                 100

gac acc atc ctg ctt ttc ggc gat gaa gat tcc gac gct gtc gtc caa   451
Asp Thr Ile Leu Leu Phe Gly Asp Glu Asp Ser Asp Ala Val Val Gln
            105                 110                 115

atc gat gac tgg ttc tcc ccc gct ttc tct gcg tac ggc ctt ccc cac   499
Ile Asp Asp Trp Phe Ser Pro Ala Phe Ser Ala Tyr Gly Leu Pro His
        120                 125                 130

ctc ctg gtg gaa gtc atg cgc ctg aag gat tcc aaa acc cct tat ctt   547
Leu Leu Val Glu Val Met Arg Leu Lys Asp Ser Lys Thr Pro Tyr Leu
    135                 140                 145

cga gtc aca ctt gct gca gat gac tcg aaa ttt atc caa acc ctt tac   595
Arg Val Thr Leu Ala Ala Asp Asp Ser Lys Phe Ile Gln Thr Leu Tyr
150                 155                 160                 165

gaa acc gac aac aaa caa tgg ttg gtg gaa acc tct tcc tcc aca ggc   643
Glu Thr Asp Asn Lys Gln Trp Leu Val Glu Thr Ser Ser Ser Thr Gly
                170                 175                 180

acg gac gaa acc cac gtg aag acc att aat gat gtg ctg gaa cgc atc   691
Thr Asp Glu Thr His Val Lys Thr Ile Asn Asp Val Leu Glu Arg Ile
            185                 190                 195

gag aca tgg ttc aac cag gag act gct gtc taaacctttt gtcgtgttct     741
Glu Thr Trp Phe Asn Gln Glu Thr Ala Val
        200                 205

ggg                                                               744
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<210> 2700
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<212> PRT
<213> Corynebacterium glutamicum

<400> 2700

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Met Ser Tyr Asp Phe Val Leu Phe Glu Thr Asp Gly Asp Pro Gly Ser
  1               5                  10                  15

Ala Arg Ile Ser Lys Thr Pro Leu Thr Glu Arg Ile Asp Phe Ala Thr
             20                  25                  30

Pro Ser Thr Thr Pro Val Leu Glu Ser Leu Ser Ala Gly Leu Ala Glu
         35                  40                  45

Thr Val Pro Asp Thr Val Lys Leu Glu Glu Asp Ala Ile His Leu Ser
     50                  55                  60

Gly Asp Arg Cys Leu Tyr Val Val Thr Asn Tyr Asn Ser Ala Glu Glu
 65                  70                  75                  80

Ala Ala Glu Trp Leu Thr Ala Ile Ala Phe Asp Tyr Gly Leu Gly Leu
                 85                  90                  95

Ala Asp Met Asn Ala Asp Thr Ile Leu Leu Phe Gly Asp Glu Asp Ser
```

```
            100                 105                 110

Asp Ala Val Val Gln Ile Asp Asp Trp Phe Ser Pro Ala Phe Ser Ala
        115                 120                 125

Tyr Gly Leu Pro His Leu Leu Val Glu Val Met Arg Leu Lys Asp Ser
    130                 135                 140

Lys Thr Pro Tyr Leu Arg Val Thr Leu Ala Ala Asp Asp Ser Lys Phe
145                 150                 155                 160

Ile Gln Thr Leu Tyr Glu Thr Asp Asn Lys Gln Trp Leu Val Glu Thr
                165                 170                 175

Ser Ser Ser Thr Gly Thr Asp Glu Thr His Val Lys Thr Ile Asn Asp
            180                 185                 190

Val Leu Glu Arg Ile Glu Thr Trp Phe Asn Gln Glu Thr Ala Val
        195                 200                 205
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<210> 2701
<211> 792
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(769)
<223> RXA02390

<400> 2701

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ggccgcgagg atctcgtagc tcgcttcgag tcataggccg gtg gag tgg acc gct   115
                                        Val Glu Trp Thr Ala
                                          1               5

ttt ggc acc ctg att ctg ctc aat ttg gtg ggc agt tta tcc ccg ggg   163
Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly Ser Leu Ser Pro Gly
                  10                  15                  20

cct gat acc ttt ttc ctc ctc cgc tta gcc acc cgc tcc aga gcg cac   211
Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr Arg Ser Arg Ala His
              25                  30                  35

gcg atc gct ggc gtc gcc ggc atc gtc acc gga ctc acg gtg tgg gtg   259
Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly Leu Thr Val Trp Val
          40                  45                  50

acg ctg acg gtc gtg gga gca gcg gcg ctg ctc acc act tat ccg tcg   307
Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu Thr Thr Tyr Pro Ser
      55                  60                  65

att ctc gga atc atc cag ctc gtc ggc ggc acg tac cta agc ttc att   355
Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr Tyr Leu Ser Phe Ile
  70                  75                  80                  85

ggg tac aag ttg ctg cgc tcg gcg tcg aga gag ctt atc gac gcc cgc   403
Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu Leu Ile Asp Ala Arg
                  90                  95                 100
```

```
cag ttc cgt ttc aac gcc gat gcc cga cct atc ccg gat gcg gta gaa   451
Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile Pro Asp Ala Val Glu
            105                 110                 115

gca ctg gga acc cgc act cag gta tat cga caa ggt ttg gcc acc aac   499
Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln Gly Leu Ala Thr Asn
        120                 125                 130

ctg tca aac cct aaa gtt gtc atg tac ttc gcg gca att ctg gct ccg   547
Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala Ala Ile Leu Ala Pro
    135                 140                 145

ttg atg cca gcg cac cca tca ccg gtg ctg gcg ttc tct atc atc gtg   595
Leu Met Pro Ala His Pro Ser Pro Val Leu Ala Phe Ser Ile Ile Val
150                 155                 160                 165

gcg att tta gtg cag acc ttt gtt acc ttc tct gct gtg tgc ctc att   643
Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser Ala Val Cys Leu Ile
                170                 175                 180

gtc tct acg gag cgt gtg cgc aaa gca atg ctg cgt gca ggt ccc tgg   691
Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu Arg Ala Gly Pro Trp
            185                 190                 195

ttt gac ctg ctt gct ggc gtt gtc ttc ctc gtt gtg ggt gtg act ctg   739
Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val Val Gly Val Thr Leu
        200                 205                 210

ctg tat gaa ggc ctg acc ggt tta ctc ggg taaaggcata aaaaatggct     789
Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly
    215                 220

tcc                                                               792
```

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<210> 2702
<211> 223
<212> PRT
<213> Corynebacterium glutamicum

<400> 2702

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Val Glu Trp Thr Ala Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly
  1               5                  10                  15

Ser Leu Ser Pro Gly Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr
             20                  25                  30

Arg Ser Arg Ala His Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly
         35                  40                  45

Leu Thr Val Trp Val Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu
     50                  55                  60

Thr Thr Tyr Pro Ser Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr
 65                  70                  75                  80

Tyr Leu Ser Phe Ile Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu
                 85                  90                  95

Leu Ile Asp Ala Arg Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile
```

```
            100                 105                 110

Pro Asp Ala Val Glu Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln
        115                 120                 125

Gly Leu Ala Thr Asn Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala
    130                 135                 140

Ala Ile Leu Ala Pro Leu Met Pro Ala His Pro Ser Pro Val Leu Ala
145                 150                 155                 160

Phe Ser Ile Ile Val Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser
                165                 170                 175

Ala Val Cys Leu Ile Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu
            180                 185                 190

Arg Ala Gly Pro Trp Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val
        195                 200                 205

Val Gly Val Thr Leu Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly
    210                 215                 220
```

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<210> 2703
<211> 405
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(382)
<223> RXA02393

<400> 2703
gccaccttca tttttcncan gccncngcaa atcagaacnc naccttctgg cactcccngc 60

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tcaaatnngg gacgtccatg cngangtttt agacatcttc atg gcg gaa tct tta   115
                                            Met Ala Glu Ser Leu
                                              1               5

gtg att atc aac atc gac gag aaa agc gcc aag ctg ctt atc gac gcc   163
Val Ile Ile Asn Ile Asp Glu Lys Ser Ala Lys Leu Leu Ile Asp Ala
                 10                  15                  20

gcc cgc cac cac atc ccc acc cgc ttc acc ggg ccc aac gcc cgg ccg   211
Ala Arg His His Ile Pro Thr Arg Phe Thr Gly Pro Asn Ala Arg Pro
             25                  30                  35

ctc agc gtc atc ccc atc gag gat ccc cgc tca cgc ccg acg ctc cac   259
Leu Ser Val Ile Pro Ile Glu Asp Pro Arg Ser Arg Pro Thr Leu His
         40                  45                  50

cca gat cat ggt tgg atg atg ccg cta agc cca cca gtg gtg gat gaa   307
Pro Asp His Gly Trp Met Met Pro Leu Ser Pro Pro Val Val Asp Glu
     55                  60                  65

ctg ctt ggc ggt ggc ttg aaa att gga gaa aca gaa cta gaa agc acc   355
Leu Leu Gly Gly Gly Leu Lys Ile Gly Glu Thr Glu Leu Glu Ser Thr
 70                  75                  80                  85
```

```
aac att gcg ttc att gtt gat gct tcc taaaaatcct gtgccgtgag          402
Asn Ile Ala Phe Ile Val Asp Ala Ser
                 90

gtt                                                                405


<210> 2704
<211> 94
<212> PRT
<213> Corynebacterium glutamicum

<400> 2704
Met Ala Glu Ser Leu Val Ile Ile Asn Ile Asp Glu Lys Ser Ala Lys
  1               5                  10                  15

Leu Leu Ile Asp Ala Ala Arg His His Ile Pro Thr Arg Phe Thr Gly
             20                  25                  30

Pro Asn Ala Arg Pro Leu Ser Val Ile Pro Ile Glu Asp Pro Arg Ser
         35                  40                  45

Arg Pro Thr Leu His Pro Asp His Gly Trp Met Met Pro Leu Ser Pro
     50                  55                  60

Pro Val Val Asp Glu Leu Leu Gly Gly Gly Leu Lys Ile Gly Glu Thr
 65                  70                  75                  80

Glu Leu Glu Ser Thr Asn Ile Ala Phe Ile Val Asp Ala Ser
                 85                  90


<210> 2705
<211> 755
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(732)
<223> RXA02395

<400> 2705
ctc atc acc atg gct atc ccc tcc ttc att ttg atc ctg gcg ttc acc   48
Leu Ile Thr Met Ala Ile Pro Ser Phe Ile Leu Ile Leu Ala Phe Thr
  1               5                  10                  15

att ttc ggt gga act gcc atc acg atg aac cgc gag aac gta gat ggt   96
Ile Phe Gly Gly Thr Ala Ile Thr Met Asn Arg Glu Asn Val Asp Gly
             20                  25                  30

ttt gac ggc agt tca tcc aag gaa cag gtg ctg ttt gat atg ttc agc   144
Phe Asp Gly Ser Ser Ser Lys Glu Gln Val Leu Phe Asp Met Phe Ser
         35                  40                  45

aac ctt ccg ctg tac tcg atc aca ccg ttc att ttg atc ttt gtg ctg   192
Asn Leu Pro Leu Tyr Ser Ile Thr Pro Phe Ile Leu Ile Phe Val Leu
     50                  55                  60

gca gta ttc ttt gtt acc tct gcc gat tcc gcc tcc gtg gtg atg gga   240
Ala Val Phe Phe Val Thr Ser Ala Asp Ser Ala Ser Val Val Met Gly
```

```
 65                  70                  75                  80

acg atg agc tcc caa ggt aac cct gca cca aac aaa tta atc gtg gtg   288
Thr Met Ser Ser Gln Gly Asn Pro Ala Pro Asn Lys Leu Ile Val Val
                 85                  90                  95

ttc tgg gga ctg tgc atg atg ggc atc gcg gtg gtc atg ctg ctt act   336
Phe Trp Gly Leu Cys Met Met Gly Ile Ala Val Val Met Leu Leu Thr
            100                 105                 110

ggt ggc gaa tcc gcg ctg act ggt ctg cag aac ctc acc att ttg atc   384
Gly Gly Glu Ser Ala Leu Thr Gly Leu Gln Asn Leu Thr Ile Leu Ile
        115                 120                 125

gcc att ccg ttt gcg ctg gtg ttg atc gtg atg gct att gcc ttt att   432
Ala Ile Pro Phe Ala Leu Val Leu Ile Val Met Ala Ile Ala Phe Ile
    130                 135                 140

aag gac tta tcc aca gac cca gcc gct att cga caa cgc tat gca aag   480
Lys Asp Leu Ser Thr Asp Pro Ala Ala Ile Arg Gln Arg Tyr Ala Lys
145                 150                 155                 160

gca gcc atc tct aac gcg gtg gtt cgt ggc ttg gaa gaa cac ggc gac   528
Ala Ala Ile Ser Asn Ala Val Val Arg Gly Leu Glu Glu His Gly Asp
                165                 170                 175

gac ttc gag ctc tcc atc gaa cct gca gag gaa ggt cgt gga gcg ggt   576
Asp Phe Glu Leu Ser Ile Glu Pro Ala Glu Glu Gly Arg Gly Ala Gly
            180                 185                 190

gct acc ttc gat tcc acc gct gat cac atc acc gac tgg tat cag cgc   624
Ala Thr Phe Asp Ser Thr Ala Asp His Ile Thr Asp Trp Tyr Gln Arg
        195                 200                 205

acc gac gaa gaa ggc aat gat gtt gat tat gac ttc acc acc ggc aaa   672
Thr Asp Glu Glu Gly Asn Asp Val Asp Tyr Asp Phe Thr Thr Gly Lys
    210                 215                 220

tgg gcc gat ggt tgg aca ccg gaa tcg acc gaa gaa ggc gaa gtg gac   720
Trp Ala Asp Gly Trp Thr Pro Glu Ser Thr Glu Glu Gly Glu Val Asp
225                 230                 235                 240

gcg aaa aag gat taaaaaataa cgactggctg gga                        755
Ala Lys Lys Asp
```

<210> 2706
<211> 244
<212> PRT
<213> Corynebacterium glutamicum

<400> 2706

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Leu Ile Thr Met Ala Ile Pro Ser Phe Ile Leu Ile Leu Ala Phe Thr
  1               5                  10                  15

Ile Phe Gly Gly Thr Ala Ile Thr Met Asn Arg Glu Asn Val Asp Gly
             20                  25                  30

Phe Asp Gly Ser Ser Ser Lys Glu Gln Val Leu Phe Asp Met Phe Ser
         35                  40                  45
```

```
Asn Leu Pro Leu Tyr Ser Ile Thr Pro Phe Ile Leu Ile Phe Val Leu
     50                  55                  60

Ala Val Phe Phe Val Thr Ser Ala Asp Ser Ala Ser Val Val Met Gly
 65                  70                  75                  80

Thr Met Ser Ser Gln Gly Asn Pro Ala Pro Asn Lys Leu Ile Val Val
                 85                  90                  95

Phe Trp Gly Leu Cys Met Met Gly Ile Ala Val Val Met Leu Leu Thr
            100                 105                 110

Gly Gly Glu Ser Ala Leu Thr Gly Leu Gln Asn Leu Thr Ile Leu Ile
        115                 120                 125

Ala Ile Pro Phe Ala Leu Val Leu Ile Val Met Ala Ile Ala Phe Ile
    130                 135                 140

Lys Asp Leu Ser Thr Asp Pro Ala Ala Ile Arg Gln Arg Tyr Ala Lys
145                 150                 155                 160

Ala Ala Ile Ser Asn Ala Val Val Arg Gly Leu Glu Glu His Gly Asp
                165                 170                 175

Asp Phe Glu Leu Ser Ile Glu Pro Ala Glu Glu Gly Arg Gly Ala Gly
            180                 185                 190

Ala Thr Phe Asp Ser Thr Ala Asp His Ile Thr Asp Trp Tyr Gln Arg
        195                 200                 205

Thr Asp Glu Glu Gly Asn Asp Val Asp Tyr Asp Phe Thr Thr Gly Lys
    210                 215                 220

Trp Ala Asp Gly Trp Thr Pro Glu Ser Thr Glu Glu Gly Glu Val Asp
225                 230                 235                 240

Ala Lys Lys Asp
```

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<210> 2707
<211> 402
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(379)
<223> RXA02396

<400> 2707
gagtgcttgt aggttgatag aaagtaaact aaagtaaaca tcaggttaac agccgggggt 60

tcaagtatta actccctcgg aaacagaaag gaacacgaca atg gct acc aca gct 115
                                              Met Ala Thr Thr Ala
                                                1   5

tcc aag atc tcc acg atc cgt cca gca cag caa gat gct ctt tgg agc 163
Ser Lys Ile Ser Thr Ile Arg Pro Ala Gln Gln Asp Ala Leu Trp Ser
                10   15   20

```
gta cgt gag gat ctt cac gct cgc ttc gat ggc ctg gtc gat cct gtc   211
Val Arg Glu Asp Leu His Ala Arg Phe Asp Gly Leu Val Asp Pro Val
            25                  30                  35

cag gta gac gca att ttg gac cat gtc gca tct aac cgc gaa gcc aag   259
Gln Val Asp Ala Ile Leu Asp His Val Ala Ser Asn Arg Glu Ala Lys
        40                  45                  50

atc acc gtc ttc agc aag att ttc atc gct cgc gag gca acc gct gca   307
Ile Thr Val Phe Ser Lys Ile Phe Ile Ala Arg Glu Ala Thr Ala Ala
    55                  60                  65

ctt cag cag att gct ggc aac gtt aac gca gac ctg ctt gac ttc att   355
Leu Gln Gln Ile Ala Gly Asn Val Asn Ala Asp Leu Leu Asp Phe Ile
70                  75                  80                  85

gcc ctc aac cgt ggc atg gca gca taagttttag ctgcccataa att         402
Ala Leu Asn Arg Gly Met Ala Ala
                90
```

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<210> 2708
<211> 93
<212> PRT
<213> Corynebacterium glutamicum

<400> 2708
Met Ala Thr Thr Ala Ser Lys Ile Ser Thr Ile Arg Pro Ala Gln Gln
1   5   10   15

Asp Ala Leu Trp Ser Val Arg Glu Asp Leu His Ala Arg Phe Asp Gly
            20   25   30

Leu Val Asp Pro Val Gln Val Asp Ala Ile Leu Asp His Val Ala Ser
        35   40   45

Asn Arg Glu Ala Lys Ile Thr Val Phe Ser Lys Ile Phe Ile Ala Arg
    50   55   60

Glu Ala Thr Ala Ala Leu Gln Gln Ile Ala Gly Asn Val Asn Ala Asp
65   70   75   80

Leu Leu Asp Phe Ile Ala Leu Asn Arg Gly Met Ala Ala
                85   90

<210> 2709
<211> 888
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(865)
<223> RXA02403

<400> 2709
gcacagaatt aaatcgctgg tgtgcgaact ttcatacctt aacgcagtag tgatgcttaa 60

ggcacaacgt gggggcaatt ccggcctata ctttggaagt atg act act ttt att   115

```
                                                    Met Thr Thr Phe Ile
                                                      1               5

acc tcc ggt ggc ttg gaa atc tcc ccc gct ggc gct cat att gtt cac   163
Thr Ser Gly Gly Leu Glu Ile Ser Pro Ala Gly Ala His Ile Val His
                10                  15                  20

gcc gaa tca cct gaa ggt gag ctg ttg ttt gtt agc tcc gct tcc caa   211
Ala Glu Ser Pro Glu Gly Glu Leu Leu Phe Val Ser Ser Ala Ser Gln
            25                  30                  35

tat ggg gag gga aat gca att agg ggt ggt gtg ccc atc att gct cca   259
Tyr Gly Glu Gly Asn Ala Ile Arg Gly Gly Val Pro Ile Ile Ala Pro
        40                  45                  50

tgg ttt ggt gga ctg ctt ggt ttg gac cct gca cat ggt tgg gcg aag   307
Trp Phe Gly Gly Leu Leu Gly Leu Asp Pro Ala His Gly Trp Ala Lys
    55                  60                  65

cgt tcc gcg tgg gac gtg act gaa cat gac ggc caa att cac gct gaa   355
Arg Ser Ala Trp Asp Val Thr Glu His Asp Gly Gln Ile His Ala Glu
70                  75                  80                  85

tat ggc cgc gat ggt tta ctg ctg gat att cgt gcg aac agc act aag   403
Tyr Gly Arg Asp Gly Leu Leu Leu Asp Ile Arg Ala Asn Ser Thr Lys
                90                  95                  100

aat ggt ttt gag atc acc ctg cgc gct tac aac gac acc gat gag gca   451
Asn Gly Phe Glu Ile Thr Leu Arg Ala Tyr Asn Asp Thr Asp Glu Ala
            105                 110                 115

cgc act gtg cag ttg gcc ttc cac cct tat ttc aag gtg gat gat gta   499
Arg Thr Val Gln Leu Ala Phe His Pro Tyr Phe Lys Val Asp Asp Val
        120                 125                 130

gaa aag atc gag gtc cgt ggc ctt gat ggg gtg gac att ctc aat cgc   547
Glu Lys Ile Glu Val Arg Gly Leu Asp Gly Val Asp Ile Leu Asn Arg
    135                 140                 145

ctg aac aat gag gtg gag acc caa gat ggt ccc gtt act ttt gat ggc   595
Leu Asn Asn Glu Val Glu Thr Gln Asp Gly Pro Val Thr Phe Asp Gly
150                 155                 160                 165

gag ttc gat cgc att gcg cta ggg act ccg gtt gtg agg att ttt gat   643
Glu Phe Asp Arg Ile Ala Leu Gly Thr Pro Val Val Arg Ile Phe Asp
                170                 175                 180

acc gat cgc atc atc acc att gag ggc gat ggt cat gat tcc act gtg   691
Thr Asp Arg Ile Ile Thr Ile Glu Gly Asp Gly His Asp Ser Thr Val
            185                 190                 195

gtg tgg aat cca ggc gaa agt cgc gcc tcc acc gtg gcc gat att ggc   739
Val Trp Asn Pro Gly Glu Ser Arg Ala Ser Thr Val Ala Asp Ile Gly
        200                 205                 210

gaa ggt gaa tgg cgc gac ttt gtg tgt gtt gaa ccg gcg ctt ttg ggt   787
Glu Gly Glu Trp Arg Asp Phe Val Cys Val Glu Pro Ala Leu Leu Gly
    215                 220                 225

gct gac caa aaa gga gtg agg gtg gct ccg ggg cag tca gtc acc gtt   835
Ala Asp Gln Lys Gly Val Arg Val Ala Pro Gly Gln Ser Val Thr Val
```

```
230                 235                 240                 245

ggg atg cag gta agc gtc gaa aag cgt gct tagtttttg ctttgaactc     885
Gly Met Gln Val Ser Val Glu Lys Arg Ala
                250                 255

gcg                                                              888


<210> 2710
<211> 255
<212> PRT
<213> Corynebacterium glutamicum

<400> 2710
Met Thr Thr Phe Ile Thr Ser Gly Gly Leu Glu Ile Ser Pro Ala Gly
  1               5                  10                  15

Ala His Ile Val His Ala Glu Ser Pro Glu Gly Glu Leu Leu Phe Val
             20                  25                  30

Ser Ser Ala Ser Gln Tyr Gly Glu Gly Asn Ala Ile Arg Gly Gly Val
         35                  40                  45

Pro Ile Ile Ala Pro Trp Phe Gly Gly Leu Leu Gly Leu Asp Pro Ala
     50                  55                  60

His Gly Trp Ala Lys Arg Ser Ala Trp Asp Val Thr Glu His Asp Gly
 65                  70                  75                  80

Gln Ile His Ala Glu Tyr Gly Arg Asp Gly Leu Leu Leu Asp Ile Arg
                 85                  90                  95

Ala Asn Ser Thr Lys Asn Gly Phe Glu Ile Thr Leu Arg Ala Tyr Asn
            100                 105                 110

Asp Thr Asp Glu Ala Arg Thr Val Gln Leu Ala Phe His Pro Tyr Phe
        115                 120                 125

Lys Val Asp Asp Val Glu Lys Ile Glu Val Arg Gly Leu Asp Gly Val
    130                 135                 140

Asp Ile Leu Asn Arg Leu Asn Asn Glu Val Glu Thr Gln Asp Gly Pro
145                 150                 155                 160

Val Thr Phe Asp Gly Glu Phe Asp Arg Ile Ala Leu Gly Thr Pro Val
                165                 170                 175

Val Arg Ile Phe Asp Thr Asp Arg Ile Ile Thr Ile Glu Gly Asp Gly
            180                 185                 190

His Asp Ser Thr Val Val Trp Asn Pro Gly Glu Ser Arg Ala Ser Thr
        195                 200                 205

Val Ala Asp Ile Gly Glu Gly Glu Trp Arg Asp Phe Val Cys Val Glu
    210                 215                 220

Pro Ala Leu Leu Gly Ala Asp Gln Lys Gly Val Arg Val Ala Pro Gly
225                 230                 235                 240

Gln Ser Val Thr Val Gly Met Gln Val Ser Val Glu Lys Arg Ala
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245 250 255

<210> 2711
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> RXA02412

<400> 2711
tgcggtgcga gcaacttcgg agactattgg ctctcctaca gctgtggcat ccgcgaaacg 60

ttcacccaaa ggcagtctca ttgggttgat cttgatcttg gtg gcc atc atc gtg 115
Val Ala Ile Ile Val
1 5

att gcg ttt gtc ttg ttg ttc aac agc ctc gtt gca cca aat aat tcc 163
Ile Ala Phe Val Leu Leu Phe Asn Ser Leu Val Ala Pro Asn Asn Ser
10 15 20

tcg agc cct gtg gca agt cca agc acc tct gaa tct gtg gag caa act 211
Ser Ser Pro Val Ala Ser Pro Ser Thr Ser Glu Ser Val Glu Gln Thr
25 30 35

att tcg gaa tcc cct gag tca ccg agc gcg aca gag gat cag ccc cca 259
Ile Ser Glu Ser Pro Glu Ser Pro Ser Ala Thr Glu Asp Gln Pro Pro
40 45 50

agc agt gca acg gaa act ccc cga aac cgc cct gcg caa cca tca ctt 307
Ser Ser Ala Thr Glu Thr Pro Arg Asn Arg Pro Ala Gln Pro Ser Leu
55 60 65

cct gcg gga gca tca cca gcc aat gat gct gct gcc acc cag acc gat 355
Pro Ala Gly Ala Ser Pro Ala Asn Asp Ala Ala Ala Thr Gln Thr Asp
70 75 80 85

gcc ggc aat tta aac aat gtg tac acc ggg tca gcg tcc acc tca gca 403
Ala Gly Asn Leu Asn Asn Val Tyr Thr Gly Ser Ala Ser Thr Ser Ala
90 95 100

ggt ttt gct caa gcc gtc cga gat gct ttt gta aac cac tat tta gac 451
Gly Phe Ala Gln Ala Val Arg Asp Ala Phe Val Asn His Tyr Leu Asp
105 110 115

acc aat gaa cta tcc ggc agg gtg aca gcc acc agc cct gtc act ggc 499
Thr Asn Glu Leu Ser Gly Arg Val Thr Ala Thr Ser Pro Val Thr Gly
120 125 130

gga aac tac acc atg aac tgc gaa gac aac ggc gag tac gtc acc tgc 547
Gly Asn Tyr Thr Met Asn Cys Glu Asp Asn Gly Glu Tyr Val Thr Cys
135 140 145

aca ggt ggc aac aac gcc gtt gtc tac att tct taaaacttct aactacaccc 600
Thr Gly Gly Asn Asn Ala Val Val Tyr Ile Ser
150 155 160

ggg 603

<210> 2712
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 2712

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Val Ala Ile Ile Val Ile Ala Phe Val Leu Leu Phe Asn Ser Leu Val
  1               5                  10                  15

Ala Pro Asn Asn Ser Ser Ser Pro Val Ala Ser Pro Ser Thr Ser Glu
             20                  25                  30

Ser Val Glu Gln Thr Ile Ser Glu Ser Pro Glu Ser Pro Ser Ala Thr
         35                  40                  45

Glu Asp Gln Pro Pro Ser Ser Ala Thr Glu Thr Pro Arg Asn Arg Pro
     50                  55                  60

Ala Gln Pro Ser Leu Pro Ala Gly Ala Ser Pro Ala Asn Asp Ala Ala
 65                  70                  75                  80

Ala Thr Gln Thr Asp Ala Gly Asn Leu Asn Asn Val Tyr Thr Gly Ser
                 85                  90                  95

Ala Ser Thr Ser Ala Gly Phe Ala Gln Ala Val Arg Asp Ala Phe Val
            100                 105                 110

Asn His Tyr Leu Asp Thr Asn Glu Leu Ser Gly Arg Val Thr Ala Thr
        115                 120                 125

Ser Pro Val Thr Gly Gly Asn Tyr Thr Met Asn Cys Glu Asp Asn Gly
    130                 135                 140

Glu Tyr Val Thr Cys Thr Gly Gly Asn Asn Ala Val Val Tyr Ile Ser
145                 150                 155                 160
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<210> 2713
<211> 2247
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2224)
<223> RXA02417

<400> 2713

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cgctgttcag aggacttccg cgggggtcga cagtataacg aattagcgtc actagaataa 60

tcgggctgtt tagttcttca caccaacata atcttatgta atg gac atg aac tct   115
                                              Met Asp Met Asn Ser
                                                1               5

tct gac cga ttg gct cta cgc acc gcg tta gag aaa ttg tcg gca tcg   163
Ser Asp Arg Leu Ala Leu Arg Thr Ala Leu Glu Lys Leu Ser Ala Ser
```

```
                  10                  15                  20

gct acc gcc atg gcg tca gcg agc aat gac atc aaa gat ctc gtt gca   211
Ala Thr Ala Met Ala Ser Ala Ser Asn Asp Ile Lys Asp Leu Val Ala
            25                  30                  35

cgc ctt gat gcc caa gag atg tcg ctt atc gac gca aac ccg gct ccc   259
Arg Leu Asp Ala Gln Glu Met Ser Leu Ile Asp Ala Asn Pro Ala Pro
        40                  45                  50

acc cca gcg ccc act gcc cca ccc gag gct cag ctt gag ccc caa cca   307
Thr Pro Ala Pro Thr Ala Pro Pro Glu Ala Gln Leu Glu Pro Gln Pro
    55                  60                  65

ctg gtg tat gca acc gcc tca acg gcg cct gca ctg gcg gat gtt tcc   355
Leu Val Tyr Ala Thr Ala Ser Thr Ala Pro Ala Leu Ala Asp Val Ser
70                  75                  80                  85

ggg acc aac cgt att cca cgt ttc gtt cgg cat cgc gcc ctg gat cca   403
Gly Thr Asn Arg Ile Pro Arg Phe Val Arg His Arg Ala Leu Asp Pro
                90                  95                  100

gcg agc gaa ggc tgg cca ctt ggc gtc gag aag caa aaa gtg cag gct   451
Ala Ser Glu Gly Trp Pro Leu Gly Val Glu Lys Gln Lys Val Gln Ala
            105                 110                 115

cct gcg tac ccg cac ccc gtc cgg cca gct cgt ccg gca aag ccg ccg   499
Pro Ala Tyr Pro His Pro Val Arg Pro Ala Arg Pro Ala Lys Pro Pro
        120                 125                 130

atg acg tcg gag gaa aag atc atg cgt ggc gtg gcg atc ggc ggt ggt   547
Met Thr Ser Glu Glu Lys Ile Met Arg Gly Val Ala Ile Gly Gly Gly
    135                 140                 145

gtg atc acc gtg gcc ggc gtg att ttg ctg gtg tcg gtg gcg att caa   595
Val Ile Thr Val Ala Gly Val Ile Leu Leu Val Ser Val Ala Ile Gln
150                 155                 160                 165

cgc ggt tgg ctt ggt ccg ctg ggt cgt gtg att ggt gcg tac ctg ctg   643
Arg Gly Trp Leu Gly Pro Leu Gly Arg Val Ile Gly Ala Tyr Leu Leu
                170                 175                 180

gcg gtg ctg ctt ctt ggc gcc gca cat tat gtg cgc aag cgc gga acc   691
Ala Val Leu Leu Leu Gly Ala Ala His Tyr Val Arg Lys Arg Gly Thr
            185                 190                 195

cgt gtg gaa gca ctc gtt gcg ttg acg gtt acc tcc cag att gcg ttt   739
Arg Val Glu Ala Leu Val Ala Leu Thr Val Thr Ser Gln Ile Ala Phe
        200                 205                 210

ctt gcc aca acg agt gca atc atc ttc att ttg gaa tgg tgg ccg cct   787
Leu Ala Thr Thr Ser Ala Ile Ile Phe Ile Leu Glu Trp Trp Pro Pro
    215                 220                 225

gga ttg ggc tcg ctg gtg gca tta ata ggc aat att ggg ttc tta atc   835
Gly Leu Gly Ser Leu Val Ala Leu Ile Gly Asn Ile Gly Phe Leu Ile
230                 235                 240                 245

gtt ggt cga ttg tgg agc cta tcc aaa acc gag aag tcc gcg gcc gaa   883
Val Gly Arg Leu Trp Ser Leu Ser Lys Thr Glu Lys Ser Ala Ala Glu
                250                 255                 260
```

```
ggc cac aca gta ttt gtg gga gcc atc gcc gtt tca gga ttc tcc gcg   931
Gly His Thr Val Phe Val Gly Ala Ile Ala Val Ser Gly Phe Ser Ala
           265                 270                 275

ata ctc ttc gcg ctc tcc gcc gat gcc tgg tgg cca att ttc tcc att   979
Ile Leu Phe Ala Leu Ser Ala Asp Ala Trp Trp Pro Ile Phe Ser Ile
       280                 285                 290

gtt gcg gca ttg ttg ctg tcg tac cgc atc tcc acg aat atc atc cga   1027
Val Ala Ala Leu Leu Leu Ser Tyr Arg Ile Ser Thr Asn Ile Ile Arg
   295                 300                 305

gcg agc atg gcg gca ttc gcg gtc att ctg cag ttt gtt ttg tcg gca   1075
Ala Ser Met Ala Ala Phe Ala Val Ile Leu Gln Phe Val Leu Ser Ala
310                 315                 320                 325

tcc tgg caa acc atg gaa tgg cca gca aca atc gtc ggc aca att act   1123
Ser Trp Gln Thr Met Glu Trp Pro Ala Thr Ile Val Gly Thr Ile Thr
               330                 335                 340

gca gtc cta ctc gta gcc ttg aca ttg tgg gat ccg ttt aag atc acc   1171
Ala Val Leu Leu Val Ala Leu Thr Leu Trp Asp Pro Phe Lys Ile Thr
           345                 350                 355

gcc acc gac agc cac gac atc gcg ttg gag gaa tac tgg cgc agc ttt   1219
Ala Thr Asp Ser His Asp Ile Ala Leu Glu Glu Tyr Trp Arg Ser Phe
       360                 365                 370

gaa acc aac cct gtt tcc acg tgg gtg ggt gct gtt tct ccg gtg ctc   1267
Glu Thr Asn Pro Val Ser Thr Trp Val Gly Ala Val Ser Pro Val Leu
   375                 380                 385

atc gtg ttc atc acc acc agc atg ttc att gca gtc gac tgg cca tgg   1315
Ile Val Phe Ile Thr Thr Ser Met Phe Ile Ala Val Asp Trp Pro Trp
390                 395                 400                 405

ctt gcc ctg ata cca gcg tgt gcg gtg gca gct ctc gga att ttc gcg   1363
Leu Ala Leu Ile Pro Ala Cys Ala Val Ala Ala Leu Gly Ile Phe Ala
               410                 415                 420

ctg cgc tca tca gac acc gcg tcc att gaa aat caa cgc atg tct cgc   1411
Leu Arg Ser Ser Asp Thr Ala Ser Ile Glu Asn Gln Arg Met Ser Arg
           425                 430                 435

ctc att gct gtt gtt ggc ctt gcg ttg att gct gaa act ttt gtc cag   1459
Leu Ile Ala Val Val Gly Leu Ala Leu Ile Ala Glu Thr Phe Val Gln
       440                 445                 450

ctg ttc tac ggc gat ctc ccc acc aac ccg ctt ctc gtc atg gtg ttc   1507
Leu Phe Tyr Gly Asp Leu Pro Thr Asn Pro Leu Leu Val Met Val Phe
   455                 460                 465

ctc atc gcc gga gct gca cta ttt atg tgg ttg cgg atg ctt cca ccg   1555
Leu Ile Ala Gly Ala Ala Leu Phe Met Trp Leu Arg Met Leu Pro Pro
470                 475                 480                 485

cag cgt caa tta ggt gtc gtc cca tgg gtc gct tgg ctg att gcc gcc   1603
Gln Arg Gln Leu Gly Val Val Pro Trp Val Ala Trp Leu Ile Ala Ala
               490                 495                 500
```

```
gtg gcg atg acc ggc gtg cta ctg cgc aat gtc gtt tca att tct cca   1651
Val Ala Met Thr Gly Val Leu Leu Arg Asn Val Val Ser Ile Ser Pro
            505                 510                 515

ctg tgg ctc acc gat acc caa gcg ctc atc caa gca ttg ctg atc ttg   1699
Leu Trp Leu Thr Asp Thr Gln Ala Leu Ile Gln Ala Leu Leu Ile Leu
        520                 525                 530

gtg ttc att gcc gcc aca atc caa gtc cgc cgc agc ttc tac gga cac   1747
Val Phe Ile Ala Ala Thr Ile Gln Val Arg Arg Ser Phe Tyr Gly His
    535                 540                 545

aaa ctg tgg ctg caa att ttg gtc ggc ttg acg ctt ctc acg ctg tcc   1795
Lys Leu Trp Leu Gln Ile Leu Val Gly Leu Thr Leu Leu Thr Leu Ser
550                 555                 560                 565

gca att tcc atc gtg acc atc aca acc ttc atc ggt cgc ctc atc gca   1843
Ala Ile Ser Ile Val Thr Ile Thr Thr Phe Ile Gly Arg Leu Ile Ala
                570                 575                 580

gga aat gcc ggc atg atg ctc gga ttc ctc atc ggc cac gcc acg gtt   1891
Gly Asn Ala Gly Met Met Leu Gly Phe Leu Ile Gly His Ala Thr Val
            585                 590                 595

tct atc ctg tgg atg gtc atc gcc gca gca ctg atg ctt aat agg aag   1939
Ser Ile Leu Trp Met Val Ile Ala Ala Ala Leu Met Leu Asn Arg Lys
        600                 605                 610

ctt ctc gac gcg ccc ggc gcc ctt tgg acc ggc gtt ggc ttg gcg gtt   1987
Leu Leu Asp Ala Pro Gly Ala Leu Trp Thr Gly Val Gly Leu Ala Val
    615                 620                 625

gcg ggc acc ttc aag ctg gtg ttc ttt gac ctg gtc gcg ctg tcc gga   2035
Ala Gly Thr Phe Lys Leu Val Phe Phe Asp Leu Val Ala Leu Ser Gly
630                 635                 640                 645

gtt ccc cgc gca att gcc ttc ctg ctc tcc ggt atc gca ctg ctg aca   2083
Val Pro Arg Ala Ile Ala Phe Leu Leu Ser Gly Ile Ala Leu Leu Thr
                650                 655                 660

atc gct gct atg agg ggc cgg aga acc tca gaa aac aag gcc gac gta   2131
Ile Ala Ala Met Arg Gly Arg Arg Thr Ser Glu Asn Lys Ala Asp Val
            665                 670                 675

gct aga cct cag gtg gct aga cat ggg gcg act agc cat aaa aat gag   2179
Ala Arg Pro Gln Val Ala Arg His Gly Ala Thr Ser His Lys Asn Glu
        680                 685                 690

gag cct tcc cat gaa agc ccc tca tct tct cct aca aca act ctt       2224
Glu Pro Ser His Glu Ser Pro Ser Ser Ser Pro Thr Thr Thr Leu
    695                 700                 705

taaggaattg gccggtgtag gaa                                        2247
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<210> 2714
<211> 708
<212> PRT
<213> Corynebacterium glutamicum

<400> 2714

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Met Asp Met Asn Ser Ser Asp Arg Leu Ala Leu Arg Thr Ala Leu Glu
 1               5                  10                  15

Lys Leu Ser Ala Ser Ala Thr Ala Met Ala Ser Ala Ser Asn Asp Ile
            20                  25                  30

Lys Asp Leu Val Ala Arg Leu Asp Ala Gln Glu Met Ser Leu Ile Asp
        35                  40                  45

Ala Asn Pro Ala Pro Thr Pro Ala Pro Thr Ala Pro Pro Glu Ala Gln
    50                  55                  60

Leu Glu Pro Gln Pro Leu Val Tyr Ala Thr Ala Ser Thr Ala Pro Ala
65                  70                  75                  80

Leu Ala Asp Val Ser Gly Thr Asn Arg Ile Pro Arg Phe Val Arg His
                85                  90                  95

Arg Ala Leu Asp Pro Ala Ser Glu Gly Trp Pro Leu Gly Val Glu Lys
            100                 105                 110

Gln Lys Val Gln Ala Pro Ala Tyr Pro His Pro Val Arg Pro Ala Arg
        115                 120                 125

Pro Ala Lys Pro Pro Met Thr Ser Glu Glu Lys Ile Met Arg Gly Val
    130                 135                 140

Ala Ile Gly Gly Gly Val Ile Thr Val Ala Gly Val Ile Leu Leu Val
145                 150                 155                 160

Ser Val Ala Ile Gln Arg Gly Trp Leu Gly Pro Leu Gly Arg Val Ile
                165                 170                 175

Gly Ala Tyr Leu Leu Ala Val Leu Leu Leu Gly Ala Ala His Tyr Val
            180                 185                 190

Arg Lys Arg Gly Thr Arg Val Glu Ala Leu Val Ala Leu Thr Val Thr
        195                 200                 205

Ser Gln Ile Ala Phe Leu Ala Thr Thr Ser Ala Ile Ile Phe Ile Leu
    210                 215                 220

Glu Trp Trp Pro Pro Gly Leu Gly Ser Leu Val Ala Leu Ile Gly Asn
225                 230                 235                 240

Ile Gly Phe Leu Ile Val Gly Arg Leu Trp Ser Leu Ser Lys Thr Glu
                245                 250                 255

Lys Ser Ala Ala Glu Gly His Thr Val Phe Val Gly Ala Ile Ala Val
            260                 265                 270

Ser Gly Phe Ser Ala Ile Leu Phe Ala Leu Ser Ala Asp Ala Trp Trp
        275                 280                 285

Pro Ile Phe Ser Ile Val Ala Ala Leu Leu Leu Ser Tyr Arg Ile Ser
    290                 295                 300

Thr Asn Ile Ile Arg Ala Ser Met Ala Ala Phe Ala Val Ile Leu Gln
305                 310                 315                 320

Phe Val Leu Ser Ala Ser Trp Gln Thr Met Glu Trp Pro Ala Thr Ile
```

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```
                325                 330                 335

Val Gly Thr Ile Thr Ala Val Leu Leu Val Ala Leu Thr Leu Trp Asp
            340                 345                 350

Pro Phe Lys Ile Thr Ala Thr Asp Ser His Asp Ile Ala Leu Glu Glu
        355                 360                 365

Tyr Trp Arg Ser Phe Glu Thr Asn Pro Val Ser Thr Trp Val Gly Ala
    370                 375                 380

Val Ser Pro Val Leu Ile Val Phe Ile Thr Thr Ser Met Phe Ile Ala
385                 390                 395                 400

Val Asp Trp Pro Trp Leu Ala Leu Ile Pro Ala Cys Ala Val Ala Ala
                405                 410                 415

Leu Gly Ile Phe Ala Leu Arg Ser Ser Asp Thr Ala Ser Ile Glu Asn
            420                 425                 430

Gln Arg Met Ser Arg Leu Ile Ala Val Val Gly Leu Ala Leu Ile Ala
        435                 440                 445

Glu Thr Phe Val Gln Leu Phe Tyr Gly Asp Leu Pro Thr Asn Pro Leu
    450                 455                 460

Leu Val Met Val Phe Leu Ile Ala Gly Ala Ala Leu Phe Met Trp Leu
465                 470                 475                 480

Arg Met Leu Pro Pro Gln Arg Gln Leu Gly Val Val Pro Trp Val Ala
                485                 490                 495

Trp Leu Ile Ala Ala Val Ala Met Thr Gly Val Leu Leu Arg Asn Val
            500                 505                 510

Val Ser Ile Ser Pro Leu Trp Leu Thr Asp Thr Gln Ala Leu Ile Gln
        515                 520                 525

Ala Leu Leu Ile Leu Val Phe Ile Ala Ala Thr Ile Gln Val Arg Arg
    530                 535                 540

Ser Phe Tyr Gly His Lys Leu Trp Leu Gln Ile Leu Val Gly Leu Thr
545                 550                 555                 560

Leu Leu Thr Leu Ser Ala Ile Ser Ile Val Thr Ile Thr Thr Phe Ile
                565                 570                 575

Gly Arg Leu Ile Ala Gly Asn Ala Gly Met Met Leu Gly Phe Leu Ile
            580                 585                 590

Gly His Ala Thr Val Ser Ile Leu Trp Met Val Ile Ala Ala Ala Leu
        595                 600                 605

Met Leu Asn Arg Lys Leu Leu Asp Ala Pro Gly Ala Leu Trp Thr Gly
    610                 615                 620

Val Gly Leu Ala Val Ala Gly Thr Phe Lys Leu Val Phe Phe Asp Leu
625                 630                 635                 640

Val Ala Leu Ser Gly Val Pro Arg Ala Ile Ala Phe Leu Leu Ser Gly
                645                 650                 655
```

```
Ile Ala Leu Leu Thr Ile Ala Ala Met Arg Gly Arg Arg Thr Ser Glu
            660                 665                 670

Asn Lys Ala Asp Val Ala Arg Pro Gln Val Ala Arg His Gly Ala Thr
        675                 680                 685

Ser His Lys Asn Glu Glu Pro Ser His Glu Ser Pro Ser Ser Ser Pro
    690                 695                 700

Thr Thr Thr Leu
705
```

<210> 2715
<211> 933
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(910)
<223> RXA02421

<400> 2715

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cggtgtactt tagcaacaag gaaaaataac tatctacggc ctgttaatag ttcaacctac 60

aggccaaacc cgccttcatt aatgaattgt gagatcgacc atg aca ttg ctc ttg   115
                                            Met Thr Leu Leu Leu
                                              1               5

aag cca att ttg cag gct gcg gga atc aat cct gaa gat gcg tta gca   163
Lys Pro Ile Leu Gln Ala Ala Gly Ile Asn Pro Glu Asp Ala Leu Ala
                  10                  15                  20

atg cgt cat gta ttt att tcg atc cac gag gac acc aat tcc aat ggt   211
Met Arg His Val Phe Ile Ser Ile His Glu Asp Thr Asn Ser Asn Gly
              25                  30                  35

att acc cgt gaa tct aaa gac gaa gag att ctc gcc tac aca gct agc   259
Ile Thr Arg Glu Ser Lys Asp Glu Glu Ile Leu Ala Tyr Thr Ala Ser
          40                  45                  50

cag tca agt gat ccg cgt aga ttc cca ctg aat ccg cca cgc ttt tgg   307
Gln Ser Ser Asp Pro Arg Arg Phe Pro Leu Asn Pro Pro Arg Phe Trp
      55                  60                  65

atg gtg ttc atc cga gaa ggt ggc tcg cag gct cga cta tgg aaa gtg   355
Met Val Phe Ile Arg Glu Gly Gly Ser Gln Ala Arg Leu Trp Lys Val
  70                  75                  80                  85

gtg gaa aac cac ggc gaa gtc acc aat gat ggc gta cgc aga gtc ttc   403
Val Glu Asn His Gly Glu Val Thr Asn Asp Gly Val Arg Arg Val Phe
                  90                  95                 100

aac ctt act gag att gaa ctc atg gat gac ctt gca ggc aga ctc gtt   451
Asn Leu Thr Glu Ile Glu Leu Met Asp Asp Leu Ala Gly Arg Leu Val
            105                 110                 115

att cgt tgg aat tca cca cgc aag tgg tgg att aag ggc act act gct   499
Ile Arg Trp Asn Ser Pro Arg Lys Trp Trp Ile Lys Gly Thr Thr Ala
```

```
        120                 125                 130

gcc cta tac acc gtg gat act att gcc gat gcg gag cct att ccg ttt   547
Ala Leu Tyr Thr Val Asp Thr Ile Ala Asp Ala Glu Pro Ile Pro Phe
    135                 140                 145

cca ggt ttc gac aat ctt gtc ctg agc tac cca ttt ctt caa gaa gtg   595
Pro Gly Phe Asp Asn Leu Val Leu Ser Tyr Pro Phe Leu Gln Glu Val
150                 155                 160                 165

atg cgt gaa cct gcc tat gct tcg tgg cgc aca gct ctt ggt gct gtc   643
Met Arg Glu Pro Ala Tyr Ala Ser Trp Arg Thr Ala Leu Gly Ala Val
                170                 175                 180

aaa ggt att tac ctc att acc gat acc cgt act ggc cgc cac tat gtc   691
Lys Gly Ile Tyr Leu Ile Thr Asp Thr Arg Thr Gly Arg His Tyr Val
            185                 190                 195

ggc aaa gct gaa gga cta gaa aac ata cgc caa cgc tgg aac agc tac   739
Gly Lys Ala Glu Gly Leu Glu Asn Ile Arg Gln Arg Trp Asn Ser Tyr
        200                 205                 210

gcc acc aat gga cat ggc gga aac gta aaa ctc aaa cag ctt aag ccc   787
Ala Thr Asn Gly His Gly Gly Asn Val Lys Leu Lys Gln Leu Lys Pro
    215                 220                 225

gac aca ttt cgt ttt tcg ttg ctt cgg gtc ttt gat ccc gca act cca   835
Asp Thr Phe Arg Phe Ser Leu Leu Arg Val Phe Asp Pro Ala Thr Pro
230                 235                 240                 245

act agc att att aac gct gct gaa agc cac ttt aaa att gct ctc gac   883
Thr Ser Ile Ile Asn Ala Ala Glu Ser His Phe Lys Ile Ala Leu Asp
                250                 255                 260

acg atc aag cac gga tta aac gca aac taatcgcagc tccccaaccc         930
Thr Ile Lys His Gly Leu Asn Ala Asn
            265                 270

caa                                                              933
```

<210> 2716
<211> 270
<212> PRT
<213> Corynebacterium glutamicum

<400> 2716

```
Met Thr Leu Leu Leu Lys Pro Ile Leu Gln Ala Ala Gly Ile Asn Pro
  1               5                  10                  15

Glu Asp Ala Leu Ala Met Arg His Val Phe Ile Ser Ile His Glu Asp
             20                  25                  30

Thr Asn Ser Asn Gly Ile Thr Arg Glu Ser Lys Asp Glu Glu Ile Leu
         35                  40                  45

Ala Tyr Thr Ala Ser Gln Ser Ser Asp Pro Arg Arg Phe Pro Leu Asn
     50                  55                  60

Pro Pro Arg Phe Trp Met Val Phe Ile Arg Glu Gly Gly Ser Gln Ala
 65                  70                  75                  80
```

```
Arg Leu Trp Lys Val Val Glu Asn His Gly Glu Val Thr Asn Asp Gly
                 85                  90                  95

Val Arg Arg Val Phe Asn Leu Thr Glu Ile Glu Leu Met Asp Asp Leu
            100                 105                 110

Ala Gly Arg Leu Val Ile Arg Trp Asn Ser Pro Arg Lys Trp Trp Ile
        115                 120                 125

Lys Gly Thr Thr Ala Ala Leu Tyr Thr Val Asp Thr Ile Ala Asp Ala
    130                 135                 140

Glu Pro Ile Pro Phe Pro Gly Phe Asp Asn Leu Val Leu Ser Tyr Pro
145                 150                 155                 160

Phe Leu Gln Glu Val Met Arg Glu Pro Ala Tyr Ala Ser Trp Arg Thr
                165                 170                 175

Ala Leu Gly Ala Val Lys Gly Ile Tyr Leu Ile Thr Asp Thr Arg Thr
            180                 185                 190

Gly Arg His Tyr Val Gly Lys Ala Glu Gly Leu Glu Asn Ile Arg Gln
        195                 200                 205

Arg Trp Asn Ser Tyr Ala Thr Asn Gly His Gly Gly Asn Val Lys Leu
    210                 215                 220

Lys Gln Leu Lys Pro Asp Thr Phe Arg Phe Ser Leu Leu Arg Val Phe
225                 230                 235                 240

Asp Pro Ala Thr Pro Thr Ser Ile Ile Asn Ala Ala Glu Ser His Phe
                245                 250                 255

Lys Ile Ala Leu Asp Thr Ile Lys His Gly Leu Asn Ala Asn
            260                 265                 270
```

<210> 2717
<211> 653
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(630)
<223> RXA02425

<400> 2717

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ccc ggc gcc ttt gat gaa tta acc agt gtt tgg gga gaa aaa ggc gga   48
Pro Gly Ala Phe Asp Glu Leu Thr Ser Val Trp Gly Glu Lys Gly Gly
  1               5                  10                  15

agt tgg gcc gct gtt atc ggc ttc ttc ggt ggc atc gcg ctg atc gcc   96
Ser Trp Ala Ala Val Ile Gly Phe Phe Gly Gly Ile Ala Leu Ile Ala
             20                  25                  30

atc atc gac cgc tta gtc ccc acg gcg att aac ccc cac gag ccc tcc   144
Ile Ile Asp Arg Leu Val Pro Thr Ala Ile Asn Pro His Glu Pro Ser
         35                  40                  45
```

```
acc gtg gga ggc gcc gtt gaa gga ttc gag cgc cgc aac cgc atg atg   192
Thr Val Gly Gly Ala Val Glu Gly Phe Glu Arg Arg Asn Arg Met Met
     50                  55                  60

aaa atg ggt gtg ctc act gcg ctg gcc atc gcg atc cac aac ttt ccc   240
Lys Met Gly Val Leu Thr Ala Leu Ala Ile Ala Ile His Asn Phe Pro
 65                  70                  75                  80

gaa ggt ttc gct aca ttc ttg gcc gga ttg tcc gat cca atg atc gcg   288
Glu Gly Phe Ala Thr Phe Leu Ala Gly Leu Ser Asp Pro Met Ile Ala
                 85                  90                  95

atc cct gtg gcc gtg gca att gcc att cac aat att cca gag ggc att   336
Ile Pro Val Ala Val Ala Ile Ala Ile His Asn Ile Pro Glu Gly Ile
            100                 105                 110

gcg gtg ccg gtg cca ctg agg gaa gct aca ggg tca cgt cga aaa gca   384
Ala Val Pro Val Pro Leu Arg Glu Ala Thr Gly Ser Arg Arg Lys Ala
        115                 120                 125

tta ggt tgg gcg acc ctc tcc ggc ctt gct gag ccc gcc ggc gcc ctc   432
Leu Gly Trp Ala Thr Leu Ser Gly Leu Ala Glu Pro Ala Gly Ala Leu
    130                 135                 140

atc gga ttc ctg ctg ctc atg ccc ttt atc gga cca gaa gca ctc ggc   480
Ile Gly Phe Leu Leu Leu Met Pro Phe Ile Gly Pro Glu Ala Leu Gly
145                 150                 155                 160

ctg tgc ttc gcc gca gtt gcc ggc gtg atg gtg ttc atc agc gtc gat   528
Leu Cys Phe Ala Ala Val Ala Gly Val Met Val Phe Ile Ser Val Asp
                165                 170                 175

gaa cta ctg ccc act gcc atc tcc agc ggc aaa cac cac acc gcc atc   576
Glu Leu Leu Pro Thr Ala Ile Ser Ser Gly Lys His His Thr Ala Ile
            180                 185                 190

tac gga ctc atc gct ggc atg gca gtc atg gcg atc agc ctg ctg ctg   624
Tyr Gly Leu Ile Ala Gly Met Ala Val Met Ala Ile Ser Leu Leu Leu
        195                 200                 205

ttt atc tagcgttcag ccgcaacaag cat                                 653
Phe Ile
    210
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Sequence Listing

<210> 2718
<211> 210
<212> PRT
<213> Corynebacterium glutamicum

<400> 2718

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Pro Gly Ala Phe Asp Glu Leu Thr Ser Val Trp Gly Glu Lys Gly Gly
  1               5                  10                  15

Ser Trp Ala Ala Val Ile Gly Phe Phe Gly Gly Ile Ala Leu Ile Ala
             20                  25                  30

Ile Ile Asp Arg Leu Val Pro Thr Ala Ile Asn Pro His Glu Pro Ser
         35                  40                  45

Thr Val Gly Gly Ala Val Glu Gly Phe Glu Arg Arg Asn Arg Met Met
```

```
     50                  55                  60

Lys Met Gly Val Leu Thr Ala Leu Ala Ile Ala Ile His Asn Phe Pro
 65                  70                  75                  80

Glu Gly Phe Ala Thr Phe Leu Ala Gly Leu Ser Asp Pro Met Ile Ala
                 85                  90                  95

Ile Pro Val Ala Val Ala Ile Ala Ile His Asn Ile Pro Glu Gly Ile
            100                 105                 110

Ala Val Pro Val Pro Leu Arg Glu Ala Thr Gly Ser Arg Arg Lys Ala
        115                 120                 125

Leu Gly Trp Ala Thr Leu Ser Gly Leu Ala Glu Pro Ala Gly Ala Leu
    130                 135                 140

Ile Gly Phe Leu Leu Leu Met Pro Phe Ile Gly Pro Glu Ala Leu Gly
145                 150                 155                 160

Leu Cys Phe Ala Ala Val Ala Gly Val Met Val Phe Ile Ser Val Asp
                165                 170                 175

Glu Leu Leu Pro Thr Ala Ile Ser Ser Gly Lys His His Thr Ala Ile
            180                 185                 190

Tyr Gly Leu Ile Ala Gly Met Ala Val Met Ala Ile Ser Leu Leu Leu
        195                 200                 205

Phe Ile
    210


<210> 2719
<211> 510
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(487)
<223> RXA02427

<400> 2719
agcgatgctg acagtgcttc acttcgggcc gcatctaatt cctgctcgat tacccaactg 60

ctcgcgcagg gaatcgtcat cgacgacgag gtgaactagc gtg gat ttt gag ttg   115
                                            Val Asp Phe Glu Leu
                                              1               5

ggt aaa cgc tgc ccc tgc gga act ggc ctt acc tac ggt gag tgc tgc   163
Gly Lys Arg Cys Pro Cys Gly Thr Gly Leu Thr Tyr Gly Glu Cys Cys
                10                  15                  20

tac cgc ttt cac tcc ggc gaa tgg gtg gcc ccc acc gct gaa gcg ctc   211
Tyr Arg Phe His Ser Gly Glu Trp Val Ala Pro Thr Ala Glu Ala Leu
            25                  30                  35

atg cga tct cgg ttc acc gcc ttt gct gtt gga aat tcc cag tac ctt   259
Met Arg Ser Arg Phe Thr Ala Phe Ala Val Gly Asn Ser Gln Tyr Leu
        40                  45                  50
```

```
ctt gac act tgg gat cca gaa acc cgg cca agc gaa ctc ggc ctc gat   307
Leu Asp Thr Trp Asp Pro Glu Thr Arg Pro Ser Glu Leu Gly Leu Asp
     55                  60                  65

atg gga att gat ttc tac cgc ctc gac atc ctc gag acc acc ggc ggt   355
Met Gly Ile Asp Phe Tyr Arg Leu Asp Ile Leu Glu Thr Thr Gly Gly
 70                  75                  80                  85

gga ccc ttc gat tcc acc ggc acc gta aaa ttc caa gcc ttc tac aag   403
Gly Pro Phe Asp Ser Thr Gly Thr Val Lys Phe Gln Ala Phe Tyr Lys
                 90                  95                 100

ggg ctc gcc tcc ggc gtc caa gaa gaa gac tcc aca ttc cgc aag gtc   451
Gly Leu Ala Ser Gly Val Gln Glu Glu Asp Ser Thr Phe Arg Lys Val
            105                 110                 115

aac ggc gcg tgg gtc tat tcc aca gga gat gtc gac tagtttcccc        497
Asn Gly Ala Trp Val Tyr Ser Thr Gly Asp Val Asp
        120                 125

acacgtgcaa tag                                                   510
```

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<210> 2720
<211> 129
<212> PRT
<213> Corynebacterium glutamicum

<400> 2720

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Val Asp Phe Glu Leu Gly Lys Arg Cys Pro Cys Gly Thr Gly Leu Thr
  1               5                  10                  15

Tyr Gly Glu Cys Cys Tyr Arg Phe His Ser Gly Glu Trp Val Ala Pro
             20                  25                  30

Thr Ala Glu Ala Leu Met Arg Ser Arg Phe Thr Ala Phe Ala Val Gly
         35                  40                  45

Asn Ser Gln Tyr Leu Leu Asp Thr Trp Asp Pro Glu Thr Arg Pro Ser
     50                  55                  60

Glu Leu Gly Leu Asp Met Gly Ile Asp Phe Tyr Arg Leu Asp Ile Leu
 65                  70                  75                  80

Glu Thr Thr Gly Gly Gly Pro Phe Asp Ser Thr Gly Thr Val Lys Phe
                 85                  90                  95

Gln Ala Phe Tyr Lys Gly Leu Ala Ser Gly Val Gln Glu Glu Asp Ser
            100                 105                 110

Thr Phe Arg Lys Val Asn Gly Ala Trp Val Tyr Ser Thr Gly Asp Val
        115                 120                 125

Asp
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<210> 2721
<211> 309
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(286)
<223> RXA02430

<400> 2721
cttgtagtca agcgtggacc aaatgcaggc gctcgattcc ttctggacca gccaaccacg 60

accgctggtc gtcacccaga aagtgacatc ttccttgatg atg tca ccc gtt tca 115
Met Ser Pro Val Ser
1 5

cgt cgc cac gca gag ttc cgc atc aat gaa ggt gaa ttt gaa gtc gtg 163
Arg Arg His Ala Glu Phe Arg Ile Asn Glu Gly Glu Phe Glu Val Val
10 15 20

gac gta ggg tcc ctc aac gga acc tac gtt aac cgc gag cca cgc aac 211
Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Arg Asn
25 30 35

gct cag gtc atg cag acc ggt gat gag atc cag att ggc aag ttc cgc 259
Ala Gln Val Met Gln Thr Gly Asp Glu Ile Gln Ile Gly Lys Phe Arg
40 45 50

ctg gtt ttc ctc gca ggc cct gct gag taaaaacact tcctaggaaa 306
Leu Val Phe Leu Ala Gly Pro Ala Glu
55 60

gtt 309

<210> 2722
<211> 62
<212> PRT
<213> Corynebacterium glutamicum

<400> 2722
Met Ser Pro Val Ser Arg Arg His Ala Glu Phe Arg Ile Asn Glu Gly
1 5 10 15

Glu Phe Glu Val Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn
20 25 30

Arg Glu Pro Arg Asn Ala Gln Val Met Gln Thr Gly Asp Glu Ile Gln
35 40 45

Ile Gly Lys Phe Arg Leu Val Phe Leu Ala Gly Pro Ala Glu
50 55 60

<210> 2723
<211> 723
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(700)
<223> RXA02433

<400> 2723
aggcacgaga tcatccatcg tcggttccat agaatgggta gctgtcgaat gctgatagat 60

atttggtgac cagagattag agcaaaggat cattttcatc gtg aag ctt ttc aag 115
Val Lys Leu Phe Lys
1 5

gca acc gca gtt act ttt act gtt gca gca gca ttg gcg ctc agc gcg 163
Ala Thr Ala Val Thr Phe Thr Val Ala Ala Ala Leu Ala Leu Ser Ala
10 15 20

tgc tcc agc agt gat gat tcc tct tcg gag tca agc acc tct tct tcc 211
Cys Ser Ser Ser Asp Asp Ser Ser Ser Glu Ser Ser Thr Ser Ser Ser
25 30 35

acc tct tcg gct gcg tct gat gct gcg act cag tac cca act gct gag 259
Thr Ser Ser Ala Ala Ser Asp Ala Ala Thr Gln Tyr Pro Thr Ala Glu
40 45 50

gaa ctg aat gca att ttg gct gtg gca acc gac cct gag gca cca atc 307
Glu Leu Asn Ala Ile Leu Ala Val Ala Thr Asp Pro Glu Ala Pro Ile
55 60 65

gag gag aag gtg aag act gtt cag ggt tct gag aac gct cct gag ctg 355
Glu Glu Lys Val Lys Thr Val Gln Gly Ser Glu Asn Ala Pro Glu Leu
70 75 80 85

ttt gag acc atg act cag gca aag gtg gag tcg ggt gct gag ttc cag 403
Phe Glu Thr Met Thr Gln Ala Lys Val Glu Ser Gly Ala Glu Phe Gln
90 95 100

gtt gtt ggt tct gtg ctt cct ggc tat gac cca acc tct gag gtt ctg 451
Val Val Gly Ser Val Leu Pro Gly Tyr Asp Pro Thr Ser Glu Val Leu
105 110 115

acc acc gtc atg ttc cag ctt ccg gac cgc gct gag cag gaa gct gaa 499
Thr Thr Val Met Phe Gln Leu Pro Asp Arg Ala Glu Gln Glu Ala Glu
120 125 130

ggc gtg gag ttt gtg aac act gat ggt aat tgg cag ctg tcc cag gat 547
Gly Val Glu Phe Val Asn Thr Asp Gly Asn Trp Gln Leu Ser Gln Asp
135 140 145

tgg gct tgt atc ttg atc acc aat act gtt gct cct gag cag gtt cct 595
Trp Ala Cys Ile Leu Ile Thr Asn Thr Val Ala Pro Glu Gln Val Pro
150 155 160 165

gca atg tgt gtt gga act gat gct tct tcc gct ggt att gaa gag gcc 643
Ala Met Cys Val Gly Thr Asp Ala Ser Ser Ala Gly Ile Glu Glu Ala
170 175 180

cca gct gaa gag ggt gct gtt gtt gag gaa gcc cct gtt gaa gag gtt 691
Pro Ala Glu Glu Gly Ala Val Val Glu Glu Ala Pro Val Glu Glu Val
185 190 195

cct gtt cag tagggtttaa cggctcaggc tga 723
Pro Val Gln
200

<210> 2724
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 2724
Val Lys Leu Phe Lys Ala Thr Ala Val Thr Phe Thr Val Ala Ala Ala
1 5 10 15

Leu Ala Leu Ser Ala Cys Ser Ser Ser Asp Asp Ser Ser Ser Glu Ser
20 25 30

Ser Thr Ser Ser Ser Thr Ser Ser Ala Ala Ser Asp Ala Ala Thr Gln
35 40 45

Tyr Pro Thr Ala Glu Glu Leu Asn Ala Ile Leu Ala Val Ala Thr Asp
50 55 60

Pro Glu Ala Pro Ile Glu Glu Lys Val Lys Thr Val Gln Gly Ser Glu
65 70 75 80

Asn Ala Pro Glu Leu Phe Glu Thr Met Thr Gln Ala Lys Val Glu Ser
85 90 95

Gly Ala Glu Phe Gln Val Val Gly Ser Val Leu Pro Gly Tyr Asp Pro
100 105 110

Thr Ser Glu Val Leu Thr Thr Val Met Phe Gln Leu Pro Asp Arg Ala
115 120 125

Glu Gln Glu Ala Glu Gly Val Glu Phe Val Asn Thr Asp Gly Asn Trp
130 135 140

Gln Leu Ser Gln Asp Trp Ala Cys Ile Leu Ile Thr Asn Thr Val Ala
145 150 155 160

Pro Glu Gln Val Pro Ala Met Cys Val Gly Thr Asp Ala Ser Ser Ala
165 170 175

Gly Ile Glu Glu Ala Pro Ala Glu Glu Gly Ala Val Val Glu Glu Ala
180 185 190

Pro Val Glu Glu Val Pro Val Gln
195 200

<210> 2725
<211> 933
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(910)
<223> RXA02437

<400> 2725
gcccatcata actacatcga gcgaaatgcc aaccacatgt cccatgcttt tactaatgtg 60

gggtcttaga agaacgcgac caatttaagg agagttgaat atg agc acg att ggc 115
Met Ser Thr Ile Gly

```
                                                    1               5

aac ctc aag tta gta gtg gat ggc gca cgt aaa gct tat gga act tat   163
Asn Leu Lys Leu Val Val Asp Gly Ala Arg Lys Ala Tyr Gly Thr Tyr
                 10                  15                  20

gcg gat tac cgc gac cgc aag gtg tct gag act tat gat gcg ttg tcc   211
Ala Asp Tyr Arg Asp Arg Lys Val Ser Glu Thr Tyr Asp Ala Leu Ser
             25                  30                  35

caa gct gct ggt gaa tat gca cca aaa gct gag cag gct gta gag act   259
Gln Ala Ala Gly Glu Tyr Ala Pro Lys Ala Glu Gln Ala Val Glu Thr
         40                  45                  50

gcg cgg gaa tca gcg aag gaa ttt tat act gag tcg cgc gat aag gct   307
Ala Arg Glu Ser Ala Lys Glu Phe Tyr Thr Glu Ser Arg Asp Lys Ala
     55                  60                  65

gga aat gtc acc aag gct gct cgt gct cgt ctg gaa aag gcg ctc gct   355
Gly Asn Val Thr Lys Ala Ala Arg Ala Arg Leu Glu Lys Ala Leu Ala
 70                  75                  80                  85

gag gct gac aag cag ggc act tct gcg ttg aag gac gca cgt gaa tcg   403
Glu Ala Asp Lys Gln Gly Thr Ser Ala Leu Lys Asp Ala Arg Glu Ser
                 90                  95                 100

ggc aag aaa ttg aac cgg aag gcg cgt cga aaa gca gac aag gcc gct   451
Gly Lys Lys Leu Asn Arg Lys Ala Arg Arg Lys Ala Asp Lys Ala Ala
             105                 110                 115

aag gca gcc cgc aag gcg act gaa aag aag gag tcg cac tgg gtg cgc   499
Lys Ala Ala Arg Lys Ala Thr Glu Lys Lys Glu Ser His Trp Val Arg
         120                 125                 130

aat ctg tcg ttg gcg gcg cta gcg acc tcc ggc atc gtc gcg gtg gcc   547
Asn Leu Ser Leu Ala Ala Leu Ala Thr Ser Gly Ile Val Ala Val Ala
     135                 140                 145

tac gcg ttt ttg aac aag acc aag aag gaa acc cca ggc acc cag cct   595
Tyr Ala Phe Leu Asn Lys Thr Lys Lys Glu Thr Pro Gly Thr Gln Pro
150                 155                 160                 165

cca cgg gtt gag gtt cag ttg aag aag gcc gtg gag cag gat gag cct   643
Pro Arg Val Glu Val Gln Leu Lys Lys Ala Val Glu Gln Asp Glu Pro
                 170                 175                 180

gag gtt gtg gct gag gct gct gtg gag gag cca gag ttg gtg tac tcc   691
Glu Val Val Ala Glu Ala Ala Val Glu Glu Pro Glu Leu Val Tyr Ser
             185                 190                 195

aca gaa agc cca gaa acc act gaa gcc cca gct gag gcc acc gaa act   739
Thr Glu Ser Pro Glu Thr Thr Glu Ala Pro Ala Glu Ala Thr Glu Thr
         200                 205                 210

cca gca gaa acc acc gaa gaa gaa gcc aaa acc gaa gct gaa cta gag   787
Pro Ala Glu Thr Thr Glu Glu Glu Ala Lys Thr Glu Ala Glu Leu Glu
     215                 220                 225

gca gag ctc gag gct gag gcc gat gcg gag cag gaa gcg gca gaa gag   835
Ala Glu Leu Glu Ala Glu Ala Asp Ala Glu Gln Glu Ala Ala Glu Glu
230                 235                 240                 245
```

```
gcg gaa gct gag gcc att cag gct gag ttt gat aag aag aat gca cct   883
Ala Glu Ala Glu Ala Ile Gln Ala Glu Phe Asp Lys Lys Asn Ala Pro
               250                 255                 260

cag cgc acc cag agc gaa aag aag aag taggttaacg cttcaattcg        930
Gln Arg Thr Gln Ser Glu Lys Lys Lys
            265                 270

tgg                                                              933
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<210> 2726
<211> 270
<212> PRT
<213> Corynebacterium glutamicum

<400> 2726

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Met Ser Thr Ile Gly Asn Leu Lys Leu Val Val Asp Gly Ala Arg Lys
  1               5                  10                  15

Ala Tyr Gly Thr Tyr Ala Asp Tyr Arg Asp Arg Lys Val Ser Glu Thr
             20                  25                  30

Tyr Asp Ala Leu Ser Gln Ala Ala Gly Glu Tyr Ala Pro Lys Ala Glu
         35                  40                  45

Gln Ala Val Glu Thr Ala Arg Glu Ser Ala Lys Glu Phe Tyr Thr Glu
     50                  55                  60

Ser Arg Asp Lys Ala Gly Asn Val Thr Lys Ala Ala Arg Ala Arg Leu
 65                  70                  75                  80

Glu Lys Ala Leu Ala Glu Ala Asp Lys Gln Gly Thr Ser Ala Leu Lys
                 85                  90                  95

Asp Ala Arg Glu Ser Gly Lys Lys Leu Asn Arg Lys Ala Arg Arg Lys
            100                 105                 110

Ala Asp Lys Ala Ala Lys Ala Ala Arg Lys Ala Thr Glu Lys Lys Glu
        115                 120                 125

Ser His Trp Val Arg Asn Leu Ser Leu Ala Ala Leu Ala Thr Ser Gly
    130                 135                 140

Ile Val Ala Val Ala Tyr Ala Phe Leu Asn Lys Thr Lys Lys Glu Thr
145                 150                 155                 160

Pro Gly Thr Gln Pro Pro Arg Val Glu Val Gln Leu Lys Lys Ala Val
                165                 170                 175

Glu Gln Asp Glu Pro Glu Val Val Ala Glu Ala Ala Val Glu Glu Pro
            180                 185                 190

Glu Leu Val Tyr Ser Thr Glu Ser Pro Glu Thr Thr Glu Ala Pro Ala
        195                 200                 205

Glu Ala Thr Glu Thr Pro Ala Glu Thr Thr Glu Glu Glu Ala Lys Thr
    210                 215                 220

Glu Ala Glu Leu Glu Ala Glu Leu Glu Ala Glu Ala Asp Ala Glu Gln
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```
225                 230                 235                 240

Glu Ala Ala Glu Glu Ala Glu Ala Glu Ala Ile Gln Ala Glu Phe Asp
                245                 250                 255

Lys Lys Asn Ala Pro Gln Arg Thr Gln Ser Glu Lys Lys Lys
            260                 265                 270


<210> 2727
<211> 1077
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1054)
<223> RXA02443

<400> 2727
caagcactgc cgcgggagcc actatcactt tgttaagtgc tgcgatattt tttgccacct 60

tattgacaaa gagtgccatt agtaggttaa acttcaccgc gtg ata ctg aaa gac   115
                                          Val Ile Leu Lys Asp
                                            1               5

att ttc aat aat ggg gag ctc ttt ggg gct tcc tcc gcg aaa aat ttc   163
Ile Phe Asn Asn Gly Glu Leu Phe Gly Ala Ser Ser Ala Lys Asn Phe
                10                  15                  20

cga aaa cta cta gct gtt cca gcc gtt gcc gcc tca cta gct ttt ggt   211
Arg Lys Leu Leu Ala Val Pro Ala Val Ala Ala Ser Leu Ala Phe Gly
            25                  30                  35

atc acc gcc tgt tcc gct gta gat gac acc cct gac att gtg gtc acc   259
Ile Thr Ala Cys Ser Ala Val Asp Asp Thr Pro Asp Ile Val Val Thr
        40                  45                  50

acc aac atc ctg ggt gat gtt gta agc cat atc gtg gga gat tcc gca   307
Thr Asn Ile Leu Gly Asp Val Val Ser His Ile Val Gly Asp Ser Ala
    55                  60                  65

gat gtc caa gta ctc atg aaa ccc aac gca gat cca cat tcc ttc gga   355
Asp Val Gln Val Leu Met Lys Pro Asn Ala Asp Pro His Ser Phe Gly
70                  75                  80                  85

gtc tca gca caa gac gcc gct gcc atg gaa cat gcc gat ctc atc gtg   403
Val Ser Ala Gln Asp Ala Ala Ala Met Glu His Ala Asp Leu Ile Val
                90                  95                  100

gcc aat gga cta gga ctt gaa gag ggc ctt caa tcc aat gtg gac aat   451
Ala Asn Gly Leu Gly Leu Glu Glu Gly Leu Gln Ser Asn Val Asp Asn
            105                 110                 115

gcc aaa agc caa ggg gtt ccc gtc ttg gaa gtc ggc gaa cac atc gat   499
Ala Lys Ser Gln Gly Val Pro Val Leu Glu Val Gly Glu His Ile Asp
        120                 125                 130

gtc att gac tac tcc ccc ggc gtt cca gat cct cac ttt tgg aca gac   547
Val Ile Asp Tyr Ser Pro Gly Val Pro Asp Pro His Phe Trp Thr Asp
    135                 140                 145
```

```
ccg gcg cgc atg atc gcc gcc acg gaa gtt ata gaa gct gaa ctg atc   595
Pro Ala Arg Met Ile Ala Ala Thr Glu Val Ile Glu Ala Glu Leu Ile
150                 155                 160                 165

aaa gaa ctc gat cct tcc ctg act gaa tcg atc aca caa tca gcc cag   643
Lys Glu Leu Asp Pro Ser Leu Thr Glu Ser Ile Thr Gln Ser Ala Gln
                170                 175                 180

cac tac cgt gag gaa ctt gtt gcc ctt gat gag gaa gtc acc gaa ttg   691
His Tyr Arg Glu Glu Leu Val Ala Leu Asp Glu Glu Val Thr Glu Leu
            185                 190                 195

ctc agc ggc gtg gcc cca gaa aac cgc aag ctg gta acc aat cac aat   739
Leu Ser Gly Val Ala Pro Glu Asn Arg Lys Leu Val Thr Asn His Asn
        200                 205                 210

gtt ttt gga tac ctg gcc agc cgg ttt aac tac acc gtc att gac acc   787
Val Phe Gly Tyr Leu Ala Ser Arg Phe Asn Tyr Thr Val Ile Asp Thr
    215                 220                 225

atc atc cca ggt gga agc aca ttg gcg gcg cct tca gca tct gac ctc   835
Ile Ile Pro Gly Gly Ser Thr Leu Ala Ala Pro Ser Ala Ser Asp Leu
230                 235                 240                 245

aat gac atc tcc acc gcc atc gaa gac aac aat gtt ccc gca atc ttc   883
Asn Asp Ile Ser Thr Ala Ile Glu Asp Asn Asn Val Pro Ala Ile Phe
                250                 255                 260

acc gat acc tca agc cca caa cgg tta gct gaa gtg ttg gcc agc aac   931
Thr Asp Thr Ser Ser Pro Gln Arg Leu Ala Glu Val Leu Ala Ser Asn
            265                 270                 275

gct ggc att gat gtt caa gtg gtg tcc att ttc acg gaa tca ctc acc   979
Ala Gly Ile Asp Val Gln Val Val Ser Ile Phe Thr Glu Ser Leu Thr
        280                 285                 290

gat gca gat ggt gaa gca ccc acc tac atc agc atg caa aaa atc aat   1027
Asp Ala Asp Gly Glu Ala Pro Thr Tyr Ile Ser Met Gln Lys Ile Asn
    295                 300                 305

gcc gag cgc att gca agc act ttg tcc taaacagtcc taaacagtct         1074
Ala Glu Arg Ile Ala Ser Thr Leu Ser
310                 315

taa                                                               1077
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<210> 2728
<211> 318
<212> PRT
<213> Corynebacterium glutamicum

<400> 2728
Val Ile Leu Lys Asp Ile Phe Asn Asn Gly Glu Leu Phe Gly Ala Ser
  1   5   10   15

Ser Ala Lys Asn Phe Arg Lys Leu Leu Ala Val Pro Ala Val Ala Ala
             20   25   30

Ser Leu Ala Phe Gly Ile Thr Ala Cys Ser Ala Val Asp Asp Thr Pro

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         35                  40                  45

Asp Ile Val Val Thr Thr Asn Ile Leu Gly Asp Val Val Ser His Ile
     50                  55                  60

Val Gly Asp Ser Ala Asp Val Gln Val Leu Met Lys Pro Asn Ala Asp
 65                  70                  75                  80

Pro His Ser Phe Gly Val Ser Ala Gln Asp Ala Ala Ala Met Glu His
                 85                  90                  95

Ala Asp Leu Ile Val Ala Asn Gly Leu Gly Leu Glu Glu Gly Leu Gln
            100                 105                 110

Ser Asn Val Asp Asn Ala Lys Ser Gln Gly Val Pro Val Leu Glu Val
        115                 120                 125

Gly Glu His Ile Asp Val Ile Asp Tyr Ser Pro Gly Val Pro Asp Pro
    130                 135                 140

His Phe Trp Thr Asp Pro Ala Arg Met Ile Ala Ala Thr Glu Val Ile
145                 150                 155                 160

Glu Ala Glu Leu Ile Lys Glu Leu Asp Pro Ser Leu Thr Glu Ser Ile
                165                 170                 175

Thr Gln Ser Ala Gln His Tyr Arg Glu Glu Leu Val Ala Leu Asp Glu
            180                 185                 190

Glu Val Thr Glu Leu Leu Ser Gly Val Ala Pro Glu Asn Arg Lys Leu
        195                 200                 205

Val Thr Asn His Asn Val Phe Gly Tyr Leu Ala Ser Arg Phe Asn Tyr
    210                 215                 220

Thr Val Ile Asp Thr Ile Ile Pro Gly Gly Ser Thr Leu Ala Ala Pro
225                 230                 235                 240

Ser Ala Ser Asp Leu Asn Asp Ile Ser Thr Ala Ile Glu Asp Asn Asn
                245                 250                 255

Val Pro Ala Ile Phe Thr Asp Thr Ser Ser Pro Gln Arg Leu Ala Glu
            260                 265                 270

Val Leu Ala Ser Asn Ala Gly Ile Asp Val Gln Val Val Ser Ile Phe
        275                 280                 285

Thr Glu Ser Leu Thr Asp Ala Asp Gly Glu Ala Pro Thr Tyr Ile Ser
    290                 295                 300

Met Gln Lys Ile Asn Ala Glu Arg Ile Ala Ser Thr Leu Ser
305                 310                 315
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<210> 2729
<211> 1401
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(1378)
<223> RXA02444

<400> 2729
aaaatcaatg ccgagcgcat tgcaagcact ttgtcctaaa cagtcctaaa cagtcttaaa 60

cagtccccgt tttactaaat gttttactaa aaggagaacc atg aaa aac tcc aag 115
Met Lys Asn Ser Lys
1 5

cta ctt ctt att gct gcg gta tcc acc gca tct atc ctg ctg gca agc 163
Leu Leu Leu Ile Ala Ala Val Ser Thr Ala Ser Ile Leu Leu Ala Ser
10 15 20

tgt ggc act gac agc tct gca gat act gca act gcg tct agc tct gca 211
Cys Gly Thr Asp Ser Ser Ala Asp Thr Ala Thr Ala Ser Ser Ser Ala
25 30 35

aca gca agc tcc gag gca cac gat cat gat ggc cac gaa gcc gaa ggc 259
Thr Ala Ser Ser Glu Ala His Asp His Asp Gly His Glu Ala Glu Gly
40 45 50

agc agc act gcc gtt gag gtg tcc tcc ccg cag gcc cgc atc gtc acc 307
Ser Ser Thr Ala Val Glu Val Ser Ser Pro Gln Ala Arg Ile Val Thr
55 60 65

acc tac gac ggt ggc atc att acc ctc gac gcc aac act ctg gaa atc 355
Thr Tyr Asp Gly Gly Ile Ile Thr Leu Asp Ala Asn Thr Leu Glu Ile
70 75 80 85

ctg gaa gac acc gaa cta gca ggt ttt aac cgc ctc aac agt gca gga 403
Leu Glu Asp Thr Glu Leu Ala Gly Phe Asn Arg Leu Asn Ser Ala Gly
90 95 100

gac gga cgc cac gta ttt gtc tcc aca ggt ggc ggc ttc cag ctc ttt 451
Asp Gly Arg His Val Phe Val Ser Thr Gly Gly Gly Phe Gln Leu Phe
105 110 115

gat acc ggc gca tgg acc gaa cca cac ggc gat cac acc cac agc tac 499
Asp Thr Gly Ala Trp Thr Glu Pro His Gly Asp His Thr His Ser Tyr
120 125 130

acc gcc acc cca gaa ctc acc gac atc acc tac tcc acc gat aag cct 547
Thr Ala Thr Pro Glu Leu Thr Asp Ile Thr Tyr Ser Thr Asp Lys Pro
135 140 145

ggt cat gta gtg aac cac gcc ggc aag acc gtg ctg ttc ggc gat ggt 595
Gly His Val Val Asn His Ala Gly Lys Thr Val Leu Phe Gly Asp Gly
150 155 160 165

gac ggc aaa atc cag atc ttc gac acc gct tcc ctc ctc aag ggc gat 643
Asp Gly Lys Ile Gln Ile Phe Asp Thr Ala Ser Leu Leu Lys Gly Asp
170 175 180

gaa gta gaa cct gag atc aaa aac gcc ctc aaa gcc cac cac ggc gtg 691
Glu Val Glu Pro Glu Ile Lys Asn Ala Leu Lys Ala His His Gly Val
185 190 195

gca gta gtc ctc gaa aac ggc gac ctg ctg cac act ttg ggc gat gag 739
Ala Val Val Leu Glu Asn Gly Asp Leu Leu His Thr Leu Gly Asp Glu
200 205 210

```
gat tcc cgc aac ggc gcc gtc gta ttc aac gca gcc ggt gaa gaa atc   787
Asp Ser Arg Asn Gly Ala Val Val Phe Asn Ala Ala Gly Glu Glu Ile
    215                 220                 225

gcc cgc aac gaa cag tgc ccc ggc gtt cac ggt gaa agc gca gca ctc   835
Ala Arg Asn Glu Gln Cys Pro Gly Val His Gly Glu Ser Ala Ala Leu
230                 235                 240                 245

ggt gac gcc atc gca gtt ggc tgt gaa gac ggt gta ctg atc tac aag   883
Gly Asp Ala Ile Ala Val Gly Cys Glu Asp Gly Val Leu Ile Tyr Lys
                250                 255                 260

gac ggc gag ttc acc aag gtc cag gca cct gat tcc tac ggt cgc atc   931
Asp Gly Glu Phe Thr Lys Val Gln Ala Pro Asp Ser Tyr Gly Arg Ile
            265                 270                 275

ggc aac caa tca ggc agc gac gtc tct cct gtc gtc ctc ggc gat tac   979
Gly Asn Gln Ser Gly Ser Asp Val Ser Pro Val Val Leu Gly Asp Tyr
        280                 285                 290

aag gta gat aaa gac gcc gac ttg gag cgc cca gag cgc gtt tcc ctc   1027
Lys Val Asp Lys Asp Ala Asp Leu Glu Arg Pro Glu Arg Val Ser Leu
    295                 300                 305

acc aac acc gag acc ggc gag ctc acc ctc gtt gac ctc ggc acc tcc   1075
Thr Asn Thr Glu Thr Gly Glu Leu Thr Leu Val Asp Leu Gly Thr Ser
310                 315                 320                 325

tac tcc ttc cgc tca ctt ggc cgt ggc cct gca ggc gaa gca gta gtt   1123
Tyr Ser Phe Arg Ser Leu Gly Arg Gly Pro Ala Gly Glu Ala Val Val
                330                 335                 340

cta ggc acc gac ggc gca ctc cac atc atc gat gcc aac acc ggc gcc   1171
Leu Gly Thr Asp Gly Ala Leu His Ile Ile Asp Ala Asn Thr Gly Ala
            345                 350                 355

atc acc aac acc tac ccc gtc atc gat gcc tgg acc gaa cca gaa gta   1219
Ile Thr Asn Thr Tyr Pro Val Ile Asp Ala Trp Thr Glu Pro Glu Val
        360                 365                 370

tgg caa gaa gca cgc cca acc ctg ttc atc aac aag gac cgc gca tac   1267
Trp Gln Glu Ala Arg Pro Thr Leu Phe Ile Asn Lys Asp Arg Ala Tyr
    375                 380                 385

gtc tcc gac cca tca aac aac gaa ctc cat gtt gtt gac ctg gcc aac   1315
Val Ser Asp Pro Ser Asn Asn Glu Leu His Val Val Asp Leu Ala Asn
390                 395                 400                 405

ggc aac atc ctt gcc agc gcc acc ctg cca gga acc ccc aac gag ctc   1363
Gly Asn Ile Leu Ala Ser Ala Thr Leu Pro Gly Thr Pro Asn Glu Leu
                410                 415                 420

acc gga gtg agc ggc taaaaagaaa ttgcttttcg acg                    1401
Thr Gly Val Ser Gly
            425
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<210> 2730
<211> 426
<212> PRT

<213> Corynebacterium glutamicum

<400> 2730

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Met Lys Asn Ser Lys Leu Leu Leu Ile Ala Ala Val Ser Thr Ala Ser
  1               5                  10                  15

Ile Leu Leu Ala Ser Cys Gly Thr Asp Ser Ser Ala Asp Thr Ala Thr
             20                  25                  30

Ala Ser Ser Ser Ala Thr Ala Ser Ser Glu Ala His Asp His Asp Gly
         35                  40                  45

His Glu Ala Glu Gly Ser Ser Thr Ala Val Glu Val Ser Ser Pro Gln
     50                  55                  60

Ala Arg Ile Val Thr Thr Tyr Asp Gly Gly Ile Ile Thr Leu Asp Ala
 65                  70                  75                  80

Asn Thr Leu Glu Ile Leu Glu Asp Thr Glu Leu Ala Gly Phe Asn Arg
                 85                  90                  95

Leu Asn Ser Ala Gly Asp Gly Arg His Val Phe Val Ser Thr Gly Gly
            100                 105                 110

Gly Phe Gln Leu Phe Asp Thr Gly Ala Trp Thr Glu Pro His Gly Asp
        115                 120                 125

His Thr His Ser Tyr Thr Ala Thr Pro Glu Leu Thr Asp Ile Thr Tyr
    130                 135                 140

Ser Thr Asp Lys Pro Gly His Val Val Asn His Ala Gly Lys Thr Val
145                 150                 155                 160

Leu Phe Gly Asp Gly Asp Gly Lys Ile Gln Ile Phe Asp Thr Ala Ser
                165                 170                 175

Leu Leu Lys Gly Asp Glu Val Glu Pro Glu Ile Lys Asn Ala Leu Lys
            180                 185                 190

Ala His His Gly Val Ala Val Val Leu Glu Asn Gly Asp Leu Leu His
        195                 200                 205

Thr Leu Gly Asp Glu Asp Ser Arg Asn Gly Ala Val Val Phe Asn Ala
    210                 215                 220

Ala Gly Glu Glu Ile Ala Arg Asn Glu Gln Cys Pro Gly Val His Gly
225                 230                 235                 240

Glu Ser Ala Ala Leu Gly Asp Ala Ile Ala Val Gly Cys Glu Asp Gly
                245                 250                 255

Val Leu Ile Tyr Lys Asp Gly Glu Phe Thr Lys Val Gln Ala Pro Asp
            260                 265                 270

Ser Tyr Gly Arg Ile Gly Asn Gln Ser Gly Ser Asp Val Ser Pro Val
        275                 280                 285

Val Leu Gly Asp Tyr Lys Val Asp Lys Asp Ala Asp Leu Glu Arg Pro
    290                 295                 300

Glu Arg Val Ser Leu Thr Asn Thr Glu Thr Gly Glu Leu Thr Leu Val
```

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305                 310                 315                 320

Asp Leu Gly Thr Ser Tyr Ser Phe Arg Ser Leu Gly Arg Gly Pro Ala
                325                 330                 335

Gly Glu Ala Val Val Leu Gly Thr Asp Gly Ala Leu His Ile Ile Asp
            340                 345                 350

Ala Asn Thr Gly Ala Ile Thr Asn Thr Tyr Pro Val Ile Asp Ala Trp
        355                 360                 365

Thr Glu Pro Glu Val Trp Gln Glu Ala Arg Pro Thr Leu Phe Ile Asn
    370                 375                 380

Lys Asp Arg Ala Tyr Val Ser Asp Pro Ser Asn Asn Glu Leu His Val
385                 390                 395                 400

Val Asp Leu Ala Asn Gly Asn Ile Leu Ala Ser Ala Thr Leu Pro Gly
                405                 410                 415

Thr Pro Asn Glu Leu Thr Gly Val Ser Gly
            420                 425
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<210> 2731
<211> 303
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(280)
<223> RXA02452

<400> 2731
tttgcgcgac taatcgccgg ataaatgaat tgattatttt aggctcccag ggattaagtc 60

tagggtggaa tgcagaaata tttcctacgg aaggtccgtt atg acg cct gca ggt 115
                                        Met Thr Pro Ala Gly
                                          1   5

cca gca caa tta ctc att gtt gct ctt gta gta att gtc ctc ttt ggt 163
Pro Ala Gln Leu Leu Ile Val Ala Leu Val Val Ile Val Leu Phe Gly
                 10   15   20

tcc aat aag ttg cct gat gtt gct cgg tcc gtt ggc cgt tcg atg cgc 211
Ser Asn Lys Leu Pro Asp Val Ala Arg Ser Val Gly Arg Ser Met Arg
             25   30   35

att ttc aaa tct gag atc aaa gag atg aac aag gat cag atc gaa agc 259
Ile Phe Lys Ser Glu Ile Lys Glu Met Asn Lys Asp Gln Ile Glu Ser
         40   45   50

tcc gat cag acc ttg aag aac taaggttcct cgcatctaaa aac   303
Ser Asp Gln Thr Leu Lys Asn
     55   60

<210> 2732
<211> 60
<212> PRT

<213> Corynebacterium glutamicum

<400> 2732

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Met Thr Pro Ala Gly Pro Ala Gln Leu Leu Ile Val Ala Leu Val Val
  1               5                  10                  15

Ile Val Leu Phe Gly Ser Asn Lys Leu Pro Asp Val Ala Arg Ser Val
             20                  25                  30

Gly Arg Ser Met Arg Ile Phe Lys Ser Glu Ile Lys Glu Met Asn Lys
         35                  40                  45

Asp Gln Ile Glu Ser Ser Asp Gln Thr Leu Lys Asn
     50                  55                  60
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<210> 2733
<211> 858
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(835)
<223> RXA02459

<400> 2733

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ggtgcgatca ttggcctcgc ggttgatggc gttcaggttg aagacattaa gaccacttcc 60

aaaactttcc ctggttttga aaatgtttgg gaggagatgg ttg gct aga cgc agc   115
                                            Leu Ala Arg Arg Ser
                                              1               5

tat gac gaa tcc gat gtt cgt gtt cgc cca ggt aaa ggt acc cgc cct   163
Tyr Asp Glu Ser Asp Val Arg Val Arg Pro Gly Lys Gly Thr Arg Pro
                 10                  15                  20

cgt acg aag gat cgg cca tcg cat gag aat gct cta gtg ggc atg gtt   211
Arg Thr Lys Asp Arg Pro Ser His Glu Asn Ala Leu Val Gly Met Val
             25                  30                  35

gtg acg aag gat cgt ggt cgt tgg ggt gtt gtt ctc gat ggt cgt caa   259
Val Thr Lys Asp Arg Gly Arg Trp Gly Val Val Leu Asp Gly Arg Gln
         40                  45                  50

gat gcc att gtg acg atg cgt gcc cgt gag ttg ggg cgt acg gct atc   307
Asp Ala Ile Val Thr Met Arg Ala Arg Glu Leu Gly Arg Thr Ala Ile
     55                  60                  65

gaa gtg ggt gat cgt gtc gga gtt gtc ggc gat acg tct ggc cgt ccg   355
Glu Val Gly Asp Arg Val Gly Val Val Gly Asp Thr Ser Gly Arg Pro
 70                  75                  80                  85

ggc tcg ttg gct cga att gtc cgc ctt gag gag cgc acg agt gtg ttg   403
Gly Ser Leu Ala Arg Ile Val Arg Leu Glu Glu Arg Thr Ser Val Leu
                 90                  95                 100

cgt cgt acg gct gat gac acg gac ccg ttt gag cgg att gtg gtg gct   451
Arg Arg Thr Ala Asp Asp Thr Asp Pro Phe Glu Arg Ile Val Val Ala
             105                 110                 115
```

```
aat gcg gat cag ttg ttg att gtt tct gct gtc gcc gat ccg ccg cct   499
Asn Ala Asp Gln Leu Leu Ile Val Ser Ala Val Ala Asp Pro Pro Pro
        120                 125                 130

cgg gcg ggt ttt gtg gag cgt gct cta att gct gcg ttt gtt ggt aat   547
Arg Ala Gly Phe Val Glu Arg Ala Leu Ile Ala Ala Phe Val Gly Asn
    135                 140                 145

ttg cag ccg gtg ttg tgt ttg acg aag tct gat ttg gcg gat cct gcg   595
Leu Gln Pro Val Leu Cys Leu Thr Lys Ser Asp Leu Ala Asp Pro Ala
150                 155                 160                 165

gag ttc gct gcg gag ttt gag gct ttg gaa gtg ccg gtt gtt gtt tgt   643
Glu Phe Ala Ala Glu Phe Glu Ala Leu Glu Val Pro Val Val Val Cys
                170                 175                 180

ggt gtt gat gat cct ctt gat cct gtt ttg gag gtc gtg gaa ggc cat   691
Gly Val Asp Asp Pro Leu Asp Pro Val Leu Glu Val Val Glu Gly His
            185                 190                 195

att acg gcg ctt att ggg caa tct ggt gtg ggt aag tcg acg ttg gtt   739
Ile Thr Ala Leu Ile Gly Gln Ser Gly Val Gly Lys Ser Thr Leu Val
        200                 205                 210

aat cgt ttg gtg ccg gaa tgc cga tcg tta aac tgg tgt cgt gtc ggg   787
Asn Arg Leu Val Pro Glu Cys Arg Ser Leu Asn Trp Cys Arg Val Gly
    215                 220                 225

ggt tgg caa ggg tcg gca tac gtc gac gca gtc ggt cgc tct tgc cat   835
Gly Trp Gln Gly Ser Ala Tyr Val Asp Ala Val Gly Arg Ser Cys His
230                 235                 240                 245

tgataatggt tggattatcg aaa                                       858
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<210> 2734
<211> 245
<212> PRT
<213> Corynebacterium glutamicum

<400> 2734

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Leu Ala Arg Arg Ser Tyr Asp Glu Ser Asp Val Arg Val Arg Pro Gly
  1               5                  10                  15

Lys Gly Thr Arg Pro Arg Thr Lys Asp Arg Pro Ser His Glu Asn Ala
             20                  25                  30

Leu Val Gly Met Val Val Thr Lys Asp Arg Gly Arg Trp Gly Val Val
         35                  40                  45

Leu Asp Gly Arg Gln Asp Ala Ile Val Thr Met Arg Ala Arg Glu Leu
     50                  55                  60

Gly Arg Thr Ala Ile Glu Val Gly Asp Arg Val Gly Val Val Gly Asp
 65                  70                  75                  80

Thr Ser Gly Arg Pro Gly Ser Leu Ala Arg Ile Val Arg Leu Glu Glu
                 85                  90                  95

Arg Thr Ser Val Leu Arg Arg Thr Ala Asp Asp Thr Asp Pro Phe Glu
            100                 105                 110
```

```
Arg Ile Val Val Ala Asn Ala Asp Gln Leu Leu Ile Val Ser Ala Val
        115                 120                 125

Ala Asp Pro Pro Pro Arg Ala Gly Phe Val Glu Arg Ala Leu Ile Ala
    130                 135                 140

Ala Phe Val Gly Asn Leu Gln Pro Val Leu Cys Leu Thr Lys Ser Asp
145                 150                 155                 160

Leu Ala Asp Pro Ala Glu Phe Ala Ala Glu Phe Glu Ala Leu Glu Val
                165                 170                 175

Pro Val Val Val Cys Gly Val Asp Asp Pro Leu Asp Pro Val Leu Glu
            180                 185                 190

Val Val Glu Gly His Ile Thr Ala Leu Ile Gly Gln Ser Gly Val Gly
        195                 200                 205

Lys Ser Thr Leu Val Asn Arg Leu Val Pro Glu Cys Arg Ser Leu Asn
    210                 215                 220

Trp Cys Arg Val Gly Gly Trp Gln Gly Ser Ala Tyr Val Asp Ala Val
225                 230                 235                 240

Gly Arg Ser Cys His
                245


<210> 2735
<211> 531
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> RXA02461

<400> 2735
agaaaatctc aaggcaaaaa acaagccacc ccaatctgtg cgacaatcaa accacagact 60

acgactatta tgtcacgaag aaaccaaaga aagggaaata atg cgc gga cta att   115
                                              Met Arg Gly Leu Ile
                                                1               5

gtt gac tac gct gga gta cta gac gga acc gat gag gac cag cgt cgc   163
Val Asp Tyr Ala Gly Val Leu Asp Gly Thr Asp Glu Asp Gln Arg Arg
                  10                  15                  20

tgg cgc aac ctg ctc gcc gca gca aag aaa aat ggc gtc gga acc gtg   211
Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn Gly Val Gly Thr Val
              25                  30                  35

atc ctc agc aac gat cca ggt ggg ctc ggc gca gcg ccg atc cgg gaa   259
Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala Ala Pro Ile Arg Glu
          40                  45                  50

ctc gaa aca aac ggg gta gtc gat aag gtg ctg ctg tcg gga gaa ctt   307
Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu Leu Ser Gly Glu Leu
      55                  60                  65
```

```
ggc gtc gaa aag cca gag gaa gca gct ttc cag gcc gcc gca gac gcc   355
Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln Ala Ala Ala Asp Ala
 70                  75                  80                  85

atc gac ctg ccc atg cgt gac tgc gtg ctt gtc gac gac tcg atc ctc   403
Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val Asp Asp Ser Ile Leu
                90                  95                 100

aac gtg cgc ggc gcc gtc gaa gcc gga ctc gta ggc gtc tac tac cag   451
Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val Gly Val Tyr Tyr Gln
            105                 110                 115

caa ttt gac cgt gca gtc gtc gaa atc gtc gga ctg ttc ggg cta gaa   499
Gln Phe Asp Arg Ala Val Val Glu Ile Val Gly Leu Phe Gly Leu Glu
        120                 125                 130

gga gaa ttc taatcttgcg cgtctacatc cca                            531
Gly Glu Phe
    135
```

Sequence Listing

<210> 2736
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 2736

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Met Arg Gly Leu Ile Val Asp Tyr Ala Gly Val Leu Asp Gly Thr Asp
  1               5                  10                  15

Glu Asp Gln Arg Arg Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn
             20                  25                  30

Gly Val Gly Thr Val Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala
         35                  40                  45

Ala Pro Ile Arg Glu Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu
     50                  55                  60

Leu Ser Gly Glu Leu Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln
 65                  70                  75                  80

Ala Ala Ala Asp Ala Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val
                 85                  90                  95

Asp Asp Ser Ile Leu Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val
            100                 105                 110

Gly Val Tyr Tyr Gln Gln Phe Asp Arg Ala Val Val Glu Ile Val Gly
        115                 120                 125

Leu Phe Gly Leu Glu Gly Glu Phe
    130                 135
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<210> 2737
<211> 348
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(325)
<223> RXA02467

<400> 2737
gtgaacgtag gtctggggct ttcagaagac acaacttaga tactatcgtt gcacggttac 60

aatagggtca ttccaataca acgattcttt taggagagct atg gat atc aag atc 115
Met Asp Ile Lys Ile
1 5

gga ttt gcc gat act gcc cgt gaa ctg gtc att tct tct gct ttg cag 163
Gly Phe Ala Asp Thr Ala Arg Glu Leu Val Ile Ser Ser Ala Leu Gln
10 15 20

cag gat gag gcc gct gcg aag gtg tcg gag gct ttg gct aat gat tct 211
Gln Asp Glu Ala Ala Ala Lys Val Ser Glu Ala Leu Ala Asn Asp Ser
25 30 35

ggc gtt tta gat ttg agc gat gaa aag ggt cgc cgt tac att att cgt 259
Gly Val Leu Asp Leu Ser Asp Glu Lys Gly Arg Arg Tyr Ile Ile Arg
40 45 50

aat agc cga atc gct tat gtt gag gtc ggc acg agt gct cct cgt act 307
Asn Ser Arg Ile Ala Tyr Val Glu Val Gly Thr Ser Ala Pro Arg Thr
55 60 65

gtc ggc ttc gct ggc gca taggggcttt tagacacgtg tcg 348
Val Gly Phe Ala Gly Ala
70 75

<210> 2738
<211> 75
<212> PRT
<213> Corynebacterium glutamicum

<400> 2738
Met Asp Ile Lys Ile Gly Phe Ala Asp Thr Ala Arg Glu Leu Val Ile
1 5 10 15

Ser Ser Ala Leu Gln Gln Asp Glu Ala Ala Ala Lys Val Ser Glu Ala
20 25 30

Leu Ala Asn Asp Ser Gly Val Leu Asp Leu Ser Asp Glu Lys Gly Arg
35 40 45

Arg Tyr Ile Ile Arg Asn Ser Arg Ile Ala Tyr Val Glu Val Gly Thr
50 55 60

Ser Ala Pro Arg Thr Val Gly Phe Ala Gly Ala
65 70 75

<210> 2739
<211> 414
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(391)
<223> RXA02472

<400> 2739
atgattctca taaggctata aacaatgtag ttaggttaca ctaatggtgt ccggttgtga 60

atagtgcagc ggacggggtt ccgctgcgga ggaggtcatc atg tca ttt gtt aac 115
Met Ser Phe Val Asn
1 5

atc acg gct ctt acg ttc cct gca ggg gct gaa aaa gaa atc gaa caa 163
Ile Thr Ala Leu Thr Phe Pro Ala Gly Ala Glu Lys Glu Ile Glu Gln
10 15 20

cgc ttc gcg gct cgt aag aag gct gta gat acg gcc aaa gga ttc caa 211
Arg Phe Ala Ala Arg Lys Lys Ala Val Asp Thr Ala Lys Gly Phe Gln
25 30 35

gaa ttt gag ttg ttg cgt cca caa ttt ggt gag gat cgc tac ttc gta 259
Glu Phe Glu Leu Leu Arg Pro Gln Phe Gly Glu Asp Arg Tyr Phe Val
40 45 50

gtt act cgt tgg gat tcc cgc gaa gac tat caa gca tgg tcg gat gcc 307
Val Thr Arg Trp Asp Ser Arg Glu Asp Tyr Gln Ala Trp Ser Asp Ala
55 60 65

cgc cct gcc ggt aac cat gct gat gat gaa caa cgt ggc atg agc gtg 355
Arg Pro Ala Gly Asn His Ala Asp Asp Glu Gln Arg Gly Met Ser Val
70 75 80 85

gaa gtt ctt ggt ttc gat gtg gtt cct ttg gaa ggc taaaagtcct 401
Glu Val Leu Gly Phe Asp Val Val Pro Leu Glu Gly
90 95

tggcgtggca tag 414

<210> 2740
<211> 97
<212> PRT
<213> Corynebacterium glutamicum

<400> 2740
Met Ser Phe Val Asn Ile Thr Ala Leu Thr Phe Pro Ala Gly Ala Glu
1 5 10 15

Lys Glu Ile Glu Gln Arg Phe Ala Ala Arg Lys Lys Ala Val Asp Thr
20 25 30

Ala Lys Gly Phe Gln Glu Phe Glu Leu Leu Arg Pro Gln Phe Gly Glu
35 40 45

Asp Arg Tyr Phe Val Val Thr Arg Trp Asp Ser Arg Glu Asp Tyr Gln
50 55 60

Ala Trp Ser Asp Ala Arg Pro Ala Gly Asn His Ala Asp Asp Glu Gln
65 70 75 80

Arg Gly Met Ser Val Glu Val Leu Gly Phe Asp Val Val Pro Leu Glu
85 90 95

Gly

<210> 2741
<211> 864
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(841)
<223> RXA02473

<400> 2741
tgcagttatg attaaactaa ctcctagcag tggccaacta catgtctggc ttaatagcct 60

atgaacgcct aagcctggag ccacaacaac cacattccga atg gtc gca gag tac 115
Met Val Ala Glu Tyr
1 5

cct gac gga tcc tcg gaa ata ttc ccg gta acg tta aat tta att ccg 163
Pro Asp Gly Ser Ser Glu Ile Phe Pro Val Thr Leu Asn Leu Ile Pro
10 15 20

gaa gat acc ctc gtt tat gac gcc gtc tac aaa ttc aaa agc atc cga 211
Glu Asp Thr Leu Val Tyr Asp Ala Val Tyr Lys Phe Lys Ser Ile Arg
25 30 35

act ggt tcc gaa gat caa ata acc cca ttt gta tca aac caa cct gat 259
Thr Gly Ser Glu Asp Gln Ile Thr Pro Phe Val Ser Asn Gln Pro Asp
40 45 50

gtg cct ttc cct gca gga aca tcg ttc aca tta act gga tat tat gaa 307
Val Pro Phe Pro Ala Gly Thr Ser Phe Thr Leu Thr Gly Tyr Tyr Glu
55 60 65

att gat cag ctg aga agt gca gga tgg aaa ttt gag ctt aat cct gta 355
Ile Asp Gln Leu Arg Ser Ala Gly Trp Lys Phe Glu Leu Asn Pro Val
70 75 80 85

aca ggt gaa ctt tca gtc aca gtt cct atc tct gta att tac cct gat 403
Thr Gly Glu Leu Ser Val Thr Val Pro Ile Ser Val Ile Tyr Pro Asp
90 95 100

ggg tct cgt gat aac aca atc gcg acc atg gaa tcc gta ggc cct gat 451
Gly Ser Arg Asp Asn Thr Ile Ala Thr Met Glu Ser Val Gly Pro Asp
105 110 115

gat tct gag ctt ttc aaa cca gac ttt gat tta atc cca ata aaa tca 499
Asp Ser Glu Leu Phe Lys Pro Asp Phe Asp Leu Ile Pro Ile Lys Ser
120 125 130

ggt gac tat ata gag ata ggt gta ctc gca cca ggg ctt cct gct ggt 547
Gly Asp Tyr Ile Glu Ile Gly Val Leu Ala Pro Gly Leu Pro Ala Gly
135 140 145

acg gaa ttc cat ctc gat tac tac gca ctt ccg gat cga ttc ttt gac 595
Thr Glu Phe His Leu Asp Tyr Tyr Ala Leu Pro Asp Arg Phe Phe Asp
150 155 160 165

```
tta ggc ggt tct aca agc ctt tca ggc aac ggt aag ttc tct ctt gga   643
Leu Gly Gly Ser Thr Ser Leu Ser Gly Asn Gly Lys Phe Ser Leu Gly
                170                 175                 180

gtt cca ctt acc tgg aat gat gat ctc cag ctc ccg atc tcg att act   691
Val Pro Leu Thr Trp Asn Asp Asp Leu Gln Leu Pro Ile Ser Ile Thr
            185                 190                 195

ttt cct gac gga agc cac aca gtt gag aat ttg cat gtt gac gta acc   739
Phe Pro Asp Gly Ser His Thr Val Glu Asn Leu His Val Asp Val Thr
        200                 205                 210

ccc gca aac ttt gct ggc aac ccc att gac gag cct aag gac gat gac   787
Pro Ala Asn Phe Ala Gly Asn Pro Ile Asp Glu Pro Lys Asp Asp Asp
    215                 220                 225

aag gat cat cca caa ccg gct cct aaa cca agt ggc agc tca ttt ggt   835
Lys Asp His Pro Gln Pro Ala Pro Lys Pro Ser Gly Ser Ser Phe Gly
230                 235                 240                 245

tct agc tagttcctac taaacagttc aaa                                864
Ser Ser
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<210> 2742
<211> 247
<212> PRT
<213> Corynebacterium glutamicum

<400> 2742

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Met Val Ala Glu Tyr Pro Asp Gly Ser Ser Glu Ile Phe Pro Val Thr
  1               5                  10                  15

Leu Asn Leu Ile Pro Glu Asp Thr Leu Val Tyr Asp Ala Val Tyr Lys
             20                  25                  30

Phe Lys Ser Ile Arg Thr Gly Ser Glu Asp Gln Ile Thr Pro Phe Val
         35                  40                  45

Ser Asn Gln Pro Asp Val Pro Phe Pro Ala Gly Thr Ser Phe Thr Leu
     50                  55                  60

Thr Gly Tyr Tyr Glu Ile Asp Gln Leu Arg Ser Ala Gly Trp Lys Phe
 65                  70                  75                  80

Glu Leu Asn Pro Val Thr Gly Glu Leu Ser Val Thr Val Pro Ile Ser
                 85                  90                  95

Val Ile Tyr Pro Asp Gly Ser Arg Asp Asn Thr Ile Ala Thr Met Glu
            100                 105                 110

Ser Val Gly Pro Asp Asp Ser Glu Leu Phe Lys Pro Asp Phe Asp Leu
        115                 120                 125

Ile Pro Ile Lys Ser Gly Asp Tyr Ile Glu Ile Gly Val Leu Ala Pro
    130                 135                 140

Gly Leu Pro Ala Gly Thr Glu Phe His Leu Asp Tyr Tyr Ala Leu Pro
145                 150                 155                 160
```

```
Asp Arg Phe Phe Asp Leu Gly Gly Ser Thr Ser Leu Ser Gly Asn Gly
                165                 170                 175

Lys Phe Ser Leu Gly Val Pro Leu Thr Trp Asn Asp Asp Leu Gln Leu
            180                 185                 190

Pro Ile Ser Ile Thr Phe Pro Asp Gly Ser His Thr Val Glu Asn Leu
        195                 200                 205

His Val Asp Val Thr Pro Ala Asn Phe Ala Gly Asn Pro Ile Asp Glu
    210                 215                 220

Pro Lys Asp Asp Asp Lys Asp His Pro Gln Pro Ala Pro Lys Pro Ser
225                 230                 235                 240

Gly Ser Ser Phe Gly Ser Ser
                245
```

<210> 2743
<211> 1278
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1255)
<223> RXA02475

<400> 2743

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tcgctcattg aggacggact cgcggaacaa aatgaggcgg gttatttcca cctgccacgg 60

taaaccactg cgcgcctgca aaaaacagta ggtttaagta atg ctt ggt ctc tct   115
                                              Met Leu Gly Leu Ser
                                                1               5

cgt cgt aag ttt gcc atg ctc gct gcc tta act gcg gga atc gtt ggc   163
Arg Arg Lys Phe Ala Met Leu Ala Ala Leu Thr Ala Gly Ile Val Gly
                  10                  15                  20

gtt gtt gcc act ggt tgt agt acg ccc gca gaa cct gaa acg atc gat   211
Val Val Ala Thr Gly Cys Ser Thr Pro Ala Glu Pro Glu Thr Ile Asp
              25                  30                  35

aat ccg gtg ttc att ggt atc tcc atc gat cca att aaa aac cta agt   259
Asn Pro Val Phe Ile Gly Ile Ser Ile Asp Pro Ile Lys Asn Leu Ser
          40                  45                  50

ccg aat cac gct gca aac ctc ttc gct tta tct gca gat ggc tcg gga   307
Pro Asn His Ala Ala Asn Leu Phe Ala Leu Ser Ala Asp Gly Ser Gly
      55                  60                  65

gga att ttc caa gaa ctc gct ccc aca tac ttt ccg tcg atc cat cga   355
Gly Ile Phe Gln Glu Leu Ala Pro Thr Tyr Phe Pro Ser Ile His Arg
  70                  75                  80                  85

tta gga aac gga ttc atc gca ccc gat aga gat tct ttg gta gtt gtc   403
Leu Gly Asn Gly Phe Ile Ala Pro Asp Arg Asp Ser Leu Val Val Val
                  90                  95                 100
```

```
gac gct tct cta aag gaa gtt tat cga cac gaa gtg gcc agg ctt ggt   451
Asp Ala Ser Leu Lys Glu Val Tyr Arg His Glu Val Ala Arg Leu Gly
            105                 110                 115

gtt gga atg caa act caa tca gct agg tct cca ctg cat aaa tca gtt   499
Val Gly Met Gln Thr Gln Ser Ala Arg Ser Pro Leu His Lys Ser Val
        120                 125                 130

gcc ttc tcc ttc aat gaa gga aca gct gaa gcc cca tat aga cac cgc   547
Ala Phe Ser Phe Asn Glu Gly Thr Ala Glu Ala Pro Tyr Arg His Arg
    135                 140                 145

atc gtc tcc gca act gag aaa aca tca gct tcc gca atg aca gat cag   595
Ile Val Ser Ala Thr Glu Lys Thr Ser Ala Ser Ala Met Thr Asp Gln
150                 155                 160                 165

cgg cac ttc gcg ctt act gca tgc gat gac gga tcc aca cgg tgg gtc   643
Arg His Phe Ala Leu Thr Ala Cys Asp Asp Gly Ser Thr Arg Trp Val
                170                 175                 180

gaa tat tcc cct gac cgc gga atg gaa gat cca atg ggc ccc ggc tca   691
Glu Tyr Ser Pro Asp Arg Gly Met Glu Asp Pro Met Gly Pro Gly Ser
            185                 190                 195

gca cgc atc gtg act ctc cag gcc gac gga gaa ctc agt gaa att gac   739
Ala Arg Ile Val Thr Leu Gln Ala Asp Gly Glu Leu Ser Glu Ile Asp
        200                 205                 210

gtt gag tgg aat ttc ccg gat cgg ccc tcc gcc cca att att ctg tct   787
Val Glu Trp Asn Phe Pro Asp Arg Pro Ser Ala Pro Ile Ile Leu Ser
    215                 220                 225

tgc gaa gat cca agc gct tat ata gtt tca gaa gaa gac atc atc tat   835
Cys Glu Asp Pro Ser Ala Tyr Ile Val Ser Glu Glu Asp Ile Ile Tyr
230                 235                 240                 245

gta aaa gac gag gta agc cct gcc gaa tcc ata gga aaa tta cct gca   883
Val Lys Asp Glu Val Ser Pro Ala Glu Ser Ile Gly Lys Leu Pro Ala
                250                 255                 260

tat gaa att ccg gac cgc gcc cga ttc gat aca gtt tcc ggc gaa gac   931
Tyr Glu Ile Pro Asp Arg Ala Arg Phe Asp Thr Val Ser Gly Glu Asp
            265                 270                 275

tac ttc gct ttt acg tca act ggg atg ctg aca cgc atc aat att ccc   979
Tyr Phe Ala Phe Thr Ser Thr Gly Met Leu Thr Arg Ile Asn Ile Pro
        280                 285                 290

caa gca aaa atc gtc tac gca caa tcc att gac ctc tac ggc aag cat   1027
Gln Ala Lys Ile Val Tyr Ala Gln Ser Ile Asp Leu Tyr Gly Lys His
    295                 300                 305

ccg gtt tcc ata act ttc gat tcc gac cgt gca tac gtg gtt act tcc   1075
Pro Val Ser Ile Thr Phe Asp Ser Asp Arg Ala Tyr Val Val Thr Ser
310                 315                 320                 325

ggg gat tcc ggg gaa agc ctt ctt gaa atc gac ttg aat gat cca aca   1123
Gly Asp Ser Gly Glu Ser Leu Leu Glu Ile Asp Leu Asn Asp Pro Thr
                330                 335                 340

tgc act tca gat cag ctc tcg ctc act ggt ttc aac aaa tta ctc aca   1171
```

```
Cys Thr Ser Asp Gln Leu Ser Leu Thr Gly Phe Asn Lys Leu Leu Thr
            345                 350                 355

gct cgg aaa cct aag cca gaa ccg tcg atc atc atc gaa acc atc ttg   1219
Ala Arg Lys Pro Lys Pro Glu Pro Ser Ile Ile Ile Glu Thr Ile Leu
        360                 365                 370

cca att gac cca aac tac tca ctg ggt tgt aag agt tagattttgg        1265
Pro Ile Asp Pro Asn Tyr Ser Leu Gly Cys Lys Ser
    375                 380                 385

acggaagtgt gta                                                   1278


<210> 2744
<211> 385
<212> PRT
<213> Corynebacterium glutamicum

<400> 2744
Met Leu Gly Leu Ser Arg Arg Lys Phe Ala Met Leu Ala Ala Leu Thr
  1               5                  10                  15

Ala Gly Ile Val Gly Val Val Ala Thr Gly Cys Ser Thr Pro Ala Glu
             20                  25                  30

Pro Glu Thr Ile Asp Asn Pro Val Phe Ile Gly Ile Ser Ile Asp Pro
         35                  40                  45

Ile Lys Asn Leu Ser Pro Asn His Ala Ala Asn Leu Phe Ala Leu Ser
     50                  55                  60

Ala Asp Gly Ser Gly Gly Ile Phe Gln Glu Leu Ala Pro Thr Tyr Phe
 65                  70                  75                  80

Pro Ser Ile His Arg Leu Gly Asn Gly Phe Ile Ala Pro Asp Arg Asp
                 85                  90                  95

Ser Leu Val Val Val Asp Ala Ser Leu Lys Glu Val Tyr Arg His Glu
            100                 105                 110

Val Ala Arg Leu Gly Val Gly Met Gln Thr Gln Ser Ala Arg Ser Pro
        115                 120                 125

Leu His Lys Ser Val Ala Phe Ser Phe Asn Glu Gly Thr Ala Glu Ala
    130                 135                 140

Pro Tyr Arg His Arg Ile Val Ser Ala Thr Glu Lys Thr Ser Ala Ser
145                 150                 155                 160

Ala Met Thr Asp Gln Arg His Phe Ala Leu Thr Ala Cys Asp Asp Gly
                165                 170                 175

Ser Thr Arg Trp Val Glu Tyr Ser Pro Asp Arg Gly Met Glu Asp Pro
            180                 185                 190

Met Gly Pro Gly Ser Ala Arg Ile Val Thr Leu Gln Ala Asp Gly Glu
        195                 200                 205

Leu Ser Glu Ile Asp Val Glu Trp Asn Phe Pro Asp Arg Pro Ser Ala
    210                 215                 220
```

```
Pro Ile Ile Leu Ser Cys Glu Asp Pro Ser Ala Tyr Ile Val Ser Glu
225                 230                 235                 240

Glu Asp Ile Ile Tyr Val Lys Asp Glu Val Ser Pro Ala Glu Ser Ile
                245                 250                 255

Gly Lys Leu Pro Ala Tyr Glu Ile Pro Asp Arg Ala Arg Phe Asp Thr
            260                 265                 270

Val Ser Gly Glu Asp Tyr Phe Ala Phe Thr Ser Thr Gly Met Leu Thr
        275                 280                 285

Arg Ile Asn Ile Pro Gln Ala Lys Ile Val Tyr Ala Gln Ser Ile Asp
    290                 295                 300

Leu Tyr Gly Lys His Pro Val Ser Ile Thr Phe Asp Ser Asp Arg Ala
305                 310                 315                 320

Tyr Val Val Thr Ser Gly Asp Ser Gly Glu Ser Leu Leu Glu Ile Asp
                325                 330                 335

Leu Asn Asp Pro Thr Cys Thr Ser Asp Gln Leu Ser Leu Thr Gly Phe
            340                 345                 350

Asn Lys Leu Leu Thr Ala Arg Lys Pro Lys Pro Glu Pro Ser Ile Ile
        355                 360                 365

Ile Glu Thr Ile Leu Pro Ile Asp Pro Asn Tyr Ser Leu Gly Cys Lys
    370                 375                 380

Ser
385
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09/30/2009 09:30:09 PM

<210> 2745
<211> 1345
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1336)
<223> RXA02478

<400> 2745
gacatcgtcg aagcgctctc cagcggcaac atcgacgatt atcgcagcgc cgtgctcgct 60

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cactacgcgc cgtttcgccg catgatttcc aacatgctcg atg cgc act agc ctc   115
                                                Met Arg Thr Ser Leu
                                                  1               5

att gcg cgc ggg ttg tac cgc att ccc gcg ctg gtc tgg gat cag ggt   163
Ile Ala Arg Gly Leu Tyr Arg Ile Pro Ala Leu Val Trp Asp Gln Gly
                 10                  15                  20

ctt tta acg ctt ttc gac gcc cgc ctc agt gtt gac gac ctc ccc gca   211
Leu Leu Thr Leu Phe Asp Ala Arg Leu Ser Val Asp Asp Leu Pro Ala
             25                  30                  35

ccc atc gac gtg gtg tca gcg cga tcc tca gac ggc atc acc tgg acc   259
```

```
Pro Ile Asp Val Val Ser Ala Arg Ser Ser Asp Gly Ile Thr Trp Thr
         40                  45                  50

acc cca gaa cca gca atc gtc gaa act gaa cac cgc ggt gtg ggc gat   307
Thr Pro Glu Pro Ala Ile Val Glu Thr Glu His Arg Gly Val Gly Asp
     55                  60                  65

gtc tgc ctt gtc acg ggc gat ctg tgc ttc cac gga ttg tcc aac ctc   355
Val Cys Leu Val Thr Gly Asp Leu Cys Phe His Gly Leu Ser Asn Leu
 70                  75                  80                  85

gca gga ttt ttt gag gat ccc acc gac ctt gaa ccc cgg ctg gcg cgc   403
Ala Gly Phe Phe Glu Asp Pro Thr Asp Leu Glu Pro Arg Leu Ala Arg
                 90                  95                 100

cgg gat gtg agt ggg tgg acg tcg ata agc atg gcc cac tat ttt gcg   451
Arg Asp Val Ser Gly Trp Thr Ser Ile Ser Met Ala His Tyr Phe Ala
            105                 110                 115

gat gtt gat gcc gcg ttc gcc tcg tcg ggg acg gga ctt gtc ctg gcg   499
Asp Val Asp Ala Ala Phe Ala Ser Ser Gly Thr Gly Leu Val Leu Ala
        120                 125                 130

gat ggg cgg tgg att cag agt ttt gtg gtg cgg cgc ggg cgc gag att   547
Asp Gly Arg Trp Ile Gln Ser Phe Val Val Arg Arg Gly Arg Glu Ile
    135                 140                 145

tcg ctt cgg att ctg cgc agc gat ggc cac atc acc gat att gcc ggc   595
Ser Leu Arg Ile Leu Arg Ser Asp Gly His Ile Thr Asp Ile Ala Gly
150                 155                 160                 165

ggt aac gaa tcc gcg atg acg cag ctg ccg agc ggt cgg att gtg ctg   643
Gly Asn Glu Ser Ala Met Thr Gln Leu Pro Ser Gly Arg Ile Val Leu
                170                 175                 180

cat tcc agg ggg gtg gga cac cgt ctg agc agt gtg tcc gat gat ttc   691
His Ser Arg Gly Val Gly His Arg Leu Ser Ser Val Ser Asp Asp Phe
            185                 190                 195

ggg gag aca ttc act ccg ctg gag cct gtg cct gaa cta atc gac ccc   739
Gly Glu Thr Phe Thr Pro Leu Glu Pro Val Pro Glu Leu Ile Asp Pro
        200                 205                 210

ggc tgc aac ggc cac gtg ttc tac tgg aaa gcg gct gga atg ctc gcc   787
Gly Cys Asn Gly His Val Phe Tyr Trp Lys Ala Ala Gly Met Leu Ala
    215                 220                 225

gca acg cac ctg gcg gac cct gat ctg cga cgc cac ttg gtg gtt gat   835
Ala Thr His Leu Ala Asp Pro Asp Leu Arg Arg His Leu Val Val Asp
230                 235                 240                 245

tta tcc agc gac gaa gga gcg acc tgg gcg cat cgc atc acc atc gag   883
Leu Ser Ser Asp Glu Gly Ala Thr Trp Ala His Arg Ile Thr Ile Glu
                250                 255                 260

cgc gaa gaa gcc gcc tat tca acc gct gcg gaa atg ccc aac gga gat   931
Arg Glu Glu Ala Ala Tyr Ser Thr Ala Ala Glu Met Pro Asn Gly Asp
            265                 270                 275

gtt gcc gtg gtg tgg gaa gca gag gga acg cgc gcg ata aaa tgc acg   979
Val Ala Val Val Trp Glu Ala Glu Gly Thr Arg Ala Ile Lys Cys Thr
```

```
        280                 285                 290

gtg atc agc gta aat gat att tcg ctg cgg atc gat gag ccc att tcc   1027
Val Ile Ser Val Asn Asp Ile Ser Leu Arg Ile Asp Glu Pro Ile Ser
    295                 300                 305

gat gcc ata tcc ctc cgc cat gtg gtg atc aac gat gac cat gac ggc   1075
Asp Ala Ile Ser Leu Arg His Val Val Ile Asn Asp Asp His Asp Gly
310                 315                 320                 325

atc gaa gtc gca ctg cct gac gca tcg caa tgg ggt gaa ggt gta ttc   1123
Ile Glu Val Ala Leu Pro Asp Ala Ser Gln Trp Gly Glu Gly Val Phe
                330                 335                 340

aaa att gtg tcc aat cca gac gcg agc acc caa aaa atc cgc act cga   1171
Lys Ile Val Ser Asn Pro Asp Ala Ser Thr Gln Lys Ile Arg Thr Arg
            345                 350                 355

ggc aag ccc gcg cga cag acc ctg gaa att ggg gat gaa ttg gtt ttt   1219
Gly Lys Pro Ala Arg Gln Thr Leu Glu Ile Gly Asp Glu Leu Val Phe
        360                 365                 370

gat atc cgc aag ggt gga gaa gtg gct tac ggc gtc acg gtt cct tat   1267
Asp Ile Arg Lys Gly Gly Glu Val Ala Tyr Gly Val Thr Val Pro Tyr
    375                 380                 385

gat ggt cgc tcg ttg ggg aag tta aac agg att ttg gag tgg ggc tgt   1315
Asp Gly Arg Ser Leu Gly Lys Leu Asn Arg Ile Leu Glu Trp Gly Cys
390                 395                 400                 405

aga ggc cga ttt gcg gtc ctt taattgcgg                            1345
Arg Gly Arg Phe Ala Val Leu
                410
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09/30/2005 09:57:50

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<210> 2746
<211> 412
<212> PRT
<213> Corynebacterium glutamicum

<400> 2746
Met Arg Thr Ser Leu Ile Ala Arg Gly Leu Tyr Arg Ile Pro Ala Leu
  1               5                  10                  15

Val Trp Asp Gln Gly Leu Leu Thr Leu Phe Asp Ala Arg Leu Ser Val
             20                  25                  30

Asp Asp Leu Pro Ala Pro Ile Asp Val Val Ser Ala Arg Ser Ser Asp
         35                  40                  45

Gly Ile Thr Trp Thr Thr Pro Glu Pro Ala Ile Val Glu Thr Glu His
     50                  55                  60

Arg Gly Val Gly Asp Val Cys Leu Val Thr Gly Asp Leu Cys Phe His
 65                  70                  75                  80

Gly Leu Ser Asn Leu Ala Gly Phe Phe Glu Asp Pro Thr Asp Leu Glu
                 85                  90                  95

Pro Arg Leu Ala Arg Arg Asp Val Ser Gly Trp Thr Ser Ile Ser Met
            100                 105                 110
```

```
Ala His Tyr Phe Ala Asp Val Asp Ala Ala Phe Ala Ser Ser Gly Thr
        115                 120                 125

Gly Leu Val Leu Ala Asp Gly Arg Trp Ile Gln Ser Phe Val Val Arg
    130                 135                 140

Arg Gly Arg Glu Ile Ser Leu Arg Ile Leu Arg Ser Asp Gly His Ile
145                 150                 155                 160

Thr Asp Ile Ala Gly Gly Asn Glu Ser Ala Met Thr Gln Leu Pro Ser
                165                 170                 175

Gly Arg Ile Val Leu His Ser Arg Gly Val Gly His Arg Leu Ser Ser
            180                 185                 190

Val Ser Asp Asp Phe Gly Glu Thr Phe Thr Pro Leu Glu Pro Val Pro
        195                 200                 205

Glu Leu Ile Asp Pro Gly Cys Asn Gly His Val Phe Tyr Trp Lys Ala
    210                 215                 220

Ala Gly Met Leu Ala Ala Thr His Leu Ala Asp Pro Asp Leu Arg Arg
225                 230                 235                 240

His Leu Val Val Asp Leu Ser Ser Asp Glu Gly Ala Thr Trp Ala His
                245                 250                 255

Arg Ile Thr Ile Glu Arg Glu Glu Ala Ala Tyr Ser Thr Ala Ala Glu
            260                 265                 270

Met Pro Asn Gly Asp Val Ala Val Val Trp Glu Ala Glu Gly Thr Arg
        275                 280                 285

Ala Ile Lys Cys Thr Val Ile Ser Val Asn Asp Ile Ser Leu Arg Ile
    290                 295                 300

Asp Glu Pro Ile Ser Asp Ala Ile Ser Leu Arg His Val Val Ile Asn
305                 310                 315                 320

Asp Asp His Asp Gly Ile Glu Val Ala Leu Pro Asp Ala Ser Gln Trp
                325                 330                 335

Gly Glu Gly Val Phe Lys Ile Val Ser Asn Pro Asp Ala Ser Thr Gln
            340                 345                 350

Lys Ile Arg Thr Arg Gly Lys Pro Ala Arg Gln Thr Leu Glu Ile Gly
        355                 360                 365

Asp Glu Leu Val Phe Asp Ile Arg Lys Gly Gly Glu Val Ala Tyr Gly
    370                 375                 380

Val Thr Val Pro Tyr Asp Gly Arg Ser Leu Gly Lys Leu Asn Arg Ile
385                 390                 395                 400

Leu Glu Trp Gly Cys Arg Gly Arg Phe Ala Val Leu
                405                 410
```

<210> 2747
<211> 933

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(910)
<223> RXA02482

<400> 2747
aaacggtggc gccttaattg ttttacgcgt gctgacagga acctttttagg tgattaacct 60

ggtttgcaac tttccaacct cagccggata aggaacacta gtg ggc gtg gct aaa 115
Val Gly Val Ala Lys
1 5

tca aag aaa tct gct tta cct aaa gtc ctg ctc acc atc gtg gtg atc 163
Ser Lys Lys Ser Ala Leu Pro Lys Val Leu Leu Thr Ile Val Val Ile
10 15 20

ctg ctc ctg ctc gtg ctg gta gca gaa ttc ggg ctg cgc ttc atg atc 211
Leu Leu Leu Leu Val Leu Val Ala Glu Phe Gly Leu Arg Phe Met Ile
25 30 35

gga aaa caa ctg aaa gat gag ttc caa gct cag gct tcc tca caa gga 259
Gly Lys Gln Leu Lys Asp Glu Phe Gln Ala Gln Ala Ser Ser Gln Gly
40 45 50

atc tct gca act gaa gag ccc tcc atc agc ttc ggc gca tcc cca ctc 307
Ile Ser Ala Thr Glu Glu Pro Ser Ile Ser Phe Gly Ala Ser Pro Leu
55 60 65

ctg tta ggc atc gct cgg gga agc atc aat gaa gtc aca atc gac acc 355
Leu Leu Gly Ile Ala Arg Gly Ser Ile Asn Glu Val Thr Ile Asp Thr
70 75 80 85

ccc gac tcc gta tcc atc act aac caa gac ggt gtc ccc tcc atc agt 403
Pro Asp Ser Val Ser Ile Thr Asn Gln Asp Gly Val Pro Ser Ile Ser
90 95 100

ggc aca cca gag tca act atc caa ctc caa ggg ctt gat atc ggt gac 451
Gly Thr Pro Glu Ser Thr Ile Gln Leu Gln Gly Leu Asp Ile Gly Asp
105 110 115

cgc gac aac cca gtc gca gac cac ctc acc tta acc aca ttg gca acc 499
Arg Asp Asn Pro Val Ala Asp His Leu Thr Leu Thr Thr Leu Ala Thr
120 125 130

gac gat ttc atc ctg gca acc atc caa cag cag atg gcc gaa gca acc 547
Asp Asp Phe Ile Leu Ala Thr Ile Gln Gln Gln Met Ala Glu Ala Thr
135 140 145

ggc ggg aac agc acc tcc caa gga ttc gca gaa cag ctt atc cag gaa 595
Gly Gly Asn Ser Thr Ser Gln Gly Phe Ala Glu Gln Leu Ile Gln Glu
150 155 160 165

ctc atc aaa gtc acc gac att act tcc gat gca gct aat caa acc atc 643
Leu Ile Lys Val Thr Asp Ile Thr Ser Asp Ala Ala Asn Gln Thr Ile
170 175 180

gaa gtt gaa ttc acc gac ggc gcc gcc cga gcc tca ctg cac ccc atc 691
Glu Val Glu Phe Thr Asp Gly Ala Ala Arg Ala Ser Leu His Pro Ile

```
            185                 190                 195

gta acg aac ggc caa ctc ggc ttt gag atc gta gat tcc caa ctc ttc   739
Val Thr Asn Gly Gln Leu Gly Phe Glu Ile Val Asp Ser Gln Leu Phe
        200                 205                 210

gga ttc ggc ctc ccc gat gaa atc tcc caa atg ctc acc gac gca ctg   787
Gly Phe Gly Leu Pro Asp Glu Ile Ser Gln Met Leu Thr Asp Ala Leu
    215                 220                 225

caa tca tca atc aat gaa gta gcc ggt ggc ctg caa atc caa agc ctc   835
Gln Ser Ser Ile Asn Glu Val Ala Gly Gly Leu Gln Ile Gln Ser Leu
230                 235                 240                 245

gaa gtt gtc gac gct ggc atc aac gtc acc ctg acc gga gac aac atc   883
Glu Val Val Asp Ala Gly Ile Asn Val Thr Leu Thr Gly Asp Asn Ile
                250                 255                 260

aac atc cag acc cta gaa gcc gca cag taaagagcgc tttcgcgtct        930
Asn Ile Gln Thr Leu Glu Ala Ala Gln
            265                 270

gtg                                                             933


<210> 2748
<211> 270
<212> PRT
<213> Corynebacterium glutamicum

<400> 2748
Val Gly Val Ala Lys Ser Lys Lys Ser Ala Leu Pro Lys Val Leu Leu
  1               5                  10                  15

Thr Ile Val Val Ile Leu Leu Leu Leu Val Leu Val Ala Glu Phe Gly
             20                  25                  30

Leu Arg Phe Met Ile Gly Lys Gln Leu Lys Asp Glu Phe Gln Ala Gln
         35                  40                  45

Ala Ser Ser Gln Gly Ile Ser Ala Thr Glu Glu Pro Ser Ile Ser Phe
     50                  55                  60

Gly Ala Ser Pro Leu Leu Leu Gly Ile Ala Arg Gly Ser Ile Asn Glu
 65                  70                  75                  80

Val Thr Ile Asp Thr Pro Asp Ser Val Ser Ile Thr Asn Gln Asp Gly
                 85                  90                  95

Val Pro Ser Ile Ser Gly Thr Pro Glu Ser Thr Ile Gln Leu Gln Gly
            100                 105                 110

Leu Asp Ile Gly Asp Arg Asp Asn Pro Val Ala Asp His Leu Thr Leu
        115                 120                 125

Thr Thr Leu Ala Thr Asp Asp Phe Ile Leu Ala Thr Ile Gln Gln Gln
    130                 135                 140

Met Ala Glu Ala Thr Gly Gly Asn Ser Thr Ser Gln Gly Phe Ala Glu
145                 150                 155                 160
```

```
Gln Leu Ile Gln Glu Leu Ile Lys Val Thr Asp Ile Thr Ser Asp Ala
                165                 170                 175

Ala Asn Gln Thr Ile Glu Val Glu Phe Thr Asp Gly Ala Ala Arg Ala
            180                 185                 190

Ser Leu His Pro Ile Val Thr Asn Gly Gln Leu Gly Phe Glu Ile Val
        195                 200                 205

Asp Ser Gln Leu Phe Gly Phe Gly Leu Pro Asp Glu Ile Ser Gln Met
    210                 215                 220

Leu Thr Asp Ala Leu Gln Ser Ser Ile Asn Glu Val Ala Gly Gly Leu
225                 230                 235                 240

Gln Ile Gln Ser Leu Glu Val Val Asp Ala Gly Ile Asn Val Thr Leu
                245                 250                 255

Thr Gly Asp Asn Ile Asn Ile Gln Thr Leu Glu Ala Ala Gln
            260                 265                 270
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Sequence Listing - 2749

<210> 2749
<211> 936
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(913)
<223> RXA02483

<400> 2749

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catgggccct gcaatcgagc ctaaggttgc cgacgcactc ggcgagctct tcgcaaacga 60

aggcgctctg accgaaaagt ggatctccga gaacctctaa atg gct gat cac gcc   115
                                              Met Ala Asp His Ala
                                                1               5

cac aat ctg cgc gcc tct ttc cgc aag ggt gca aac gga aag cag aag   163
His Asn Leu Arg Ala Ser Phe Arg Lys Gly Ala Asn Gly Lys Gln Lys
                  10                  15                  20

cca atc ggc gtg atc acc cgc ggc acc acc ggt gtg aac cgc cta cgg   211
Pro Ile Gly Val Ile Thr Arg Gly Thr Thr Gly Val Asn Arg Leu Arg
              25                  30                  35

cgc ttc gat cgg tgg tgc ttt cat cat ccc aaa ata cgt tcg ctt ctc   259
Arg Phe Asp Arg Trp Cys Phe His His Pro Lys Ile Arg Ser Leu Leu
          40                  45                  50

gac gcc act tcc ctg gcg tta gat gtc ggg tac ggc gcc agc cac aca   307
Asp Ala Thr Ser Leu Ala Leu Asp Val Gly Tyr Gly Ala Ser His Thr
      55                  60                  65

acc acc gtc gaa tgg gga cgt tgg ctc cac cgc ctc caa ccc gac atg   355
Thr Thr Val Glu Trp Gly Arg Trp Leu His Arg Leu Gln Pro Asp Met
  70                  75                  80                  85

gat gtc atc ggc cta gaa atc aac ccc gaa cga gtc ctc gaa ccc caa   403
Asp Val Ile Gly Leu Glu Ile Asn Pro Glu Arg Val Leu Glu Pro Gln
```

```
                  90                  95                 100

aac ggc gtg tcc ttt gaa ctc ggc gga ttc gaa ctt gcc ggc tac acc   451
Asn Gly Val Ser Phe Glu Leu Gly Gly Phe Glu Leu Ala Gly Tyr Thr
            105                 110                 115

cca caa ctc gtg cgc gcc ttc aac gtg ctg cgc caa tac gac gtg gac   499
Pro Gln Leu Val Arg Ala Phe Asn Val Leu Arg Gln Tyr Asp Val Asp
        120                 125                 130

caa gtc gaa gcc gca tgg gaa acc gtc acc tcc aga ctt gcc cca ggc   547
Gln Val Glu Ala Ala Trp Glu Thr Val Thr Ser Arg Leu Ala Pro Gly
    135                 140                 145

gga ctg ttt ttc gaa ggc acc tgc gat gaa atc ggc aaa cgc tgc acc   595
Gly Leu Phe Phe Glu Gly Thr Cys Asp Glu Ile Gly Lys Arg Cys Thr
150                 155                 160                 165

tgg atc aca ctt aac tca gac ggc cca caa gaa ctc acc ctt gca tgg   643
Trp Ile Thr Leu Asn Ser Asp Gly Pro Gln Glu Leu Thr Leu Ala Trp
                170                 175                 180

gat cct tgg gga atc tcc acc ccc tcc gat gtg gcc gaa cga ctg ccc   691
Asp Pro Trp Gly Ile Ser Thr Pro Ser Asp Val Ala Glu Arg Leu Pro
            185                 190                 195

aaa atg ctc atc cac cgc aac att cct ggt gaa aag att cac gca ctg   739
Lys Met Leu Ile His Arg Asn Ile Pro Gly Glu Lys Ile His Ala Leu
        200                 205                 210

cta gca gcc gct gat tta gcc tgg gac tac tgc gcc ggc tgg gaa ccc   787
Leu Ala Ala Ala Asp Leu Ala Trp Asp Tyr Cys Ala Gly Trp Glu Pro
    215                 220                 225

cac gga ccg cgc gtg cgc tgg gaa aaa gcc cgc gag atg ctc atc gac   835
His Gly Pro Arg Val Arg Trp Glu Lys Ala Arg Glu Met Leu Ile Asp
230                 235                 240                 245

caa ggt tgg ccc atc gca gtg tcc agg cga cgc gtg ggc gat agc ctg   883
Gln Gly Trp Pro Ile Ala Val Ser Arg Arg Arg Val Gly Asp Ser Leu
                250                 255                 260

ctg act gta ccg tgg gaa acg gtg gcg cct taattgtttt acgcgtgctg     933
Leu Thr Val Pro Trp Glu Thr Val Ala Pro
            265                 270

aca                                                               936
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<210> 2750
<211> 271
<212> PRT
<213> Corynebacterium glutamicum

<400> 2750

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Met Ala Asp His Ala His Asn Leu Arg Ala Ser Phe Arg Lys Gly Ala
  1               5                  10                  15

Asn Gly Lys Gln Lys Pro Ile Gly Val Ile Thr Arg Gly Thr Thr Gly
             20                  25                  30
```

```
Val Asn Arg Leu Arg Arg Phe Asp Arg Trp Cys Phe His His Pro Lys
         35                  40                  45

Ile Arg Ser Leu Leu Asp Ala Thr Ser Leu Ala Leu Asp Val Gly Tyr
     50                  55                  60

Gly Ala Ser His Thr Thr Thr Val Glu Trp Gly Arg Trp Leu His Arg
 65                  70                  75                  80

Leu Gln Pro Asp Met Asp Val Ile Gly Leu Glu Ile Asn Pro Glu Arg
                 85                  90                  95

Val Leu Glu Pro Gln Asn Gly Val Ser Phe Glu Leu Gly Gly Phe Glu
            100                 105                 110

Leu Ala Gly Tyr Thr Pro Gln Leu Val Arg Ala Phe Asn Val Leu Arg
        115                 120                 125

Gln Tyr Asp Val Asp Gln Val Glu Ala Ala Trp Glu Thr Val Thr Ser
    130                 135                 140

Arg Leu Ala Pro Gly Gly Leu Phe Phe Glu Gly Thr Cys Asp Glu Ile
145                 150                 155                 160

Gly Lys Arg Cys Thr Trp Ile Thr Leu Asn Ser Asp Gly Pro Gln Glu
                165                 170                 175

Leu Thr Leu Ala Trp Asp Pro Trp Gly Ile Ser Thr Pro Ser Asp Val
            180                 185                 190

Ala Glu Arg Leu Pro Lys Met Leu Ile His Arg Asn Ile Pro Gly Glu
        195                 200                 205

Lys Ile His Ala Leu Leu Ala Ala Ala Asp Leu Ala Trp Asp Tyr Cys
    210                 215                 220

Ala Gly Trp Glu Pro His Gly Pro Arg Val Arg Trp Glu Lys Ala Arg
225                 230                 235                 240

Glu Met Leu Ile Asp Gln Gly Trp Pro Ile Ala Val Ser Arg Arg Arg
                245                 250                 255

Val Gly Asp Ser Leu Leu Thr Val Pro Trp Glu Thr Val Ala Pro
            260                 265                 270
```

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<210> 2751
<211> 624
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(601)
<223> RXA02484

<400> 2751
cggcgaaagt gacttccgaa tcgagttcga cgccgtcgat cgcggcgatt tcctgggcta 60

gcgatgaatc caacacccca ctaacggtag tcttatcctc atg gca acg cgt aca 115
Met Ala Thr Arg Thr

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                                                    1               5

gaa aac acc att acg atc aat cag ccc gtc ggc aag gtg cac caa gca   163
Glu Asn Thr Ile Thr Ile Asn Gln Pro Val Gly Lys Val His Gln Ala
                 10                  15                  20

ctg acc acc gaa gcc tac tgg gca tac atc gca gag aac ctc tcc ccc   211
Leu Thr Thr Glu Ala Tyr Trp Ala Tyr Ile Ala Glu Asn Leu Ser Pro
            25                  30                  35

gaa gct ggc gag gtc aac gag ttc acc gca gct gac ggt ggc gca acc   259
Glu Ala Gly Glu Val Asn Glu Phe Thr Ala Ala Asp Gly Gly Ala Thr
         40                  45                  50

gca acc ctt ttt gag gtc ctc cca ctc gag gtc ctc cca gag gca gtt   307
Ala Thr Leu Phe Glu Val Leu Pro Leu Glu Val Leu Pro Glu Ala Val
     55                  60                  65

cgc gca atg atc agc cag gca ctg aag gtc aag cga gtc ctc acg gtt   355
Arg Ala Met Ile Ser Gln Ala Leu Lys Val Lys Arg Val Leu Thr Val
 70                  75                  80                  85

cct gca ctg acc aac aac gcc aca acc gtc gag tac aac gct gac gtc   403
Pro Ala Leu Thr Asn Asn Ala Thr Thr Val Glu Tyr Asn Ala Asp Val
                 90                  95                 100

aag ggc acc cct gtt gat ttc aag ggc acc atc gcc atc aac ggc gac   451
Lys Gly Thr Pro Val Asp Phe Lys Gly Thr Ile Ala Ile Asn Gly Asp
            105                 110                 115

gac gca gca acc acc ttc gac tac agc aac gaa gtg tcc gtg aac atc   499
Asp Ala Ala Thr Thr Phe Asp Tyr Ser Asn Glu Val Ser Val Asn Ile
        120                 125                 130

cca ttc atg ggc cct gca atc gag cct aag gtt gcc gac gca ctc ggc   547
Pro Phe Met Gly Pro Ala Ile Glu Pro Lys Val Ala Asp Ala Leu Gly
    135                 140                 145

gag ctc ttc gca aac gaa ggc gct ctg acc gaa aag tgg atc tcc gag   595
Glu Leu Phe Ala Asn Glu Gly Ala Leu Thr Glu Lys Trp Ile Ser Glu
150                 155                 160                 165

aac ctc taaatggctg atcacgccca caa                                624
Asn Leu
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<210> 2752
<211> 167
<212> PRT
<213> Corynebacterium glutamicum

<400> 2752

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Met Ala Thr Arg Thr Glu Asn Thr Ile Thr Ile Asn Gln Pro Val Gly
  1               5                  10                  15

Lys Val His Gln Ala Leu Thr Thr Glu Ala Tyr Trp Ala Tyr Ile Ala
            20                  25                  30

Glu Asn Leu Ser Pro Glu Ala Gly Glu Val Asn Glu Phe Thr Ala Ala
         35                  40                  45
```

```
Asp Gly Gly Ala Thr Ala Thr Leu Phe Glu Val Leu Pro Leu Glu Val
     50                  55                  60

Leu Pro Glu Ala Val Arg Ala Met Ile Ser Gln Ala Leu Lys Val Lys
 65                  70                  75                  80

Arg Val Leu Thr Val Pro Ala Leu Thr Asn Asn Ala Thr Thr Val Glu
                 85                  90                  95

Tyr Asn Ala Asp Val Lys Gly Thr Pro Val Asp Phe Lys Gly Thr Ile
            100                 105                 110

Ala Ile Asn Gly Asp Asp Ala Ala Thr Thr Phe Asp Tyr Ser Asn Glu
        115                 120                 125

Val Ser Val Asn Ile Pro Phe Met Gly Pro Ala Ile Glu Pro Lys Val
    130                 135                 140

Ala Asp Ala Leu Gly Glu Leu Phe Ala Asn Glu Gly Ala Leu Thr Glu
145                 150                 155                 160

Lys Trp Ile Ser Glu Asn Leu
                165
```

<210> 2753
<211> 759
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(736)
<223> RXA02486

<400> 2753

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accctcgtcc cagaacccgt ctggattgga atcagcatcg atg act gaa ttt tcc   115
                                          Met Thr Glu Phe Ser
                                            1               5

gac gtc cct ggc acc gcc gcc cca ctg cac agg gcg ttg gaa aat gcc   163
Asp Val Pro Gly Thr Ala Ala Pro Leu His Arg Ala Leu Glu Asn Ala
                 10                  15                  20

gga tac tcc act tta gaa tcc ctc gac ggt gtt ccc tac aag acg ttg   211
Gly Tyr Ser Thr Leu Glu Ser Leu Asp Gly Val Pro Tyr Lys Thr Leu
             25                  30                  35

att gcc ctg cat ggt gtc gga aaa act ggc ctc ggc agg atc cag gca   259
Ile Ala Leu His Gly Val Gly Lys Thr Gly Leu Gly Arg Ile Gln Ala
         40                  45                  50

gca ttg ttg gaa cgt ggc ctt tcc ctg ggg gaa gaa aca aaa ggc gcc   307
Ala Leu Leu Glu Arg Gly Leu Ser Leu Gly Glu Glu Thr Lys Gly Ala
     55                  60                  65

acc atc acc cca ggt cac acc ggt aaa gtg gcc tca gat atc aaa act   355
Thr Ile Thr Pro Gly His Thr Gly Lys Val Ala Ser Asp Ile Lys Thr
```

```
 70                  75                  80                  85

cac atc act tcc gtg gat ccc gtc gca tac gtc gat ggt cta gag ggg   403
His Ile Thr Ser Val Asp Pro Val Ala Tyr Val Asp Gly Leu Glu Gly
                 90                  95                 100

cgt cgg gtt gct cac ggg cac caa ttg cta tcg atc ttc ggt cgc gtc   451
Arg Arg Val Ala His Gly His Gln Leu Leu Ser Ile Phe Gly Arg Val
            105                 110                 115

acc ggc gcg gaa ccc aaa atg tgg gga ccc tcc atg atc gga tac ggc   499
Thr Gly Ala Glu Pro Lys Met Trp Gly Pro Ser Met Ile Gly Tyr Gly
        120                 125                 130

tca gtc cac tac gtt tcc cac acc gga agg gaa ggc gat tgg ttt cag   547
Ser Val His Tyr Val Ser His Thr Gly Arg Glu Gly Asp Trp Phe Gln
    135                 140                 145

tgt ggt ttc agc ccg gcg aag tcc aaa atc tgc ctg tat ggc ctg aag   595
Cys Gly Phe Ser Pro Ala Lys Ser Lys Ile Cys Leu Tyr Gly Leu Lys
150                 155                 160                 165

gat tcg cct cgc ggt gag gaa ttg ctg cag aaa ctt gga aaa tac acc   643
Asp Ser Pro Arg Gly Glu Glu Leu Leu Gln Lys Leu Gly Lys Tyr Thr
                170                 175                 180

gaa ggc cgc gga tgc gtg tac atc aat aaa ccg gaa gac atc gat ttg   691
Glu Gly Arg Gly Cys Val Tyr Ile Asn Lys Pro Glu Asp Ile Asp Leu
            185                 190                 195

gat gtt tta gag gcc atg atc agc gag tca tgg gcc ggc caa ggc       736
Asp Val Leu Glu Ala Met Ile Ser Glu Ser Trp Ala Gly Gln Gly
        200                 205                 210

taggttgcaa atccccacca caa                                        759


<210> 2754
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 2754
Met Thr Glu Phe Ser Asp Val Pro Gly Thr Ala Ala Pro Leu His Arg
  1               5                  10                  15

Ala Leu Glu Asn Ala Gly Tyr Ser Thr Leu Glu Ser Leu Asp Gly Val
             20                  25                  30

Pro Tyr Lys Thr Leu Ile Ala Leu His Gly Val Gly Lys Thr Gly Leu
         35                  40                  45

Gly Arg Ile Gln Ala Ala Leu Leu Glu Arg Gly Leu Ser Leu Gly Glu
     50                  55                  60

Glu Thr Lys Gly Ala Thr Ile Thr Pro Gly His Thr Gly Lys Val Ala
 65                  70                  75                  80

Ser Asp Ile Lys Thr His Ile Thr Ser Val Asp Pro Val Ala Tyr Val
                 85                  90                  95
```

```
Asp Gly Leu Glu Gly Arg Arg Val Ala His Gly His Gln Leu Leu Ser
            100                 105                 110

Ile Phe Gly Arg Val Thr Gly Ala Glu Pro Lys Met Trp Gly Pro Ser
        115                 120                 125

Met Ile Gly Tyr Gly Ser Val His Tyr Val Ser His Thr Gly Arg Glu
    130                 135                 140

Gly Asp Trp Phe Gln Cys Gly Phe Ser Pro Ala Lys Ser Lys Ile Cys
145                 150                 155                 160

Leu Tyr Gly Leu Lys Asp Ser Pro Arg Gly Glu Glu Leu Leu Gln Lys
                165                 170                 175

Leu Gly Lys Tyr Thr Glu Gly Arg Gly Cys Val Tyr Ile Asn Lys Pro
            180                 185                 190

Glu Asp Ile Asp Leu Asp Val Leu Glu Ala Met Ile Ser Glu Ser Trp
        195                 200                 205

Ala Gly Gln Gly
    210


<210> 2755
<211> 392
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(369)
<223> RXA02488

<400> 2755
aag ctg act gca act ggt gtc gat gtc atg ggc acc ttc tac cca gaa   48
Lys Leu Thr Ala Thr Gly Val Asp Val Met Gly Thr Phe Tyr Pro Glu
  1               5                  10                  15

ggt gaa gca ctt gcg cca atc act ttg aac ctc acc aac gaa gtt gta   96
Gly Glu Ala Leu Ala Pro Ile Thr Leu Asn Leu Thr Asn Glu Val Val
             20                  25                  30

tgc gac gag cct gaa acc ccc gtt gag cct gag gtt cct gta gag cct   144
Cys Asp Glu Pro Glu Thr Pro Val Glu Pro Glu Val Pro Val Glu Pro
         35                  40                  45

gag act cca gta gat ccg gaa acc tcg gtc gac cca gag act cca gta   192
Glu Thr Pro Val Asp Pro Glu Thr Ser Val Asp Pro Glu Thr Pro Val
     50                  55                  60

gat ccg gaa acc tcg gtc gac cca gaa aag cct ggc gat gac aac aag   240
Asp Pro Glu Thr Ser Val Asp Pro Glu Lys Pro Gly Asp Asp Asn Lys
 65                  70                  75                  80

gat gac gga agc aac agc agc agc aac ggc gat atc ctc gga atc ttg   288
Asp Asp Gly Ser Asn Ser Ser Ser Asn Gly Asp Ile Leu Gly Ile Leu
                 85                  90                  95

ggc atc ctc gca gcg ctt ggt ggc gtt ggt gca ctt gtg tac aac ttc   336
```

```
Gly Ile Leu Ala Ala Leu Gly Gly Val Gly Ala Leu Val Tyr Asn Phe
            100                 105                 110

ctg gta gct agc gga ttc ctt gca gcg ttt aag taaatgaatc gttttcctag 389
Leu Val Ala Ser Gly Phe Leu Ala Ala Phe Lys
        115                 120

tgc                                                               392


<210> 2756
<211> 123
<212> PRT
<213> Corynebacterium glutamicum

<400> 2756
Lys Leu Thr Ala Thr Gly Val Asp Val Met Gly Thr Phe Tyr Pro Glu
  1               5                  10                  15

Gly Glu Ala Leu Ala Pro Ile Thr Leu Asn Leu Thr Asn Glu Val Val
             20                  25                  30

Cys Asp Glu Pro Glu Thr Pro Val Glu Pro Glu Val Pro Val Glu Pro
         35                  40                  45

Glu Thr Pro Val Asp Pro Glu Thr Ser Val Asp Pro Glu Thr Pro Val
     50                  55                  60

Asp Pro Glu Thr Ser Val Asp Pro Glu Lys Pro Gly Asp Asp Asn Lys
 65                  70                  75                  80

Asp Asp Gly Ser Asn Ser Ser Ser Asn Gly Asp Ile Leu Gly Ile Leu
                 85                  90                  95

Gly Ile Leu Ala Ala Leu Gly Gly Val Gly Ala Leu Val Tyr Asn Phe
            100                 105                 110

Leu Val Ala Ser Gly Phe Leu Ala Ala Phe Lys
        115                 120


<210> 2757
<211> 724
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(724)
<223> RXA02489

<400> 2757
tatcctcgga atcttgggca tcctcgcagc gcttggtggc gttggtgcac ttgtgtacaa 60

cttcctggta gctagcggat tccttgcagc gtttaagtaa atg aat cgt ttt cct   115
                                               Met Asn Arg Phe Pro
                                                 1               5

agt gcc tta tta gca gcc tct gtc gcg ggg gct gcg ttg gcc att cca   163
Ser Ala Leu Leu Ala Ala Ser Val Ala Gly Ala Ala Leu Ala Ile Pro
                10                  15                  20
```

```
gcg acc tct gca cat gca gca gaa tct att tgt aca ttc acc ggc gat   211
Ala Thr Ser Ala His Ala Ala Glu Ser Ile Cys Thr Phe Thr Gly Asp
            25                  30                  35

gtt ggg tgg aat gtg cgc gat tct ttc aac agt tat ctt ttg gga aac   259
Val Gly Trp Asn Val Arg Asp Ser Phe Asn Ser Tyr Leu Leu Gly Asn
        40                  45                  50

atc gca aat ggt agt gct tat aaa tat aag ggc ggg ttg gac gtt cgt   307
Ile Ala Asn Gly Ser Ala Tyr Lys Tyr Lys Gly Gly Leu Asp Val Arg
    55                  60                  65

gac ggc gtc cag acc gac ggt aac ggc aaa act cca gca ctg acc tgg   355
Asp Gly Val Gln Thr Asp Gly Asn Gly Lys Thr Pro Ala Leu Thr Trp
70                  75                  80                  85

cca gtt gat tcg gtg acg tct tcg aag att tcc act tcc gga ggc gcg   403
Pro Val Asp Ser Val Thr Ser Ser Lys Ile Ser Thr Ser Gly Gly Ala
                90                  95                  100

cac tgg acc gga cac aac ctg tac ccc ggt gat gac ctc gcg gaa gtc   451
His Trp Thr Gly His Asn Leu Tyr Pro Gly Asp Asp Leu Ala Glu Val
            105                 110                 115

cct aac aat ttc acg ttg gat ctt gat ttt tcc aac atc act gtg gag   499
Pro Asn Asn Phe Thr Leu Asp Leu Asp Phe Ser Asn Ile Thr Val Glu
        120                 125                 130

ctg agt ggt tct aca ggt cgg ttg ttg gtg gat tac aca tct cgg gaa   547
Leu Ser Gly Ser Thr Gly Arg Leu Leu Val Asp Tyr Thr Ser Arg Glu
    135                 140                 145

tac atc aac acc cac acg ttg ggt gag ttt caa act ggt gaa cag gct   595
Tyr Ile Asn Thr His Thr Leu Gly Glu Phe Gln Thr Gly Glu Gln Ala
150                 155                 160                 165

gag ctt gcc acg att act ttt gcc aaa gct cca gac ctc acc tct aat   643
Glu Leu Ala Thr Ile Thr Phe Ala Lys Ala Pro Asp Leu Thr Ser Asn
                170                 175                 180

tca gtc aac gtg act ggc gat gtg gca ttg act gct gat ggt gtg gaa   691
Ser Val Asn Val Thr Gly Asp Val Ala Leu Thr Ala Asp Gly Val Glu
            185                 190                 195

gtt ttc ggt ggt ttc tac acg gca ggg gag gag                      724
Val Phe Gly Gly Phe Tyr Thr Ala Gly Glu Glu
        200                 205
```

20050176090

<210> 2758
<211> 208
<212> PRT
<213> Corynebacterium glutamicum

<400> 2758

```
Met Asn Arg Phe Pro Ser Ala Leu Leu Ala Ala Ser Val Ala Gly Ala
  1               5                  10                  15

Ala Leu Ala Ile Pro Ala Thr Ser Ala His Ala Ala Glu Ser Ile Cys
            20                  25                  30
```

```
Thr Phe Thr Gly Asp Val Gly Trp Asn Val Arg Asp Ser Phe Asn Ser
         35                  40                  45

Tyr Leu Leu Gly Asn Ile Ala Asn Gly Ser Ala Tyr Lys Tyr Lys Gly
     50                  55                  60

Gly Leu Asp Val Arg Asp Gly Val Gln Thr Asp Gly Asn Gly Lys Thr
 65                  70                  75                  80

Pro Ala Leu Thr Trp Pro Val Asp Ser Val Thr Ser Ser Lys Ile Ser
                 85                  90                  95

Thr Ser Gly Gly Ala His Trp Thr Gly His Asn Leu Tyr Pro Gly Asp
            100                 105                 110

Asp Leu Ala Glu Val Pro Asn Asn Phe Thr Leu Asp Leu Asp Phe Ser
        115                 120                 125

Asn Ile Thr Val Glu Leu Ser Gly Ser Thr Gly Arg Leu Leu Val Asp
    130                 135                 140

Tyr Thr Ser Arg Glu Tyr Ile Asn Thr His Thr Leu Gly Glu Phe Gln
145                 150                 155                 160

Thr Gly Glu Gln Ala Glu Leu Ala Thr Ile Thr Phe Ala Lys Ala Pro
                165                 170                 175

Asp Leu Thr Ser Asn Ser Val Asn Val Thr Gly Asp Val Ala Leu Thr
            180                 185                 190

Ala Asp Gly Val Glu Val Phe Gly Gly Phe Tyr Thr Ala Gly Glu Glu
        195                 200                 205
```

<210> 2759
<211> 2691
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2668)
<223> RXA02495

<400> 2759

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aaggaggaaa attatcaccg tcttaaaaac ggctaaggct tttctaaatt cgccgctgcg 60

caccatcacg tggcgcagcg ttgtggcgaa taaactccgc atg gca tta aca gtg   115
                                          Met Ala Leu Thr Val
                                            1               5

ctt tcg gtt gtg cta gga acc gca ttt ttg tgt ggc tcc ctc ctc ctc   163
Leu Ser Val Val Leu Gly Thr Ala Phe Leu Cys Gly Ser Leu Leu Leu
                 10                  15                  20

aca cat tcc ctt gaa aga aca ttt tcc tcc atc gtt gat gcc ggc gtg   211
Thr His Ser Leu Glu Arg Thr Phe Ser Ser Ile Val Asp Ala Gly Val
```

```
                25                  30                  35

gag ggc gtt gac gtg ggc gtt atc gcg caa caa aac aac ccc gac ggc   259
Glu Gly Val Asp Val Gly Val Ile Ala Gln Gln Asn Asn Pro Asp Gly
          40                  45                  50

gta cct ttc tcc gtc atc gcc gaa att gag cag tat ccg gaa gtc cgc   307
Val Pro Phe Ser Val Ile Ala Glu Ile Glu Gln Tyr Pro Glu Val Arg
     55                  60                  65

gcc gtc aac atc atc ggc gac ggc ccc ggc atg ccc tcc ggc acc acc   355
Ala Val Asn Ile Ile Gly Asp Gly Pro Gly Met Pro Ser Gly Thr Thr
 70                  75                  80                  85

atg acc ggc caa tcc gcg ctg atc ctc acc gac tcc gac ggc aat ccc   403
Met Thr Gly Gln Ser Ala Leu Ile Leu Thr Asp Ser Asp Gly Asn Pro
                 90                  95                 100

ctg caa gca ggc agc tcc ggc acg cac ccg cta gcc att tat ccg cag   451
Leu Gln Ala Gly Ser Ser Gly Thr His Pro Leu Ala Ile Tyr Pro Gln
            105                 110                 115

ggc gag tgg gtc tcg ccc gag cca acg ctt atc gac ggc cac ttc ccc   499
Gly Glu Trp Val Ser Pro Glu Pro Thr Leu Ile Asp Gly His Phe Pro
        120                 125                 130

aca aaa ccc gac gag gta gta gtc aac gct tcg gcc gcc aaa cgt ggc   547
Thr Lys Pro Asp Glu Val Val Val Asn Ala Ser Ala Ala Lys Arg Gly
    135                 140                 145

ggg ctc tcc ctc ggt gat cac cta acg atc gtc aca ccc acc gaa cgc   595
Gly Leu Ser Leu Gly Asp His Leu Thr Ile Val Thr Pro Thr Glu Arg
150                 155                 160                 165

atc gac gcc acc ctg tct gga acc ttc gaa tca aac acc gac gtc gca   643
Ile Asp Ala Thr Leu Ser Gly Thr Phe Glu Ser Asn Thr Asp Val Ala
                170                 175                 180

ggc tgg gtc gga gtc gga ttc acc cca cag cgc tac gtc gaa ctg ctc   691
Gly Trp Val Gly Val Gly Phe Thr Pro Gln Arg Tyr Val Glu Leu Leu
            185                 190                 195

acc aac ggc acc gac gcc agc caa atc acc atc gca gtc aac gac ggc   739
Thr Asn Gly Thr Asp Ala Ser Gln Ile Thr Ile Ala Val Asn Asp Gly
        200                 205                 210

gcc gac ccc atg gca gtc cgc aac cgc atc ggc aaa aac cac cgg gac   787
Ala Asp Pro Met Ala Val Arg Asn Arg Ile Gly Lys Asn His Arg Asp
    215                 220                 225

ctg ctg ccc ctg ctg ccc gag caa atc atc gac caa acc acc ggc gac   835
Leu Leu Pro Leu Leu Pro Glu Gln Ile Ile Asp Gln Thr Thr Gly Asp
230                 235                 240                 245

acc gac cgc caa ctg gag ttc atg acc tac gtg ctc ctg gca ttc gcc   883
Thr Asp Arg Gln Leu Glu Phe Met Thr Tyr Val Leu Leu Ala Phe Ala
                250                 255                 260

gcg atc gca ctg att gtt ggc tcg ttc atc att gcc aac acc ttc gcg   931
Ala Ile Ala Leu Ile Val Gly Ser Phe Ile Ile Ala Asn Thr Phe Ala
            265                 270                 275
```

```
atg atc gtc gcc caa cgc acc ggc gaa ttc gcc ctc ctc cgt tcc att   979
Met Ile Val Ala Gln Arg Thr Gly Glu Phe Ala Leu Leu Arg Ser Ile
        280                 285                 290

ggt gtc tcc acg ttc caa atc gga ttc tcc gtg att atg gaa gca gta   1027
Gly Val Ser Thr Phe Gln Ile Gly Phe Ser Val Ile Met Glu Ala Val
    295                 300                 305

ttc gtc gga ctt atc ggc ggt ttc atc ggc atc gca gtt ggc ttc gga   1075
Phe Val Gly Leu Ile Gly Gly Phe Ile Gly Ile Ala Val Gly Phe Gly
310                 315                 320                 325

gtg gtc aat gca ctt gtc caa gtg ctc aac caa ttc ggc gac acc ctc   1123
Val Val Asn Ala Leu Val Gln Val Leu Asn Gln Phe Gly Asp Thr Leu
                330                 335                 340

tcc tcc atc gac atc acc tac aac gcc gga tcc ttc atc ttc cct gtc   1171
Ser Ser Ile Asp Ile Thr Tyr Asn Ala Gly Ser Phe Ile Phe Pro Val
            345                 350                 355

ctc ttc gcc gtc act gcc acc gta cta agc tcc ata tcg cct gct cac   1219
Leu Phe Ala Val Thr Ala Thr Val Leu Ser Ser Ile Ser Pro Ala His
        360                 365                 370

cgc gcc ggt aac ctc cca cca gtc caa gca ttc gaa tcc tcc gat gca   1267
Arg Ala Gly Asn Leu Pro Pro Val Gln Ala Phe Glu Ser Ser Asp Ala
    375                 380                 385

cgc agc gac gcc ctc gga agg atc cgc ttc ctc gtc gcc gcc gtc atg   1315
Arg Ser Asp Ala Leu Gly Arg Ile Arg Phe Leu Val Ala Ala Val Met
390                 395                 400                 405

ctc acc ctt gga atc agc ctg acg atc gca ggt gcc gtg gta tcc gcc   1363
Leu Thr Leu Gly Ile Ser Leu Thr Ile Ala Gly Ala Val Val Ser Ala
                410                 415                 420

atc aac gga gat gaa ttc aaa aca gaa aca cgc ctc gca ttc atc ggc   1411
Ile Asn Gly Asp Glu Phe Lys Thr Glu Thr Arg Leu Ala Phe Ile Gly
            425                 430                 435

gct gga ctt ctc tta gtg ttc ttc tca ctc tcc ctg tcc ggt ccc gca   1459
Ala Gly Leu Leu Leu Val Phe Phe Ser Leu Ser Leu Ser Gly Pro Ala
        440                 445                 450

ctg atg gtg gcg acc tct cag act ctt ggc gtg gcg ata atg tcg ccg   1507
Leu Met Val Ala Thr Ser Gln Thr Leu Gly Val Ala Ile Met Ser Pro
    455                 460                 465

ttc cga gcc gtc ggc aag ctc gca caa cgc aac acc ctg cgc aat ccg   1555
Phe Arg Ala Val Gly Lys Leu Ala Gln Arg Asn Thr Leu Arg Asn Pro
470                 475                 480                 485

cga cgc tcc gca acc acc gca ctg gcc gtc act ttg agc gtt ggc ctc   1603
Arg Arg Ser Ala Thr Thr Ala Leu Ala Val Thr Leu Ser Val Gly Leu
                490                 495                 500

gtc gcc tgc gtt gga gtc atc ggc gcc acc acc cgc gcc agc gtc ttc   1651
Val Ala Cys Val Gly Val Ile Gly Ala Thr Thr Arg Ala Ser Val Phe
            505                 510                 515
```

```
ggg tcc atg gaa tcc acc atc aaa tcc cca tat gtc ctc gac agc atc   1699
Gly Ser Met Glu Ser Thr Ile Lys Ser Pro Tyr Val Leu Asp Ser Ile
        520                 525                 530

ggt ggc acc atg atc cct gga caa ccc gcc ggc ggt tca agg tca ctg   1747
Gly Gly Thr Met Ile Pro Gly Gln Pro Ala Gly Gly Ser Arg Ser Leu
    535                 540                 545

tcc atg tcc gca gcc gtc gca cag gaa atc gca caa acc cgc gga gtc   1795
Ser Met Ser Ala Ala Val Ala Gln Glu Ile Ala Gln Thr Arg Gly Val
550                 555                 560                 565

ggc aaa gtg ggc acc ctc atg acc ggc agc gtc caa gtc aac gga tgg   1843
Gly Lys Val Gly Thr Leu Met Thr Gly Ser Val Gln Val Asn Gly Trp
                570                 575                 580

gac aac gaa aac acc aca att ttc gac ggc gac ctc tct cag ttc ctc   1891
Asp Asn Glu Asn Thr Thr Ile Phe Asp Gly Asp Leu Ser Gln Phe Leu
            585                 590                 595

gac ctc gca gtc cgc tcc ggc gac gcc ttc gac gac gaa acc ccc ggc   1939
Asp Leu Ala Val Arg Ser Gly Asp Ala Phe Asp Asp Glu Thr Pro Gly
        600                 605                 610

gtc atg atc tcc acc acc tac gcc gac caa tcc gac ctc gaa gta ggc   1987
Val Met Ile Ser Thr Thr Tyr Ala Asp Gln Ser Asp Leu Glu Val Gly
    615                 620                 625

gac acc gtc acc gtc aac ccc tac gga tcc gac gac ggc atc cgc gtc   2035
Asp Thr Val Thr Val Asn Pro Tyr Gly Ser Asp Asp Gly Ile Arg Val
630                 635                 640                 645

ccc atc acc ggc atc tac gca gaa acc aac ctc gtc gga cac ctc atg   2083
Pro Ile Thr Gly Ile Tyr Ala Glu Thr Asn Leu Val Gly His Leu Met
                650                 655                 660

gtc aac gca gcc gcc acc aac cga gtc ctc acc tcc gcg gac acc tac   2131
Val Asn Ala Ala Ala Thr Asn Arg Val Leu Thr Ser Ala Asp Thr Tyr
            665                 670                 675

cac cgg tcc caa atc ttc gtc aac ggc gac ggc tcc acc acc aac gaa   2179
His Arg Ser Gln Ile Phe Val Asn Gly Asp Gly Ser Thr Thr Asn Glu
        680                 685                 690

gaa ctc cgc gac atc ctc gtc gac gcc gta gcc ccc ttc ctc atc gtc   2227
Glu Leu Arg Asp Ile Leu Val Asp Ala Val Ala Pro Phe Leu Ile Val
    695                 700                 705

caa gtg aaa tcc aaa gat gaa ttc cgc gga agc ctc ggc acc caa atc   2275
Gln Val Lys Ser Lys Asp Glu Phe Arg Gly Ser Leu Gly Thr Gln Ile
710                 715                 720                 725

aac caa ttg ctc ggc atc atc tac gga ctg ctc gcc ctg gca gtg atc   2323
Asn Gln Leu Leu Gly Ile Ile Tyr Gly Leu Leu Ala Leu Ala Val Ile
                730                 735                 740

atc gca gtc ctg gga atc gtc aac aca ctg ttc ctc tcc atc agc gaa   2371
Ile Ala Val Leu Gly Ile Val Asn Thr Leu Phe Leu Ser Ile Ser Glu
            745                 750                 755

cgc acc cgc gaa atc gga atc ctc cgc gcc acc ggc gtc caa cga gga   2419
```

```
Arg Thr Arg Glu Ile Gly Ile Leu Arg Ala Thr Gly Val Gln Arg Gly
        760                 765                 770

caa atc cgc cgc atg att acc ctc gaa tcc gtc atc ctc tcc atc cac   2467
Gln Ile Arg Arg Met Ile Thr Leu Glu Ser Val Ile Leu Ser Ile His
    775                 780                 785

ggc gca atc cac gga ctc ctc cta ggt aca ttt atc ggc tgg gca atc   2515
Gly Ala Ile His Gly Leu Leu Leu Gly Thr Phe Ile Gly Trp Ala Ile
790                 795                 800                 805

gtc agt tgt ctc cgc acc cga ggc atg gca ccc gtc gaa ttc ccc tgg   2563
Val Ser Cys Leu Arg Thr Arg Gly Met Ala Pro Val Glu Phe Pro Trp
                810                 815                 820

acc caa atc gga tta atg ctc atc tcc gca atc atc atc gga ggc ata   2611
Thr Gln Ile Gly Leu Met Leu Ile Ser Ala Ile Ile Ile Gly Gly Ile
            825                 830                 835

gca gcc ctc atc cca gcc aac cga gcc tcc cga atc tcc cct ttg gaa   2659
Ala Ala Leu Ile Pro Ala Asn Arg Ala Ser Arg Ile Ser Pro Leu Glu
        840                 845                 850

gca atc aac taacagtctg catcggcaac ctc                            2691
Ala Ile Asn
    855
```

<210> 2760
<211> 856
<212> PRT
<213> Corynebacterium glutamicum

<400> 2760

```
Met Ala Leu Thr Val Leu Ser Val Val Leu Gly Thr Ala Phe Leu Cys
  1               5                  10                  15

Gly Ser Leu Leu Leu Thr His Ser Leu Glu Arg Thr Phe Ser Ser Ile
            20                  25                  30

Val Asp Ala Gly Val Glu Gly Val Asp Val Gly Val Ile Ala Gln Gln
        35                  40                  45

Asn Asn Pro Asp Gly Val Pro Phe Ser Val Ile Ala Glu Ile Glu Gln
    50                  55                  60

Tyr Pro Glu Val Arg Ala Val Asn Ile Ile Gly Asp Gly Pro Gly Met
65                  70                  75                  80

Pro Ser Gly Thr Thr Met Thr Gly Gln Ser Ala Leu Ile Leu Thr Asp
                85                  90                  95

Ser Asp Gly Asn Pro Leu Gln Ala Gly Ser Ser Gly Thr His Pro Leu
            100                 105                 110

Ala Ile Tyr Pro Gln Gly Glu Trp Val Ser Pro Glu Pro Thr Leu Ile
        115                 120                 125

Asp Gly His Phe Pro Thr Lys Pro Asp Glu Val Val Val Asn Ala Ser
    130                 135                 140
```

```
Ala Ala Lys Arg Gly Gly Leu Ser Leu Gly Asp His Leu Thr Ile Val
145                 150                 155                 160

Thr Pro Thr Glu Arg Ile Asp Ala Thr Leu Ser Gly Thr Phe Glu Ser
                165                 170                 175

Asn Thr Asp Val Ala Gly Trp Val Gly Val Gly Phe Thr Pro Gln Arg
            180                 185                 190

Tyr Val Glu Leu Leu Thr Asn Gly Thr Asp Ala Ser Gln Ile Thr Ile
        195                 200                 205

Ala Val Asn Asp Gly Ala Asp Pro Met Ala Val Arg Asn Arg Ile Gly
    210                 215                 220

Lys Asn His Arg Asp Leu Leu Pro Leu Leu Pro Glu Gln Ile Ile Asp
225                 230                 235                 240

Gln Thr Thr Gly Asp Thr Asp Arg Gln Leu Glu Phe Met Thr Tyr Val
                245                 250                 255

Leu Leu Ala Phe Ala Ala Ile Ala Leu Ile Val Gly Ser Phe Ile Ile
            260                 265                 270

Ala Asn Thr Phe Ala Met Ile Val Ala Gln Arg Thr Gly Glu Phe Ala
        275                 280                 285

Leu Leu Arg Ser Ile Gly Val Ser Thr Phe Gln Ile Gly Phe Ser Val
    290                 295                 300

Ile Met Glu Ala Val Phe Val Gly Leu Ile Gly Gly Phe Ile Gly Ile
305                 310                 315                 320

Ala Val Gly Phe Gly Val Val Asn Ala Leu Val Gln Val Leu Asn Gln
                325                 330                 335

Phe Gly Asp Thr Leu Ser Ser Ile Asp Ile Thr Tyr Asn Ala Gly Ser
            340                 345                 350

Phe Ile Phe Pro Val Leu Phe Ala Val Thr Ala Thr Val Leu Ser Ser
        355                 360                 365

Ile Ser Pro Ala His Arg Ala Gly Asn Leu Pro Pro Val Gln Ala Phe
    370                 375                 380

Glu Ser Ser Asp Ala Arg Ser Asp Ala Leu Gly Arg Ile Arg Phe Leu
385                 390                 395                 400

Val Ala Ala Val Met Leu Thr Leu Gly Ile Ser Leu Thr Ile Ala Gly
                405                 410                 415

Ala Val Val Ser Ala Ile Asn Gly Asp Glu Phe Lys Thr Glu Thr Arg
            420                 425                 430

Leu Ala Phe Ile Gly Ala Gly Leu Leu Leu Val Phe Phe Ser Leu Ser
        435                 440                 445

Leu Ser Gly Pro Ala Leu Met Val Ala Thr Ser Gln Thr Leu Gly Val
    450                 455                 460

Ala Ile Met Ser Pro Phe Arg Ala Val Gly Lys Leu Ala Gln Arg Asn
```

```
465                 470                 475                 480

Thr Leu Arg Asn Pro Arg Arg Ser Ala Thr Thr Ala Leu Ala Val Thr
                485                 490                 495

Leu Ser Val Gly Leu Val Ala Cys Val Gly Val Ile Gly Ala Thr Thr
            500                 505                 510

Arg Ala Ser Val Phe Gly Ser Met Glu Ser Thr Ile Lys Ser Pro Tyr
        515                 520                 525

Val Leu Asp Ser Ile Gly Gly Thr Met Ile Pro Gly Gln Pro Ala Gly
    530                 535                 540

Gly Ser Arg Ser Leu Ser Met Ser Ala Ala Val Ala Gln Glu Ile Ala
545                 550                 555                 560

Gln Thr Arg Gly Val Gly Lys Val Gly Thr Leu Met Thr Gly Ser Val
                565                 570                 575

Gln Val Asn Gly Trp Asp Asn Glu Asn Thr Thr Ile Phe Asp Gly Asp
            580                 585                 590

Leu Ser Gln Phe Leu Asp Leu Ala Val Arg Ser Gly Asp Ala Phe Asp
        595                 600                 605

Asp Glu Thr Pro Gly Val Met Ile Ser Thr Thr Tyr Ala Asp Gln Ser
    610                 615                 620

Asp Leu Glu Val Gly Asp Thr Val Thr Val Asn Pro Tyr Gly Ser Asp
625                 630                 635                 640

Asp Gly Ile Arg Val Pro Ile Thr Gly Ile Tyr Ala Glu Thr Asn Leu
                645                 650                 655

Val Gly His Leu Met Val Asn Ala Ala Ala Thr Asn Arg Val Leu Thr
            660                 665                 670

Ser Ala Asp Thr Tyr His Arg Ser Gln Ile Phe Val Asn Gly Asp Gly
        675                 680                 685

Ser Thr Thr Asn Glu Glu Leu Arg Asp Ile Leu Val Asp Ala Val Ala
    690                 695                 700

Pro Phe Leu Ile Val Gln Val Lys Ser Lys Asp Glu Phe Arg Gly Ser
705                 710                 715                 720

Leu Gly Thr Gln Ile Asn Gln Leu Leu Gly Ile Ile Tyr Gly Leu Leu
                725                 730                 735

Ala Leu Ala Val Ile Ile Ala Val Leu Gly Ile Val Asn Thr Leu Phe
            740                 745                 750

Leu Ser Ile Ser Glu Arg Thr Arg Glu Ile Gly Ile Leu Arg Ala Thr
        755                 760                 765

Gly Val Gln Arg Gly Gln Ile Arg Arg Met Ile Thr Leu Glu Ser Val
    770                 775                 780

Ile Leu Ser Ile His Gly Ala Ile His Gly Leu Leu Leu Gly Thr Phe
785                 790                 795                 800
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Ile Gly Trp Ala Ile Val Ser Cys Leu Arg Thr Arg Gly Met Ala Pro
                805                 810                 815

Val Glu Phe Pro Trp Thr Gln Ile Gly Leu Met Leu Ile Ser Ala Ile
            820                 825                 830

Ile Ile Gly Gly Ile Ala Ala Leu Ile Pro Ala Asn Arg Ala Ser Arg
        835                 840                 845

Ile Ser Pro Leu Glu Ala Ile Asn
    850                 855


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<213> Corynebacterium glutamicum

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<222> (101)..(907)
<223> RXA02496

<400> 2761
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atctcacacc taaaggttag acggtctagg gtggcaaagt gtg aat cgg tca aat   115
                                          Val Asn Arg Ser Asn
                                            1               5

tct tct tcg gta ttt tta ggt ttc ccc gag tct tcg cca gcg gcg gca   163
Ser Ser Ser Val Phe Leu Gly Phe Pro Glu Ser Ser Pro Ala Ala Ala
                10                  15                  20

tcg att cgt gct ggg gag gaa ctc cct ctt gat ttc cca cgt gaa tgg   211
Ser Ile Arg Ala Gly Glu Glu Leu Pro Leu Asp Phe Pro Arg Glu Trp
            25                  30                  35

tat gaa ttc acg gat cca act gat att gag cat gta ttt agc atc gat   259
Tyr Glu Phe Thr Asp Pro Thr Asp Ile Glu His Val Phe Ser Ile Asp
        40                  45                  50

tta acg tgg ctt gag tct aat tgg aat tgc acc ttt ggt acc ccc gat   307
Leu Thr Trp Leu Glu Ser Asn Trp Asn Cys Thr Phe Gly Thr Pro Asp
    55                  60                  65

tgt tta ggt att gat tcc gaa aac gcc gac gtg ggt tgt tgc ggc cac   355
Cys Leu Gly Ile Asp Ser Glu Asn Ala Asp Val Gly Cys Cys Gly His
70                  75                  80                  85

ggt gca ttc tta gca gat gag aca gat cga gat cag ctt tat gat gcc   403
Gly Ala Phe Leu Ala Asp Glu Thr Asp Arg Asp Gln Leu Tyr Asp Ala
                90                  95                  100

gtt gct cag atg ccc gct aag tat tgg cag cta cgc ccc gcc tcc acg   451
Val Ala Gln Met Pro Ala Lys Tyr Trp Gln Leu Arg Pro Ala Ser Thr
            105                 110                 115

gac tcg ttt tta gca tcc gat gac ggc acc gac att gag ccg tgg ctg   499
Asp Ser Phe Leu Ala Ser Asp Asp Gly Thr Asp Ile Glu Pro Trp Leu
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        120                 125                 130

aca tgg gat gaa tta gat gat gaa gac ggc aat ccc gag ccc gct ttg   547
Thr Trp Asp Glu Leu Asp Asp Glu Asp Gly Asn Pro Glu Pro Ala Leu
    135                 140                 145

aag aca act gtg gtc aac ggc gcc tgt att ttt gcc aac agg gcg ggt   595
Lys Thr Thr Val Val Asn Gly Ala Cys Ile Phe Ala Asn Arg Ala Gly
150                 155                 160                 165

tgg gaa aca ggc gcg ggg tgt gcg ctg cat cag tgg ggc gtg aac gca   643
Trp Glu Thr Gly Ala Gly Cys Ala Leu His Gln Trp Gly Val Asn Ala
                170                 175                 180

aat gag gat cta acc gtc gtc aag cct gaa gtt tgt tgg cag ctc ccg   691
Asn Glu Asp Leu Thr Val Val Lys Pro Glu Val Cys Trp Gln Leu Pro
            185                 190                 195

ctg cgc cgc ctg gag gcc tgg gaa gag cgc ccc gac ggg caa gaa atc   739
Leu Arg Arg Leu Glu Ala Trp Glu Glu Arg Pro Asp Gly Gln Glu Ile
        200                 205                 210

ttg cgc acc aca att act gaa tac aac cgg cgc ggc tgg ggc aac ggc   787
Leu Arg Thr Thr Ile Thr Glu Tyr Asn Arg Arg Gly Trp Gly Asn Gly
    215                 220                 225

ggc gag gat ttc gac tgg tac tgc acc acc tct ccg cgc tgc cac acc   835
Gly Glu Asp Phe Asp Trp Tyr Cys Thr Thr Ser Pro Arg Cys His Thr
230                 235                 240                 245

aat gcc gaa ccc atg tgg aaa aca cag gaa aca gaa ctc cgt gca ctc   883
Asn Ala Glu Pro Met Trp Lys Thr Gln Glu Thr Glu Leu Arg Ala Leu
                250                 255                 260

atg gga cca aac tcc tac gag gtg tgacgtaaat atttggaagc acg         930
Met Gly Pro Asn Ser Tyr Glu Val
            265
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<210> 2762
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<212> PRT
<213> Corynebacterium glutamicum

<400> 2762

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Val Asn Arg Ser Asn Ser Ser Ser Val Phe Leu Gly Phe Pro Glu Ser
  1               5                  10                  15

Ser Pro Ala Ala Ala Ser Ile Arg Ala Gly Glu Glu Leu Pro Leu Asp
             20                  25                  30

Phe Pro Arg Glu Trp Tyr Glu Phe Thr Asp Pro Thr Asp Ile Glu His
         35                  40                  45

Val Phe Ser Ile Asp Leu Thr Trp Leu Glu Ser Asn Trp Asn Cys Thr
     50                  55                  60

Phe Gly Thr Pro Asp Cys Leu Gly Ile Asp Ser Glu Asn Ala Asp Val
 65                  70                  75                  80

Gly Cys Cys Gly His Gly Ala Phe Leu Ala Asp Glu Thr Asp Arg Asp
```

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                 85                  90                  95

Gln Leu Tyr Asp Ala Val Ala Gln Met Pro Ala Lys Tyr Trp Gln Leu
            100                 105                 110

Arg Pro Ala Ser Thr Asp Ser Phe Leu Ala Ser Asp Asp Gly Thr Asp
        115                 120                 125

Ile Glu Pro Trp Leu Thr Trp Asp Glu Leu Asp Asp Glu Asp Gly Asn
    130                 135                 140

Pro Glu Pro Ala Leu Lys Thr Thr Val Val Asn Gly Ala Cys Ile Phe
145                 150                 155                 160

Ala Asn Arg Ala Gly Trp Glu Thr Gly Ala Gly Cys Ala Leu His Gln
                165                 170                 175

Trp Gly Val Asn Ala Asn Glu Asp Leu Thr Val Val Lys Pro Glu Val
            180                 185                 190

Cys Trp Gln Leu Pro Leu Arg Arg Leu Glu Ala Trp Glu Glu Arg Pro
        195                 200                 205

Asp Gly Gln Glu Ile Leu Arg Thr Thr Ile Thr Glu Tyr Asn Arg Arg
    210                 215                 220

Gly Trp Gly Asn Gly Gly Glu Asp Phe Asp Trp Tyr Cys Thr Thr Ser
225                 230                 235                 240

Pro Arg Cys His Thr Asn Ala Glu Pro Met Trp Lys Thr Gln Glu Thr
                245                 250                 255

Glu Leu Arg Ala Leu Met Gly Pro Asn Ser Tyr Glu Val
            260                 265
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CCTGAGCCAACTATTGATGTGACATCCATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCAATGCCGATATCCTGCCGATCACCGGTGCCGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACAGTTACCGCATAACCTGACGTTTATGCGCCGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCAAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCGGGTACCGAGCTCGAATTCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTTCAAGAATTCTCATGTTTGACAGCTTATCATCGATAAGCTTTAATGCGGTAGTTTATCACAGTTAAATTGCTAACGCAGTCAGGCACCGTGTATGAAATCTAACAATGCGCTCATCGTCATCCTCGGCACCGTCACCCTGGATGCTGTAGGCATAGGCTTGGTTATGCCGGTACTGCCGGGCCTCTTGCGGGATATCGTCCATTCCGACAGCATCGCCAGTCACTATGGCGTGCTGCTAGCGCTATATGCGTTGATGCAATTTCTATGCGCACCCGTTCTCGGAGCACTGTCCGACCGCTTTGGCCGCCGCCCAGTCCTGCTCGCTTCGCTACTTGGAGCCACTATCGACTACGCGATCATGGCGACCACACCCGTCCTGTGGATCTATCGAATCTAAATGTAAGTTAAAATCTCTAAAATCGTGTTATCTACAATAACTATGCGGGCATCAAAGCAGATTACTTCGCGCTGTTTAAAGGACAATCAACTTTCACAACGTGGAGCCGCCAGCAACACAGGGGCGCAGGTGATGCCGGCGCACATCGCCATTCCGGATGAGCATTCATCAGGCGGGCAAGAATGTGAATAAAGGCCGGATAAAACTTGTGCTTATTTTTCTTTACGGTCTTTAAAAAGGCCGTAATATCCAGCTGAACGGTCTGGTTATAGGTACATTGAGCAACTGACTGAAATGCCTCAAAATGTTCTTTACGATGCCATTGGGATATATCAACGGTGGTATATCCAGTGATTTTTTTCTCCATTTTAGCTTCCTTAGCTCCTGAAAATCTCGATAACTCAAAAAATACGCCCGGTAGTGATCTTATTTCATTATGGTGAAAGTTGGAACCTCTTACGTGCCGATCAACGTCTCATTTTCGCCAAAAGTTGGCCCAGGGCTTCCCGGTATCAACAGGGACACCAGGATTTATTTATTCTGCGAAGTGATCTTCCGTCACAGGTATTTATTCGGCGCAAAGTGCGTCGGGTGATGCTGCCAACTTACTGATTTAGTGTATGATGGTGTTTTTGAGGTGCTCCAGTGGCTTCTGTTTCTATCAGCTGTCCCTCCTGTTCAGCTACTGACGGGGTGGTGCGTAACGGCAAAAGCACCGCCGGACATCAGCGCTAGCGGAGTGTATACTGGCTTACTATGTTGGCACTGATGAGGGTGTCAGTGAAGTGCTTCATGTGGCAGGAGAAAAAAGGCTGCACCGGTGCGTCAGCAGAATATGTGATACAGGATATATTCCGCTTCCTCGCTCACTGACTCGCTACGCTCGGTCGTTCGACTGCGGCGAGCGGAAATGGCTTACGAACGGGGCGGAGATTTCCTGGAAGATGCCAGGAAGATACTTAACAGGGAAGTGAGAGGGCCGCGGCAAAGC

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gta tcc gtt gct gag ctg acc ggc tcc att cct gcc gtt aag gaa aag   259
Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro Ala Val Lys Glu Lys
         40                  45                  50

ccc gcg gag tcc aag cac tcc agc gtg ccc atc gat gca cca gca gaa   307
Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile Asp Ala Pro Ala Glu
     55                  60                  65

cct gag gtt gtt gag gcc ccc aag cct gag ccc gcc gaa gaa gta gaa   355
Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro Ala Glu Glu Val Glu
 70                  75                  80                  85

gtg gct tcg gtg gag ggc gac gtc gat aag cag gaa acc cct gag cgt   403
Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln Glu Thr Pro Glu Arg
                 90                  95                 100

ccg gcg ccg agc aac gaa gaa acc atg gtg ctg cgc atc gtg gat gaa   451
Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu Arg Ile Val Asp Glu
            105                 110                 115

aaa gat cca att agc ttg acg acg ggc gcg ttc ccc gtg gtt ccg gca   499
Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe Pro Val Val Pro Ala
        120                 125                 130

gtt gcc gcc aag ccg gcg ccc gta gtg cgc gcg gag aag gac gcc gat   547
Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala Glu Lys Asp Ala Asp
    135                 140                 145

gtg gag act gcc gta aag gca gat ttc gca gag gtg gaa gtc gat aac   595
Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu Val Glu Val Asp Asn
150                 155                 160                 165

act gac acc acg cag atg gct gtg gtg gaa gaa gtt gac gag gag cca   643
Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu Val Asp Glu Glu Pro
                170                 175                 180

gag caa gaa aac aaa atg tcc gta ttc gcg atc atc atg atg gcg atc   691
Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile Ile Met Met Ala Ile
            185                 190                 195

gtc gga gtt gtt ctc ggt gtc gtt gta ttc ctc ggc ttt gaa atg ctg   739
Val Gly Val Val Leu Gly Val Val Val Phe Leu Gly Phe Glu Met Leu
        200                 205                 210

tgg gag cgc ctg aac aag tgg atc gtc gct gtt ctg gca gtc ggc gtg   787
Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val Leu Ala Val Gly Val
    215                 220                 225

acc ttg gga atg gtg ggc atc atc cac gct ttg cgc acc tca cgt gat   835
Thr Leu Gly Met Val Gly Ile Ile His Ala Leu Arg Thr Ser Arg Asp
230                 235                 240                 245

ggt ttc agc atg gtt ctc gca gga atc gtg ggc ctg gtc atg acg ttc   883
Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly Leu Val Met Thr Phe
                250                 255                 260

ggg ccg ctg gca atc gtc atg taatttgtcg ttttgggccc ccg             927
Gly Pro Leu Ala Ile Val Met
            265
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<213> Corynebacterium glutamicum

<400> 2764
Met Ser Glu Glu Lys Leu Thr Val Ala Glu Leu Met Ala Arg Ala Ala
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Lys Glu Gly Arg Ser Thr Asp Ala Pro Arg Arg Arg Arg Arg Arg Ser
20 25 30

Ile Glu Asp Gly Gly Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro
35 40 45

Ala Val Lys Glu Lys Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile
50 55 60

Asp Ala Pro Ala Glu Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro
65 70 75 80

Ala Glu Glu Val Glu Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln
85 90 95

Glu Thr Pro Glu Arg Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu
100 105 110

Arg Ile Val Asp Glu Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe
115 120 125

Pro Val Val Pro Ala Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala
130 135 140

Glu Lys Asp Ala Asp Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu
145 150 155 160

Val Glu Val Asp Asn Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu
165 170 175

Val Asp Glu Glu Pro Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile
180 185 190

Ile Met Met Ala Ile Val Gly Val Val Leu Gly Val Val Val Phe Leu
195 200 205

Gly Phe Glu Met Leu Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val
210 215 220

Leu Ala Val Gly Val Thr Leu Gly Met Val Gly Ile Ile His Ala Leu
225 230 235 240

Arg Thr Ser Arg Asp Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly
245 250 255

Leu Val Met Thr Phe Gly Pro Leu Ala Ile Val Met
260 265

<210> 2765
<211> 222
<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS
<222> (101)..(199)
<223> RXA02500

<400> 2765
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ttttgtacgt acaacatcga tttaagcgag ggaaaccgta atg ggt tct gtc atc 115
Met Gly Ser Val Ile
1 5

aag aag cgc cgc aag cgc atg tcc aag aag aag cac cgc aag atg ctg 163
Lys Lys Arg Arg Lys Arg Met Ser Lys Lys Lys His Arg Lys Met Leu
10 15 20

cgc cgt act cgt gtc cag cgt aga aaa ttg ggc aag taagccttca 209
Arg Arg Thr Arg Val Gln Arg Arg Lys Leu Gly Lys
25 30

attgagcttc aaa 222

<210> 2766
<211> 33
<212> PRT
<213> Corynebacterium glutamicum

<400> 2766
Met Gly Ser Val Ile Lys Lys Arg Arg Lys Arg Met Ser Lys Lys Lys
1 5 10 15

His Arg Lys Met Leu Arg Arg Thr Arg Val Gln Arg Arg Lys Leu Gly
20 25 30

Lys

<210> 2767
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<212> DNA
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<220>
<221> CDS
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<223> RXA02506

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cctttccctg aactctaagc aattgtgatc tatagtacaa atgcataaac attaaccgtg 60

atatccatct cttgcatacc ggccgaaagg tttagcacac atg cac ctc aat cag 115
Met His Leu Asn Gln
1 5

ctc gaa ttt ttc atc gca gta gcc caa cac gga cag atc aac cgc gcc 163
Leu Glu Phe Phe Ile Ala Val Ala Gln His Gly Gln Ile Asn Arg Ala
10 15 20

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gcc gaa gaa ctc ctc att tcc caa ccc gct ctc agc cga cag atc tcc   211
Ala Glu Glu Leu Leu Ile Ser Gln Pro Ala Leu Ser Arg Gln Ile Ser
             25                  30                  35

gca ctt gaa aaa tcc gtc gga gct cca ctc ttc gaa cgc cat tcc cgc   259
Ala Leu Glu Lys Ser Val Gly Ala Pro Leu Phe Glu Arg His Ser Arg
         40                  45                  50

ggt gtc tcc ctc aca aag gcc gga gaa atc ctc cac gaa gaa gcc ctc   307
Gly Val Ser Leu Thr Lys Ala Gly Glu Ile Leu His Glu Glu Ala Leu
     55                  60                  65

cga acg ctt agc agg atg caa tcg gta gtc gat gaa atc caa tcc ggt   355
Arg Thr Leu Ser Arg Met Gln Ser Val Val Asp Glu Ile Gln Ser Gly
 70                  75                  80                  85

gag cac ctc atc acc agc atc aac atc gga gtt ccc cct gga atc ccc   403
Glu His Leu Ile Thr Ser Ile Asn Ile Gly Val Pro Pro Gly Ile Pro
                 90                  95                 100

atc gac tgg ttg cgc tgc caa ctc atc gat tta ggc ccc gag acc cgc   451
Ile Asp Trp Leu Arg Cys Gln Leu Ile Asp Leu Gly Pro Glu Thr Arg
            105                 110                 115

att tca ctg atc gaa tcc ccc acc gat gat cag cta aaa ctt ctt aaa   499
Ile Ser Leu Ile Glu Ser Pro Thr Asp Asp Gln Leu Lys Leu Leu Lys
        120                 125                 130

caa cgc gaa ctc gac atc gcc ctt tgt cga cgc caa agc gag gcc ttt   547
Gln Arg Glu Leu Asp Ile Ala Leu Cys Arg Arg Gln Ser Glu Ala Phe
    135                 140                 145

gcc acc aca ctt gtc cac gaa caa gaa ctg gga atc gtc gtc cga aaa   595
Ala Thr Thr Leu Val His Glu Gln Glu Leu Gly Ile Val Val Arg Lys
150                 155                 160                 165

aac tcc gaa ctg cac caa aaa gtc gca gga aaa gac aac gcc aca ctc   643
Asn Ser Glu Leu His Gln Lys Val Ala Gly Lys Asp Asn Ala Thr Leu
                170                 175                 180

ttc gat ctt gaa ggg ctt cga gtc ctc gca cac tcc cgc ggt gaa gta   691
Phe Asp Leu Glu Gly Leu Arg Val Leu Ala His Ser Arg Gly Glu Val
            185                 190                 195

aga att cag gaa gaa atc ctc aaa aac gcc atg ctc gcc gca gga gtt   739
Arg Ile Gln Glu Glu Ile Leu Lys Asn Ala Met Leu Ala Ala Gly Val
        200                 205                 210

aat gcc acg tgg atc ttc cga aaa ttt ggg caa tat agc tca ctg atc   787
Asn Ala Thr Trp Ile Phe Arg Lys Phe Gly Gln Tyr Ser Ser Leu Ile
    215                 220                 225

gca gac ctt gtc cag gcc gat gtc gca ctc aca aca gag gaa tcc gcc   835
Ala Asp Leu Val Gln Ala Asp Val Ala Leu Thr Thr Glu Glu Ser Ala
230                 235                 240                 245

cgc acc aac ttc ccc agc tgg caa tgg gtc ccc atc gaa ggc gaa gac   883
Arg Thr Asn Phe Pro Ser Trp Gln Trp Val Pro Ile Glu Gly Glu Asp
                250                 255                 260
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gcc tcc gga aat gac ctt gtt gtt cgc acc tgg atc acc tgg aac ccc   931
Ala Ser Gly Asn Asp Leu Val Val Arg Thr Trp Ile Thr Trp Asn Pro
            265                 270                 275

caa ccc acc ccc gcg gtg aag gcc ctg atc cag aaa ttt att gac gga   979
Gln Pro Thr Pro Ala Val Lys Ala Leu Ile Gln Lys Phe Ile Asp Gly
        280                 285                 290

aac tgagttctaa acagccgcca tga                                    1005
Asn
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<210> 2768
<211> 294
<212> PRT
<213> Corynebacterium glutamicum

<400> 2768

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Met His Leu Asn Gln Leu Glu Phe Phe Ile Ala Val Ala Gln His Gly
  1               5                  10                  15

Gln Ile Asn Arg Ala Ala Glu Glu Leu Leu Ile Ser Gln Pro Ala Leu
             20                  25                  30

Ser Arg Gln Ile Ser Ala Leu Glu Lys Ser Val Gly Ala Pro Leu Phe
         35                  40                  45

Glu Arg His Ser Arg Gly Val Ser Leu Thr Lys Ala Gly Glu Ile Leu
     50                  55                  60

His Glu Glu Ala Leu Arg Thr Leu Ser Arg Met Gln Ser Val Val Asp
 65                  70                  75                  80

Glu Ile Gln Ser Gly Glu His Leu Ile Thr Ser Ile Asn Ile Gly Val
                 85                  90                  95

Pro Pro Gly Ile Pro Ile Asp Trp Leu Arg Cys Gln Leu Ile Asp Leu
            100                 105                 110

Gly Pro Glu Thr Arg Ile Ser Leu Ile Glu Ser Pro Thr Asp Asp Gln
        115                 120                 125

Leu Lys Leu Leu Lys Gln Arg Glu Leu Asp Ile Ala Leu Cys Arg Arg
    130                 135                 140

Gln Ser Glu Ala Phe Ala Thr Thr Leu Val His Glu Gln Glu Leu Gly
145                 150                 155                 160

Ile Val Val Arg Lys Asn Ser Glu Leu His Gln Lys Val Ala Gly Lys
                165                 170                 175

Asp Asn Ala Thr Leu Phe Asp Leu Glu Gly Leu Arg Val Leu Ala His
            180                 185                 190

Ser Arg Gly Glu Val Arg Ile Gln Glu Glu Ile Leu Lys Asn Ala Met
        195                 200                 205

Leu Ala Ala Gly Val Asn Ala Thr Trp Ile Phe Arg Lys Phe Gly Gln
    210                 215                 220
```

```
Tyr Ser Ser Leu Ile Ala Asp Leu Val Gln Ala Asp Val Ala Leu Thr
225                 230                 235                 240

Thr Glu Glu Ser Ala Arg Thr Asn Phe Pro Ser Trp Gln Trp Val Pro
                245                 250                 255

Ile Glu Gly Glu Asp Ala Ser Gly Asn Asp Leu Val Val Arg Thr Trp
            260                 265                 270

Ile Thr Trp Asn Pro Gln Pro Thr Pro Ala Val Lys Ala Leu Ile Gln
        275                 280                 285

Lys Phe Ile Asp Gly Asn
    290
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<210> 2769
<211> 860
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(837)
<223> RXA02514

<400> 2769

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aac tcc cac aac cca acc cca gta acc atc acg gtt act ggc aag ggt   48
Asn Ser His Asn Pro Thr Pro Val Thr Ile Thr Val Thr Gly Lys Gly
  1               5                  10                  15

gaa ggc gtt acc tct ttc ggc gca atc tcc atc gag gtt gaa gcg ggc   96
Glu Gly Val Thr Ser Phe Gly Ala Ile Ser Ile Glu Val Glu Ala Gly
            20                  25                  30

gca gac gct atc gtc gca ctg cag tac gtc gga tcc ggc acc cac gct   144
Ala Asp Ala Ile Val Ala Leu Gln Tyr Val Gly Ser Gly Thr His Ala
        35                  40                  45

gac aac gtc gaa ttc atc gtt ggc gac aac gca cgc ctg acc gtc atc   192
Asp Asn Val Glu Phe Ile Val Gly Asp Asn Ala Arg Leu Thr Val Ile
    50                  55                  60

acg gac acc cac tgg aac gct gac gca gtt cac ctg agc aac cag ctt   240
Thr Asp Thr His Trp Asn Ala Asp Ala Val His Leu Ser Asn Gln Leu
65                  70                  75                  80

gca cag ctg gga cgc gac gca act cta cgc cac acc gtg gca acc ttc   288
Ala Gln Leu Gly Arg Asp Ala Thr Leu Arg His Thr Val Ala Thr Phe
                85                  90                  95

ggt gga gaa gta gtc cgc atc gtc cca cgc gtg cgt ttc acc gca cca   336
Gly Gly Glu Val Val Arg Ile Val Pro Arg Val Arg Phe Thr Ala Pro
            100                 105                 110

ggt ggc gac gca gaa atg ctc ggc gtc tac ttc gca gat gat gga cag   384
Gly Gly Asp Ala Glu Met Leu Gly Val Tyr Phe Ala Asp Asp Gly Gln
        115                 120                 125

tac ttc gag cag cgc ctg ctg gtt gac cac gct gta cca aac tgt cgc   432
Tyr Phe Glu Gln Arg Leu Leu Val Asp His Ala Val Pro Asn Cys Arg
```

```
    130                 135                 140

tcc aac gtc ttg tac aag ggc gca ctt cag ggt gac aag aac tct gac   480
Ser Asn Val Leu Tyr Lys Gly Ala Leu Gln Gly Asp Lys Asn Ser Asp
145                 150                 155                 160

aag cca gat gcc cgt acc tgc tgg gtt ggc gat gtg ctc atc cgc tca   528
Lys Pro Asp Ala Arg Thr Cys Trp Val Gly Asp Val Leu Ile Arg Ser
                165                 170                 175

aac gcc cac ggc act gac acc tac gaa gct aac cgc tca ctc gtc ctc   576
Asn Ala His Gly Thr Asp Thr Tyr Glu Ala Asn Arg Ser Leu Val Leu
            180                 185                 190

acc gag ggt gca cgc gca gac gct att cca aac ctc gag att gaa acc   624
Thr Glu Gly Ala Arg Ala Asp Ala Ile Pro Asn Leu Glu Ile Glu Thr
        195                 200                 205

ggc cag atc gtt ggc gca gga cac gca gca acc gtc ggt cgt ttc gac   672
Gly Gln Ile Val Gly Ala Gly His Ala Ala Thr Val Gly Arg Phe Asp
    210                 215                 220

gac gag cac gtg ttc tac ctc cag gcc cgt ggt att cct gca gag gaa   720
Asp Glu His Val Phe Tyr Leu Gln Ala Arg Gly Ile Pro Ala Glu Glu
225                 230                 235                 240

gca cgc cgc ctc atc gtc cgc ggt ttc ttc aac gaa gtg atc aac aag   768
Ala Arg Arg Leu Ile Val Arg Gly Phe Phe Asn Glu Val Ile Asn Lys
                245                 250                 255

gtc cca gtt gaa tcc atc cgc ggg gaa ttg gac aac cga gtc agc tcg   816
Val Pro Val Glu Ser Ile Arg Gly Glu Leu Asp Asn Arg Val Ser Ser
            260                 265                 270

gaa ctc gca gtt ctt ggc atg taattaagcc aaagtaacta agc             860
Glu Leu Ala Val Leu Gly Met
        275
```

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<210> 2770
<211> 279
<212> PRT
<213> Corynebacterium glutamicum

<400> 2770

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Asn Ser His Asn Pro Thr Pro Val Thr Ile Thr Val Thr Gly Lys Gly
  1               5                  10                  15

Glu Gly Val Thr Ser Phe Gly Ala Ile Ser Ile Glu Val Glu Ala Gly
             20                  25                  30

Ala Asp Ala Ile Val Ala Leu Gln Tyr Val Gly Ser Gly Thr His Ala
         35                  40                  45

Asp Asn Val Glu Phe Ile Val Gly Asp Asn Ala Arg Leu Thr Val Ile
     50                  55                  60

Thr Asp Thr His Trp Asn Ala Asp Ala Val His Leu Ser Asn Gln Leu
 65                  70                  75                  80

Ala Gln Leu Gly Arg Asp Ala Thr Leu Arg His Thr Val Ala Thr Phe
```

```
                 85                  90                  95

Gly Gly Glu Val Val Arg Ile Val Pro Arg Val Arg Phe Thr Ala Pro
            100                 105                 110

Gly Gly Asp Ala Glu Met Leu Gly Val Tyr Phe Ala Asp Asp Gly Gln
        115                 120                 125

Tyr Phe Glu Gln Arg Leu Leu Val Asp His Ala Val Pro Asn Cys Arg
    130                 135                 140

Ser Asn Val Leu Tyr Lys Gly Ala Leu Gln Gly Asp Lys Asn Ser Asp
145                 150                 155                 160

Lys Pro Asp Ala Arg Thr Cys Trp Val Gly Asp Val Leu Ile Arg Ser
                165                 170                 175

Asn Ala His Gly Thr Asp Thr Tyr Glu Ala Asn Arg Ser Leu Val Leu
            180                 185                 190

Thr Glu Gly Ala Arg Ala Asp Ala Ile Pro Asn Leu Glu Ile Glu Thr
        195                 200                 205

Gly Gln Ile Val Gly Ala Gly His Ala Ala Thr Val Gly Arg Phe Asp
    210                 215                 220

Asp Glu His Val Phe Tyr Leu Gln Ala Arg Gly Ile Pro Ala Glu Glu
225                 230                 235                 240

Ala Arg Arg Leu Ile Val Arg Gly Phe Phe Asn Glu Val Ile Asn Lys
                245                 250                 255

Val Pro Val Glu Ser Ile Arg Gly Glu Leu Asp Asn Arg Val Ser Ser
            260                 265                 270

Glu Leu Ala Val Leu Gly Met
        275
```

US20050153417A1

<210> 2771
<211> 534
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> RXA02518

<400> 2771
cgcgtgaagt gcgcgctgct tgggtggaag gctttccagg cggcaaccgc tgacgctgtt 60

gcgcacgcac attagcccgc tgtattaatt ggaggaaacc atg agc gag cac acc 115
                                                Met Ser Glu His Thr
                                                  1   5

gag aac acg aca gag gtt gaa gac cag aac gct tcc acc ttt gaa gca 163
Glu Asn Thr Thr Glu Val Glu Asp Gln Asn Ala Ser Thr Phe Glu Ala
                 10   15   20

caa agc tct gag cgc cca gag cag tcc gag gca gac ctg gct aag gcc 211

```
Gln Ser Ser Glu Arg Pro Glu Gln Ser Glu Ala Asp Leu Ala Lys Ala
             25                  30                  35

agc gat gtt gag gag tac atg cgc gac gtt att gac cct gaa ctg ggc   259
Ser Asp Val Glu Glu Tyr Met Arg Asp Val Ile Asp Pro Glu Leu Gly
         40                  45                  50

att aac gtt gtt gac ctg ggc ctt gtc tac gat att tac atc atc aac   307
Ile Asn Val Val Asp Leu Gly Leu Val Tyr Asp Ile Tyr Ile Ile Asn
     55                  60                  65

ggc aac gaa gct cac atc gat atg act ctg act tca cca gct tgc ccg   355
Gly Asn Glu Ala His Ile Asp Met Thr Leu Thr Ser Pro Ala Cys Pro
 70                  75                  80                  85

ctg act gac gtc atc gaa gat cag gca cgc acc gca atc gtc ggc aac   403
Leu Thr Asp Val Ile Glu Asp Gln Ala Arg Thr Ala Ile Val Gly Asn
                 90                  95                 100

ggc att gca gag aag atg tcc ctg aac tgg gta tgg atg cca cct tgg   451
Gly Ile Ala Glu Lys Met Ser Leu Asn Trp Val Trp Met Pro Pro Trp
            105                 110                 115

ggt cca cac atg att acc gaa gag ggc cgc gct cag ctg cag gcc cta   499
Gly Pro His Met Ile Thr Glu Glu Gly Arg Ala Gln Leu Gln Ala Leu
        120                 125                 130

gga ttc gcg gtt taaaaggctg cttatcgacg cca                        534
Gly Phe Ala Val
    135


<210> 2772
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 2772
Met Ser Glu His Thr Glu Asn Thr Thr Glu Val Glu Asp Gln Asn Ala
  1               5                  10                  15

Ser Thr Phe Glu Ala Gln Ser Ser Glu Arg Pro Glu Gln Ser Glu Ala
             20                  25                  30

Asp Leu Ala Lys Ala Ser Asp Val Glu Glu Tyr Met Arg Asp Val Ile
         35                  40                  45

Asp Pro Glu Leu Gly Ile Asn Val Val Asp Leu Gly Leu Val Tyr Asp
     50                  55                  60

Ile Tyr Ile Ile Asn Gly Asn Glu Ala His Ile Asp Met Thr Leu Thr
 65                  70                  75                  80

Ser Pro Ala Cys Pro Leu Thr Asp Val Ile Glu Asp Gln Ala Arg Thr
                 85                  90                  95

Ala Ile Val Gly Asn Gly Ile Ala Glu Lys Met Ser Leu Asn Trp Val
            100                 105                 110

Trp Met Pro Pro Trp Gly Pro His Met Ile Thr Glu Glu Gly Arg Ala
        115                 120                 125
```

```
Gln Leu Gln Ala Leu Gly Phe Ala Val
    130                 135


<210> 2773
<211> 1566
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1543)
<223> RXA02521

<400> 2773
gcacacgcaa ccattggcaa caatcgcgga cggccacggc atctgcacaa caaatattgc 60

attgacaccc atcaaacact cctgatgaaa ggagcggatc atg act tcg gca acg   115
                                           Met Thr Ser Ala Thr
                                             1               5

acg aac cca ggg gtt aac gag ccc ttg acc gat gac cag atc att gaa   163
Thr Asn Pro Gly Val Asn Glu Pro Leu Thr Asp Asp Gln Ile Ile Glu
                 10                  15                  20

tcc atc ggt ccg tac aac tat ggt tgg cac gac tcc gac gac gct ggt   211
Ser Ile Gly Pro Tyr Asn Tyr Gly Trp His Asp Ser Asp Asp Ala Gly
             25                  30                  35

gca tcc gca cag cgt ggt ctc agc gag gat gtc gta cgc gac atc tct   259
Ala Ser Ala Gln Arg Gly Leu Ser Glu Asp Val Val Arg Asp Ile Ser
         40                  45                  50

gcg aag aag agc gag cca gaa tgg atg ctt cag cag cgc ctc aag gcc   307
Ala Lys Lys Ser Glu Pro Glu Trp Met Leu Gln Gln Arg Leu Lys Ala
     55                  60                  65

ctg agc att ttt gat aag aag cca gtt cca acc tgg ggt gca gac ctt   355
Leu Ser Ile Phe Asp Lys Lys Pro Val Pro Thr Trp Gly Ala Asp Leu
 70                  75                  80                  85

tca ggc att gac ttc gac aac att aaa tac ttc gtc cgc tcc act gag   403
Ser Gly Ile Asp Phe Asp Asn Ile Lys Tyr Phe Val Arg Ser Thr Glu
                 90                  95                 100

aag cag gca cag tcc tgg gag gat ctc cca gaa gac atc aag aat acc   451
Lys Gln Ala Gln Ser Trp Glu Asp Leu Pro Glu Asp Ile Lys Asn Thr
            105                 110                 115

tac gac aag ctg ggt att cct gag gcc gag aag cag cgc ctc gtt gca   499
Tyr Asp Lys Leu Gly Ile Pro Glu Ala Glu Lys Gln Arg Leu Val Ala
        120                 125                 130

ggt gtt gca gct cag tac gag tct gag gtt gtc tac cac cag atc cgc   547
Gly Val Ala Ala Gln Tyr Glu Ser Glu Val Val Tyr His Gln Ile Arg
    135                 140                 145

gag gac ctg gag gaa aag gga gtt atc ttc ctt gac acc gat acc gca   595
Glu Asp Leu Glu Glu Lys Gly Val Ile Phe Leu Asp Thr Asp Thr Ala
150                 155                 160                 165
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```
ctg aaa gag cac cct gag atc ttc cag gag tac ttc ggc acc gtc att   643
Leu Lys Glu His Pro Glu Ile Phe Gln Glu Tyr Phe Gly Thr Val Ile
                170                 175                 180

cca gca ggc gac aac aag ttc tcc gca ctg aac tcc gct gtc tgg tcc   691
Pro Ala Gly Asp Asn Lys Phe Ser Ala Leu Asn Ser Ala Val Trp Ser
            185                 190                 195

ggt gga tct ttc atc tac gtg cca aag ggt gtc cac gtg gac att cct   739
Gly Gly Ser Phe Ile Tyr Val Pro Lys Gly Val His Val Asp Ile Pro
        200                 205                 210

ctg cag gct tac ttc cgc atc aac acc gag aac atg ggt cag ttc gaa   787
Leu Gln Ala Tyr Phe Arg Ile Asn Thr Glu Asn Met Gly Gln Phe Glu
    215                 220                 225

cgc acc ctg atc atc gtt gat gag gat gcc tac gtt cac tac gtt gag   835
Arg Thr Leu Ile Ile Val Asp Glu Asp Ala Tyr Val His Tyr Val Glu
230                 235                 240                 245

ggc tgt acc gca cct att tac aag tcc gac tcc ctg cac tcc gca gtc   883
Gly Cys Thr Ala Pro Ile Tyr Lys Ser Asp Ser Leu His Ser Ala Val
                250                 255                 260

gtt gag atc atc gtg aag aag ggt gga cgc tgc cgc tac acc acc att   931
Val Glu Ile Ile Val Lys Lys Gly Gly Arg Cys Arg Tyr Thr Thr Ile
            265                 270                 275

cag aac tgg tcc aac aac gtc tac aac ctg gtg acc aag cgc acc aag   979
Gln Asn Trp Ser Asn Asn Val Tyr Asn Leu Val Thr Lys Arg Thr Lys
        280                 285                 290

gtt gaa gag ggc ggc acc atg gaa tgg gtc gat ggc aac atc ggc tcc   1027
Val Glu Glu Gly Gly Thr Met Glu Trp Val Asp Gly Asn Ile Gly Ser
    295                 300                 305

aag gtc acc atg aag tac cca gct gtc tgg atg act ggc cca cac gca   1075
Lys Val Thr Met Lys Tyr Pro Ala Val Trp Met Thr Gly Pro His Ala
310                 315                 320                 325

aag ggc gaa gtt ctc tcc gtc gct ttc gca ggt gag gga cag ttc cag   1123
Lys Gly Glu Val Leu Ser Val Ala Phe Ala Gly Glu Gly Gln Phe Gln
                330                 335                 340

gac acc ggc gcc aag atg acc cac atg gct cct tac act tcc tcc aac   1171
Asp Thr Gly Ala Lys Met Thr His Met Ala Pro Tyr Thr Ser Ser Asn
            345                 350                 355

atc gtg tcc aag tct gtg gca cgt ggc ggt gga cgt gcg gct tac cgt   1219
Ile Val Ser Lys Ser Val Ala Arg Gly Gly Gly Arg Ala Ala Tyr Arg
        360                 365                 370

ggt ctg gtt cag atc aac gca aac gct cac cac tca acc tcc aac gtt   1267
Gly Leu Val Gln Ile Asn Ala Asn Ala His His Ser Thr Ser Asn Val
    375                 380                 385

gag tgt gac gca ctg ctg gtc gat gac atc tcc cgt tct gac acc tac   1315
Glu Cys Asp Ala Leu Leu Val Asp Asp Ile Ser Arg Ser Asp Thr Tyr
390                 395                 400                 405
```

```
cca tac aac gac atc cgt aac gat cac gtg tca ctc ggc cac gag gca   1363
Pro Tyr Asn Asp Ile Arg Asn Asp His Val Ser Leu Gly His Glu Ala
                410                 415                 420

act gtt tcc cag gtt tct gaa gag cag ctg ttc tac ctc atg agc cgc   1411
Thr Val Ser Gln Val Ser Glu Glu Gln Leu Phe Tyr Leu Met Ser Arg
            425                 430                 435

gga ctt gcg gaa gaa gaa gca atg gca atg atc gtt cgt ggc ttc gtt   1459
Gly Leu Ala Glu Glu Glu Ala Met Ala Met Ile Val Arg Gly Phe Val
        440                 445                 450

gag cca atc gct aag gaa ctc cca atg gag tac gcc ctt gag ctc aac   1507
Glu Pro Ile Ala Lys Glu Leu Pro Met Glu Tyr Ala Leu Glu Leu Asn
    455                 460                 465

cga ctg atc gaa ctg cag atg gaa gga tcg gtg ggc taagcccaat        1553
Arg Leu Ile Glu Leu Gln Met Glu Gly Ser Val Gly
470                 475                 480

gactgaagta gca                                                   1566
```

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<210> 2774
<211> 481
<212> PRT
<213> Corynebacterium glutamicum

<400> 2774

```
Met Thr Ser Ala Thr Thr Asn Pro Gly Val Asn Glu Pro Leu Thr Asp
  1               5                  10                  15

Asp Gln Ile Ile Glu Ser Ile Gly Pro Tyr Asn Tyr Gly Trp His Asp
             20                  25                  30

Ser Asp Asp Ala Gly Ala Ser Ala Gln Arg Gly Leu Ser Glu Asp Val
         35                  40                  45

Val Arg Asp Ile Ser Ala Lys Lys Ser Glu Pro Glu Trp Met Leu Gln
     50                  55                  60

Gln Arg Leu Lys Ala Leu Ser Ile Phe Asp Lys Lys Pro Val Pro Thr
 65                  70                  75                  80

Trp Gly Ala Asp Leu Ser Gly Ile Asp Phe Asp Asn Ile Lys Tyr Phe
                 85                  90                  95

Val Arg Ser Thr Glu Lys Gln Ala Gln Ser Trp Glu Asp Leu Pro Glu
            100                 105                 110

Asp Ile Lys Asn Thr Tyr Asp Lys Leu Gly Ile Pro Glu Ala Glu Lys
        115                 120                 125

Gln Arg Leu Val Ala Gly Val Ala Ala Gln Tyr Glu Ser Glu Val Val
    130                 135                 140

Tyr His Gln Ile Arg Glu Asp Leu Glu Glu Lys Gly Val Ile Phe Leu
145                 150                 155                 160

Asp Thr Asp Thr Ala Leu Lys Glu His Pro Glu Ile Phe Gln Glu Tyr
                165                 170                 175
```

```
Phe Gly Thr Val Ile Pro Ala Gly Asp Asn Lys Phe Ser Ala Leu Asn
            180                 185                 190

Ser Ala Val Trp Ser Gly Gly Ser Phe Ile Tyr Val Pro Lys Gly Val
        195                 200                 205

His Val Asp Ile Pro Leu Gln Ala Tyr Phe Arg Ile Asn Thr Glu Asn
    210                 215                 220

Met Gly Gln Phe Glu Arg Thr Leu Ile Ile Val Asp Glu Asp Ala Tyr
225                 230                 235                 240

Val His Tyr Val Glu Gly Cys Thr Ala Pro Ile Tyr Lys Ser Asp Ser
                245                 250                 255

Leu His Ser Ala Val Val Glu Ile Ile Val Lys Lys Gly Gly Arg Cys
            260                 265                 270

Arg Tyr Thr Thr Ile Gln Asn Trp Ser Asn Asn Val Tyr Asn Leu Val
        275                 280                 285

Thr Lys Arg Thr Lys Val Glu Glu Gly Gly Thr Met Glu Trp Val Asp
    290                 295                 300

Gly Asn Ile Gly Ser Lys Val Thr Met Lys Tyr Pro Ala Val Trp Met
305                 310                 315                 320

Thr Gly Pro His Ala Lys Gly Glu Val Leu Ser Val Ala Phe Ala Gly
                325                 330                 335

Glu Gly Gln Phe Gln Asp Thr Gly Ala Lys Met Thr His Met Ala Pro
            340                 345                 350

Tyr Thr Ser Ser Asn Ile Val Ser Lys Ser Val Ala Arg Gly Gly Gly
        355                 360                 365

Arg Ala Ala Tyr Arg Gly Leu Val Gln Ile Asn Ala Asn Ala His His
    370                 375                 380

Ser Thr Ser Asn Val Glu Cys Asp Ala Leu Leu Val Asp Asp Ile Ser
385                 390                 395                 400

Arg Ser Asp Thr Tyr Pro Tyr Asn Asp Ile Arg Asn Asp His Val Ser
                405                 410                 415

Leu Gly His Glu Ala Thr Val Ser Gln Val Ser Glu Glu Gln Leu Phe
            420                 425                 430

Tyr Leu Met Ser Arg Gly Leu Ala Glu Glu Glu Ala Met Ala Met Ile
        435                 440                 445

Val Arg Gly Phe Val Glu Pro Ile Ala Lys Glu Leu Pro Met Glu Tyr
    450                 455                 460

Ala Leu Glu Leu Asn Arg Leu Ile Glu Leu Gln Met Glu Gly Ser Val
465                 470                 475                 480

Gly
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<210> 2775
<211> 813
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(790)
<223> RXA02524

<400> 2775
gacgcgatca ggcgctccta cgcacccagg caattaggcc tgagcttatc gacgcatccc 60

tcctcgattc caccgacctc aaagtattgg gactggacaa atg aca gag acc aca 115
Met Thr Glu Thr Thr
1 5

cct caa ccc cca aag cca gag ccc gag ctc ccg aaa ttt ctc agc aac 163
Pro Gln Pro Pro Lys Pro Glu Pro Glu Leu Pro Lys Phe Leu Ser Asn
10 15 20

cca gaa cgc gcc gac atc att ttg ttc atc gca ctc att gtg atg ggc 211
Pro Glu Arg Ala Asp Ile Ile Leu Phe Ile Ala Leu Ile Val Met Gly
25 30 35

att ttc tcc ctc tgc atg atc cca ctg cgc gcc tgg atg ctc acc caa 259
Ile Phe Ser Leu Cys Met Ile Pro Leu Arg Ala Trp Met Leu Thr Gln
40 45 50

cct ctg gcc tac acc ctc atc gtc ggt ggt tac acc agt gca gtc gtg 307
Pro Leu Ala Tyr Thr Leu Ile Val Gly Gly Tyr Thr Ser Ala Val Val
55 60 65

ggc ggc gcg aac gct tcg gta gaa aac ggc atc tgg tgg gtc tac tgg 355
Gly Gly Ala Asn Ala Ser Val Glu Asn Gly Ile Trp Trp Val Tyr Trp
70 75 80 85

ctc tgc acc ctg atc ggc gcg ctg aag ttc atg ccc gtc tat tgg ctg 403
Leu Cys Thr Leu Ile Gly Ala Leu Lys Phe Met Pro Val Tyr Trp Leu
90 95 100

atg ggt aag cgc tgg ggc atg gaa ttt atc gac atg tcc ctc caa tac 451
Met Gly Lys Arg Trp Gly Met Glu Phe Ile Asp Met Ser Leu Gln Tyr
105 110 115

atg ccc cgc ttc cac cgc atg ttc aaa aaa tcc gtc gac tcc gaa tcc 499
Met Pro Arg Phe His Arg Met Phe Lys Lys Ser Val Asp Ser Glu Ser
120 125 130

acc cgc ctc tac gcc tgg atc atc ggc ctc att cca ctc gca tac ctc 547
Thr Arg Leu Tyr Ala Trp Ile Ile Gly Leu Ile Pro Leu Ala Tyr Leu
135 140 145

cca gga cca gtg ccg gga acc atc ctt aac gca gtg gct ggg ctg gtg 595
Pro Gly Pro Val Pro Gly Thr Ile Leu Asn Ala Val Ala Gly Leu Val
150 155 160 165

aaa atc ccc ttc tgg atc atc atg gcc tgg aat gcg atc tgc gta cta 643
Lys Ile Pro Phe Trp Ile Ile Met Ala Trp Asn Ala Ile Cys Val Leu
170 175 180

```
tcg gtc aac gga cta ttc atg tgg ctg gga tac acc ttc ggc gaa caa   691
Ser Val Asn Gly Leu Phe Met Trp Leu Gly Tyr Thr Phe Gly Glu Gln
            185                 190                 195

gtc ctc gac atc gtc aac gtg gtc aac cgc tac atg ctt tgg ata acc   739
Val Leu Asp Ile Val Asn Val Val Asn Arg Tyr Met Leu Trp Ile Thr
        200                 205                 210

tta gga ttg ctg gcg ctg atg ttt ttc cgc gca cgg aag caa ttt gcc   787
Leu Gly Leu Leu Ala Leu Met Phe Phe Arg Ala Arg Lys Gln Phe Ala
    215                 220                 225

aag taaatggttg aaaggaatat gac                                    813
Lys
230
```

<210> 2776
<211> 230
<212> PRT
<213> Corynebacterium glutamicum

<400> 2776

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Met Thr Glu Thr Thr Pro Gln Pro Pro Lys Pro Glu Pro Glu Leu Pro
  1               5                  10                  15

Lys Phe Leu Ser Asn Pro Glu Arg Ala Asp Ile Ile Leu Phe Ile Ala
             20                  25                  30

Leu Ile Val Met Gly Ile Phe Ser Leu Cys Met Ile Pro Leu Arg Ala
         35                  40                  45

Trp Met Leu Thr Gln Pro Leu Ala Tyr Thr Leu Ile Val Gly Gly Tyr
     50                  55                  60

Thr Ser Ala Val Val Gly Gly Ala Asn Ala Ser Val Glu Asn Gly Ile
 65                  70                  75                  80

Trp Trp Val Tyr Trp Leu Cys Thr Leu Ile Gly Ala Leu Lys Phe Met
                 85                  90                  95

Pro Val Tyr Trp Leu Met Gly Lys Arg Trp Gly Met Glu Phe Ile Asp
            100                 105                 110

Met Ser Leu Gln Tyr Met Pro Arg Phe His Arg Met Phe Lys Lys Ser
        115                 120                 125

Val Asp Ser Glu Ser Thr Arg Leu Tyr Ala Trp Ile Ile Gly Leu Ile
    130                 135                 140

Pro Leu Ala Tyr Leu Pro Gly Pro Val Pro Gly Thr Ile Leu Asn Ala
145                 150                 155                 160

Val Ala Gly Leu Val Lys Ile Pro Phe Trp Ile Ile Met Ala Trp Asn
                165                 170                 175

Ala Ile Cys Val Leu Ser Val Asn Gly Leu Phe Met Trp Leu Gly Tyr
            180                 185                 190

Thr Phe Gly Glu Gln Val Leu Asp Ile Val Asn Val Val Asn Arg Tyr
```

```
        195                 200                 205

Met Leu Trp Ile Thr Leu Gly Leu Leu Ala Leu Met Phe Phe Arg Ala
    210                 215                 220

Arg Lys Gln Phe Ala Lys
225                 230


<210> 2777
<211> 501
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(478)
<223> RXA02525

<400> 2777
cgtggtcaac cgctacatgc tttggataac cttaggattg ctggcgctga tgtttttccg 60

cgcacggaag caatttgcca agtaaatggt tgaaaggaat atg acc acc atg cga   115
                                          Met Thr Thr Met Arg
                                            1               5

gaa gtt tca acc gac ctc aac atc ctc atc gtc ccc agc gaa tgg gaa   163
Glu Val Ser Thr Asp Leu Asn Ile Leu Ile Val Pro Ser Glu Trp Glu
                  10                  15                  20

aaa gta cta gaa aac cta cca gcg aca ttg agt gag tcc gga ttc gta   211
Lys Val Leu Glu Asn Leu Pro Ala Thr Leu Ser Glu Ser Gly Phe Val
             25                  30                  35

gcc tct gaa atc cac tcc cag atc gtc gac ctc acc tgc gaa ccc gac   259
Ala Ser Glu Ile His Ser Gln Ile Val Asp Leu Thr Cys Glu Pro Asp
         40                  45                  50

aac atg ctt gtc acc cag ttc tcc cag cta gag ggc cac cca cca att   307
Asn Met Leu Val Thr Gln Phe Ser Gln Leu Glu Gly His Pro Pro Ile
     55                  60                  65

gtg gaa gtg ctc cac cgc cta gta att aac ggc tcc tcc gac ctg gag   355
Val Glu Val Leu His Arg Leu Val Ile Asn Gly Ser Ser Asp Leu Glu
 70                  75                  80                  85

ctt aaa gac ctc acc aaa aag gtg gtg ggg gcg ttg cct cag ggg acc   403
Leu Lys Asp Leu Thr Lys Lys Val Val Gly Ala Leu Pro Gln Gly Thr
                 90                  95                 100

tac tgg tat gga act tcc ctt gaa ggt gcg acc gaa cct ggc gtt aac   451
Tyr Trp Tyr Gly Thr Ser Leu Glu Gly Ala Thr Glu Pro Gly Val Asn
            105                 110                 115

gca tca tgc gcg tgg cag cat cgg ggc tagttttccg cgtttagtca         498
Ala Ser Cys Ala Trp Gln His Arg Gly
        120                 125

gtt                                                               501
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<210> 2778
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 2778
Met Thr Thr Met Arg Glu Val Ser Thr Asp Leu Asn Ile Leu Ile Val
1 5 10 15

Pro Ser Glu Trp Glu Lys Val Leu Glu Asn Leu Pro Ala Thr Leu Ser
20 25 30

Glu Ser Gly Phe Val Ala Ser Glu Ile His Ser Gln Ile Val Asp Leu
35 40 45

Thr Cys Glu Pro Asp Asn Met Leu Val Thr Gln Phe Ser Gln Leu Glu
50 55 60

Gly His Pro Pro Ile Val Glu Val Leu His Arg Leu Val Ile Asn Gly
65 70 75 80

Ser Ser Asp Leu Glu Leu Lys Asp Leu Thr Lys Lys Val Val Gly Ala
85 90 95

Leu Pro Gln Gly Thr Tyr Trp Tyr Gly Thr Ser Leu Glu Gly Ala Thr
100 105 110

Glu Pro Gly Val Asn Ala Ser Cys Ala Trp Gln His Arg Gly
115 120 125

<210> 2779
<211> 561
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(538)
<223> RXA02540

<400> 2779
gcatatgctg aagcagaaac taattcaggt tttgatcccc gcgctaactg ggcgggccag 60

aaccgctaga cgttctcttt gagaaaggag gtgacgaaac atg gca tcc aca ccg 115
Met Ala Ser Thr Pro
1 5

aaa aaa tcc aac gat gaa ggt cag ttt gac cgt gtc gat ttt caa ggg 163
Lys Lys Ser Asn Asp Glu Gly Gln Phe Asp Arg Val Asp Phe Gln Gly
10 15 20

gaa gtc ttc gtt atc tct gtc gca gcc gag ctt gcc ggc atg cat gcc 211
Glu Val Phe Val Ile Ser Val Ala Ala Glu Leu Ala Gly Met His Ala
25 30 35

caa act ttg cga acc tac gat cgc atg ggt ttg gtc acc ccg ata cgc 259
Gln Thr Leu Arg Thr Tyr Asp Arg Met Gly Leu Val Thr Pro Ile Arg
40 45 50

act cgc gga ggc ggt cgc cgt tac tcc cgc gct gac gtg gaa tta ctc 307

```
Thr Arg Gly Gly Gly Arg Arg Tyr Ser Arg Ala Asp Val Glu Leu Leu
     55                  60                  65

cga gaa att cag cac ctc agc cag gag gaa ggc gta aac ctc gcc gga   355
Arg Glu Ile Gln His Leu Ser Gln Glu Glu Gly Val Asn Leu Ala Gly
 70                  75                  80                  85

atc aag gcg atc atc gag ctc ggc gaa gaa aac cga aac ctc aaa gaa   403
Ile Lys Ala Ile Ile Glu Leu Gly Glu Glu Asn Arg Asn Leu Lys Glu
                 90                  95                 100

tcc ctg cgt aag gtc aca gct gag aat gag cag ctc aaa gat caa tta   451
Ser Leu Arg Lys Val Thr Ala Glu Asn Glu Gln Leu Lys Asp Gln Leu
            105                 110                 115

cgc agc ggg cgt ccg cgt ggc gag ctg gtg cac gtg ccc cgc tcc acc   499
Arg Ser Gly Arg Pro Arg Gly Glu Leu Val His Val Pro Arg Ser Thr
        120                 125                 130

gcg gtg gtc atg tgg gaa cgc cgc aag ggg cgt tcc aag taaaaacatg    548
Ala Val Val Met Trp Glu Arg Arg Lys Gly Arg Ser Lys
    135                 140                 145

cttgtcgacg cca                                                   561


<210> 2780
<211> 146
<212> PRT
<213> Corynebacterium glutamicum

<400> 2780
Met Ala Ser Thr Pro Lys Lys Ser Asn Asp Glu Gly Gln Phe Asp Arg
  1               5                  10                  15

Val Asp Phe Gln Gly Glu Val Phe Val Ile Ser Val Ala Ala Glu Leu
             20                  25                  30

Ala Gly Met His Ala Gln Thr Leu Arg Thr Tyr Asp Arg Met Gly Leu
         35                  40                  45

Val Thr Pro Ile Arg Thr Arg Gly Gly Gly Arg Arg Tyr Ser Arg Ala
     50                  55                  60

Asp Val Glu Leu Leu Arg Glu Ile Gln His Leu Ser Gln Glu Glu Gly
 65                  70                  75                  80

Val Asn Leu Ala Gly Ile Lys Ala Ile Ile Glu Leu Gly Glu Glu Asn
                 85                  90                  95

Arg Asn Leu Lys Glu Ser Leu Arg Lys Val Thr Ala Glu Asn Glu Gln
            100                 105                 110

Leu Lys Asp Gln Leu Arg Ser Gly Arg Pro Arg Gly Glu Leu Val His
        115                 120                 125

Val Pro Arg Ser Thr Ala Val Val Met Trp Glu Arg Arg Lys Gly Arg
    130                 135                 140

Ser Lys
145
```

<210> 2781
<211> 1551
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1528)
<223> RXA02544

<400> 2781
ccaatcaggg aagataagag ctgttttcaa caggtcccac tcaactttga caccaagtct 60

cacgcaaaat taacagccat aaactttaga aggacaccct gtg tcc cac acc tgt 115
Val Ser His Thr Cys
1 5

ggc ata gtg att ttt gtg agc aca gaa tca gga aac acc cca aaa agg 163
Gly Ile Val Ile Phe Val Ser Thr Glu Ser Gly Asn Thr Pro Lys Arg
10 15 20

gat gat gca aaa agc acc atc cct ccg aaa gat ttg cct gac acc gtc 211
Asp Asp Ala Lys Ser Thr Ile Pro Pro Lys Asp Leu Pro Asp Thr Val
25 30 35

tta gac gcg att gaa ggc aat ttt gag cca ccg cta aat acc cag aag 259
Leu Asp Ala Ile Glu Gly Asn Phe Glu Pro Pro Leu Asn Thr Gln Lys
40 45 50

tcg gcg gtt ccc cct aat gcc gaa gca act gtc gag gct gat tct gaa 307
Ser Ala Val Pro Pro Asn Ala Glu Ala Thr Val Glu Ala Asp Ser Glu
55 60 65

gga act acc gac cgc tct gtc att ttg ggc agg gac ggc cgc tgg ctg 355
Gly Thr Thr Asp Arg Ser Val Ile Leu Gly Arg Asp Gly Arg Trp Leu
70 75 80 85

tcc gga tgg gca ttg cgc ttc atc gtg ctg gtt atc gcc ggc gtc att 403
Ser Gly Trp Ala Leu Arg Phe Ile Val Leu Val Ile Ala Gly Val Ile
90 95 100

gca ctt cgt atg ctg ggc ttc atc tgg gtt ggc atc ctc cca gtc gtc 451
Ala Leu Arg Met Leu Gly Phe Ile Trp Val Gly Ile Leu Pro Val Val
105 110 115

ctc gca ctt cta gtc tgc acc gtg cta tgg cca cca gtg aaa tgg ctg 499
Leu Ala Leu Leu Val Cys Thr Val Leu Trp Pro Pro Val Lys Trp Leu
120 125 130

cgc gag cat aag att ccc acg gcg ctc gcc gtt gtc atc aca att ttg 547
Arg Glu His Lys Ile Pro Thr Ala Leu Ala Val Val Ile Thr Ile Leu
135 140 145

ggt ttc ttc gcc ctc atc ggc gga gtt ttt gca gcc atc gcg cca agc 595
Gly Phe Phe Ala Leu Ile Gly Gly Val Phe Ala Ala Ile Ala Pro Ser
150 155 160 165

gtg tct tcc cag aca aag caa gtg gta gac caa gca act gtt ggt atc 643
Val Ser Ser Gln Thr Lys Gln Val Val Asp Gln Ala Thr Val Gly Ile

```
                170                 175                 180

gaa gat cta atg gat tgg gtt cag ggc cca cct ttt aac tta gat atc   691
Glu Asp Leu Met Asp Trp Val Gln Gly Pro Pro Phe Asn Leu Asp Ile
            185                 190                 195

tca cag ttt gaa ggc gcg ctc aat gac cta aca tcc atg ctg caa tca   739
Ser Gln Phe Glu Gly Ala Leu Asn Asp Leu Thr Ser Met Leu Gln Ser
        200                 205                 210

cag tct tcc acc att gct tct ggt gtg ttc tct gga ctg tca acg gca   787
Gln Ser Ser Thr Ile Ala Ser Gly Val Phe Ser Gly Leu Ser Thr Ala
    215                 220                 225

tca tcc atc gtt gtc aca cta gca gtg atg ctg gtg ttg acc ttc ttc   835
Ser Ser Ile Val Val Thr Leu Ala Val Met Leu Val Leu Thr Phe Phe
230                 235                 240                 245

ttc ctc aaa gac ggt cct cgt ttc ctg cca tgg atg cgc ggc ttc act   883
Phe Leu Lys Asp Gly Pro Arg Phe Leu Pro Trp Met Arg Gly Phe Thr
                250                 255                 260

ggt gaa aac gca ggt tgg cac ctc aca gaa gtc ctg acc cgt acc tgg   931
Gly Glu Asn Ala Gly Trp His Leu Thr Glu Val Leu Thr Arg Thr Trp
            265                 270                 275

aat acc ttg gcc gga ttc atc cgt gct cag gca ttg gtg tcc atg gtt   979
Asn Thr Leu Ala Gly Phe Ile Arg Ala Gln Ala Leu Val Ser Met Val
        280                 285                 290

gac gca ata ttc att ggt atc gga ttg ctg ctt ctt ggc gtc cca atg   1027
Asp Ala Ile Phe Ile Gly Ile Gly Leu Leu Leu Leu Gly Val Pro Met
    295                 300                 305

gcc ctc gcg ctc gcg gtc atc aca ttc ttc gcg ggc ttc atc ccc atc   1075
Ala Leu Ala Leu Ala Val Ile Thr Phe Phe Ala Gly Phe Ile Pro Ile
310                 315                 320                 325

gtc ggt gcg gtg tct gca ggc gcc ctg gct gtc atc atc gcg cta gtt   1123
Val Gly Ala Val Ser Ala Gly Ala Leu Ala Val Ile Ile Ala Leu Val
                330                 335                 340

acc aac ggc gtg acc aat gcg ctt ttg gta ctt gta ttg atc ctg gcg   1171
Thr Asn Gly Val Thr Asn Ala Leu Leu Val Leu Val Leu Ile Leu Ala
            345                 350                 355

gtt cag cag atc gag ggc aat atc ttg tcc cca ttc ctg cag tcc aag   1219
Val Gln Gln Ile Glu Gly Asn Ile Leu Ser Pro Phe Leu Gln Ser Lys
        360                 365                 370

gct atg aac ctg cac gca gcg gtt gtt ttg cta tcc gtc acc gtc ggc   1267
Ala Met Asn Leu His Ala Ala Val Val Leu Leu Ser Val Thr Val Gly
    375                 380                 385

tcc acc atg ttc ggc atc atc ggc gca ttc ttg gct gtt cca gta gcc   1315
Ser Thr Met Phe Gly Ile Ile Gly Ala Phe Leu Ala Val Pro Val Ala
390                 395                 400                 405

gcg acg ttg gct gtc tgg gtg cgc tac cac tct gaa atg gtt gct ttg   1363
Ala Thr Leu Ala Val Trp Val Arg Tyr His Ser Glu Met Val Ala Leu
                410                 415                 420
```

```
cgc gcc ggt gag atc acc agt gat gac att gag atc gcc acg acg aaa   1411
Arg Ala Gly Glu Ile Thr Ser Asp Asp Ile Glu Ile Ala Thr Thr Lys
            425                 430                 435

ggt tcc cca acc agc ctc aat ggc caa gaa acc ctt gct gcc att cga   1459
Gly Ser Pro Thr Ser Leu Asn Gly Gln Glu Thr Leu Ala Ala Ile Arg
        440                 445                 450

agc aga ttc gcc atc ctt ggc cgc aag aag ccg aca tct gcc act gca   1507
Ser Arg Phe Ala Ile Leu Gly Arg Lys Lys Pro Thr Ser Ala Thr Ala
    455                 460                 465

gaa aaa gca gac tca gaa agc tagccaataa tgctcactcc cga             1551
Glu Lys Ala Asp Ser Glu Ser
470                 475
```

<210> 2782
<211> 476
<212> PRT
<213> Corynebacterium glutamicum

<400> 2782

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Val Ser His Thr Cys Gly Ile Val Ile Phe Val Ser Thr Glu Ser Gly
  1               5                  10                  15

Asn Thr Pro Lys Arg Asp Asp Ala Lys Ser Thr Ile Pro Pro Lys Asp
             20                  25                  30

Leu Pro Asp Thr Val Leu Asp Ala Ile Glu Gly Asn Phe Glu Pro Pro
         35                  40                  45

Leu Asn Thr Gln Lys Ser Ala Val Pro Pro Asn Ala Glu Ala Thr Val
     50                  55                  60

Glu Ala Asp Ser Glu Gly Thr Thr Asp Arg Ser Val Ile Leu Gly Arg
 65                  70                  75                  80

Asp Gly Arg Trp Leu Ser Gly Trp Ala Leu Arg Phe Ile Val Leu Val
                 85                  90                  95

Ile Ala Gly Val Ile Ala Leu Arg Met Leu Gly Phe Ile Trp Val Gly
            100                 105                 110

Ile Leu Pro Val Val Leu Ala Leu Leu Val Cys Thr Val Leu Trp Pro
        115                 120                 125

Pro Val Lys Trp Leu Arg Glu His Lys Ile Pro Thr Ala Leu Ala Val
    130                 135                 140

Val Ile Thr Ile Leu Gly Phe Phe Ala Leu Ile Gly Gly Val Phe Ala
145                 150                 155                 160

Ala Ile Ala Pro Ser Val Ser Ser Gln Thr Lys Gln Val Val Asp Gln
                165                 170                 175

Ala Thr Val Gly Ile Glu Asp Leu Met Asp Trp Val Gln Gly Pro Pro
            180                 185                 190

Phe Asn Leu Asp Ile Ser Gln Phe Glu Gly Ala Leu Asn Asp Leu Thr
```

```
        195                 200                 205

Ser Met Leu Gln Ser Gln Ser Ser Thr Ile Ala Ser Gly Val Phe Ser
    210                 215                 220

Gly Leu Ser Thr Ala Ser Ser Ile Val Val Thr Leu Ala Val Met Leu
225                 230                 235                 240

Val Leu Thr Phe Phe Phe Leu Lys Asp Gly Pro Arg Phe Leu Pro Trp
                245                 250                 255

Met Arg Gly Phe Thr Gly Glu Asn Ala Gly Trp His Leu Thr Glu Val
            260                 265                 270

Leu Thr Arg Thr Trp Asn Thr Leu Ala Gly Phe Ile Arg Ala Gln Ala
        275                 280                 285

Leu Val Ser Met Val Asp Ala Ile Phe Ile Gly Ile Gly Leu Leu Leu
    290                 295                 300

Leu Gly Val Pro Met Ala Leu Ala Leu Ala Val Ile Thr Phe Phe Ala
305                 310                 315                 320

Gly Phe Ile Pro Ile Val Gly Ala Val Ser Ala Gly Ala Leu Ala Val
                325                 330                 335

Ile Ile Ala Leu Val Thr Asn Gly Val Thr Asn Ala Leu Leu Val Leu
            340                 345                 350

Val Leu Ile Leu Ala Val Gln Gln Ile Glu Gly Asn Ile Leu Ser Pro
        355                 360                 365

Phe Leu Gln Ser Lys Ala Met Asn Leu His Ala Ala Val Val Leu Leu
    370                 375                 380

Ser Val Thr Val Gly Ser Thr Met Phe Gly Ile Ile Gly Ala Phe Leu
385                 390                 395                 400

Ala Val Pro Val Ala Ala Thr Leu Ala Val Trp Val Arg Tyr His Ser
                405                 410                 415

Glu Met Val Ala Leu Arg Ala Gly Glu Ile Thr Ser Asp Asp Ile Glu
            420                 425                 430

Ile Ala Thr Thr Lys Gly Ser Pro Thr Ser Leu Asn Gly Gln Glu Thr
        435                 440                 445

Leu Ala Ala Ile Arg Ser Arg Phe Ala Ile Leu Gly Arg Lys Lys Pro
    450                 455                 460

Thr Ser Ala Thr Ala Glu Lys Ala Asp Ser Glu Ser
465                 470                 475
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<210> 2783
<211> 681
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(658)
<223> RXA02545

<400> 2783
aagaaatcga gaaagtaatt cgtgggtgaa gttgtttcag agttgttttt tattaaacaa 60

ctcagcctgt aacctcttgg tcgttctatg cttggtcacc atg act gag act ctt 115
Met Thr Glu Thr Leu
1 5

ttt gta tcc gcc aca act gag gaa gcg gtg tat ctt cca gat gga atc 163
Phe Val Ser Ala Thr Thr Glu Glu Ala Val Tyr Leu Pro Asp Gly Ile
10 15 20

gac ttg ctg gtg act ggc atc gga acg acc gca gca acg atg att ttg 211
Asp Leu Leu Val Thr Gly Ile Gly Thr Thr Ala Ala Thr Met Ile Leu
25 30 35

act aag gag ttg gct act cgg gag gtg ctt cct gcc cga att gtc aat 259
Thr Lys Glu Leu Ala Thr Arg Glu Val Leu Pro Ala Arg Ile Val Asn
40 45 50

att ggt acg gcg gga gct ttg gtg gat gga ttg gct ggc gta tac gag 307
Ile Gly Thr Ala Gly Ala Leu Val Asp Gly Leu Ala Gly Val Tyr Glu
55 60 65

atc gaa tac gtt ctg cag cat gat ttc agt agc gag tta atc gct gaa 355
Ile Glu Tyr Val Leu Gln His Asp Phe Ser Ser Glu Leu Ile Ala Glu
70 75 80 85

atg aca gga aag cca tgc tca aat ggt tca act ttg gcc acg agt ggg 403
Met Thr Gly Lys Pro Cys Ser Asn Gly Ser Thr Leu Ala Thr Ser Gly
90 95 100

cac ttc cca gta gcg agt ttg gca aca gga aac tca ttt att gca gat 451
His Phe Pro Val Ala Ser Leu Ala Thr Gly Asn Ser Phe Ile Ala Asp
105 110 115

tca gaa acc cgc aac cac ctg gcc acc cgg gcc tcc ctc tgc gat atg 499
Ser Glu Thr Arg Asn His Leu Ala Thr Arg Ala Ser Leu Cys Asp Met
120 125 130

gag ggc gcg gcg ctg gtg ggc gtc gca aag cat ttt ggt gtt ccg att 547
Glu Gly Ala Ala Leu Val Gly Val Ala Lys His Phe Gly Val Pro Ile
135 140 145

acg ctg ctg aag cag gtt agt gac agc gcg gat gag gag gct tcg ggg 595
Thr Leu Leu Lys Gln Val Ser Asp Ser Ala Asp Glu Glu Ala Ser Gly
150 155 160 165

tcg tgg ttt gat gcg gtc gat gcg ggc gca cga cag ttg gcg gag gct 643
Ser Trp Phe Asp Ala Val Asp Ala Gly Ala Arg Gln Leu Ala Glu Ala
170 175 180

gtg aag gag ttt aaa taacaaaaac ccgatgcctg gcg 681
Val Lys Glu Phe Lys
185

<210> 2784
<211> 186

<212> PRT
<213> Corynebacterium glutamicum

<400> 2784
Met Thr Glu Thr Leu Phe Val Ser Ala Thr Thr Glu Glu Ala Val Tyr
1 5 10 15

Leu Pro Asp Gly Ile Asp Leu Leu Val Thr Gly Ile Gly Thr Thr Ala
20 25 30

Ala Thr Met Ile Leu Thr Lys Glu Leu Ala Thr Arg Glu Val Leu Pro
35 40 45

Ala Arg Ile Val Asn Ile Gly Thr Ala Gly Ala Leu Val Asp Gly Leu
50 55 60

Ala Gly Val Tyr Glu Ile Glu Tyr Val Leu Gln His Asp Phe Ser Ser
65 70 75 80

Glu Leu Ile Ala Glu Met Thr Gly Lys Pro Cys Ser Asn Gly Ser Thr
85 90 95

Leu Ala Thr Ser Gly His Phe Pro Val Ala Ser Leu Ala Thr Gly Asn
100 105 110

Ser Phe Ile Ala Asp Ser Glu Thr Arg Asn His Leu Ala Thr Arg Ala
115 120 125

Ser Leu Cys Asp Met Glu Gly Ala Ala Leu Val Gly Val Ala Lys His
130 135 140

Phe Gly Val Pro Ile Thr Leu Leu Lys Gln Val Ser Asp Ser Ala Asp
145 150 155 160

Glu Glu Ala Ser Gly Ser Trp Phe Asp Ala Val Asp Ala Gly Ala Arg
165 170 175

Gln Leu Ala Glu Ala Val Lys Glu Phe Lys
180 185

<210> 2785
<211> 1227
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1204)
<223> RXA02546

<400> 2785
gattatgtcg gctccaccat cgtggtcagc tacaccgaaa aaccaaacgc ccagggcgca 60

attcagggca attccagttt ctctaggatc gagaaataac atg cca ttg ttt atc 115
Met Pro Leu Phe Ile
1 5

gac gac gcc ctc cac cgc agc aaa aaa tac ttc cac gcg cac tta agc 163
Asp Asp Ala Leu His Arg Ser Lys Lys Tyr Phe His Ala His Leu Ser
10 15 20

```
gag ctg ctc ctc ggc gaa ttt gca ggc ctc agc ctg ccc ctg cac cca   211
Glu Leu Leu Leu Gly Glu Phe Ala Gly Leu Ser Leu Pro Leu His Pro
             25                  30                  35

ccg acg gca gct aaa gcc gcc gcc gat att gat gcc acg agg gaa ttt   259
Pro Thr Ala Ala Lys Ala Ala Ala Asp Ile Asp Ala Thr Arg Glu Phe
         40                  45                  50

atc cgc caa tgg gag ggg cgt gat gat gtg gaa tat gcc att cga aac   307
Ile Arg Gln Trp Glu Gly Arg Asp Asp Val Glu Tyr Ala Ile Arg Asn
     55                  60                  65

tgg tct cct gtg ggc tta ggt aaa act gaa gta ccc gtt agg ctg acg   355
Trp Ser Pro Val Gly Leu Gly Lys Thr Glu Val Pro Val Arg Leu Thr
 70                  75                  80                  85

ttg aac acg act gag gaa tta gtt gtg ttt gcg cag gta gag gat gaa   403
Leu Asn Thr Thr Glu Glu Leu Val Val Phe Ala Gln Val Glu Asp Glu
                 90                  95                 100

tgg tct tca ctt cac gag agg ttt tca cag ctg tct ggt ttt aca gcg   451
Trp Ser Ser Leu His Glu Arg Phe Ser Gln Leu Ser Gly Phe Thr Ala
            105                 110                 115

gag gtg gtg gcg aaa cat gtg tcg ctg tgg cgt tcg ctg tct aac gat   499
Glu Val Val Ala Lys His Val Ser Leu Trp Arg Ser Leu Ser Asn Asp
        120                 125                 130

gat ctc tct aag gca gtg tta gtt gtg gat tgg ttt ttg aaa cac cct   547
Asp Leu Ser Lys Ala Val Leu Val Val Asp Trp Phe Leu Lys His Pro
    135                 140                 145

aac tct ggc ctg ctg aaa cgc gcc gtc gca gtt gaa ggc gtg cat acc   595
Asn Ser Gly Leu Leu Lys Arg Ala Val Ala Val Glu Gly Val His Thr
150                 155                 160                 165

aaa tgg ctc gaa aac cac cgc gta ctc att gaa acg tta gtg gcc gac   643
Lys Trp Leu Glu Asn His Arg Val Leu Ile Glu Thr Leu Val Ala Asp
                170                 175                 180

aaa cgt ggt gaa cct ggt cgt gcc gat ctt gga ctt ggt gac gcc gaa   691
Lys Arg Gly Glu Pro Gly Arg Ala Asp Leu Gly Leu Gly Asp Ala Glu
            185                 190                 195

gct cgc gtc cgg ctc cgc ttc cat tcc gta gat gct ccc gct ggg ctc   739
Ala Arg Val Arg Leu Arg Phe His Ser Val Asp Ala Pro Ala Gly Leu
        200                 205                 210

aca gac att gaa gta ccg ctt tcc aac ctg tgt gaa tta caa gaa ccg   787
Thr Asp Ile Glu Val Pro Leu Ser Asn Leu Cys Glu Leu Gln Glu Pro
    215                 220                 225

caa gta att ctg atg gtg gaa aac ctc gat tca ttt ctc gct tta ccc   835
Gln Val Ile Leu Met Val Glu Asn Leu Asp Ser Phe Leu Ala Leu Pro
230                 235                 240                 245

act tgg ccg ggc gta aca att gct tgg ggt gcg ggc tac cgt gca gta   883
Thr Trp Pro Gly Val Thr Ile Ala Trp Gly Ala Gly Tyr Arg Ala Val
                250                 255                 260
```

```
gac att gtt cga gga ccc tac ttt tct aat ggt cgg ttg ctg tac tgg   931
Asp Ile Val Arg Gly Pro Tyr Phe Ser Asn Gly Arg Leu Leu Tyr Trp
            265                 270                 275

ggt gac ctt gac ctg gac ggt ttc aaa att ctc gac ggc gtc cgc agc   979
Gly Asp Leu Asp Leu Asp Gly Phe Lys Ile Leu Asp Gly Val Arg Ser
        280                 285                 290

cat gtt cct cac acc gaa tcc gtg ctg atg aac tct gaa acc gtc tcc   1027
His Val Pro His Thr Glu Ser Val Leu Met Asn Ser Glu Thr Val Ser
    295                 300                 305

cgc tgg cgc tac ctt ggc gtt gcc gac cga gaa ttc aag gca gag agc   1075
Arg Trp Arg Tyr Leu Gly Val Ala Asp Arg Glu Phe Lys Ala Glu Ser
310                 315                 320                 325

ttt gac aac ctt cat gat ttt gaa tct gac gca ctt gac cta ctc att   1123
Phe Asp Asn Leu His Asp Phe Glu Ser Asp Ala Leu Asp Leu Leu Ile
                330                 335                 340

aca gac ggt gag ctc cgc att gaa caa gaa cgc atc cgc ctc gat gtt   1171
Thr Asp Gly Glu Leu Arg Ile Glu Gln Glu Arg Ile Arg Leu Asp Val
            345                 350                 355

gct gtt gaa gaa atc gag aaa gta att cgt ggg tgaagttgtt tcagagttgt 1224
Ala Val Glu Glu Ile Glu Lys Val Ile Arg Gly
        360                 365

ttt                                                               1227
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<210> 2786
<211> 368
<212> PRT
<213> Corynebacterium glutamicum

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<400> 2786
Met Pro Leu Phe Ile Asp Asp Ala Leu His Arg Ser Lys Lys Tyr Phe
  1               5                  10                  15

His Ala His Leu Ser Glu Leu Leu Leu Gly Glu Phe Ala Gly Leu Ser
             20                  25                  30

Leu Pro Leu His Pro Pro Thr Ala Ala Lys Ala Ala Ala Asp Ile Asp
         35                  40                  45

Ala Thr Arg Glu Phe Ile Arg Gln Trp Glu Gly Arg Asp Asp Val Glu
     50                  55                  60

Tyr Ala Ile Arg Asn Trp Ser Pro Val Gly Leu Gly Lys Thr Glu Val
 65                  70                  75                  80

Pro Val Arg Leu Thr Leu Asn Thr Thr Glu Glu Leu Val Val Phe Ala
                 85                  90                  95

Gln Val Glu Asp Glu Trp Ser Ser Leu His Glu Arg Phe Ser Gln Leu
            100                 105                 110

Ser Gly Phe Thr Ala Glu Val Val Ala Lys His Val Ser Leu Trp Arg
        115                 120                 125
```

```
Ser Leu Ser Asn Asp Asp Leu Ser Lys Ala Val Leu Val Val Asp Trp
    130                 135                 140

Phe Leu Lys His Pro Asn Ser Gly Leu Leu Lys Arg Ala Val Ala Val
145                 150                 155                 160

Glu Gly Val His Thr Lys Trp Leu Glu Asn His Arg Val Leu Ile Glu
                165                 170                 175

Thr Leu Val Ala Asp Lys Arg Gly Glu Pro Gly Arg Ala Asp Leu Gly
            180                 185                 190

Leu Gly Asp Ala Glu Ala Arg Val Arg Leu Arg Phe His Ser Val Asp
        195                 200                 205

Ala Pro Ala Gly Leu Thr Asp Ile Glu Val Pro Leu Ser Asn Leu Cys
    210                 215                 220

Glu Leu Gln Glu Pro Gln Val Ile Leu Met Val Glu Asn Leu Asp Ser
225                 230                 235                 240

Phe Leu Ala Leu Pro Thr Trp Pro Gly Val Thr Ile Ala Trp Gly Ala
                245                 250                 255

Gly Tyr Arg Ala Val Asp Ile Val Arg Gly Pro Tyr Phe Ser Asn Gly
            260                 265                 270

Arg Leu Leu Tyr Trp Gly Asp Leu Asp Leu Asp Gly Phe Lys Ile Leu
        275                 280                 285

Asp Gly Val Arg Ser His Val Pro His Thr Glu Ser Val Leu Met Asn
    290                 295                 300

Ser Glu Thr Val Ser Arg Trp Arg Tyr Leu Gly Val Ala Asp Arg Glu
305                 310                 315                 320

Phe Lys Ala Glu Ser Phe Asp Asn Leu His Asp Phe Glu Ser Asp Ala
                325                 330                 335

Leu Asp Leu Leu Ile Thr Asp Gly Glu Leu Arg Ile Glu Gln Glu Arg
            340                 345                 350

Ile Arg Leu Asp Val Ala Val Glu Glu Ile Glu Lys Val Ile Arg Gly
        355                 360                 365
```

<210> 2787
<211> 1326
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1326)
<223> RXA02549

<400> 2787
acc ctc act gca atc tcc tcc gaa act tgg cct atc atg ctc gcg cca 48

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Thr Leu Thr Ala Ile Ser Ser Glu Thr Trp Pro Ile Met Leu Ala Pro
  1               5                  10                  15

tgg gta tgt ctg cct ctg ctt tcg cga aat gtg gat gca cgg gcc atc   96
Trp Val Cys Leu Pro Leu Leu Ser Arg Asn Val Asp Ala Arg Ala Ile
            20                  25                  30

gcg ttg tcc tta ctt ccc gcg gca tgc atg ggt gca gtt aat gcc acc   144
Ala Leu Ser Leu Leu Pro Ala Ala Cys Met Gly Ala Val Asn Ala Thr
        35                  40                  45

gcc acg atg gca gca ctc atc ccg gca gcg ctg atc ttg ctg tat aga   192
Ala Thr Met Ala Ala Leu Ile Pro Ala Ala Leu Ile Leu Leu Tyr Arg
    50                  55                  60

ggg ctc ttc tta agg ctg ctt ctg tgg gga atg ggc gtt ctc gct gtt   240
Gly Leu Phe Leu Arg Leu Leu Leu Trp Gly Met Gly Val Leu Ala Val
65                  70                  75                  80

aat tca tgg tgg atc gga cct ttg ttg gtg ctt ggc aaa tac gcc ccg   288
Asn Ser Trp Trp Ile Gly Pro Leu Leu Val Leu Gly Lys Tyr Ala Pro
                85                  90                  95

ccc ttc acc gaa ttc atc gaa agt tcc tcc gtc acc act tcc tgg ctc   336
Pro Phe Thr Glu Phe Ile Glu Ser Ser Ser Val Thr Thr Ser Trp Leu
            100                 105                 110

aac cca gta gaa ata ctc cgc gga acc acc agt tgg aca ccc ttc gta   384
Asn Pro Val Glu Ile Leu Arg Gly Thr Thr Ser Trp Thr Pro Phe Val
        115                 120                 125

gac act gaa cga caa gcc gga tat ctc ctg gtc aac gat gct ctc ttt   432
Asp Thr Glu Arg Gln Ala Gly Tyr Leu Leu Val Asn Asp Ala Leu Phe
    130                 135                 140

gtc acc ctc agc gtt ctc gtc gca gcc ctc ggc ttg atc ggc ctc acc   480
Val Thr Leu Ser Val Leu Val Ala Ala Leu Gly Leu Ile Gly Leu Thr
145                 150                 155                 160

ttg atg aaa cac cgt gga ctg tgg gca ttc atg ctg gcc atc gga ctc   528
Leu Met Lys His Arg Gly Leu Trp Ala Phe Met Leu Ala Ile Gly Leu
                165                 170                 175

ctc atc ctc ggc agc gcc cac cta acg gct gtt caa gaa ttc ctc gac   576
Leu Ile Leu Gly Ser Ala His Leu Thr Ala Val Gln Glu Phe Leu Asp
            180                 185                 190

ggc cca ggc gca gca ctt cga aac atc cac aaa ttt gat cta tta gtc   624
Gly Pro Gly Ala Ala Leu Arg Asn Ile His Lys Phe Asp Leu Leu Val
        195                 200                 205

cgc atg ccg ttg atg gtg ggc gtt gcc gca ttg ggg tcg cat atc agt   672
Arg Met Pro Leu Met Val Gly Val Ala Ala Leu Gly Ser His Ile Ser
    210                 215                 220

ctg ccc ttg ctt ggg acg act gca ttg acc agc gga caa ggc aaa cac   720
Leu Pro Leu Leu Gly Thr Thr Ala Leu Thr Ser Gly Gln Gly Lys His
225                 230                 235                 240

cac acc atc ccg ctg cct ctc caa aaa cgc caa gcc gca gga ctc ctc   768
His Thr Ile Pro Leu Pro Leu Gln Lys Arg Gln Ala Ala Gly Leu Leu
```

```
                245                 250                 255

gtg gtg atc atc gct gtc ggt gct ctt gct ccc gca tgg tcg gca cgg   816
Val Val Ile Ile Ala Val Gly Ala Leu Ala Pro Ala Trp Ser Ala Arg
            260                 265                 270

ctg cta cct cag gga acg tgg gat gaa gtg cct gac tac tgg tac gaa   864
Leu Leu Pro Gln Gly Thr Trp Asp Glu Val Pro Asp Tyr Trp Tyr Glu
        275                 280                 285

gcc aca gaa ttc ctc aac caa aac gcc aca ggc acc cgc acg ttg att   912
Ala Thr Glu Phe Leu Asn Gln Asn Ala Thr Gly Thr Arg Thr Leu Ile
    290                 295                 300

tgg cct agc tcg ccg ttt gcc cgc cag gac tgg gga tgg act cgg gat   960
Trp Pro Ser Ser Pro Phe Ala Arg Gln Asp Trp Gly Trp Thr Arg Asp
305                 310                 315                 320

gaa cca gct caa cca ctt ctt gat gtt ccg tgg gct gtc cgc gat gcc   1008
Glu Pro Ala Gln Pro Leu Leu Asp Val Pro Trp Ala Val Arg Asp Ala
                325                 330                 335

att cct ttg gtt ccc ccg gag gcg att cgc gga tta gat ggt ctc gac   1056
Ile Pro Leu Val Pro Pro Glu Ala Ile Arg Gly Leu Asp Gly Leu Asp
            340                 345                 350

gac cta ggc act cta ggc acc ggt cta aac gac gag gct tta aaa cgt   1104
Asp Leu Gly Thr Leu Gly Thr Gly Leu Asn Asp Glu Ala Leu Lys Arg
        355                 360                 365

cta ggc atc ggc gca gta ctg gtg agg cat gat ctg gaa gcc gac cca   1152
Leu Gly Ile Gly Ala Val Leu Val Arg His Asp Leu Glu Ala Asp Pro
    370                 375                 380

gat att gag gtg gat ctg cct ggg gaa aag cac act ttt ggc tcc caa   1200
Asp Ile Glu Val Asp Leu Pro Gly Glu Lys His Thr Phe Gly Ser Gln
385                 390                 395                 400

ggc caa gta gac gtc tac ctc acc gac ccc gac cgc aat atg tgg atc   1248
Gly Gln Val Asp Val Tyr Leu Thr Asp Pro Asp Arg Asn Met Trp Ile
                405                 410                 415

act tcc ggc aca tcc aag cag ctg ccc acc gtc gct ggc ggc ggc gaa   1296
Thr Ser Gly Thr Ser Lys Gln Leu Pro Thr Val Ala Gly Gly Gly Glu
            420                 425                 430

atc ctc tcg ctc cta gac acc atc aac ggc                          1326
Ile Leu Ser Leu Leu Asp Thr Ile Asn Gly
        435                 440
```

<210> 2788
<211> 442
<212> PRT
<213> Corynebacterium glutamicum

<400> 2788

```
Thr Leu Thr Ala Ile Ser Ser Glu Thr Trp Pro Ile Met Leu Ala Pro
  1               5                  10                  15

Trp Val Cys Leu Pro Leu Leu Ser Arg Asn Val Asp Ala Arg Ala Ile
```

```
            20                  25                  30

Ala Leu Ser Leu Leu Pro Ala Ala Cys Met Gly Ala Val Asn Ala Thr
         35                  40                  45

Ala Thr Met Ala Ala Leu Ile Pro Ala Ala Leu Ile Leu Leu Tyr Arg
     50                  55                  60

Gly Leu Phe Leu Arg Leu Leu Leu Trp Gly Met Gly Val Leu Ala Val
 65                  70                  75                  80

Asn Ser Trp Trp Ile Gly Pro Leu Leu Val Leu Gly Lys Tyr Ala Pro
                 85                  90                  95

Pro Phe Thr Glu Phe Ile Glu Ser Ser Ser Val Thr Thr Ser Trp Leu
            100                 105                 110

Asn Pro Val Glu Ile Leu Arg Gly Thr Thr Ser Trp Thr Pro Phe Val
        115                 120                 125

Asp Thr Glu Arg Gln Ala Gly Tyr Leu Leu Val Asn Asp Ala Leu Phe
    130                 135                 140

Val Thr Leu Ser Val Leu Val Ala Ala Leu Gly Leu Ile Gly Leu Thr
145                 150                 155                 160

Leu Met Lys His Arg Gly Leu Trp Ala Phe Met Leu Ala Ile Gly Leu
                165                 170                 175

Leu Ile Leu Gly Ser Ala His Leu Thr Ala Val Gln Glu Phe Leu Asp
            180                 185                 190

Gly Pro Gly Ala Ala Leu Arg Asn Ile His Lys Phe Asp Leu Leu Val
        195                 200                 205

Arg Met Pro Leu Met Val Gly Val Ala Ala Leu Gly Ser His Ile Ser
    210                 215                 220

Leu Pro Leu Leu Gly Thr Thr Ala Leu Thr Ser Gly Gln Gly Lys His
225                 230                 235                 240

His Thr Ile Pro Leu Pro Leu Gln Lys Arg Gln Ala Ala Gly Leu Leu
                245                 250                 255

Val Val Ile Ile Ala Val Gly Ala Leu Ala Pro Ala Trp Ser Ala Arg
            260                 265                 270

Leu Leu Pro Gln Gly Thr Trp Asp Glu Val Pro Asp Tyr Trp Tyr Glu
        275                 280                 285

Ala Thr Glu Phe Leu Asn Gln Asn Ala Thr Gly Thr Arg Thr Leu Ile
    290                 295                 300

Trp Pro Ser Ser Pro Phe Ala Arg Gln Asp Trp Gly Trp Thr Arg Asp
305                 310                 315                 320

Glu Pro Ala Gln Pro Leu Leu Asp Val Pro Trp Ala Val Arg Asp Ala
                325                 330                 335

Ile Pro Leu Val Pro Pro Glu Ala Ile Arg Gly Leu Asp Gly Leu Asp
            340                 345                 350
```

```
Asp Leu Gly Thr Leu Gly Thr Gly Leu Asn Asp Glu Ala Leu Lys Arg
        355                 360                 365

Leu Gly Ile Gly Ala Val Leu Val Arg His Asp Leu Glu Ala Asp Pro
    370                 375                 380

Asp Ile Glu Val Asp Leu Pro Gly Glu Lys His Thr Phe Gly Ser Gln
385                 390                 395                 400

Gly Gln Val Asp Val Tyr Leu Thr Asp Pro Asp Arg Asn Met Trp Ile
                405                 410                 415

Thr Ser Gly Thr Ser Lys Gln Leu Pro Thr Val Ala Gly Gly Gly Glu
            420                 425                 430

Ile Leu Ser Leu Leu Asp Thr Ile Asn Gly
        435                 440
```

<210> 2789
<211> 918
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(895)
<223> RXA02552

<400> 2789

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tccttaaata cccactgtcc tctattctgg gttaggcttc actgggtaaa agtgcctgcc 60

tatgcctgaa acttgagcat ggcaacagca aggagacacc gtg gga aaa cat gca   115
                                              Val Gly Lys His Ala
                                                1               5

gct gaa aca tcg gaa ccg aag aaa aat tca ccg tgg cgc att ggt ttg   163
Ala Glu Thr Ser Glu Pro Lys Lys Asn Ser Pro Trp Arg Ile Gly Leu
                  10                  15                  20

ttg acg ttt ttg att tct tca gtt gtc gtg acg ctg gtg ggc atg gtg   211
Leu Thr Phe Leu Ile Ser Ser Val Val Val Thr Leu Val Gly Met Val
              25                  30                  35

atg ctg tgg ccg gat tct gat gat gtg gtg ttg gcg gat aac ttt tcg   259
Met Leu Trp Pro Asp Ser Asp Asp Val Val Leu Ala Asp Asn Phe Ser
          40                  45                  50

cag acg ttt gcg gga aat cat gag cag gtg gat gga acg atc acg ctc   307
Gln Thr Phe Ala Gly Asn His Glu Gln Val Asp Gly Thr Ile Thr Leu
      55                  60                  65

gtt gat aat tct gcg tgt aat tcg cca gac acc ggc cga gtt ttt gcg   355
Val Asp Asn Ser Ala Cys Asn Ser Pro Asp Thr Gly Arg Val Phe Ala
 70                  75                  80                  85

gaa agc ccc acg att tct gcg gag ccg gca acg ttg gag tgc gtg cgt   403
Glu Ser Pro Thr Ile Ser Ala Glu Pro Ala Thr Leu Glu Cys Val Arg
                  90                  95                 100
```

```
gca ctc gta gac atc aca tcg ggt gcc aat gag ggg cag aaa act cag   451
Ala Leu Val Asp Ile Thr Ser Gly Ala Asn Glu Gly Gln Lys Thr Gln
            105                 110                 115

ctg atc act tac gcg caa cct ggt gat ccg gag ttt tcc gag ggc gac   499
Leu Ile Thr Tyr Ala Gln Pro Gly Asp Pro Glu Phe Ser Glu Gly Asp
        120                 125                 130

aag atc cgc atg gtg gaa aca ccg gat aca aat ggc gag atc atc tac   547
Lys Ile Arg Met Val Glu Thr Pro Asp Thr Asn Gly Glu Ile Ile Tyr
    135                 140                 145

acc ttt gct gat tac cag cgc gga ccg gcg ttg atc att tgg ggt gtg   595
Thr Phe Ala Asp Tyr Gln Arg Gly Pro Ala Leu Ile Ile Trp Gly Val
150                 155                 160                 165

gtt ctc att gtg gcg atg gga gct ttc gcg gcg tgg cga ggt gtg cgt   643
Val Leu Ile Val Ala Met Gly Ala Phe Ala Ala Trp Arg Gly Val Arg
                170                 175                 180

gcg ctg gtt ggt ttg gtc gtc acc ttg gga att gtt ggt att ttc ttg   691
Ala Leu Val Gly Leu Val Val Thr Leu Gly Ile Val Gly Ile Phe Leu
            185                 190                 195

ctg cca gga ttg gcc agc ggg cac gat gcg atg tgg ttg gcg ctg gtg   739
Leu Pro Gly Leu Ala Ser Gly His Asp Ala Met Trp Leu Ala Leu Val
        200                 205                 210

tgt ggc gcg gcg atc ttg ttg att gtg gtg ccg atg gtt cac gga atc   787
Cys Gly Ala Ala Ile Leu Leu Ile Val Val Pro Met Val His Gly Ile
    215                 220                 225

aac tgg aaa tcg gca gct gcg ttg gcg ggc acg ctg gtg gca ttg ttg   835
Asn Trp Lys Ser Ala Ala Ala Leu Ala Gly Thr Leu Val Ala Leu Leu
230                 235                 240                 245

ttg tcg gcg gtg ttg tcg tgg gcg tcg atc gtc acc act gaa ttt gcg   883
Leu Ser Ala Val Leu Ser Trp Ala Ser Ile Val Thr Thr Glu Phe Ala
                250                 255                 260

cgg act ggg cga tgagaatcat ctgaagatca tca                        918
Arg Thr Gly Arg
            265
```

<210> 2790
<211> 265
<212> PRT
<213> Corynebacterium glutamicum

<400> 2790

```
Val Gly Lys His Ala Ala Glu Thr Ser Glu Pro Lys Lys Asn Ser Pro
  1               5                  10                  15

Trp Arg Ile Gly Leu Leu Thr Phe Leu Ile Ser Ser Val Val Val Thr
             20                  25                  30

Leu Val Gly Met Val Met Leu Trp Pro Asp Ser Asp Asp Val Val Leu
         35                  40                  45

Ala Asp Asn Phe Ser Gln Thr Phe Ala Gly Asn His Glu Gln Val Asp
```

```
     50                  55                  60

Gly Thr Ile Thr Leu Val Asp Asn Ser Ala Cys Asn Ser Pro Asp Thr
 65                  70                  75                  80

Gly Arg Val Phe Ala Glu Ser Pro Thr Ile Ser Ala Glu Pro Ala Thr
                 85                  90                  95

Leu Glu Cys Val Arg Ala Leu Val Asp Ile Thr Ser Gly Ala Asn Glu
            100                 105                 110

Gly Gln Lys Thr Gln Leu Ile Thr Tyr Ala Gln Pro Gly Asp Pro Glu
        115                 120                 125

Phe Ser Glu Gly Asp Lys Ile Arg Met Val Glu Thr Pro Asp Thr Asn
    130                 135                 140

Gly Glu Ile Ile Tyr Thr Phe Ala Asp Tyr Gln Arg Gly Pro Ala Leu
145                 150                 155                 160

Ile Ile Trp Gly Val Val Leu Ile Val Ala Met Gly Ala Phe Ala Ala
                165                 170                 175

Trp Arg Gly Val Arg Ala Leu Val Gly Leu Val Val Thr Leu Gly Ile
            180                 185                 190

Val Gly Ile Phe Leu Leu Pro Gly Leu Ala Ser Gly His Asp Ala Met
        195                 200                 205

Trp Leu Ala Leu Val Cys Gly Ala Ala Ile Leu Leu Ile Val Val Pro
    210                 215                 220

Met Val His Gly Ile Asn Trp Lys Ser Ala Ala Ala Leu Ala Gly Thr
225                 230                 235                 240

Leu Val Ala Leu Leu Leu Ser Ala Val Leu Ser Trp Ala Ser Ile Val
                245                 250                 255

Thr Thr Glu Phe Ala Arg Thr Gly Arg
            260                 265
```

20050070703

<210> 2791
<211> 747
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(724)
<223> RXA02554

<400> 2791
gcttttgaag tgtgtcgcgt gtgcggactg aaatagtttc cgcttcaact tggttgctaa 60

ggataggctc cataaaaata accaaaggcg gaaaatttca atg tca cac act aag 115
                                                Met Ser His Thr Lys
                                                  1   5

cca tcc att gcc atc ctc ggt gct ggc cga gtg ggt tct tca ctt gcc 163
Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val Gly Ser Ser Leu Ala

```
                  10                  15                  20

agg tca gcg gtc gcc gca ggc tat gag gta aag gtt gct ggt tca ggt   211
Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys Val Ala Gly Ser Gly
             25                  30                  35

gct gtg gac aaa atc gct ctt acc gct gag atc ctt atg ccc ggc gcg   259
Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile Leu Met Pro Gly Ala
         40                  45                  50

gtt cca agc act gct gac cag gct gta aag gat gca gat att gtg ttc   307
Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp Ala Asp Ile Val Phe
     55                  60                  65

ttg gct gtt ccc ctg cat aaa ttc cgc agt gtc aat cca gcc act tta   355
Leu Ala Val Pro Leu His Lys Phe Arg Ser Val Asn Pro Ala Thr Leu
 70                  75                  80                  85

gag ggc aag atc gtt att gac acg atg aac cac tgg gtt ccg gtc aat   403
Glu Gly Lys Ile Val Ile Asp Thr Met Asn His Trp Val Pro Val Asn
                 90                  95                 100

ggt gag ttg gag gaa att gat cag gat ccg cgc agc act tcg gag att   451
Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg Ser Thr Ser Glu Ile
            105                 110                 115

att gcg gag ttt ttc gcg gga tca acc atg gtg aag tct ttt aac cac   499
Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val Lys Ser Phe Asn His
        120                 125                 130

att ggt tat cac gag att gag cag gat gcg ggt acc ggg cgt gcg att   547
Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly Thr Gly Arg Ala Ile
    135                 140                 145

gcg tat gcc acg gat gat gtg gat gca ggt gcc cag gtt gca cag cta   595
Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala Gln Val Ala Gln Leu
150                 155                 160                 165

att aag agt ttt ggg ttt gtt cct tta aat att ggc gca ttg gaa aac   643
Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile Gly Ala Leu Glu Asn
                170                 175                 180

ggc cgt att ctg gaa cct ggc caa gaa gct ttc ggc gcg cac ctt aat   691
Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe Gly Ala His Leu Asn
            185                 190                 195

aaa gat tcg cgc cta gaa ctt gtt aat cag cgg tagtacctcg atcttcagcc 744
Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
        200                 205

aac                                                               747
```

<210> 2792
<211> 208
<212> PRT
<213> Corynebacterium glutamicum

<400> 2792

```
Met Ser His Thr Lys Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val
  1               5                  10                  15
```

```
Gly Ser Ser Leu Ala Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys
              20                  25                  30

Val Ala Gly Ser Gly Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile
          35                  40                  45

Leu Met Pro Gly Ala Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp
      50                  55                  60

Ala Asp Ile Val Phe Leu Ala Val Pro Leu His Lys Phe Arg Ser Val
  65                  70                  75                  80

Asn Pro Ala Thr Leu Glu Gly Lys Ile Val Ile Asp Thr Met Asn His
                  85                  90                  95

Trp Val Pro Val Asn Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg
             100                 105                 110

Ser Thr Ser Glu Ile Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val
         115                 120                 125

Lys Ser Phe Asn His Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly
     130                 135                 140

Thr Gly Arg Ala Ile Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala
145                 150                 155                 160

Gln Val Ala Gln Leu Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile
                165                 170                 175

Gly Ala Leu Glu Asn Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe
             180                 185                 190

Gly Ala His Leu Asn Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
         195                 200                 205
```

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<210> 2793
<211> 854
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (82)..(831)
<223> RXA02569

<400> 2793

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aatcttcaaa tcgttcccgc aagcaaaagg tgacatactg ctggcttgtt tttgcattcg 60

acgatctgca tggggattac tatg tca cgc tca tct aaa att tcg gtc gcg    111
                      Met Ser Arg Ser Ser Lys Ile Ser Val Ala
                        1               5                  10

ttt ggt ggc cta ctc atc gct gct acc tgg ctg tat ttg gtc ttg gtc   159
Phe Gly Gly Leu Leu Ile Ala Ala Thr Trp Leu Tyr Leu Val Leu Val
                15                  20                  25
```

```
agg cct acc gat tgg gaa tca gtg ggt ggt tcc acg gaa gcg ttg atc   207
Arg Pro Thr Asp Trp Glu Ser Val Gly Gly Ser Thr Glu Ala Leu Ile
            30                  35                  40

acg ttg gtg ggc tat gtt gcc ggc acg atc gcg ttg ttg gtt ggt gtg   255
Thr Leu Val Gly Tyr Val Ala Gly Thr Ile Ala Leu Leu Val Gly Val
        45                  50                  55

ctg cct acg ctt cca gcc agg acc att gcg atc att cct gtg gct ttg   303
Leu Pro Thr Leu Pro Ala Arg Thr Ile Ala Ile Ile Pro Val Ala Leu
    60                  65                  70

gtg ctc aat att ttg tta ggc caa gtc act ggt tct ttt gtc att ccg   351
Val Leu Asn Ile Leu Leu Gly Gln Val Thr Gly Ser Phe Val Ile Pro
75                  80                  85                  90

ctg tat tta gat gcg gtg ggc aca gtg ctg gtc gca gct ctt gct ggt   399
Leu Tyr Leu Asp Ala Val Gly Thr Val Leu Val Ala Ala Leu Ala Gly
                95                  100                 105

cct agt gct ggt ttg gca aca ggt gct tta agt tct gtg gtg tgg gcg   447
Pro Ser Ala Gly Leu Ala Thr Gly Ala Leu Ser Ser Val Val Trp Ala
            110                 115                 120

ttg ttc aat ccg ctg gct ttg ccg ttt gct gca ggt tcc gcg ctg act   495
Leu Phe Asn Pro Leu Ala Leu Pro Phe Ala Ala Gly Ser Ala Leu Thr
        125                 130                 135

ggt tgg ttg acc ggt gtg gtg att aaa aag ggt gcg ttt aag aat atc   543
Gly Trp Leu Thr Gly Val Val Ile Lys Lys Gly Ala Phe Lys Asn Ile
    140                 145                 150

ttc gcc acc atc atc tct ggt gcg gtc att ggt ttg atc acg ggt gct   591
Phe Ala Thr Ile Ile Ser Gly Ala Val Ile Gly Leu Ile Thr Gly Ala
155                 160                 165                 170

gtc gct gcc ccg gtt gcg gcg ttt gtt tat ggc gga acc gcc ggt gtg   639
Val Ala Ala Pro Val Ala Ala Phe Val Tyr Gly Gly Thr Ala Gly Val
                175                 180                 185

gga act ggt gcg gtg gtt agc ctc ttc cgc gaa atg ggt aac tct ttg   687
Gly Thr Gly Ala Val Val Ser Leu Phe Arg Glu Met Gly Asn Ser Leu
            190                 195                 200

ctc gca tcg gta acc tgg cag tcg ttt att tcc gat cct ttg gat aag   735
Leu Ala Ser Val Thr Trp Gln Ser Phe Ile Ser Asp Pro Leu Asp Lys
        205                 210                 215

gcc att gtt atg ctc att gtg ttt gtg gtg gtc aag tcg cta ccc aag   783
Ala Ile Val Met Leu Ile Val Phe Val Val Val Lys Ser Leu Pro Lys
    220                 225                 230

cgc acc act agg gca ttg gtt ccg cag cgg gtt ccg gag gac gtc gct   831
Arg Thr Thr Arg Ala Leu Val Pro Gln Arg Val Pro Glu Asp Val Ala
235                 240                 245                 250

taaacatgaa tcctttgaca tgg                                        854
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<210> 2794

<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 2794

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Met Ser Arg Ser Ser Lys Ile Ser Val Ala Phe Gly Gly Leu Leu Ile
  1               5                  10                  15

Ala Ala Thr Trp Leu Tyr Leu Val Leu Val Arg Pro Thr Asp Trp Glu
             20                  25                  30

Ser Val Gly Gly Ser Thr Glu Ala Leu Ile Thr Leu Val Gly Tyr Val
         35                  40                  45

Ala Gly Thr Ile Ala Leu Leu Val Gly Val Leu Pro Thr Leu Pro Ala
     50                  55                  60

Arg Thr Ile Ala Ile Ile Pro Val Ala Leu Val Leu Asn Ile Leu Leu
 65                  70                  75                  80

Gly Gln Val Thr Gly Ser Phe Val Ile Pro Leu Tyr Leu Asp Ala Val
                 85                  90                  95

Gly Thr Val Leu Val Ala Ala Leu Ala Gly Pro Ser Ala Gly Leu Ala
            100                 105                 110

Thr Gly Ala Leu Ser Ser Val Val Trp Ala Leu Phe Asn Pro Leu Ala
        115                 120                 125

Leu Pro Phe Ala Ala Gly Ser Ala Leu Thr Gly Trp Leu Thr Gly Val
    130                 135                 140

Val Ile Lys Lys Gly Ala Phe Lys Asn Ile Phe Ala Thr Ile Ile Ser
145                 150                 155                 160

Gly Ala Val Ile Gly Leu Ile Thr Gly Ala Val Ala Ala Pro Val Ala
                165                 170                 175

Ala Phe Val Tyr Gly Gly Thr Ala Gly Val Gly Thr Gly Ala Val Val
            180                 185                 190

Ser Leu Phe Arg Glu Met Gly Asn Ser Leu Leu Ala Ser Val Thr Trp
        195                 200                 205

Gln Ser Phe Ile Ser Asp Pro Leu Asp Lys Ala Ile Val Met Leu Ile
    210                 215                 220

Val Phe Val Val Val Lys Ser Leu Pro Lys Arg Thr Thr Arg Ala Leu
225                 230                 235                 240

Val Pro Gln Arg Val Pro Glu Asp Val Ala
                245                 250
```

<210> 2795
<211> 765
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(742)
<223> RXA02570

<400> 2795
ccattgttat gctcattgtg tttgtggtgg tcaagtcgct acccaagcgc accactaggg 60

cattggttcc gcagcgggtt ccggaggacg tcgcttaaac atg aat cct ttg aca 115
Met Asn Pro Leu Thr
1 5

tgg atc att ggc gca ttc agc atg tgg atc gtg gtg ctg ggc gtt aat 163
Trp Ile Ile Gly Ala Phe Ser Met Trp Ile Val Val Leu Gly Val Asn
10 15 20

aag ctt ggt tta agc atc gca gtg atc atc atc gcg cag gtc gtg gcg 211
Lys Leu Gly Leu Ser Ile Ala Val Ile Ile Ile Ala Gln Val Val Ala
25 30 35

atg att cgg gtg cgc aat gta tct gtg ttg gct tca aca gca ttg tta 259
Met Ile Arg Val Arg Asn Val Ser Val Leu Ala Ser Thr Ala Leu Leu
40 45 50

tcg gtt cct gca ttg gcc tcg atg gcg ctg att cac atg ccg tat tct 307
Ser Val Pro Ala Leu Ala Ser Met Ala Leu Ile His Met Pro Tyr Ser
55 60 65

tcc gac ggc tgg ttg att gct ctt acc ttg acg gct cgt ttt agt gcg 355
Ser Asp Gly Trp Leu Ile Ala Leu Thr Leu Thr Ala Arg Phe Ser Ala
70 75 80 85

ttg atg tct att ttc ctc ctt gca gca aca gcg att act att cct gag 403
Leu Met Ser Ile Phe Leu Leu Ala Ala Thr Ala Ile Thr Ile Pro Glu
90 95 100

ctg gtg aaa tcc cta tat cgt tgg ccc aag ctg gcg tat atc gtg ggt 451
Leu Val Lys Ser Leu Tyr Arg Trp Pro Lys Leu Ala Tyr Ile Val Gly
105 110 115

tct gca ttg cag atg att ccg cag ggt aaa cag acc ttg gcg ttg gtt 499
Ser Ala Leu Gln Met Ile Pro Gln Gly Lys Gln Thr Leu Ala Leu Val
120 125 130

cgt gat gcc aat gct ttg cgc ggg cgc agc gtt aaa ggt ccc gtg cgc 547
Arg Asp Ala Asn Ala Leu Arg Gly Arg Ser Val Lys Gly Pro Val Arg
135 140 145

gcg gtg aaa tat gtg ggt ttg ccc ctg att aca cat tta ctt agt gca 595
Ala Val Lys Tyr Val Gly Leu Pro Leu Ile Thr His Leu Leu Ser Ala
150 155 160 165

ggt gcc gcg cga gcg att ccc ttg gag gtc gca ggc ctg gac agg ccg 643
Gly Ala Ala Arg Ala Ile Pro Leu Glu Val Ala Gly Leu Asp Arg Pro
170 175 180

ggg ccg cgt acg gtg ttg gtt gag gtg gtg gag ggg cgc gtc gaa aag 691
Gly Pro Arg Thr Val Leu Val Glu Val Val Glu Gly Arg Val Glu Lys
185 190 195

cat tgt cgc tgg ttg ttg ccg ctt ttg gca gtc ggg atg gcg tgg tgg 739
His Cys Arg Trp Leu Leu Pro Leu Leu Ala Val Gly Met Ala Trp Trp
200 205 210

ctc taactcaaat cgtcggaccg tcc 765
Leu

<210> 2796
<211> 214
<212> PRT
<213> Corynebacterium glutamicum

<400> 2796
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Val Leu Gly Val Asn Lys Leu Gly Leu Ser Ile Ala Val Ile Ile Ile
20 25 30

Ala Gln Val Val Ala Met Ile Arg Val Arg Asn Val Ser Val Leu Ala
35 40 45

Ser Thr Ala Leu Leu Ser Val Pro Ala Leu Ala Ser Met Ala Leu Ile
50 55 60

His Met Pro Tyr Ser Ser Asp Gly Trp Leu Ile Ala Leu Thr Leu Thr
65 70 75 80

Ala Arg Phe Ser Ala Leu Met Ser Ile Phe Leu Leu Ala Ala Thr Ala
85 90 95

Ile Thr Ile Pro Glu Leu Val Lys Ser Leu Tyr Arg Trp Pro Lys Leu
100 105 110

Ala Tyr Ile Val Gly Ser Ala Leu Gln Met Ile Pro Gln Gly Lys Gln
115 120 125

Thr Leu Ala Leu Val Arg Asp Ala Asn Ala Leu Arg Gly Arg Ser Val
130 135 140

Lys Gly Pro Val Arg Ala Val Lys Tyr Val Gly Leu Pro Leu Ile Thr
145 150 155 160

His Leu Leu Ser Ala Gly Ala Ala Arg Ala Ile Pro Leu Glu Val Ala
165 170 175

Gly Leu Asp Arg Pro Gly Pro Arg Thr Val Leu Val Glu Val Val Glu
180 185 190

Gly Arg Val Glu Lys His Cys Arg Trp Leu Leu Pro Leu Leu Ala Val
195 200 205

Gly Met Ala Trp Trp Leu
210

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<212> DNA
<213> Corynebacterium glutamicum

<220>

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<222> (101)..(544)
<223> RXA02573

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gaagtgaagt actttccgaa agattcacag ggagcatgca atg acg aac aaa acc 115
Met Thr Asn Lys Thr
1 5

atg ctg gtt gct ttt gat ggc tca ccg gaa tcc cgg cgc gct ttg gaa 163
Met Leu Val Ala Phe Asp Gly Ser Pro Glu Ser Arg Arg Ala Leu Glu
10 15 20

tat gcg gcg aaa ttg ttg cag ccg cgc acc gtg gaa att tta act gcg 211
Tyr Ala Ala Lys Leu Leu Gln Pro Arg Thr Val Glu Ile Leu Thr Ala
25 30 35

tgg gag cca ttg cat cgg caa gct gcg cgc tcg gtt tcg ttg atc acc 259
Trp Glu Pro Leu His Arg Gln Ala Ala Arg Ser Val Ser Leu Ile Thr
40 45 50

ttg ggg gtg gaa ccc gaa gac ccc gcc cat tcc gct gca cta aaa acc 307
Leu Gly Val Glu Pro Glu Asp Pro Ala His Ser Ala Ala Leu Lys Thr
55 60 65

tgc cag gaa ggc gta gag cta gcc caa tct cta ggt ctg gaa gcg cga 355
Cys Gln Glu Gly Val Glu Leu Ala Gln Ser Leu Gly Leu Glu Ala Arg
70 75 80 85

gcc cac atg gtg gaa tcc gca acg gcc gtg tgg agc gcc atc gtt gat 403
Ala His Met Val Glu Ser Ala Thr Ala Val Trp Ser Ala Ile Val Asp
90 95 100

gct gct gac gag ctc cgc ccc gac gtg att gtc acc ggc acc cgc ggg 451
Ala Ala Asp Glu Leu Arg Pro Asp Val Ile Val Thr Gly Thr Arg Gly
105 110 115

atc tcc gga tgg aaa tcc ctg tgg caa tcc tcc acc tca gac agc gtg 499
Ile Ser Gly Trp Lys Ser Leu Trp Gln Ser Ser Thr Ser Asp Ser Val
120 125 130

ctc cac cac gcc gac gta cca gtt ttt gtc gtt cca ccc ctg gac 544
Leu His His Ala Asp Val Pro Val Phe Val Val Pro Pro Leu Asp
135 140 145

taaaaccgag acgagaacca aga 567

<210> 2798
<211> 148
<212> PRT
<213> Corynebacterium glutamicum

<400> 2798
Met Thr Asn Lys Thr Met Leu Val Ala Phe Asp Gly Ser Pro Glu Ser
1 5 10 15

Arg Arg Ala Leu Glu Tyr Ala Ala Lys Leu Leu Gln Pro Arg Thr Val
20 25 30

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Glu Ile Leu Thr Ala Trp Glu Pro Leu His Arg Gln Ala Ala Arg Ser
          35                  40                  45

Val Ser Leu Ile Thr Leu Gly Val Glu Pro Glu Asp Pro Ala His Ser
      50                  55                  60

Ala Ala Leu Lys Thr Cys Gln Glu Gly Val Glu Leu Ala Gln Ser Leu
 65                  70                  75                  80

Gly Leu Glu Ala Arg Ala His Met Val Glu Ser Ala Thr Ala Val Trp
                 85                  90                  95

Ser Ala Ile Val Asp Ala Ala Asp Glu Leu Arg Pro Asp Val Ile Val
            100                 105                 110

Thr Gly Thr Arg Gly Ile Ser Gly Trp Lys Ser Leu Trp Gln Ser Ser
        115                 120                 125

Thr Ser Asp Ser Val Leu His His Ala Asp Val Pro Val Phe Val Val
    130                 135                 140

Pro Pro Leu Asp
145


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<213> Corynebacterium glutamicum

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<223> RXA02575

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tgagtaggaa tttcgcatca gtgcaactag cctttcaggt gtg aag aac tct ggg   115
                                            Val Lys Asn Ser Gly
                                              1               5

aaa aat tcg gca aag aat cgg acc aaa ggg atc cta atc ggg gtt ctc   163
Lys Asn Ser Ala Lys Asn Arg Thr Lys Gly Ile Leu Ile Gly Val Leu
                 10                  15                  20

gtt ggt ctg att gcc att ttt gca ggc atc tat gcg gtc gat gtt ttc   211
Val Gly Leu Ile Ala Ile Phe Ala Gly Ile Tyr Ala Val Asp Val Phe
             25                  30                  35

ctc aac aag gac aac atc cct cgt gga aca acc gtc ggt ggc gtc agt   259
Leu Asn Lys Asp Asn Ile Pro Arg Gly Thr Thr Val Gly Gly Val Ser
         40                  45                  50

att tcc aac ctc agt gca caa gaa gcc cgc aca aag ttg gaa acc gaa   307
Ile Ser Asn Leu Ser Ala Gln Glu Ala Arg Thr Lys Leu Glu Thr Glu
     55                  60                  65

ctg gcc aat gat gtg gtg cag ccc gtc acc gtg acg gca ggg gag cag   355
Leu Ala Asn Asp Val Val Gln Pro Val Thr Val Thr Ala Gly Glu Gln
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 70                  75                  80                  85

agc acc act ttt gat cca gtt gcc tcc ggc gtc ggc atc gat tgg gac   403
Ser Thr Thr Phe Asp Pro Val Ala Ser Gly Val Gly Ile Asp Trp Asp
                 90                  95                 100

gca acc atc gaa ggc acc ggc gag cag tct tgg aac ccc att acc cgc   451
Ala Thr Ile Glu Gly Thr Gly Glu Gln Ser Trp Asn Pro Ile Thr Arg
            105                 110                 115

ttc gtg gcg ctg ttc aaa gaa tcc gaa tct ccc atc gtg agc acc gtc   499
Phe Val Ala Leu Phe Lys Glu Ser Glu Ser Pro Ile Val Ser Thr Val
        120                 125                 130

gat ccc gca gcc ttc ggc ccg acc ctt gat cgc atg gtc ggc gaa ctc   547
Asp Pro Ala Ala Phe Gly Pro Thr Leu Asp Arg Met Val Gly Glu Leu
    135                 140                 145

tat cga gat ccc att tcc gga aac ctg cat atc gac gcc ggc acc ctc   595
Tyr Arg Asp Pro Ile Ser Gly Asn Leu His Ile Asp Ala Gly Thr Leu
150                 155                 160                 165

gtg gtc aac gac acc atc gac gga caa gcc gta gac cgc acc att ttg   643
Val Val Asn Asp Thr Ile Asp Gly Gln Ala Val Asp Arg Thr Ile Leu
                170                 175                 180

gaa caa gca gtc aca gaa aac tgg ctc aac cca gag ggc gta aaa gcc   691
Glu Gln Ala Val Thr Glu Asn Trp Leu Asn Pro Glu Gly Val Lys Ala
            185                 190                 195

gag cca tac gtt gtt ccc gct gcg atc agc caa gac acc atc gat aaa   739
Glu Pro Tyr Val Val Pro Ala Ala Ile Ser Gln Asp Thr Ile Asp Lys
        200                 205                 210

ctt gca gaa ggc gcc gga gct aaa gca gta tct agc cct ttc gtc gtc   787
Leu Ala Glu Gly Ala Gly Ala Lys Ala Val Ser Ser Pro Phe Val Val
    215                 220                 225

cga ggc gat gac gga att gaa ggc acc atc ccc gtc gag cgc atg ggt   835
Arg Gly Asp Asp Gly Ile Glu Gly Thr Ile Pro Val Glu Arg Met Gly
230                 235                 240                 245

gaa gtg gtg agt ttc cca gaa gaa aac ggc acc atc cgc gtc gac atc   883
Glu Val Val Ser Phe Pro Glu Glu Asn Gly Thr Ile Arg Val Asp Ile
                250                 255                 260

aat gca gaa gca gca aca gca atg ctg gcc gaa ggt ctc aaa gaa aca   931
Asn Ala Glu Ala Ala Thr Ala Met Leu Ala Glu Gly Leu Lys Glu Thr
            265                 270                 275

gag atc gag ccc acc aac gct caa atc agt ttc tcc tca ggc tcc cgc   979
Glu Ile Glu Pro Thr Asn Ala Gln Ile Ser Phe Ser Ser Gly Ser Arg
        280                 285                 290

gta gtc acc cca gaa gtc acc gga cac gga atc aac tgg gaa gaa acc   1027
Val Val Thr Pro Glu Val Thr Gly His Gly Ile Asn Trp Glu Glu Thr
    295                 300                 305

ctg gcc gat ctg ccc aac aac ctc acc ggc gat ggc ccc cgc acc atc   1075
Leu Ala Asp Leu Pro Asn Asn Leu Thr Gly Asp Gly Pro Arg Thr Ile
310                 315                 320                 325
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gac gca atc tac gag gac acc cca gca aca ttc acc gcc acc gac gcc   1123
Asp Ala Ile Tyr Glu Asp Thr Pro Ala Thr Phe Thr Ala Thr Asp Ala
                330                 335                 340

caa aac gct acc ttc aat gag gtc atg ggc gag ttc acc acc ggc ggc   1171
Gln Asn Ala Thr Phe Asn Glu Val Met Gly Glu Phe Thr Thr Gly Gly
            345                 350                 355

ttc tct gct gcc tcc gga aca aac atc cgc ctc acc gcg caa atg gtc   1219
Phe Ser Ala Ala Ser Gly Thr Asn Ile Arg Leu Thr Ala Gln Met Val
        360                 365                 370

gac ggc gca gtc gtt tca cct ggc gat aca ttc tcc ctc               1258
Asp Gly Ala Val Val Ser Pro Gly Asp Thr Phe Ser Leu
    375                 380                 385


<210> 2800
<211> 386
<212> PRT
<213> Corynebacterium glutamicum

<400> 2800
Val Lys Asn Ser Gly Lys Asn Ser Ala Lys Asn Arg Thr Lys Gly Ile
  1               5                  10                  15

Leu Ile Gly Val Leu Val Gly Leu Ile Ala Ile Phe Ala Gly Ile Tyr
             20                  25                  30

Ala Val Asp Val Phe Leu Asn Lys Asp Asn Ile Pro Arg Gly Thr Thr
         35                  40                  45

Val Gly Gly Val Ser Ile Ser Asn Leu Ser Ala Gln Glu Ala Arg Thr
     50                  55                  60

Lys Leu Glu Thr Glu Leu Ala Asn Asp Val Val Gln Pro Val Thr Val
 65                  70                  75                  80

Thr Ala Gly Glu Gln Ser Thr Thr Phe Asp Pro Val Ala Ser Gly Val
                 85                  90                  95

Gly Ile Asp Trp Asp Ala Thr Ile Glu Gly Thr Gly Glu Gln Ser Trp
            100                 105                 110

Asn Pro Ile Thr Arg Phe Val Ala Leu Phe Lys Glu Ser Glu Ser Pro
        115                 120                 125

Ile Val Ser Thr Val Asp Pro Ala Ala Phe Gly Pro Thr Leu Asp Arg
    130                 135                 140

Met Val Gly Glu Leu Tyr Arg Asp Pro Ile Ser Gly Asn Leu His Ile
145                 150                 155                 160

Asp Ala Gly Thr Leu Val Val Asn Asp Thr Ile Asp Gly Gln Ala Val
                165                 170                 175

Asp Arg Thr Ile Leu Glu Gln Ala Val Thr Glu Asn Trp Leu Asn Pro
            180                 185                 190

Glu Gly Val Lys Ala Glu Pro Tyr Val Val Pro Ala Ala Ile Ser Gln
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        195                 200                 205

Asp Thr Ile Asp Lys Leu Ala Glu Gly Ala Gly Ala Lys Ala Val Ser
    210                 215                 220

Ser Pro Phe Val Val Arg Gly Asp Asp Gly Ile Glu Gly Thr Ile Pro
225                 230                 235                 240

Val Glu Arg Met Gly Glu Val Val Ser Phe Pro Glu Glu Asn Gly Thr
                245                 250                 255

Ile Arg Val Asp Ile Asn Ala Glu Ala Ala Thr Ala Met Leu Ala Glu
            260                 265                 270

Gly Leu Lys Glu Thr Glu Ile Glu Pro Thr Asn Ala Gln Ile Ser Phe
        275                 280                 285

Ser Ser Gly Ser Arg Val Val Thr Pro Glu Val Thr Gly His Gly Ile
    290                 295                 300

Asn Trp Glu Glu Thr Leu Ala Asp Leu Pro Asn Asn Leu Thr Gly Asp
305                 310                 315                 320

Gly Pro Arg Thr Ile Asp Ala Ile Tyr Glu Asp Thr Pro Ala Thr Phe
                325                 330                 335

Thr Ala Thr Asp Ala Gln Asn Ala Thr Phe Asn Glu Val Met Gly Glu
            340                 345                 350

Phe Thr Thr Gly Gly Phe Ser Ala Ala Ser Gly Thr Asn Ile Arg Leu
        355                 360                 365

Thr Ala Gln Met Val Asp Gly Ala Val Val Ser Pro Gly Asp Thr Phe
    370                 375                 380

Ser Leu
385
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CURRENT SEQUENCE LISTING

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<211> 1545
<212> DNA
<213> Corynebacterium glutamicum

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<221> CDS
<222> (101)..(1522)
<223> RXA02576

<400> 2801

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gctgatgagc actgtgaata aactcaggag ttaaatcctt atg acc ccg acc cgc   115
                                              Met Thr Pro Thr Arg
                                                1               5

cgt atc ctg ctg tgg gca tgg acg act gtg ctt ttg ggt tct ttg ctg   163
Arg Ile Leu Leu Trp Ala Trp Thr Thr Val Leu Leu Gly Ser Leu Leu
                 10                  15                  20

tgg ccg ttg gct gcg cct ggc gag ttg ttg ttg cgg gat atg tcg gtg   211
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Trp Pro Leu Ala Ala Pro Gly Glu Leu Leu Leu Arg Asp Met Ser Val
             25                  30                  35

gtg gac cat cct gcg ttg tcg ttg aat gcg ttg ggt ttt ggt gat ttg   259
Val Asp His Pro Ala Leu Ser Leu Asn Ala Leu Gly Phe Gly Asp Leu
         40                  45                  50

ccg tcg cgg aac gcc ccg cag gat ggt gtg ctg gcg ttg ctt ggc ttt   307
Pro Ser Arg Asn Ala Pro Gln Asp Gly Val Leu Ala Leu Leu Gly Phe
     55                  60                  65

ttg ccg gtg agt tgg atc gtt cga acc atg ctg ctt gtg gcg ggt ttc   355
Leu Pro Val Ser Trp Ile Val Arg Thr Met Leu Leu Val Ala Gly Phe
 70                  75                  80                  85

gcg ggc gcg tgg ggt gcg atg cgc ctt ggg cct tcc aag ttt ttg gcc   403
Ala Gly Ala Trp Gly Ala Met Arg Leu Gly Pro Ser Lys Phe Leu Ala
                 90                  95                 100

gtt acc gtg gcg att tac aat ccc ttc gtg gtg gag cgt ctg ctg cag   451
Val Thr Val Ala Ile Tyr Asn Pro Phe Val Val Glu Arg Leu Leu Gln
            105                 110                 115

ggc cat tgg tcg ttg gtg atg gcg gtg tgg ctg ttc ccg ctg gtt gtg   499
Gly His Trp Ser Leu Val Met Ala Val Trp Leu Phe Pro Leu Val Val
        120                 125                 130

gcg ctg cgc agg cat ccg cgt tgg cag gtt gtg gcg atc tgg gcg gcg   547
Ala Leu Arg Arg His Pro Arg Trp Gln Val Val Ala Ile Trp Ala Ala
    135                 140                 145

tcg ttg acg ccc acg ggt gcg gtg gtt gcg gcg gtc acg ggc gtg gcg   595
Ser Leu Thr Pro Thr Gly Ala Val Val Ala Ala Val Thr Gly Val Ala
150                 155                 160                 165

agt tct aaa aga aaa cgc ttt acg acg cta tgt tcc ttc ctt tcg tgg   643
Ser Ser Lys Arg Lys Arg Phe Thr Thr Leu Cys Ser Phe Leu Ser Trp
                170                 175                 180

ctt cct tgg cta ata cct gcg ctt ctt gcc acc ccc act tcg gga ggt   691
Leu Pro Trp Leu Ile Pro Ala Leu Leu Ala Thr Pro Thr Ser Gly Gly
            185                 190                 195

gcg ctg acc ttc gcc att cgt tct gaa aca tat gca gga acg ttg gga   739
Ala Leu Thr Phe Ala Ile Arg Ser Glu Thr Tyr Ala Gly Thr Leu Gly
        200                 205                 210

act gcg ctg ggc ctg ggt gga att tgg aac gcg ggg gcc gtg ccg gcc   787
Thr Ala Leu Gly Leu Gly Gly Ile Trp Asn Ala Gly Ala Val Pro Ala
    215                 220                 225

tca cgc gaa ctg ggt ttc gcg gtt gct gga att ttg tta ttt gcg att   835
Ser Arg Glu Leu Gly Phe Ala Val Ala Gly Ile Leu Leu Phe Ala Ile
230                 235                 240                 245

ctg ctg gcg ggt ttc aaa aac tgt ccg tgg gtt ctc gca ctg ctg gcg   883
Leu Leu Ala Gly Phe Lys Asn Cys Pro Trp Val Leu Ala Leu Leu Ala
                250                 255                 260

gtc gta ggt ttt atg ggg gcg atc ggt ccg tgg ctg atg ccg aat ctg   931
Val Val Gly Phe Met Gly Ala Ile Gly Pro Trp Leu Met Pro Asn Leu
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            265                 270                 275

ttc acg tgg acc atc gca tat gtt cca ggc gcc gcg ctg ttt agg gat   979
Phe Thr Trp Thr Ile Ala Tyr Val Pro Gly Ala Ala Leu Phe Arg Asp
        280                 285                 290

tct caa aaa ctc ctc atg ctg gct atc cct gcc tat gtg tgt ttg gcc   1027
Ser Gln Lys Leu Leu Met Leu Ala Ile Pro Ala Tyr Val Cys Leu Ala
    295                 300                 305

gcc ggg gtg aaa agc cca ctg tcg tgg gtg gct acc ggt ttg gcg ttg   1075
Ala Gly Val Lys Ser Pro Leu Ser Trp Val Ala Thr Gly Leu Ala Leu
310                 315                 320                 325

ctc cag att cct gat gca cca cgt gag gtt tcc gtg ata cgc cca agt   1123
Leu Gln Ile Pro Asp Ala Pro Arg Glu Val Ser Val Ile Arg Pro Ser
                330                 335                 340

tca gcg cat gtg gaa tca gtg gaa gca ctg gca gaa atc gct gat ggc   1171
Ser Ala His Val Glu Ser Val Glu Ala Leu Ala Glu Ile Ala Asp Gly
            345                 350                 355

cgc gac atc tta atc atc ggc caa ggc ccc ttg gtg acc cgc gag gat   1219
Arg Asp Ile Leu Ile Ile Gly Gln Gly Pro Leu Val Thr Arg Glu Asp
        360                 365                 370

ggg atc ccg gtt gtc gat ccc aaa acc aaa gcc ctc tcc gtg gtg gaa   1267
Gly Ile Pro Val Val Asp Pro Lys Thr Lys Ala Leu Ser Val Val Glu
    375                 380                 385

tcc ggc gaa ctg cgt gtg gac gga atc atc acc gac gcg ccc tca cag   1315
Ser Gly Glu Leu Arg Val Asp Gly Ile Ile Thr Asp Ala Pro Ser Gln
390                 395                 400                 405

cgg tgg acc gaa gca acg cag gca tgg gcg gcc ggg gat atc gag cgc   1363
Arg Trp Thr Glu Ala Thr Gln Ala Trp Ala Ala Gly Asp Ile Glu Arg
                410                 415                 420

ctt gaa gaa ctt ggc gtt ggt gtc gtg gtg gat gga gat acg atc aca   1411
Leu Glu Glu Leu Gly Val Gly Val Val Val Asp Gly Asp Thr Ile Thr
            425                 430                 435

gaa act ggc gca cca ccg cag cat ggc tgg aaa tac tac ctc ggt gtg   1459
Glu Thr Gly Ala Pro Pro Gln His Gly Trp Lys Tyr Tyr Leu Gly Val
        440                 445                 450

ggc ctg acc gtg ctg tgg atg gcg ttg ccg ctg gga cta ctt ttt cga   1507
Gly Leu Thr Val Leu Trp Met Ala Leu Pro Leu Gly Leu Leu Phe Arg
    455                 460                 465

cgc aag acc aag aag tagttcctcg aactgcgctc ccg                    1545
Arg Lys Thr Lys Lys
470
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<210> 2802
<211> 474
<212> PRT
<213> Corynebacterium glutamicum

<400> 2802

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Leu Gly Ser Leu Leu Trp Pro Leu Ala Ala Pro Gly Glu Leu Leu Leu
            20                  25                  30

Arg Asp Met Ser Val Val Asp His Pro Ala Leu Ser Leu Asn Ala Leu
        35                  40                  45

Gly Phe Gly Asp Leu Pro Ser Arg Asn Ala Pro Gln Asp Gly Val Leu
    50                  55                  60

Ala Leu Leu Gly Phe Leu Pro Val Ser Trp Ile Val Arg Thr Met Leu
65                  70                  75                  80

Leu Val Ala Gly Phe Ala Gly Ala Trp Gly Ala Met Arg Leu Gly Pro
                85                  90                  95

Ser Lys Phe Leu Ala Val Thr Val Ala Ile Tyr Asn Pro Phe Val Val
            100                 105                 110

Glu Arg Leu Leu Gln Gly His Trp Ser Leu Val Met Ala Val Trp Leu
        115                 120                 125

Phe Pro Leu Val Val Ala Leu Arg Arg His Pro Arg Trp Gln Val Val
    130                 135                 140

Ala Ile Trp Ala Ala Ser Leu Thr Pro Thr Gly Ala Val Val Ala Ala
145                 150                 155                 160

Val Thr Gly Val Ala Ser Ser Lys Arg Lys Arg Phe Thr Thr Leu Cys
                165                 170                 175

Ser Phe Leu Ser Trp Leu Pro Trp Leu Ile Pro Ala Leu Leu Ala Thr
            180                 185                 190

Pro Thr Ser Gly Gly Ala Leu Thr Phe Ala Ile Arg Ser Glu Thr Tyr
        195                 200                 205

Ala Gly Thr Leu Gly Thr Ala Leu Gly Leu Gly Gly Ile Trp Asn Ala
    210                 215                 220

Gly Ala Val Pro Ala Ser Arg Glu Leu Gly Phe Ala Val Ala Gly Ile
225                 230                 235                 240

Leu Leu Phe Ala Ile Leu Leu Ala Gly Phe Lys Asn Cys Pro Trp Val
                245                 250                 255

Leu Ala Leu Leu Ala Val Val Gly Phe Met Gly Ala Ile Gly Pro Trp
            260                 265                 270

Leu Met Pro Asn Leu Phe Thr Trp Thr Ile Ala Tyr Val Pro Gly Ala
        275                 280                 285

Ala Leu Phe Arg Asp Ser Gln Lys Leu Leu Met Leu Ala Ile Pro Ala
    290                 295                 300

Tyr Val Cys Leu Ala Ala Gly Val Lys Ser Pro Leu Ser Trp Val Ala
305                 310                 315                 320

Thr Gly Leu Ala Leu Leu Gln Ile Pro Asp Ala Pro Arg Glu Val Ser
```

```
                325                 330                 335

Val Ile Arg Pro Ser Ser Ala His Val Glu Ser Val Glu Ala Leu Ala
            340                 345                 350

Glu Ile Ala Asp Gly Arg Asp Ile Leu Ile Ile Gly Gln Gly Pro Leu
        355                 360                 365

Val Thr Arg Glu Asp Gly Ile Pro Val Val Asp Pro Lys Thr Lys Ala
    370                 375                 380

Leu Ser Val Val Glu Ser Gly Glu Leu Arg Val Asp Gly Ile Ile Thr
385                 390                 395                 400

Asp Ala Pro Ser Gln Arg Trp Thr Glu Ala Thr Gln Ala Trp Ala Ala
                405                 410                 415

Gly Asp Ile Glu Arg Leu Glu Glu Leu Gly Val Gly Val Val Val Asp
            420                 425                 430

Gly Asp Thr Ile Thr Glu Thr Gly Ala Pro Pro Gln His Gly Trp Lys
        435                 440                 445

Tyr Tyr Leu Gly Val Gly Leu Thr Val Leu Trp Met Ala Leu Pro Leu
    450                 455                 460

Gly Leu Leu Phe Arg Arg Lys Thr Lys Lys
465                 470


<210> 2803
<211> 1008
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(985)
<223> RXA02577

<400> 2803
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gcgtagtccc tcgagtgagc tgatgaatcc gcgatggcgg atg ggt gca tat gat   115
                                              Met Gly Ala Tyr Asp
                                                1               5

tgg gta gac att att tca aca tgc gag ttt agc gga aag gtg tgg gct   163
Trp Val Asp Ile Ile Ser Thr Cys Glu Phe Ser Gly Lys Val Trp Ala
                10                  15                  20

gtt ttt atg aag cga tct gca acg gtc ctc att att gcg ggc gtg ctg   211
Val Phe Met Lys Arg Ser Ala Thr Val Leu Ile Ile Ala Gly Val Leu
            25                  30                  35

ttc ctc att ttt gcc ttc acg gta ccg ccg tat gtg act ggt cag gcg   259
Phe Leu Ile Phe Ala Phe Thr Val Pro Pro Tyr Val Thr Gly Gln Ala
        40                  45                  50

cgg acg att ccg aag gat ttg gat ctg acg ttg gtg agc gaa agt ccg   307
Arg Thr Ile Pro Lys Asp Leu Asp Leu Thr Leu Val Ser Glu Ser Pro
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     55                  60                  65

cag ggg ttt gtg cgc act gaa cat att gtg act gct ccg acg gaa aag   355
Gln Gly Phe Val Arg Thr Glu His Ile Val Thr Ala Pro Thr Glu Lys
 70                  75                  80                  85

gtc gat gag atc gcg acg cat gtg gat cag aca gtt acg gat gtg cag   403
Val Asp Glu Ile Ala Thr His Val Asp Gln Thr Val Thr Asp Val Gln
                 90                  95                 100

ggg aaa act gtt gcg gaa att tcg gat gat gtg gtg ttg att gga cac   451
Gly Lys Thr Val Ala Glu Ile Ser Asp Asp Val Val Leu Ile Gly His
            105                 110                 115

tct cgt tat ccg gtg att aag ccg act gcc acc att tcg ggt tcg ccg   499
Ser Arg Tyr Pro Val Ile Lys Pro Thr Ala Thr Ile Ser Gly Ser Pro
        120                 125                 130

gcg gat agt agc aat gtg gtg cgg gag ggg ttg cat tac ttc ttc ccg   547
Ala Asp Ser Ser Asn Val Val Arg Glu Gly Leu His Tyr Phe Phe Pro
    135                 140                 145

gct aat acg ttg cgg aat tct tat ccc tat tat gac atc gta ttg ggt   595
Ala Asn Thr Leu Arg Asn Ser Tyr Pro Tyr Tyr Asp Ile Val Leu Gly
150                 155                 160                 165

gag gat tcc ccg gtg gat tat gtc tcg cgc gag ggc aat act tat acc   643
Glu Asp Ser Pro Val Asp Tyr Val Ser Arg Glu Gly Asn Thr Tyr Thr
                170                 175                 180

ttc tac cag cat ctt cgt tat gtt cca ttg gat gat tct cac acc tat   691
Phe Tyr Gln His Leu Arg Tyr Val Pro Leu Asp Asp Ser His Thr Tyr
            185                 190                 195

tcg gtg gag cgg acc ctg aaa gtg gat cgt ttt tcc ggc atc att gtg   739
Ser Val Glu Arg Thr Leu Lys Val Asp Arg Phe Ser Gly Ile Ile Val
        200                 205                 210

gct aaa gat gag gcg atg acg ttt cat ggc cca gac ggc gat gac aca   787
Ala Lys Asp Glu Ala Met Thr Phe His Gly Pro Asp Gly Asp Asp Thr
    215                 220                 225

gta gaa ttc act tat act gcg gat acg ttg aag ctt ctg cag gat cat   835
Val Glu Phe Thr Tyr Thr Ala Asp Thr Leu Lys Leu Leu Gln Asp His
230                 235                 240                 245

gcg cat gat att gat cag cgg ttg tcg tgg gct aag ggg ttt gat ttc   883
Ala His Asp Ile Asp Gln Arg Leu Ser Trp Ala Lys Gly Phe Asp Phe
                250                 255                 260

ttt tct aaa ttc tta ggc ctg tcg ttg ctt gcg att ggt gtg ttc ctc   931
Phe Ser Lys Phe Leu Gly Leu Ser Leu Leu Ala Ile Gly Val Phe Leu
            265                 270                 275

acg gga att ttc aag cgc ggc cag ctg atg agc act gtg aat aaa ctc   979
Thr Gly Ile Phe Lys Arg Gly Gln Leu Met Ser Thr Val Asn Lys Leu
        280                 285                 290

agg agt taaatcctta tgaccccgac ccg                                1008
Arg Ser
    295
```

<210> 2804
<211> 295
<212> PRT
<213> Corynebacterium glutamicum

<400> 2804

```
Met Gly Ala Tyr Asp Trp Val Asp Ile Ile Ser Thr Cys Glu Phe Ser
  1               5                  10                  15

Gly Lys Val Trp Ala Val Phe Met Lys Arg Ser Ala Thr Val Leu Ile
             20                  25                  30

Ile Ala Gly Val Leu Phe Leu Ile Phe Ala Phe Thr Val Pro Pro Tyr
         35                  40                  45

Val Thr Gly Gln Ala Arg Thr Ile Pro Lys Asp Leu Asp Leu Thr Leu
     50                  55                  60

Val Ser Glu Ser Pro Gln Gly Phe Val Arg Thr Glu His Ile Val Thr
 65                  70                  75                  80

Ala Pro Thr Glu Lys Val Asp Glu Ile Ala Thr His Val Asp Gln Thr
                 85                  90                  95

Val Thr Asp Val Gln Gly Lys Thr Val Ala Glu Ile Ser Asp Asp Val
            100                 105                 110

Val Leu Ile Gly His Ser Arg Tyr Pro Val Ile Lys Pro Thr Ala Thr
        115                 120                 125

Ile Ser Gly Ser Pro Ala Asp Ser Ser Asn Val Val Arg Glu Gly Leu
    130                 135                 140

His Tyr Phe Phe Pro Ala Asn Thr Leu Arg Asn Ser Tyr Pro Tyr Tyr
145                 150                 155                 160

Asp Ile Val Leu Gly Glu Asp Ser Pro Val Asp Tyr Val Ser Arg Glu
                165                 170                 175

Gly Asn Thr Tyr Thr Phe Tyr Gln His Leu Arg Tyr Val Pro Leu Asp
            180                 185                 190

Asp Ser His Thr Tyr Ser Val Glu Arg Thr Leu Lys Val Asp Arg Phe
        195                 200                 205

Ser Gly Ile Ile Val Ala Lys Asp Glu Ala Met Thr Phe His Gly Pro
    210                 215                 220

Asp Gly Asp Asp Thr Val Glu Phe Thr Tyr Thr Ala Asp Thr Leu Lys
225                 230                 235                 240

Leu Leu Gln Asp His Ala His Asp Ile Asp Gln Arg Leu Ser Trp Ala
                245                 250                 255

Lys Gly Phe Asp Phe Phe Ser Lys Phe Leu Gly Leu Ser Leu Leu Ala
            260                 265                 270

Ile Gly Val Phe Leu Thr Gly Ile Phe Lys Arg Gly Gln Leu Met Ser
        275                 280                 285
```

```
Thr Val Asn Lys Leu Arg Ser
    290                 295


<210> 2805
<211> 474
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(451)
<223> RXA02584

<400> 2805
gactcaaggc caatgaatcc ctggatgtgg aacaggatac gattaactca gactctaacc 60

gacagtccgc aattgaaagg ccagatacgt gaaccgctgg atg tcc ttg ctg tgt   115
                                        Met Ser Leu Leu Cys
                                          1               5

gat tcc atc gcc atc ggt ctc ttc gca ctc ttc gcc cgc gtc gcc cac   163
Asp Ser Ile Ala Ile Gly Leu Phe Ala Leu Phe Ala Arg Val Ala His
                 10                  15                  20

caa agc gcc gac atg cca cta aat gtg cag ggc tgg ttt ttc aca tgg   211
Gln Ser Ala Asp Met Pro Leu Asn Val Gln Gly Trp Phe Phe Thr Trp
             25                  30                  35

ctg cca ttc ctc gca ggt gtg ttc atc gcc tac ctg gtg gca atc ctc   259
Leu Pro Phe Leu Ala Gly Val Phe Ile Ala Tyr Leu Val Ala Ile Leu
         40                  45                  50

cct gcg aag ctt ccc agc gaa cgc atc cgc ccc gct ggc ctg acc gtg   307
Pro Ala Lys Leu Pro Ser Glu Arg Ile Arg Pro Ala Gly Leu Thr Val
     55                  60                  65

tgg ata ctc gcg gta att gtg gga ctt gtg att tgg ggc ttc aac aat   355
Trp Ile Leu Ala Val Ile Val Gly Leu Val Ile Trp Gly Phe Asn Asn
 70                  75                  80                  85

ggt ggg gtt cca cac tgg tcc ttc atg att gtc gca acg acc gcc tcc   403
Gly Gly Val Pro His Trp Ser Phe Met Ile Val Ala Thr Thr Ala Ser
                 90                  95                 100

gcc att ttg gtt ctc ggc tgg cga gcg ttg ttt aag gtg aca atg cgc   451
Ala Ile Leu Val Leu Gly Trp Arg Ala Leu Phe Lys Val Thr Met Arg
            105                 110                 115

taagtgcttt taaaaaatgg gag                                        474


<210> 2806
<211> 117
<212> PRT
<213> Corynebacterium glutamicum

<400> 2806
Met Ser Leu Leu Cys Asp Ser Ile Ala Ile Gly Leu Phe Ala Leu Phe
  1               5                  10                  15
```

```
Ala Arg Val Ala His Gln Ser Ala Asp Met Pro Leu Asn Val Gln Gly
             20                  25                  30

Trp Phe Phe Thr Trp Leu Pro Phe Leu Ala Gly Val Phe Ile Ala Tyr
         35                  40                  45

Leu Val Ala Ile Leu Pro Ala Lys Leu Pro Ser Glu Arg Ile Arg Pro
     50                  55                  60

Ala Gly Leu Thr Val Trp Ile Leu Ala Val Ile Val Gly Leu Val Ile
 65                  70                  75                  80

Trp Gly Phe Asn Asn Gly Gly Val Pro His Trp Ser Phe Met Ile Val
                 85                  90                  95

Ala Thr Thr Ala Ser Ala Ile Leu Val Leu Gly Trp Arg Ala Leu Phe
            100                 105                 110

Lys Val Thr Met Arg
        115
```

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<210> 2807
<211> 1104
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1081)
<223> RXA02585

<400> 2807

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gcgaggattt ttcagcaacc cctggattcg ttgggctttg tccctggcgt ttctaggggt 60

gatcctattt ttcctgaggg atcagctgga tttcctcaaa atg ggc atc caa caa   115
                                            Met Gly Ile Gln Gln
                                              1               5

atc cgc cac gtc agc ccc gta ggc gtt gcc ctc acc atg gtg gcg ttg   163
Ile Arg His Val Ser Pro Val Gly Val Ala Leu Thr Met Val Ala Leu
             10                  15                  20

gtg ttg tca ttc gtt gcg atg gcc aga gtc atg cag atc atg ttg aaa   211
Val Leu Ser Phe Val Ala Met Ala Arg Val Met Gln Ile Met Leu Lys
         25                  30                  35

gcc gga ggt agt cct gcg act ctc aaa gcc acc acg gct tta act ttt   259
Ala Gly Gly Ser Pro Ala Thr Leu Lys Ala Thr Thr Ala Leu Thr Phe
     40                  45                  50

gcg gct aac tcc tgg tcc gcg acc ctt cct ggc ggc ccg gcg ttt tcc   307
Ala Ala Asn Ser Trp Ser Ala Thr Leu Pro Gly Gly Pro Ala Phe Ser
 55                  60                  65

gcg att ctc acc tat aaa gtg cag cgc agc tgg ggt gcc agc gcc gtg   355
Ala Ile Leu Thr Tyr Lys Val Gln Arg Ser Trp Gly Ala Ser Ala Val
 70                  75                  80                  85

ctg tgt tcg tgg ttt ttc ctg ctc tcc agt gcc cta tcg acc gtc tgg   403
```

```
Leu Cys Ser Trp Phe Phe Leu Leu Ser Ser Ala Leu Ser Thr Val Trp
                 90                  95                 100

ttg gtt gct ctc ggt gtc atc gcc gtg ttt tat atg ggc gca tcg ctg   451
Leu Val Ala Leu Gly Val Ile Ala Val Phe Tyr Met Gly Ala Ser Leu
            105                 110                 115

aac tta tgg tca ctg atc gcc aca ttc atc gcc atg gtc ggg ctg tct   499
Asn Leu Trp Ser Leu Ile Ala Thr Phe Ile Ala Met Val Gly Leu Ser
        120                 125                 130

ggc gcc gtt tat tgg gca gcc aac aac ccc gac tcc ttg gct cgg tgg   547
Gly Ala Val Tyr Trp Ala Ala Asn Asn Pro Asp Ser Leu Ala Arg Trp
    135                 140                 145

gtg cga aaa ttg acg aaa aac agg gag tgg ggc ttc gtc gaa aag ctt   595
Val Arg Lys Leu Thr Lys Asn Arg Glu Trp Gly Phe Val Glu Lys Leu
150                 155                 160                 165

ctt gga agc att gag cag ctg cgc tcg gtc tcg ctc acc ggg ccg caa   643
Leu Gly Ser Ile Glu Gln Leu Arg Ser Val Ser Leu Thr Gly Pro Gln
                170                 175                 180

ttc gcg gcc agc acc gcg tgg tct tta ggc aat agg ctt ttc gac gcc   691
Phe Ala Ala Ser Thr Ala Trp Ser Leu Gly Asn Arg Leu Phe Asp Ala
            185                 190                 195

atc tcc ctc tgg att tgc atc tgg gcg gtc acc ggc act gcc ccg atg   739
Ile Ser Leu Trp Ile Cys Ile Trp Ala Val Thr Gly Thr Ala Pro Met
        200                 205                 210

ttt gaa cca gaa ccc aac aac acc acc atc gca ggc gta ctg ttg gcg   787
Phe Glu Pro Glu Pro Asn Asn Thr Thr Ile Ala Gly Val Leu Leu Ala
    215                 220                 225

tac acc acc gca aaa atc gca ggc tca atc caa gcc acc cca ggc gga   835
Tyr Thr Thr Ala Lys Ile Ala Gly Ser Ile Gln Ala Thr Pro Gly Gly
230                 235                 240                 245

atc ggc ccc atc gaa gcc gcc tac atc gca gcc ctc gta gcc acc ggt   883
Ile Gly Pro Ile Glu Ala Ala Tyr Ile Ala Ala Leu Val Ala Thr Gly
                250                 255                 260

atg acc gca gtg gaa gcc gcc gga gct gtc ata atc tac cgt tta tgc   931
Met Thr Ala Val Glu Ala Ala Gly Ala Val Ile Ile Tyr Arg Leu Cys
            265                 270                 275

tca ttt atc atc atg gcg att gtc gga tgg gtc atc tat ttt atc tat   979
Ser Phe Ile Ile Met Ala Ile Val Gly Trp Val Ile Tyr Phe Ile Tyr
        280                 285                 290

ttc acc ccc cag gga ctc aag gcc aat gaa tcc ctg gat gtg gaa cag   1027
Phe Thr Pro Gln Gly Leu Lys Ala Asn Glu Ser Leu Asp Val Glu Gln
    295                 300                 305

gat acg att aac tca gac tct aac cga cag tcc gca att gaa agg cca   1075
Asp Thr Ile Asn Ser Asp Ser Asn Arg Gln Ser Ala Ile Glu Arg Pro
310                 315                 320                 325

gat acg tgaaccgctg gatgtccttg ctg                                 1104
Asp Thr
```

<210> 2808
<211> 327
<212> PRT
<213> Corynebacterium glutamicum

<400> 2808
Met Gly Ile Gln Gln Ile Arg His Val Ser Pro Val Gly Val Ala Leu
1 5 10 15

Thr Met Val Ala Leu Val Leu Ser Phe Val Ala Met Ala Arg Val Met
20 25 30

Gln Ile Met Leu Lys Ala Gly Gly Ser Pro Ala Thr Leu Lys Ala Thr
35 40 45

Thr Ala Leu Thr Phe Ala Ala Asn Ser Trp Ser Ala Thr Leu Pro Gly
50 55 60

Gly Pro Ala Phe Ser Ala Ile Leu Thr Tyr Lys Val Gln Arg Ser Trp
65 70 75 80

Gly Ala Ser Ala Val Leu Cys Ser Trp Phe Phe Leu Leu Ser Ser Ala
85 90 95

Leu Ser Thr Val Trp Leu Val Ala Leu Gly Val Ile Ala Val Phe Tyr
100 105 110

Met Gly Ala Ser Leu Asn Leu Trp Ser Leu Ile Ala Thr Phe Ile Ala
115 120 125

Met Val Gly Leu Ser Gly Ala Val Tyr Trp Ala Ala Asn Asn Pro Asp
130 135 140

Ser Leu Ala Arg Trp Val Arg Lys Leu Thr Lys Asn Arg Glu Trp Gly
145 150 155 160

Phe Val Glu Lys Leu Leu Gly Ser Ile Glu Gln Leu Arg Ser Val Ser
165 170 175

Leu Thr Gly Pro Gln Phe Ala Ala Ser Thr Ala Trp Ser Leu Gly Asn
180 185 190

Arg Leu Phe Asp Ala Ile Ser Leu Trp Ile Cys Ile Trp Ala Val Thr
195 200 205

Gly Thr Ala Pro Met Phe Glu Pro Glu Pro Asn Asn Thr Thr Ile Ala
210 215 220

Gly Val Leu Leu Ala Tyr Thr Thr Ala Lys Ile Ala Gly Ser Ile Gln
225 230 235 240

Ala Thr Pro Gly Gly Ile Gly Pro Ile Glu Ala Ala Tyr Ile Ala Ala
245 250 255

Leu Val Ala Thr Gly Met Thr Ala Val Glu Ala Ala Gly Ala Val Ile
260 265 270

Ile Tyr Arg Leu Cys Ser Phe Ile Ile Met Ala Ile Val Gly Trp Val

```
        275                 280                 285

Ile Tyr Phe Ile Tyr Phe Thr Pro Gln Gly Leu Lys Ala Asn Glu Ser
    290                 295                 300

Leu Asp Val Glu Gln Asp Thr Ile Asn Ser Asp Ser Asn Arg Gln Ser
305                 310                 315                 320

Ala Ile Glu Arg Pro Asp Thr
                325
```

<210> 2809
<211> 807
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(784)
<223> RXA02588

<400> 2809

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ctcagctgac tgaccgtcag gtcatcacca agtttgaagg caaaggcttg gaaaaagatc 60

acgtgatcaa tgagtacttg tggcagaagg tgcaaaacta atg tct gat gtg cat   115
                                              Met Ser Asp Val His
                                                1               5

gag gtc att cat agc tac aat ccc act gac aaa gaa ggc cct gaa agt   163
Glu Val Ile His Ser Tyr Asn Pro Thr Asp Lys Glu Gly Pro Glu Ser
                  10                  15                  20

gtc ctt cta gtg tgg gac gct ccc aac cta gat atg ggt ttg ggc gct   211
Val Leu Leu Val Trp Asp Ala Pro Asn Leu Asp Met Gly Leu Gly Ala
              25                  30                  35

att ttg ggt ggt cgc cca acc gct gcg tac cga cct cgc ttt gat gcc   259
Ile Leu Gly Gly Arg Pro Thr Ala Ala Tyr Arg Pro Arg Phe Asp Ala
          40                  45                  50

atc ggt cgg tgg ttg ctt gct cgc gca ggt cgc agg gca cat gag ttg   307
Ile Gly Arg Trp Leu Leu Ala Arg Ala Gly Arg Arg Ala His Glu Leu
      55                  60                  65

ggc cgc cac att gag cct gag gca acg gtg ttt gcc aac atc acc cca   355
Gly Arg His Ile Glu Pro Glu Ala Thr Val Phe Ala Asn Ile Thr Pro
  70                  75                  80                  85

ggt ggc tct gat gtt gtt cga cct tgg gtg gaa gcg ctg cgt aac gtt   403
Gly Gly Ser Asp Val Val Arg Pro Trp Val Glu Ala Leu Arg Asn Val
                  90                  95                 100

ggt ttc gcg gtc ttc gct aag cct aag atc ggc gag gat tcc gat gtc   451
Gly Phe Ala Val Phe Ala Lys Pro Lys Ile Gly Glu Asp Ser Asp Val
              105                 110                 115

gat ccg gac atg att gat cac att cgc agg cgc tat gaa gaa ggc gtg   499
Asp Pro Asp Met Ile Asp His Ile Arg Arg Arg Tyr Glu Glu Gly Val
          120                 125                 130
```

```
ctg cgg ggt gtc atc gtg gcc agt gca gat ggt cag aac ttc cgt gag   547
Leu Arg Gly Val Ile Val Ala Ser Ala Asp Gly Gln Asn Phe Arg Glu
    135                 140                 145

act ctc gag gag ctc gtt gca gag ggc att cct gcc acg gtc att ggt   595
Thr Leu Glu Glu Leu Val Ala Glu Gly Ile Pro Ala Thr Val Ile Gly
150                 155                 160                 165

ttc cac gag cac gcg tca tgg gct gta gct cat gac acc atc gag ttt   643
Phe His Glu His Ala Ser Trp Ala Val Ala His Asp Thr Ile Glu Phe
                170                 175                 180

gtt gat ctg gag gaa atc ccc ggc gtc ttc cgt gag ccg ctt cct cgc   691
Val Asp Leu Glu Glu Ile Pro Gly Val Phe Arg Glu Pro Leu Pro Arg
            185                 190                 195

gtc agc ctg gat aac ctg cca gac ggt ggc gca tgg ctg cag ccg ttc   739
Val Ser Leu Asp Asn Leu Pro Asp Gly Gly Ala Trp Leu Gln Pro Phe
        200                 205                 210

cgc cct ctg act gcc ttg tta tcc aac cgc cac aat tcc cag gag       784
Arg Pro Leu Thr Ala Leu Leu Ser Asn Arg His Asn Ser Gln Glu
    215                 220                 225

taatccaccc gtgttttcta aat                                        807
```

<210> 2810
<211> 228
<212> PRT
<213> Corynebacterium glutamicum

<400> 2810

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Met Ser Asp Val His Glu Val Ile His Ser Tyr Asn Pro Thr Asp Lys
  1               5                  10                  15

Glu Gly Pro Glu Ser Val Leu Leu Val Trp Asp Ala Pro Asn Leu Asp
             20                  25                  30

Met Gly Leu Gly Ala Ile Leu Gly Gly Arg Pro Thr Ala Ala Tyr Arg
         35                  40                  45

Pro Arg Phe Asp Ala Ile Gly Arg Trp Leu Leu Ala Arg Ala Gly Arg
     50                  55                  60

Arg Ala His Glu Leu Gly Arg His Ile Glu Pro Glu Ala Thr Val Phe
 65                  70                  75                  80

Ala Asn Ile Thr Pro Gly Gly Ser Asp Val Val Arg Pro Trp Val Glu
                 85                  90                  95

Ala Leu Arg Asn Val Gly Phe Ala Val Phe Ala Lys Pro Lys Ile Gly
            100                 105                 110

Glu Asp Ser Asp Val Asp Pro Asp Met Ile Asp His Ile Arg Arg Arg
        115                 120                 125

Tyr Glu Glu Gly Val Leu Arg Gly Val Ile Val Ala Ser Ala Asp Gly
    130                 135                 140

Gln Asn Phe Arg Glu Thr Leu Glu Glu Leu Val Ala Glu Gly Ile Pro
```

```
145                 150                 155                 160

Ala Thr Val Ile Gly Phe His Glu His Ala Ser Trp Ala Val Ala His
                165                 170                 175

Asp Thr Ile Glu Phe Val Asp Leu Glu Glu Ile Pro Gly Val Phe Arg
            180                 185                 190

Glu Pro Leu Pro Arg Val Ser Leu Asp Asn Leu Pro Asp Gly Gly Ala
        195                 200                 205

Trp Leu Gln Pro Phe Arg Pro Leu Thr Ala Leu Leu Ser Asn Arg His
    210                 215                 220

Asn Ser Gln Glu
225
```

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<210> 2811
<211> 1953
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1930)
<223> RXA02591

<400> 2811

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atgtgtccgt tgtctcacct aaagttttaa ctagttctgt atctgaaagc tacgctaggg 60

ggcgagaact ctgtcgaatg acacaaaatc tggagaagta atg act act gct gca   115
                                            Met Thr Thr Ala Ala
                                              1               5

atc agg ggc ctt cag ggc gag gcg ccg acc aag aat aag gaa ctg ctg   163
Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys Asn Lys Glu Leu Leu
                  10                  15                  20

aac tgg atc gca gac gcc gtc gag ctc ttc cag cct gag gct gtt gtg   211
Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln Pro Glu Ala Val Val
              25                  30                  35

ttc gtt gat gga tcc cag gct gag tgg gat cgc atg gcg gag gat ctt   259
Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg Met Ala Glu Asp Leu
          40                  45                  50

gtt gaa gcc ggt acc ctc atc aag ctc aac gag gaa aag cgt ccg aac   307
Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu Glu Lys Arg Pro Asn
      55                  60                  65

agc tac cta gct cgt tcc aac cca tct gac gtt gcg cgc gtt gag tcc   355
Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val Ala Arg Val Glu Ser
  70                  75                  80                  85

cgc acc ttc atc tgc tcc gag aag gaa gaa gat gct ggc cca acc aac   403
Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp Ala Gly Pro Thr Asn
                  90                  95                 100

aac tgg gct cca cca cag gca atg aag gac gaa atg tcc aag cat tac   451
Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu Met Ser Lys His Tyr
```

```
                105                 110                 115

gct ggt tcc atg aag ggg cgc acc atg tac gtc gtg cct ttc tgc atg   499
Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val Val Pro Phe Cys Met
        120                 125                 130

ggt cca atc agc gat ccg gac cct aag ctt ggt gtg cag ctc act gac   547
Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly Val Gln Leu Thr Asp
    135                 140                 145

tcc gag tac gtt gtc atg tcc atg cgc atc atg acc cgc atg ggt att   595
Ser Glu Tyr Val Val Met Ser Met Arg Ile Met Thr Arg Met Gly Ile
150                 155                 160                 165

gaa gcg ctg gac aag atc ggc gcg aac ggc agc ttc gtc agg tgc ctc   643
Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser Phe Val Arg Cys Leu
                170                 175                 180

cac tcc gtt ggt gct cct ttg gag cca ggc cag gaa gac gtt gca tgg   691
His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln Glu Asp Val Ala Trp
            185                 190                 195

cct tgc aac gac acc aag tac atc acc cag ttc cca gag acc aag gaa   739
Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe Pro Glu Thr Lys Glu
        200                 205                 210

att tgg tcc tac ggt tcc ggc tac ggc gga aac gca atc ctg gca aag   787
Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn Ala Ile Leu Ala Lys
    215                 220                 225

aag tgc tac gca ctg cgt atc gca tct gtc atg gct cgc gaa gaa gga   835
Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met Ala Arg Glu Glu Gly
230                 235                 240                 245

tgg atg gct gag cac atg ctc atc ctg aag ctg atc aac cca gag ggc   883
Trp Met Ala Glu His Met Leu Ile Leu Lys Leu Ile Asn Pro Glu Gly
                250                 255                 260

aag gcg tac cac atc gca gca gca ttc cca tct gct tgt ggc aag acc   931
Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser Ala Cys Gly Lys Thr
            265                 270                 275

aac ctc gcc atg atc act cca acc atc cca ggc tgg acc gct cag gtt   979
Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly Trp Thr Ala Gln Val
        280                 285                 290

gtt ggc gac gac atc gct tgg ctg aag ctg cgc gag gac ggc ctc tac   1027
Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg Glu Asp Gly Leu Tyr
    295                 300                 305

gca gtt aac cca gaa aat ggt ttc ttc ggt gtt gct cca ggc acc aac   1075
Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val Ala Pro Gly Thr Asn
310                 315                 320                 325

tac gca tcc aac cca atc gcg atg aag acc atg gaa cca ggc aac acc   1123
Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met Glu Pro Gly Asn Thr
                330                 335                 340

ctg ttc acc aac gtg gca ctc acc gac gac ggc gac atc tgg tgg gaa   1171
Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly Asp Ile Trp Trp Glu
            345                 350                 355
```

```
ggc atg gac ggc gac gcc cca gct cac ctc att gac tgg atg ggc aac   1219
Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile Asp Trp Met Gly Asn
        360                 365                 370

gac tgg acc cca gag tcc gac gaa aac gct gct cac cct aac tcc cgt   1267
Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala His Pro Asn Ser Arg
    375                 380                 385

tac tgc gta gca atc gac cag tcc cca gca gca gca cct gag ttc aac   1315
Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala Ala Pro Glu Phe Asn
390                 395                 400                 405

gac tgg gaa ggc gtc aag atc gac gca atc ctc ttc ggt gga cgt cgc   1363
Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu Phe Gly Gly Arg Arg
                410                 415                 420

gca gac acc gtc cca ctg gtt acc cag acc tac gac tgg gag cac ggc   1411
Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr Asp Trp Glu His Gly
            425                 430                 435

acc atg gtt ggt gca ctg ctc gca tcc ggt cag acc gca gct tcc gca   1459
Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln Thr Ala Ala Ser Ala
        440                 445                 450

gaa gca aag gtc ggc aca ctc cgc cac gac cca atg gca atg ctc cca   1507
Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro Met Ala Met Leu Pro
    455                 460                 465

ttc att ggc tac aac gct ggt gaa tac ctg cag aac tgg att gac atg   1555
Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln Asn Trp Ile Asp Met
470                 475                 480                 485

ggt aac aag ggt ggc gac aag atg cca tcc atc ttc ctg gtc aac tgg   1603
Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile Phe Leu Val Asn Trp
                490                 495                 500

ttc cgc cgt ggc gaa gat gga cgc ttc ctg tgg cct ggc ttc ggc gac   1651
Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp Pro Gly Phe Gly Asp
            505                 510                 515

aac tct cgc gtt ctg aag tgg gtc atc gac cgc atc gaa ggc cac gtt   1699
Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg Ile Glu Gly His Val
        520                 525                 530

ggc gca gac gag acc gtt gtt gga cac acc gct aag gcc gaa gac ctc   1747
Gly Ala Asp Glu Thr Val Val Gly His Thr Ala Lys Ala Glu Asp Leu
    535                 540                 545

gac ctc gac ggc ctc gac acc cca att gag gat gtc aag gaa gca ctg   1795
Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp Val Lys Glu Ala Leu
550                 555                 560                 565

acc gct cct gca gag cag tgg gca aac gac gtt gaa gac aac gcc gag   1843
Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val Glu Asp Asn Ala Glu
                570                 575                 580

tac ctc act ttc ctc gga cca cgt gtt cct gca gag gtt cac agc cag   1891
Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala Glu Val His Ser Gln
            585                 590                 595
```

```
ttc gat gct ctg aag gcc cgc att tca gca gct cac gct taaagttcac    1940
Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala His Ala
        600                 605                 610

gcttaagaac tgc                                                   1953
```

<210> 2812
<211> 610
<212> PRT
<213> Corynebacterium glutamicum

<400> 2812

```
Met Thr Thr Ala Ala Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys
  1               5                  10                  15

Asn Lys Glu Leu Leu Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln
             20                  25                  30

Pro Glu Ala Val Val Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg
         35                  40                  45

Met Ala Glu Asp Leu Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu
     50                  55                  60

Glu Lys Arg Pro Asn Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val
 65                  70                  75                  80

Ala Arg Val Glu Ser Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp
                 85                  90                  95

Ala Gly Pro Thr Asn Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu
            100                 105                 110

Met Ser Lys His Tyr Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val
        115                 120                 125

Val Pro Phe Cys Met Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly
    130                 135                 140

Val Gln Leu Thr Asp Ser Glu Tyr Val Val Met Ser Met Arg Ile Met
145                 150                 155                 160

Thr Arg Met Gly Ile Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser
                165                 170                 175

Phe Val Arg Cys Leu His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln
            180                 185                 190

Glu Asp Val Ala Trp Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe
        195                 200                 205

Pro Glu Thr Lys Glu Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn
    210                 215                 220

Ala Ile Leu Ala Lys Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met
225                 230                 235                 240

Ala Arg Glu Glu Gly Trp Met Ala Glu His Met Leu Ile Leu Lys Leu
                245                 250                 255
```

```
Ile Asn Pro Glu Gly Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser
            260                 265                 270

Ala Cys Gly Lys Thr Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly
        275                 280                 285

Trp Thr Ala Gln Val Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg
    290                 295                 300

Glu Asp Gly Leu Tyr Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val
305                 310                 315                 320

Ala Pro Gly Thr Asn Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met
                325                 330                 335

Glu Pro Gly Asn Thr Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly
            340                 345                 350

Asp Ile Trp Trp Glu Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile
        355                 360                 365

Asp Trp Met Gly Asn Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala
    370                 375                 380

His Pro Asn Ser Arg Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala
385                 390                 395                 400

Ala Pro Glu Phe Asn Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu
                405                 410                 415

Phe Gly Gly Arg Arg Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr
            420                 425                 430

Asp Trp Glu His Gly Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln
        435                 440                 445

Thr Ala Ala Ser Ala Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro
    450                 455                 460

Met Ala Met Leu Pro Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln
465                 470                 475                 480

Asn Trp Ile Asp Met Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile
                485                 490                 495

Phe Leu Val Asn Trp Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp
            500                 505                 510

Pro Gly Phe Gly Asp Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg
        515                 520                 525

Ile Glu Gly His Val Gly Ala Asp Glu Thr Val Val Gly His Thr Ala
    530                 535                 540

Lys Ala Glu Asp Leu Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp
545                 550                 555                 560

Val Lys Glu Ala Leu Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val
                565                 570                 575

Glu Asp Asn Ala Glu Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala
```

```
            580                 585                 590

Glu Val His Ser Gln Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala
        595                 600                 605

His Ala
    610


<210> 2813
<211> 714
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(691)
<223> RXA02598

<400> 2813
ctttgggaaa gtacccccta tgacggaaaa ctggatggat cctgtggttg aaccacagtc 60

aacgggagag gggaaatcgg acactatatg gttggagatc gtg aca act gac caa   115
                                            Val Thr Thr Asp Gln
                                              1               5

aac aaa aga agt ctc agt gag ctt gcg gcc aga atc gtt agt gaa atc   163
Asn Lys Arg Ser Leu Ser Glu Leu Ala Ala Arg Ile Val Ser Glu Ile
                  10                  15                  20

tgt gca ccg tgg gta ctc aac atc gga ttt ttc ctc atc ctg ggc ggc   211
Cys Ala Pro Trp Val Leu Asn Ile Gly Phe Phe Leu Ile Leu Gly Gly
              25                  30                  35

gta aca ggc gcc tgg acg cta gga att gtg gcg gca atc gga acc gga   259
Val Thr Gly Ala Trp Thr Leu Gly Ile Val Ala Ala Ile Gly Thr Gly
          40                  45                  50

atc gtt ccg atg atc tta att ttg ggc ttg atg aag ctc ggc agg gta   307
Ile Val Pro Met Ile Leu Ile Leu Gly Leu Met Lys Leu Gly Arg Val
      55                  60                  65

gga aac cac cat gtg acg acc cga aat cag cgc ggc ctt gtg ttt gtg   355
Gly Asn His His Val Thr Thr Arg Asn Gln Arg Gly Leu Val Phe Val
  70                  75                  80                  85

ggc atc att gtt tgt gtc atc att ttg att ttt atc ctc aga gcc ctt   403
Gly Ile Ile Val Cys Val Ile Ile Leu Ile Phe Ile Leu Arg Ala Leu
                  90                  95                 100

gaa gca cct cag ctg att tgg gat ggc atg ttc tca gca ctg att ttc   451
Glu Ala Pro Gln Leu Ile Trp Asp Gly Met Phe Ser Ala Leu Ile Phe
              105                 110                 115

tta gtt ctg ttt gca caa gtg acg ttg aaa att aaa gcc tca gtt cat   499
Leu Val Leu Phe Ala Gln Val Thr Leu Lys Ile Lys Ala Ser Val His
          120                 125                 130

gtt ggg ctg tgg gtg tgt tta gtg atg ttc ctc ggt ctg acg gtt tct   547
Val Gly Leu Trp Val Cys Leu Val Met Phe Leu Gly Leu Thr Val Ser
      135                 140                 145
```

```
tcg tgg tgg tta ctc ggg ttg ctg ttt acc cca gtc acc gcg tgg gca   595
Ser Trp Trp Leu Leu Gly Leu Leu Phe Thr Pro Val Thr Ala Trp Ala
150                 155                 160                 165

cgt atg cgg atc aag cat cat acg atg tcg gag att gtg gcg ggc gtt   643
Arg Met Arg Ile Lys His His Thr Met Ser Glu Ile Val Ala Gly Val
                170                 175                 180

gtt aca gga gca gtt gca acc ggc att tgt tat gca ctc cta ctt gcg   691
Val Thr Gly Ala Val Ala Thr Gly Ile Cys Tyr Ala Leu Leu Leu Ala
            185                 190                 195

taaaggagaa ttatggatca gct                                       714
```

<210> 2814
<211> 197
<212> PRT
<213> Corynebacterium glutamicum

<400> 2814

```
Val Thr Thr Asp Gln Asn Lys Arg Ser Leu Ser Glu Leu Ala Ala Arg
  1               5                  10                  15

Ile Val Ser Glu Ile Cys Ala Pro Trp Val Leu Asn Ile Gly Phe Phe
             20                  25                  30

Leu Ile Leu Gly Gly Val Thr Gly Ala Trp Thr Leu Gly Ile Val Ala
         35                  40                  45

Ala Ile Gly Thr Gly Ile Val Pro Met Ile Leu Ile Leu Gly Leu Met
     50                  55                  60

Lys Leu Gly Arg Val Gly Asn His His Val Thr Thr Arg Asn Gln Arg
 65                  70                  75                  80

Gly Leu Val Phe Val Gly Ile Ile Val Cys Val Ile Ile Leu Ile Phe
                 85                  90                  95

Ile Leu Arg Ala Leu Glu Ala Pro Gln Leu Ile Trp Asp Gly Met Phe
            100                 105                 110

Ser Ala Leu Ile Phe Leu Val Leu Phe Ala Gln Val Thr Leu Lys Ile
        115                 120                 125

Lys Ala Ser Val His Val Gly Leu Trp Val Cys Leu Val Met Phe Leu
    130                 135                 140

Gly Leu Thr Val Ser Ser Trp Trp Leu Leu Gly Leu Leu Phe Thr Pro
145                 150                 155                 160

Val Thr Ala Trp Ala Arg Met Arg Ile Lys His His Thr Met Ser Glu
                165                 170                 175

Ile Val Ala Gly Val Val Thr Gly Ala Val Ala Thr Gly Ile Cys Tyr
            180                 185                 190

Ala Leu Leu Leu Ala
        195
```

<210> 2815
<211> 1521
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1498)
<223> RXA02600

<400> 2815
gattttgctt ttcgacgcac cgttcggccg ttatctagat ctggtcacaa tgtcggtttt 60

tcatggattc atgtccttta tcggacgtac tgtggggagt atg caa cct ttt cca 115
Met Gln Pro Phe Pro
1 5

ctg tcc tta acc aac agc tcc gtc gct ggt att gca gcg gga gcg ttg 163
Leu Ser Leu Thr Asn Ser Ser Val Ala Gly Ile Ala Ala Gly Ala Leu
10 15 20

ctg ttt ctc tcc gtc cct ttc gca tcg cct gtt cac gcg caa acc ata 211
Leu Phe Leu Ser Val Pro Phe Ala Ser Pro Val His Ala Gln Thr Ile
25 30 35

ctg caa gac acc ctt gaa gtg act gtg ttg gat aat gcc gac gag ctc 259
Leu Gln Asp Thr Leu Glu Val Thr Val Leu Asp Asn Ala Asp Glu Leu
40 45 50

gct cca gag gat gag gat ttc ctc agc acg gaa aca ccc aag att gat 307
Ala Pro Glu Asp Glu Asp Phe Leu Ser Thr Glu Thr Pro Lys Ile Asp
55 60 65

ttc cct gac tca gtt acc gca gtc cgg tac atc acg ctc acg gac aac 355
Phe Pro Asp Ser Val Thr Ala Val Arg Tyr Ile Thr Leu Thr Asp Asn
70 75 80 85

act gac aaa atc aat gat gac gtt gaa aat tac ctg cgc gcc gaa cac 403
Thr Asp Lys Ile Asn Asp Asp Val Glu Asn Tyr Leu Arg Ala Glu His
90 95 100

ccc gag tgg atc caa aca aac tct ttc gcc cct ggt gaa gtg atc atc 451
Pro Glu Trp Ile Gln Thr Asn Ser Phe Ala Pro Gly Glu Val Ile Ile
105 110 115

gca gtc ggt ttc gac ccc aac acc atg ggt gcc tac gcg ggt aac gat 499
Ala Val Gly Phe Asp Pro Asn Thr Met Gly Ala Tyr Ala Gly Asn Asp
120 125 130

gtg gcc gca gag act ggg atc gca gaa caa gac cgc atc gac ggc acc 547
Val Ala Ala Glu Thr Gly Ile Ala Glu Gln Asp Arg Ile Asp Gly Thr
135 140 145

acc gat gcg atg cgc cca tta ctc caa gac ggt cgc att gcc cta ggc 595
Thr Asp Ala Met Arg Pro Leu Leu Gln Asp Gly Arg Ile Ala Leu Gly
150 155 160 165

atg ttg gag ggt gca aaa tcg gtt gct gat acc tct gtc gtt cgg gaa 643
Met Leu Glu Gly Ala Lys Ser Val Ala Asp Thr Ser Val Val Arg Glu
170 175 180

```
agc tca gct cca agt ggt gga gta atc gcc gct att ttg ggt ggc atc   691
Ser Ser Ala Pro Ser Gly Gly Val Ile Ala Ala Ile Leu Gly Gly Ile
            185                 190                 195

gct gct ctc gtg gca att att gtc gcg tgg gct acg agt tac gcg aat   739
Ala Ala Leu Val Ala Ile Ile Val Ala Trp Ala Thr Ser Tyr Ala Asn
        200                 205                 210

aag aag aag gca gaa aag gct cgt gag cag ttt gat tat gca tca cgc   787
Lys Lys Lys Ala Glu Lys Ala Arg Glu Gln Phe Asp Tyr Ala Ser Arg
    215                 220                 225

cat tat ggt gag gtc gcc cag caa ctc gac ggt atc aac gtg cga gcg   835
His Tyr Gly Glu Val Ala Gln Gln Leu Asp Gly Ile Asn Val Arg Ala
230                 235                 240                 245

cac tcg cta act tcc cca ctg gct gat gat gag ctc cgc agg caa tgg   883
His Ser Leu Thr Ser Pro Leu Ala Asp Asp Glu Leu Arg Arg Gln Trp
                250                 255                 260

gac gat gta aat tct cgt ttt ctt gaa gtc aat gat att ttt ggc agg   931
Asp Asp Val Asn Ser Arg Phe Leu Glu Val Asn Asp Ile Phe Gly Arg
            265                 270                 275

ctc gaa ggt ttg acc tcg acc tca gaa aac aag gca ttt cga aaa gcc   979
Leu Glu Gly Leu Thr Ser Thr Ser Glu Asn Lys Ala Phe Arg Lys Ala
        280                 285                 290

ttg cca gat att gaa aaa gct cat act gcc gtg act caa atg gag atc   1027
Leu Pro Asp Ile Glu Lys Ala His Thr Ala Val Thr Gln Met Glu Ile
    295                 300                 305

gca cag aaa aac att gac acg ctc tac gat atg gag cac ggc cat gaa   1075
Ala Gln Lys Asn Ile Asp Thr Leu Tyr Asp Met Glu His Gly His Glu
310                 315                 320                 325

gac acc cgt cgc agg gaa tta act agg ctg cgt gcc gat atg cag gaa   1123
Asp Thr Arg Arg Arg Glu Leu Thr Arg Leu Arg Ala Asp Met Gln Glu
                330                 335                 340

gcc cgt caa gat atc aac gat aaa gat gca gtt gtt gac gat att ctc   1171
Ala Arg Gln Asp Ile Asn Asp Lys Asp Ala Val Val Asp Asp Ile Leu
            345                 350                 355

cgc acg ctg atc cag cgc acg gaa act atc gca ccg tcc gca cct gat   1219
Arg Thr Leu Ile Gln Arg Thr Glu Thr Ile Ala Pro Ser Ala Pro Asp
        360                 365                 370

ttc atg gac caa tac gcc cgc ttg atc cgt gat tat gcc gtg gcg ctt   1267
Phe Met Asp Gln Tyr Ala Arg Leu Ile Arg Asp Tyr Ala Val Ala Leu
    375                 380                 385

caa ggt gtg gaa aag aac ctc gag cag gtt aaa cag acc acc gag cgc   1315
Gln Gly Val Glu Lys Asn Leu Glu Gln Val Lys Gln Thr Thr Glu Arg
390                 395                 400                 405

aat gct cca gcc atc tac gac gac aat tgg cgc gtg ggc act ggc tac   1363
Asn Ala Pro Ala Ile Tyr Asp Asp Asn Trp Arg Val Gly Thr Gly Tyr
                410                 415                 420
```

```
aac tcg tgg gtc ccg tac tac atg atc agt tct tgg cac gca gct gat   1411
Asn Ser Trp Val Pro Tyr Tyr Met Ile Ser Ser Trp His Ala Ala Asp
            425                 430                 435

gtc agt gct gca tcg tca gct tct tcc agt tca gca aat acc act ttc   1459
Val Ser Ala Ala Ser Ser Ala Ser Ser Ser Ser Ala Asn Thr Thr Phe
        440                 445                 450

agc agt ggt ttc agc ggc gct gga gga ggt tcc agc tgg taaacaccac    1508
Ser Ser Gly Phe Ser Gly Ala Gly Gly Gly Ser Ser Trp
    455                 460                 465

cactgaagtc aac                                                   1521
```

<210> 2816
<211> 466
<212> PRT
<213> Corynebacterium glutamicum

<400> 2816

```
Met Gln Pro Phe Pro Leu Ser Leu Thr Asn Ser Ser Val Ala Gly Ile
  1               5                  10                  15

Ala Ala Gly Ala Leu Leu Phe Leu Ser Val Pro Phe Ala Ser Pro Val
             20                  25                  30

His Ala Gln Thr Ile Leu Gln Asp Thr Leu Glu Val Thr Val Leu Asp
         35                  40                  45

Asn Ala Asp Glu Leu Ala Pro Glu Asp Glu Asp Phe Leu Ser Thr Glu
     50                  55                  60

Thr Pro Lys Ile Asp Phe Pro Asp Ser Val Thr Ala Val Arg Tyr Ile
 65                  70                  75                  80

Thr Leu Thr Asp Asn Thr Asp Lys Ile Asn Asp Asp Val Glu Asn Tyr
                 85                  90                  95

Leu Arg Ala Glu His Pro Glu Trp Ile Gln Thr Asn Ser Phe Ala Pro
            100                 105                 110

Gly Glu Val Ile Ile Ala Val Gly Phe Asp Pro Asn Thr Met Gly Ala
        115                 120                 125

Tyr Ala Gly Asn Asp Val Ala Ala Glu Thr Gly Ile Ala Glu Gln Asp
    130                 135                 140

Arg Ile Asp Gly Thr Thr Asp Ala Met Arg Pro Leu Leu Gln Asp Gly
145                 150                 155                 160

Arg Ile Ala Leu Gly Met Leu Glu Gly Ala Lys Ser Val Ala Asp Thr
                165                 170                 175

Ser Val Val Arg Glu Ser Ser Ala Pro Ser Gly Gly Val Ile Ala Ala
            180                 185                 190

Ile Leu Gly Gly Ile Ala Ala Leu Val Ala Ile Ile Val Ala Trp Ala
        195                 200                 205

Thr Ser Tyr Ala Asn Lys Lys Lys Ala Glu Lys Ala Arg Glu Gln Phe
```

```
    210                 215                 220

Asp Tyr Ala Ser Arg His Tyr Gly Glu Val Ala Gln Gln Leu Asp Gly
225                 230                 235                 240

Ile Asn Val Arg Ala His Ser Leu Thr Ser Pro Leu Ala Asp Asp Glu
                245                 250                 255

Leu Arg Arg Gln Trp Asp Asp Val Asn Ser Arg Phe Leu Glu Val Asn
            260                 265                 270

Asp Ile Phe Gly Arg Leu Glu Gly Leu Thr Ser Thr Ser Glu Asn Lys
        275                 280                 285

Ala Phe Arg Lys Ala Leu Pro Asp Ile Glu Lys Ala His Thr Ala Val
    290                 295                 300

Thr Gln Met Glu Ile Ala Gln Lys Asn Ile Asp Thr Leu Tyr Asp Met
305                 310                 315                 320

Glu His Gly His Glu Asp Thr Arg Arg Arg Glu Leu Thr Arg Leu Arg
                325                 330                 335

Ala Asp Met Gln Glu Ala Arg Gln Asp Ile Asn Asp Lys Asp Ala Val
            340                 345                 350

Val Asp Asp Ile Leu Arg Thr Leu Ile Gln Arg Thr Glu Thr Ile Ala
        355                 360                 365

Pro Ser Ala Pro Asp Phe Met Asp Gln Tyr Ala Arg Leu Ile Arg Asp
    370                 375                 380

Tyr Ala Val Ala Leu Gln Gly Val Glu Lys Asn Leu Glu Gln Val Lys
385                 390                 395                 400

Gln Thr Thr Glu Arg Asn Ala Pro Ala Ile Tyr Asp Asp Asn Trp Arg
                405                 410                 415

Val Gly Thr Gly Tyr Asn Ser Trp Val Pro Tyr Tyr Met Ile Ser Ser
            420                 425                 430

Trp His Ala Ala Asp Val Ser Ala Ala Ser Ser Ala Ser Ser Ser Ser
        435                 440                 445

Ala Asn Thr Thr Phe Ser Ser Gly Phe Ser Gly Ala Gly Gly Gly Ser
    450                 455                 460

Ser Trp
465


<210> 2817
<211> 2112
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2089)
<223> RXA02601
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<400> 2817
ctcatacaat tgccaggatc ttccatggcg gatacggcgc gtaagttctg tgaatgcggg 60

gtccggatac tacgcttagg caagataaat tgtgagttca atg aag ggt gaa gat 115
Met Lys Gly Glu Asp
1 5

acg tca atg agc gca aca aac ctg gcg gtt gag cag cta cag cga gtg 163
Thr Ser Met Ser Ala Thr Asn Leu Ala Val Glu Gln Leu Gln Arg Val
10 15 20

ctc ctg ccg agg cgc ggc gag cca gca gat gtc agg tcg ttg tac ctg 211
Leu Leu Pro Arg Arg Gly Glu Pro Ala Asp Val Arg Ser Leu Tyr Leu
25 30 35

ttg gaa gca gaa agt aat aag gaa cgc ctg gaa tgg gaa gat cgt ttt 259
Leu Glu Ala Glu Ser Asn Lys Glu Arg Leu Glu Trp Glu Asp Arg Phe
40 45 50

agc gtt tcc gtc ccc gct ggc gcc gag gtg tct ttt cag acc tac ttc 307
Ser Val Ser Val Pro Ala Gly Ala Glu Val Ser Phe Gln Thr Tyr Phe
55 60 65

aat gca ttt cct gca agc tac tgg cgt cgc tgg tca cag cta gat tct 355
Asn Ala Phe Pro Ala Ser Tyr Trp Arg Arg Trp Ser Gln Leu Asp Ser
70 75 80 85

gtc gta ctg aaa ctg aaa gtt tcc ggc gaa gcg cgc gtc gac ctc tac 403
Val Val Leu Lys Leu Lys Val Ser Gly Glu Ala Arg Val Asp Leu Tyr
90 95 100

cga tcc aag atc gat gga gca cgc atc gga att acc ggt tcc gta gtc 451
Arg Ser Lys Ile Asp Gly Ala Arg Ile Gly Ile Thr Gly Ser Val Val
105 110 115

aaa gat gac ttc atc gaa ttt gaa gtt tca tta gcc cca ttc gaa gac 499
Lys Asp Asp Phe Ile Glu Phe Glu Val Ser Leu Ala Pro Phe Glu Asp
120 125 130

ggc ggc tgg atc tgg ttc gac ctc acc gct gaa acc gac gca acc gtc 547
Gly Gly Trp Ile Trp Phe Asp Leu Thr Ala Glu Thr Asp Ala Thr Val
135 140 145

gaa gaa gca ggc tgg tac gct cca cac gcg cca aaa gcc cag atc atg 595
Glu Glu Ala Gly Trp Tyr Ala Pro His Ala Pro Lys Ala Gln Ile Met
150 155 160 165

cca gat gga tct gaa gtc ggc cca ttt gaa gcc cgt gca acc gtc gga 643
Pro Asp Gly Ser Glu Val Gly Pro Phe Glu Ala Arg Ala Thr Val Gly
170 175 180

atc ccg acc ttc aac cgc cca gct gat gca gtt gca gca ctg gaa gca 691
Ile Pro Thr Phe Asn Arg Pro Ala Asp Ala Val Ala Ala Leu Glu Ala
185 190 195

ctt gcc tcc gac cca gca gtt gac gcc gtc att gat acc gtc atc atg 739
Leu Ala Ser Asp Pro Ala Val Asp Ala Val Ile Asp Thr Val Ile Met
200 205 210

cct gat caa ggc aac aag cac cct gcc gac gag cca ggt tac aag gca 787
Pro Asp Gln Gly Asn Lys His Pro Ala Asp Glu Pro Gly Tyr Lys Ala

```
    215                 220                 225

gct gtt gag cac ttc ggc gac cgc ttc ttc gaa ttc cgc cag ggc aac   835
Ala Val Glu His Phe Gly Asp Arg Phe Phe Glu Phe Arg Gln Gly Asn
230                 235                 240                 245

ctc ggc gga tcc ggc ggt tac tcc cgc atc atg ttc gaa gcc ctt ggc   883
Leu Gly Gly Ser Gly Gly Tyr Ser Arg Ile Met Phe Glu Ala Leu Gly
                250                 255                 260

gga gtc gac ggc aag ggc gaa gca ggc gct gcc aag agc cca tac atc   931
Gly Val Asp Gly Lys Gly Glu Ala Gly Ala Ala Lys Ser Pro Tyr Ile
            265                 270                 275

ctg tac atg gat gac gac att gct att gag cca gac tca gtg ctg cgt   979
Leu Tyr Met Asp Asp Asp Ile Ala Ile Glu Pro Asp Ser Val Leu Arg
        280                 285                 290

gcg ctt cag gta gcc cgc tac gca aaa tcc ccc atc ctc gtt ggc gga   1027
Ala Leu Gln Val Ala Arg Tyr Ala Lys Ser Pro Ile Leu Val Gly Gly
    295                 300                 305

caa atg ctc aac ctg caa gag cgc agc cac ctt cac acc atg ggc gaa   1075
Gln Met Leu Asn Leu Gln Glu Arg Ser His Leu His Thr Met Gly Glu
310                 315                 320                 325

gta gtt ggc gga cac gac ttc atg tgg acc gcc gca cca cac gtg cac   1123
Val Val Gly Gly His Asp Phe Met Trp Thr Ala Ala Pro His Val His
                330                 335                 340

tac gac cac gac ttc tct gca cac cca cta cat gat cgc ggt aaa ttc   1171
Tyr Asp His Asp Phe Ser Ala His Pro Leu His Asp Arg Gly Lys Phe
            345                 350                 355

gac gac aag cca gac gca cca aac tcc cgc gac ctg cac cgc cgc atc   1219
Asp Asp Lys Pro Asp Ala Pro Asn Ser Arg Asp Leu His Arg Arg Ile
        360                 365                 370

gac gtt gac ttc aac ggc tgg tgg atg tgc atg atc cca cgc gtt gtc   1267
Asp Val Asp Phe Asn Gly Trp Trp Met Cys Met Ile Pro Arg Val Val
    375                 380                 385

gcc gaa cag atc ggc caa cca ctc cca ctc ttt atc aag tgg gac gac   1315
Ala Glu Gln Ile Gly Gln Pro Leu Pro Leu Phe Ile Lys Trp Asp Asp
390                 395                 400                 405

gcc gaa tac ggt cta cgc gca cgc aaa gct gga ttc ccc aca gca acc   1363
Ala Glu Tyr Gly Leu Arg Ala Arg Lys Ala Gly Phe Pro Thr Ala Thr
                410                 415                 420

tgg cca gga atc gca atc tgg cac atg gcc tgg tcc gac aaa gac gac   1411
Trp Pro Gly Ile Ala Ile Trp His Met Ala Trp Ser Asp Lys Asp Asp
            425                 430                 435

gcc atc gac tgg cag gcc tac ttc cac ctc cgc aac cgc ctc gtg gtt   1459
Ala Ile Asp Trp Gln Ala Tyr Phe His Leu Arg Asn Arg Leu Val Val
        440                 445                 450

gcc gcg atg tac cac caa ggc agc gtc gac ggc att gtc cga tcg atg   1507
Ala Ala Met Tyr His Gln Gly Ser Val Asp Gly Ile Val Arg Ser Met
    455                 460                 465
```

```
caa aaa gcc acc ttc aag cac ctg ctg tgc ctg gaa tac tcc acc gtg   1555
Gln Lys Ala Thr Phe Lys His Leu Leu Cys Leu Glu Tyr Ser Thr Val
470                 475                 480                 485

gca atc caa aac gaa gca atg aag gac ttc ctt gca gga cca gat cag   1603
Ala Ile Gln Asn Glu Ala Met Lys Asp Phe Leu Ala Gly Pro Asp Gln
                490                 495                 500

ctc ttc tcg atc ctg gac acc tca cta cct cga att gca gcg att cgc   1651
Leu Phe Ser Ile Leu Asp Thr Ser Leu Pro Arg Ile Ala Ala Ile Arg
            505                 510                 515

aaa acc tat cca gac gcc gtt gtg ctg cca agc gcc acc gaa ctg cca   1699
Lys Thr Tyr Pro Asp Ala Val Val Leu Pro Ser Ala Thr Glu Leu Pro
        520                 525                 530

cga gca acc ggc gcg ccg ggt gtc cca acc aag gac atc ggt gga cgc   1747
Arg Ala Thr Gly Ala Pro Gly Val Pro Thr Lys Asp Ile Gly Gly Arg
    535                 540                 545

ctg gcc cca atc aag aag gca atg tgg ctg gct aag ggc ctg aag cac   1795
Leu Ala Pro Ile Lys Lys Ala Met Trp Leu Ala Lys Gly Leu Lys His
550                 555                 560                 565

tcc ctg tct aag gaa gat gcc tcc cac cac gag gtg cca cag gcc aac   1843
Ser Leu Ser Lys Glu Asp Ala Ser His His Glu Val Pro Gln Ala Asn
                570                 575                 580

ttc gca cca atc gaa gca cgt tgg ttc agc ctg tcc cga gtc gat ggc   1891
Phe Ala Pro Ile Glu Ala Arg Trp Phe Ser Leu Ser Arg Val Asp Gly
            585                 590                 595

gca aca gtt acc acc gcg gat ggc cgc ggc gtg gtc tac cgc aag cgc   1939
Ala Thr Val Thr Thr Ala Asp Gly Arg Gly Val Val Tyr Arg Lys Arg
        600                 605                 610

gac cgc gac aaa gct aaa gaa ctt ggc aaa gaa gca cgc gca ctg caa   1987
Asp Arg Asp Lys Ala Lys Glu Leu Gly Lys Glu Ala Arg Ala Leu Gln
    615                 620                 625

aag caa gta gca gag cgt ttc gac gaa ctc agt cgc gcc tac cgc aac   2035
Lys Gln Val Ala Glu Arg Phe Asp Glu Leu Ser Arg Ala Tyr Arg Asn
630                 635                 640                 645

gct cat cct gag ctt gtg agc cgt gaa gcc tgg gga aag gtc ttc gat   2083
Ala His Pro Glu Leu Val Ser Arg Glu Ala Trp Gly Lys Val Phe Asp
                650                 655                 660

gag caa taaggaagta cagattctgg tag                                2112
Glu Gln
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<210> 2818
<211> 663
<212> PRT
<213> Corynebacterium glutamicum

<400> 2818
Met Lys Gly Glu Asp Thr Ser Met Ser Ala Thr Asn Leu Ala Val Glu

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  1               5                  10                  15
Gln Leu Gln Arg Val Leu Leu Pro Arg Arg Gly Glu Pro Ala Asp Val
            20                  25                  30
Arg Ser Leu Tyr Leu Leu Glu Ala Glu Ser Asn Lys Glu Arg Leu Glu
        35                  40                  45
Trp Glu Asp Arg Phe Ser Val Ser Val Pro Ala Gly Ala Glu Val Ser
    50                  55                  60
Phe Gln Thr Tyr Phe Asn Ala Phe Pro Ala Ser Tyr Trp Arg Arg Trp
65                  70                  75                  80
Ser Gln Leu Asp Ser Val Val Leu Lys Leu Lys Val Ser Gly Glu Ala
                85                  90                  95
Arg Val Asp Leu Tyr Arg Ser Lys Ile Asp Gly Ala Arg Ile Gly Ile
            100                 105                 110
Thr Gly Ser Val Val Lys Asp Asp Phe Ile Glu Phe Glu Val Ser Leu
        115                 120                 125
Ala Pro Phe Glu Asp Gly Gly Trp Ile Trp Phe Asp Leu Thr Ala Glu
    130                 135                 140
Thr Asp Ala Thr Val Glu Glu Ala Gly Trp Tyr Ala Pro His Ala Pro
145                 150                 155                 160
Lys Ala Gln Ile Met Pro Asp Gly Ser Glu Val Gly Pro Phe Glu Ala
                165                 170                 175
Arg Ala Thr Val Gly Ile Pro Thr Phe Asn Arg Pro Ala Asp Ala Val
            180                 185                 190
Ala Ala Leu Glu Ala Leu Ala Ser Asp Pro Ala Val Asp Ala Val Ile
        195                 200                 205
Asp Thr Val Ile Met Pro Asp Gln Gly Asn Lys His Pro Ala Asp Glu
    210                 215                 220
Pro Gly Tyr Lys Ala Ala Val Glu His Phe Gly Asp Arg Phe Phe Glu
225                 230                 235                 240
Phe Arg Gln Gly Asn Leu Gly Gly Ser Gly Gly Tyr Ser Arg Ile Met
                245                 250                 255
Phe Glu Ala Leu Gly Gly Val Asp Gly Lys Gly Glu Ala Gly Ala Ala
            260                 265                 270
Lys Ser Pro Tyr Ile Leu Tyr Met Asp Asp Asp Ile Ala Ile Glu Pro
        275                 280                 285
Asp Ser Val Leu Arg Ala Leu Gln Val Ala Arg Tyr Ala Lys Ser Pro
    290                 295                 300
Ile Leu Val Gly Gly Gln Met Leu Asn Leu Gln Glu Arg Ser His Leu
305                 310                 315                 320
His Thr Met Gly Glu Val Val Gly Gly His Asp Phe Met Trp Thr Ala
                325                 330                 335
```

```
Ala Pro His Val His Tyr Asp His Asp Phe Ser Ala His Pro Leu His
            340                 345                 350

Asp Arg Gly Lys Phe Asp Asp Lys Pro Asp Ala Pro Asn Ser Arg Asp
        355                 360                 365

Leu His Arg Arg Ile Asp Val Asp Phe Asn Gly Trp Trp Met Cys Met
    370                 375                 380

Ile Pro Arg Val Val Ala Glu Gln Ile Gly Gln Pro Leu Pro Leu Phe
385                 390                 395                 400

Ile Lys Trp Asp Asp Ala Glu Tyr Gly Leu Arg Ala Arg Lys Ala Gly
                405                 410                 415

Phe Pro Thr Ala Thr Trp Pro Gly Ile Ala Ile Trp His Met Ala Trp
            420                 425                 430

Ser Asp Lys Asp Asp Ala Ile Asp Trp Gln Ala Tyr Phe His Leu Arg
        435                 440                 445

Asn Arg Leu Val Val Ala Ala Met Tyr His Gln Gly Ser Val Asp Gly
    450                 455                 460

Ile Val Arg Ser Met Gln Lys Ala Thr Phe Lys His Leu Leu Cys Leu
465                 470                 475                 480

Glu Tyr Ser Thr Val Ala Ile Gln Asn Glu Ala Met Lys Asp Phe Leu
                485                 490                 495

Ala Gly Pro Asp Gln Leu Phe Ser Ile Leu Asp Thr Ser Leu Pro Arg
            500                 505                 510

Ile Ala Ala Ile Arg Lys Thr Tyr Pro Asp Ala Val Val Leu Pro Ser
        515                 520                 525

Ala Thr Glu Leu Pro Arg Ala Thr Gly Ala Pro Gly Val Pro Thr Lys
    530                 535                 540

Asp Ile Gly Gly Arg Leu Ala Pro Ile Lys Lys Ala Met Trp Leu Ala
545                 550                 555                 560

Lys Gly Leu Lys His Ser Leu Ser Lys Glu Asp Ala Ser His His Glu
                565                 570                 575

Val Pro Gln Ala Asn Phe Ala Pro Ile Glu Ala Arg Trp Phe Ser Leu
            580                 585                 590

Ser Arg Val Asp Gly Ala Thr Val Thr Thr Ala Asp Gly Arg Gly Val
        595                 600                 605

Val Tyr Arg Lys Arg Asp Arg Asp Lys Ala Lys Glu Leu Gly Lys Glu
    610                 615                 620

Ala Arg Ala Leu Gln Lys Gln Val Ala Glu Arg Phe Asp Glu Leu Ser
625                 630                 635                 640

Arg Ala Tyr Arg Asn Ala His Pro Glu Leu Val Ser Arg Glu Ala Trp
                645                 650                 655
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Gly Lys Val Phe Asp Glu Gln
            660


<210> 2819
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> RXA02602

<400> 2819
ctgcaaaagc aagtagcaga gcgtttcgac gaactcagtc gcgcctaccg caacgctcat 60

cctgagcttg tgagccgtga agcctgggga aaggtcttcg atg agc aat aag gaa   115
                                        Met Ser Asn Lys Glu
                                          1               5

gta cag att ctg gta gca atc cag gat caa ctc atg gat gcc cca gga   163
Val Gln Ile Leu Val Ala Ile Gln Asp Gln Leu Met Asp Ala Pro Gly
                 10                  15                  20

gta ctg ccc acc gca cga gga ctc agc ctg ctc ggc gaa cat gct gca   211
Val Leu Pro Thr Ala Arg Gly Leu Ser Leu Leu Gly Glu His Ala Ala
             25                  30                  35

ggc tgg ctg gca ctc ggc gct ggc ggt gct gtt gtg gac aaa aaa cgt   259
Gly Trp Leu Ala Leu Gly Ala Gly Gly Ala Val Val Asp Lys Lys Arg
         40                  45                  50

cgc cgc tcc tgg gct gga ctc ttc atc gct gca ctg gga agc cac gca   307
Arg Arg Ser Trp Ala Gly Leu Phe Ile Ala Ala Leu Gly Ser His Ala
     55                  60                  65

gca tca gtg atc atc aaa cga gtt gtc cgc cgc gct cgg cca cat gac   355
Ala Ser Val Ile Ile Lys Arg Val Val Arg Arg Ala Arg Pro His Asp
 70                  75                  80                  85

cca gcc atc agg att ggt gtg ggc acc ccc tca aag cta agc ttt cct   403
Pro Ala Ile Arg Ile Gly Val Gly Thr Pro Ser Lys Leu Ser Phe Pro
                 90                  95                 100

tct tca cat gcg acc tcg aca acc gca act atg gtt tat ctt gcg cgc   451
Ser Ser His Ala Thr Ser Thr Thr Ala Thr Met Val Tyr Leu Ala Arg
            105                 110                 115

atc acc aag tca cca gtg cca ctg cta gga atc ccc atc atg gtg cta   499
Ile Thr Lys Ser Pro Val Pro Leu Leu Gly Ile Pro Ile Met Val Leu
        120                 125                 130

tca cgc atg gtg ctt ggc gtg cat tac cca acc gat gtg cta gcc ggc   547
Ser Arg Met Val Leu Gly Val His Tyr Pro Thr Asp Val Leu Ala Gly
    135                 140                 145

gcg ttg ttg gga gca gcg acc gca gag gcc gtc cat aag atc gaa agg   595
Ala Leu Leu Gly Ala Ala Thr Ala Glu Ala Val His Lys Ile Glu Arg
150                 155                 160                 165
```

gct acg aag tgagcgaaca cgccgctgaa cat 627
Ala Thr Lys

<210> 2820
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 2820
Met Ser Asn Lys Glu Val Gln Ile Leu Val Ala Ile Gln Asp Gln Leu
1 5 10 15

Met Asp Ala Pro Gly Val Leu Pro Thr Ala Arg Gly Leu Ser Leu Leu
20 25 30

Gly Glu His Ala Ala Gly Trp Leu Ala Leu Gly Ala Gly Gly Ala Val
35 40 45

Val Asp Lys Lys Arg Arg Arg Ser Trp Ala Gly Leu Phe Ile Ala Ala
50 55 60

Leu Gly Ser His Ala Ala Ser Val Ile Ile Lys Arg Val Val Arg Arg
65 70 75 80

Ala Arg Pro His Asp Pro Ala Ile Arg Ile Gly Val Gly Thr Pro Ser
85 90 95

Lys Leu Ser Phe Pro Ser Ser His Ala Thr Ser Thr Thr Ala Thr Met
100 105 110

Val Tyr Leu Ala Arg Ile Thr Lys Ser Pro Val Pro Leu Leu Gly Ile
115 120 125

Pro Ile Met Val Leu Ser Arg Met Val Leu Gly Val His Tyr Pro Thr
130 135 140

Asp Val Leu Ala Gly Ala Leu Leu Gly Ala Ala Thr Ala Glu Ala Val
145 150 155 160

His Lys Ile Glu Arg Ala Thr Lys
165

<210> 2821
<211> 2199
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2176)
<223> RXA02604

<400> 2821
tctgcatcgt gatggctgtg tacatcatgc cgatgttttg aatatttacc aatgaacatg 60

ctctgaccag catgtccatt aacgtttgag gccacatgcg gtg cta gca tgt ggc 115
Val Leu Ala Cys Gly
1 5

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ctc atg acg ttt agc ccc cag cgt ccg gag ttt gag acc ggt aag cag   163
Leu Met Thr Phe Ser Pro Gln Arg Pro Glu Phe Glu Thr Gly Lys Gln
                 10                  15                  20

cca gat cca gaa act gaa cac gca ggt gac ttc ttt gaa gaa acc tca   211
Pro Asp Pro Glu Thr Glu His Ala Gly Asp Phe Phe Glu Glu Thr Ser
             25                  30                  35

agc agt gct cct cgc gcc gca tct aac ggt tct tct ggt ccg aac tac   259
Ser Ser Ala Pro Arg Ala Ala Ser Asn Gly Ser Ser Gly Pro Asn Tyr
         40                  45                  50

acc ctc att aca acg ttt cta gcg gcc ctt act gct ggc atc ttt gct   307
Thr Leu Ile Thr Thr Phe Leu Ala Ala Leu Thr Ala Gly Ile Phe Ala
     55                  60                  65

ttc tgg gca ggc tgg acc cgc aaa tgg atc agc gac gac gga ctg atc   355
Phe Trp Ala Gly Trp Thr Arg Lys Trp Ile Ser Asp Asp Gly Leu Ile
 70                  75                  80                  85

gtc cta cgc acc gtc cga aac ctc ctg gct gga aac ggg cca gta ttc   403
Val Leu Arg Thr Val Arg Asn Leu Leu Ala Gly Asn Gly Pro Val Phe
                 90                  95                 100

aac gct ggc gaa cgc gtc gaa gcc aac aca tct act ctg tgg caa tac   451
Asn Ala Gly Glu Arg Val Glu Ala Asn Thr Ser Thr Leu Trp Gln Tyr
             105                 110                 115

tgc atc tat ctg gtt gcc tta gta act gac tat cgc ctc gaa gat att   499
Cys Ile Tyr Leu Val Ala Leu Val Thr Asp Tyr Arg Leu Glu Asp Ile
         120                 125                 130

gct ctg tgg ctt gcg ctg ctg ttc acc acc gca gcg tcc atc atc ggt   547
Ala Leu Trp Leu Ala Leu Leu Phe Thr Thr Ala Ala Ser Ile Ile Gly
     135                 140                 145

gtc ctg ggt acc gcg cat ctc cac cgc aaa cgc att gcc gta ttg ctt   595
Val Leu Gly Thr Ala His Leu His Arg Lys Arg Ile Ala Val Leu Leu
150                 155                 160                 165

cct gca ggc gtg atc ggc tac ttc agc ctt tcc ccg gcg cga gac ttt   643
Pro Ala Gly Val Ile Gly Tyr Phe Ser Leu Ser Pro Ala Arg Asp Phe
                 170                 175                 180

gcc act tcc gga ttg gag tgg ggc cta tct ttg atg tgg att tcc atc   691
Ala Thr Ser Gly Leu Glu Trp Gly Leu Ser Leu Met Trp Ile Ser Ile
             185                 190                 195

caa tgg ctg ctg ctg gtg ttg tgg gcg act tcg ggc aag acc tcg ggc   739
Gln Trp Leu Leu Leu Val Leu Trp Ala Thr Ser Gly Lys Thr Ser Gly
         200                 205                 210

aag aag gct tcg ggc gca aaa act tca aat cct atc gtt aat gcc ggt   787
Lys Lys Ala Ser Gly Ala Lys Thr Ser Asn Pro Ile Val Asn Ala Gly
     215                 220                 225

gca ata acc tat gct ttg gcc ttt tgg tca ggc ttg agc tgg ctg gtt   835
Ala Ile Thr Tyr Ala Leu Ala Phe Trp Ser Gly Leu Ser Trp Leu Val
230                 235                 240                 245
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cgc cca gaa ctg gcg atg tat ggc ggt ttg act gga gtg ttg ctg ctg   883
Arg Pro Glu Leu Ala Met Tyr Gly Gly Leu Thr Gly Val Leu Leu Leu
                250                 255                 260

ctt act gcg cca cga tgg cgg gta gtt ttg ggg atc ctg gtg gcg gct   931
Leu Thr Ala Pro Arg Trp Arg Val Val Leu Gly Ile Leu Val Ala Ala
            265                 270                 275

ttg cct ctt cca gct gcg tac caa atc ttc cgc atg ggt tat tac ggg   979
Leu Pro Leu Pro Ala Ala Tyr Gln Ile Phe Arg Met Gly Tyr Tyr Gly
        280                 285                 290

ctg atg gtg ccg cac acg gct gta gcg aaa tca gcc tca gat gcg gtg   1027
Leu Met Val Pro His Thr Ala Val Ala Lys Ser Ala Ser Asp Ala Val
    295                 300                 305

tgg ggg act ggt tgg gaa tat gtt gag gat ttc acg ggg cct tac aac   1075
Trp Gly Thr Gly Trp Glu Tyr Val Glu Asp Phe Thr Gly Pro Tyr Asn
310                 315                 320                 325

ctg tgg ctc ggt ttg gcc ttg ctg ttg gcc gca ggc gcg ttg aca gtg   1123
Leu Trp Leu Gly Leu Ala Leu Leu Leu Ala Ala Gly Ala Leu Thr Val
                330                 335                 340

tgg aaa act gac aag cac tta gcg ata ccg aag ggg cgg ctg ggg ctg   1171
Trp Lys Thr Asp Lys His Leu Ala Ile Pro Lys Gly Arg Leu Gly Leu
            345                 350                 355

cgc act ccg ggt atg gct ata gcg ttg ctg gtt atc tgt gcg ctc gtc   1219
Arg Thr Pro Gly Met Ala Ile Ala Leu Leu Val Ile Cys Ala Leu Val
        360                 365                 370

cac ttc ctt tac gtt atc cgt gtt ggt ggc gac ttc atg cat gga cgc   1267
His Phe Leu Tyr Val Ile Arg Val Gly Gly Asp Phe Met His Gly Arg
    375                 380                 385

atg ctg ctc ctt cca ctt ttt gcc att ctg ctg cct gtt tct gtc att   1315
Met Leu Leu Leu Pro Leu Phe Ala Ile Leu Leu Pro Val Ser Val Ile
390                 395                 400                 405

ccg gtc aat gtt gtt gat cga ggt tgg cag gat ttg gtt gcg ctg gtt   1363
Pro Val Asn Val Val Asp Arg Gly Trp Gln Asp Leu Val Ala Leu Val
                410                 415                 420

ctc gtt ttc tct acg tgg gtg tgg tcc act gtg gtt ttt gtg cag ggg   1411
Leu Val Phe Ser Thr Trp Val Trp Ser Thr Val Val Phe Val Gln Gly
            425                 430                 435

cac caa tgg gaa aat acc ggc cag cat gtg gtt gat gag cgt gat ttt   1459
His Gln Trp Glu Asn Thr Gly Gln His Val Val Asp Glu Arg Asp Phe
        440                 445                 450

tgg att gat ttc acc aac cga gat gaa gat cat cct ccg ctt tat gca   1507
Trp Ile Asp Phe Thr Asn Arg Asp Glu Asp His Pro Pro Leu Tyr Ala
    455                 460                 465

gag gat ttc ctc act gtt gat tcc atg aat gat tac gca gag gtt atg   1555
Glu Asp Phe Leu Thr Val Asp Ser Met Asn Asp Tyr Ala Glu Val Met
470                 475                 480                 485

cgc gat cag acg ttg gtt aat cca aca ggc cag caa ctc aat att ctg   1603
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Arg Asp Gln Thr Leu Val Asn Pro Thr Gly Gln Gln Leu Asn Ile Leu
                490                 495                 500

gcc agc agt gac ccg acc act tat tcg tgg atc acc aca cct cgc gtg   1651
Ala Ser Ser Asp Pro Thr Thr Tyr Ser Trp Ile Thr Thr Pro Arg Val
            505                 510                 515

gag ggg gtt gaa gcc ggt gat ttg gct aac ctc tcg cca act gtt ttc   1699
Glu Gly Val Glu Ala Gly Asp Leu Ala Asn Leu Ser Pro Thr Val Phe
        520                 525                 530

cat gtg aac ctc ggc atg acc tcc atg aac gca ccg ctc aac gtg cgt   1747
His Val Asn Leu Gly Met Thr Ser Met Asn Ala Pro Leu Asn Val Arg
    535                 540                 545

gtg aca gac ctg att ggt ttg gca acg cca ctg gca gcc cgc cag cca   1795
Val Thr Asp Leu Ile Gly Leu Ala Thr Pro Leu Ala Ala Arg Gln Pro
550                 555                 560                 565

cgc att gaa ggt ggt cga atc ggc cac gat aaa ttg atg gac ttg gaa   1843
Arg Ile Glu Gly Gly Arg Ile Gly His Asp Lys Leu Met Asp Leu Glu
                570                 575                 580

tgg cag gtc gcg gaa tcc gcc act ccg ctg gcg tac aca ccg ggt tgg   1891
Trp Gln Val Ala Glu Ser Ala Thr Pro Leu Ala Tyr Thr Pro Gly Trp
            585                 590                 595

ttg gat act caa aag act tat gag gcc cgc cag gcg cta cgc cac cca   1939
Leu Asp Thr Gln Lys Thr Tyr Glu Ala Arg Gln Ala Leu Arg His Pro
        600                 605                 610

gaa ttg gtt cac ctt ttc cag act tac cgt gag cca atg tcc tac cac   1987
Glu Leu Val His Leu Phe Gln Thr Tyr Arg Glu Pro Met Ser Tyr His
    615                 620                 625

cgg ttt gtg gac aat att aaa tac gca ctc act acc gga aga aca ctg   2035
Arg Phe Val Asp Asn Ile Lys Tyr Ala Leu Thr Thr Gly Arg Thr Leu
630                 635                 640                 645

gaa att tca gat aat cct gaa gat ctt ttg aaa gaa ttt aac ccg acc   2083
Glu Ile Ser Asp Asn Pro Glu Asp Leu Leu Lys Glu Phe Asn Pro Thr
                650                 655                 660

cct gca gag att cag gac ggg tta gaa act att gct tgg cct ggg gaa   2131
Pro Ala Glu Ile Gln Asp Gly Leu Glu Thr Ile Ala Trp Pro Gly Glu
            665                 670                 675

att aaa ctt gat gaa cct cgc gga gaa cct tta tat agc tct cag       2176
Ile Lys Leu Asp Glu Pro Arg Gly Glu Pro Leu Tyr Ser Ser Gln
        680                 685                 690

taaacactta ttcgcaaatc att                                        2199


<210> 2822
<211> 692
<212> PRT
<213> Corynebacterium glutamicum

<400> 2822
Val Leu Ala Cys Gly Leu Met Thr Phe Ser Pro Gln Arg Pro Glu Phe
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  1               5                  10                  15
Glu Thr Gly Lys Gln Pro Asp Pro Glu Thr Glu His Ala Gly Asp Phe
            20                  25                  30
Phe Glu Glu Thr Ser Ser Ser Ala Pro Arg Ala Ala Ser Asn Gly Ser
        35                  40                  45
Ser Gly Pro Asn Tyr Thr Leu Ile Thr Thr Phe Leu Ala Ala Leu Thr
    50                  55                  60
Ala Gly Ile Phe Ala Phe Trp Ala Gly Trp Thr Arg Lys Trp Ile Ser
65                  70                  75                  80
Asp Asp Gly Leu Ile Val Leu Arg Thr Val Arg Asn Leu Leu Ala Gly
                85                  90                  95
Asn Gly Pro Val Phe Asn Ala Gly Glu Arg Val Glu Ala Asn Thr Ser
            100                 105                 110
Thr Leu Trp Gln Tyr Cys Ile Tyr Leu Val Ala Leu Val Thr Asp Tyr
        115                 120                 125
Arg Leu Glu Asp Ile Ala Leu Trp Leu Ala Leu Leu Phe Thr Thr Ala
    130                 135                 140
Ala Ser Ile Ile Gly Val Leu Gly Thr Ala His Leu His Arg Lys Arg
145                 150                 155                 160
Ile Ala Val Leu Leu Pro Ala Gly Val Ile Gly Tyr Phe Ser Leu Ser
                165                 170                 175
Pro Ala Arg Asp Phe Ala Thr Ser Gly Leu Glu Trp Gly Leu Ser Leu
            180                 185                 190
Met Trp Ile Ser Ile Gln Trp Leu Leu Leu Val Leu Trp Ala Thr Ser
        195                 200                 205
Gly Lys Thr Ser Gly Lys Lys Ala Ser Gly Ala Lys Thr Ser Asn Pro
    210                 215                 220
Ile Val Asn Ala Gly Ala Ile Thr Tyr Ala Leu Ala Phe Trp Ser Gly
225                 230                 235                 240
Leu Ser Trp Leu Val Arg Pro Glu Leu Ala Met Tyr Gly Gly Leu Thr
                245                 250                 255
Gly Val Leu Leu Leu Leu Thr Ala Pro Arg Trp Arg Val Val Leu Gly
            260                 265                 270
Ile Leu Val Ala Ala Leu Pro Leu Pro Ala Ala Tyr Gln Ile Phe Arg
        275                 280                 285
Met Gly Tyr Tyr Gly Leu Met Val Pro His Thr Ala Val Ala Lys Ser
    290                 295                 300
Ala Ser Asp Ala Val Trp Gly Thr Gly Trp Glu Tyr Val Glu Asp Phe
305                 310                 315                 320
Thr Gly Pro Tyr Asn Leu Trp Leu Gly Leu Ala Leu Leu Leu Ala Ala
                325                 330                 335
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Gly Ala Leu Thr Val Trp Lys Thr Asp Lys His Leu Ala Ile Pro Lys
            340                 345                 350

Gly Arg Leu Gly Leu Arg Thr Pro Gly Met Ala Ile Ala Leu Leu Val
        355                 360                 365

Ile Cys Ala Leu Val His Phe Leu Tyr Val Ile Arg Val Gly Gly Asp
    370                 375                 380

Phe Met His Gly Arg Met Leu Leu Leu Pro Leu Phe Ala Ile Leu Leu
385                 390                 395                 400

Pro Val Ser Val Ile Pro Val Asn Val Val Asp Arg Gly Trp Gln Asp
                405                 410                 415

Leu Val Ala Leu Val Leu Val Phe Ser Thr Trp Val Trp Ser Thr Val
            420                 425                 430

Val Phe Val Gln Gly His Gln Trp Glu Asn Thr Gly Gln His Val Val
        435                 440                 445

Asp Glu Arg Asp Phe Trp Ile Asp Phe Thr Asn Arg Asp Glu Asp His
    450                 455                 460

Pro Pro Leu Tyr Ala Glu Asp Phe Leu Thr Val Asp Ser Met Asn Asp
465                 470                 475                 480

Tyr Ala Glu Val Met Arg Asp Gln Thr Leu Val Asn Pro Thr Gly Gln
                485                 490                 495

Gln Leu Asn Ile Leu Ala Ser Ser Asp Pro Thr Thr Tyr Ser Trp Ile
            500                 505                 510

Thr Thr Pro Arg Val Glu Gly Val Glu Ala Gly Asp Leu Ala Asn Leu
        515                 520                 525

Ser Pro Thr Val Phe His Val Asn Leu Gly Met Thr Ser Met Asn Ala
    530                 535                 540

Pro Leu Asn Val Arg Val Thr Asp Leu Ile Gly Leu Ala Thr Pro Leu
545                 550                 555                 560

Ala Ala Arg Gln Pro Arg Ile Glu Gly Gly Arg Ile Gly His Asp Lys
                565                 570                 575

Leu Met Asp Leu Glu Trp Gln Val Ala Glu Ser Ala Thr Pro Leu Ala
            580                 585                 590

Tyr Thr Pro Gly Trp Leu Asp Thr Gln Lys Thr Tyr Glu Ala Arg Gln
        595                 600                 605

Ala Leu Arg His Pro Glu Leu Val His Leu Phe Gln Thr Tyr Arg Glu
    610                 615                 620

Pro Met Ser Tyr His Arg Phe Val Asp Asn Ile Lys Tyr Ala Leu Thr
625                 630                 635                 640

Thr Gly Arg Thr Leu Glu Ile Ser Asp Asn Pro Glu Asp Leu Leu Lys
                645                 650                 655
```

```
Glu Phe Asn Pro Thr Pro Ala Glu Ile Gln Asp Gly Leu Glu Thr Ile
            660                 665                 670

Ala Trp Pro Gly Glu Ile Lys Leu Asp Glu Pro Arg Gly Glu Pro Leu
        675                 680                 685

Tyr Ser Ser Gln
    690


<210> 2823
<211> 372
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(349)
<223> RXA02609

<400> 2823
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cggggcagcc gaggaaatcg acggcctgcc cgaggtgacc gtg gaa cgc agc gct   115
                                              Val Glu Arg Ser Ala
                                                1               5

gag gcg caa gcg ttc ctg gat gcg ctg aaa gat gaa aaa atc gac atc   163
Glu Ala Gln Ala Phe Leu Asp Ala Leu Lys Asp Glu Lys Ile Asp Ile
                  10                  15                  20

tcc ggc gtg gag gac cag ttg att gcg act gcg cga aat tac tgc agt   211
Ser Gly Val Glu Asp Gln Leu Ile Ala Thr Ala Arg Asn Tyr Cys Ser
              25                  30                  35

tcg gaa aac aag gac caa aac gtc act gtc gat gcg gtt gca ggc cag   259
Ser Glu Asn Lys Asp Gln Asn Val Thr Val Asp Ala Val Ala Gly Gln
          40                  45                  50

ctc atc gtg cag gga cgc acc agc gtg aag gaa gat caa gca gcg gaa   307
Leu Ile Val Gln Gly Arg Thr Ser Val Lys Glu Asp Gln Ala Ala Glu
     55                  60                  65

att tct acg ctg ctg aag gaa tct gcg gat cgg acg tat tgt           349
Ile Ser Thr Leu Leu Lys Glu Ser Ala Asp Arg Thr Tyr Cys
 70                  75                  80

taaccgatga ggaaaaccat cac                                        372


<210> 2824
<211> 83
<212> PRT
<213> Corynebacterium glutamicum

<400> 2824
Val Glu Arg Ser Ala Glu Ala Gln Ala Phe Leu Asp Ala Leu Lys Asp
  1               5                  10                  15

Glu Lys Ile Asp Ile Ser Gly Val Glu Asp Gln Leu Ile Ala Thr Ala
             20                  25                  30
```

```
Arg Asn Tyr Cys Ser Ser Glu Asn Lys Asp Gln Asn Val Thr Val Asp
          35                  40                  45

Ala Val Ala Gly Gln Leu Ile Val Gln Gly Arg Thr Ser Val Lys Glu
      50                  55                  60

Asp Gln Ala Ala Glu Ile Ser Thr Leu Leu Lys Glu Ser Ala Asp Arg
 65                  70                  75                  80

Thr Tyr Cys
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<210> 2825
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(607)
<223> RXA02617

<400> 2825

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ctctttaatt aacttttggg cgacccttta cggtcgtcct cttgcgttcc caaaacatac 60

ccagtaagtt actgggtatc caactcttga ttggggaaca atg tcc ata aaa cat   115
                                            Met Ser Ile Lys His
                                              1               5

gca ctc ttg gtg ctc atg ctc gac gaa cca acc tcg gca agt cag ctg   163
Ala Leu Leu Val Leu Met Leu Asp Glu Pro Thr Ser Ala Ser Gln Leu
                 10                  15                  20

caa acc aag ttt gaa gaa aca atg ggg atc tgg cag ctc aat atc ggc   211
Gln Thr Lys Phe Glu Glu Thr Met Gly Ile Trp Gln Leu Asn Ile Gly
             25                  30                  35

caa gtc acc caa acc atc cag cgg cta cag cgc gac ggc ctg gcg gaa   259
Gln Val Thr Gln Thr Ile Gln Arg Leu Gln Arg Asp Gly Leu Ala Glu
         40                  45                  50

acc gca ggc acc acc gtc agt tcc aac ggc cgc acc gta gat act ttc   307
Thr Ala Gly Thr Thr Val Ser Ser Asn Gly Arg Thr Val Asp Thr Phe
     55                  60                  65

cag ccc acg gac tta ggt cgc gaa ctt gtc gcg cag tgg ttc gaa agt   355
Gln Pro Thr Asp Leu Gly Arg Glu Leu Val Ala Gln Trp Phe Glu Ser
 70                  75                  80                  85

ccc gtc acc gtc aca ctg tcc gaa cgc gat gaa tta gtc acc aaa atc   403
Pro Val Thr Val Thr Leu Ser Glu Arg Asp Glu Leu Val Thr Lys Ile
                 90                  95                 100

gcc atc gca gaa tca cgt ggc ctc aat ttg att cca ctt tta gac att   451
Ala Ile Ala Glu Ser Arg Gly Leu Asn Leu Ile Pro Leu Leu Asp Ile
            105                 110                 115

caa cgc aac aca gtc atg gcg gaa cta cgc gca ctc aac aaa tcc agc   499
Gln Arg Asn Thr Val Met Ala Glu Leu Arg Ala Leu Asn Lys Ser Ser
```

```
        120                 125                 130

cgc gat ctc gcc gaa acc aga aac acc cag cgg ctc ctc gtc gaa aag   547
Arg Asp Leu Ala Glu Thr Arg Asn Thr Gln Arg Leu Leu Val Glu Lys
    135                 140                 145

cga atc ttt gaa cta gaa gcc cag gca cgt tgg ctc gac cga att gaa   595
Arg Ile Phe Glu Leu Glu Ala Gln Ala Arg Trp Leu Asp Arg Ile Glu
150                 155                 160                 165

gca ttg gag cag taaatgacaa acacgccttt ccc                        630
Ala Leu Glu Gln
```

<210> 2826
<211> 169
<212> PRT
<213> Corynebacterium glutamicum

<400> 2826

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Met Ser Ile Lys His Ala Leu Leu Val Leu Met Leu Asp Glu Pro Thr
  1               5                  10                  15

Ser Ala Ser Gln Leu Gln Thr Lys Phe Glu Glu Thr Met Gly Ile Trp
             20                  25                  30

Gln Leu Asn Ile Gly Gln Val Thr Gln Thr Ile Gln Arg Leu Gln Arg
         35                  40                  45

Asp Gly Leu Ala Glu Thr Ala Gly Thr Thr Val Ser Ser Asn Gly Arg
     50                  55                  60

Thr Val Asp Thr Phe Gln Pro Thr Asp Leu Gly Arg Glu Leu Val Ala
 65                  70                  75                  80

Gln Trp Phe Glu Ser Pro Val Thr Val Thr Leu Ser Glu Arg Asp Glu
                 85                  90                  95

Leu Val Thr Lys Ile Ala Ile Ala Glu Ser Arg Gly Leu Asn Leu Ile
            100                 105                 110

Pro Leu Leu Asp Ile Gln Arg Asn Thr Val Met Ala Glu Leu Arg Ala
        115                 120                 125

Leu Asn Lys Ser Ser Arg Asp Leu Ala Glu Thr Arg Asn Thr Gln Arg
    130                 135                 140

Leu Leu Val Glu Lys Arg Ile Phe Glu Leu Glu Ala Gln Ala Arg Trp
145                 150                 155                 160

Leu Asp Arg Ile Glu Ala Leu Glu Gln
                165
```

<210> 2827
<211> 1023
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(1000)
<223> RXA02619

<400> 2827
agcgacttct caaagaacca ccccactcat ttcgagtgcg ggtggttttt tctatgccta 60

attctatgcc taattctatg tctgattcta ttggtgtcgc atg cgc agt gta gtt 115
Met Arg Ser Val Val
1 5

tta gaa cta cta gag aac tgg aag gaa tca ctc gtg ctt cac ccc tca 163
Leu Glu Leu Leu Glu Asn Trp Lys Glu Ser Leu Val Leu His Pro Ser
10 15 20

ttg act gag cta gcg gat gct gcc cca ctt gca cag gat ttt gcc acc 211
Leu Thr Glu Leu Ala Asp Ala Ala Pro Leu Ala Gln Asp Phe Ala Thr
25 30 35

gtc cgc ggt gtg ctg aag gaa tcg ctg gat ttg ttg ggc aat gca ctg 259
Val Arg Gly Val Leu Lys Glu Ser Leu Asp Leu Leu Gly Asn Ala Leu
40 45 50

aac cac ggt gaa gag ccc gcg gag ctt gca ggg tgg ctg tca caa gtt 307
Asn His Gly Glu Glu Pro Ala Glu Leu Ala Gly Trp Leu Ser Gln Val
55 60 65

att act gat gtt ttg cac tcc cct ggc ttg gat gcc cac gtg gtg ctc 355
Ile Thr Asp Val Leu His Ser Pro Gly Leu Asp Ala His Val Val Leu
70 75 80 85

acc ggc ccc gtg ggg cgt gga gac gca ctg cct acc tcg ccc gtg agg 403
Thr Gly Pro Val Gly Arg Gly Asp Ala Leu Pro Thr Ser Pro Val Arg
90 95 100

tgg ctg gcg gtc gtc gat agc caa gaa gat ccg aat gaa aag att tca 451
Trp Leu Ala Val Val Asp Ser Gln Glu Asp Pro Asn Glu Lys Ile Ser
105 110 115

gcg ctg tta act gag gtg ggc ttc att gcg gag ccg atc ggt gcg gca 499
Ala Leu Leu Thr Glu Val Gly Phe Ile Ala Glu Pro Ile Gly Ala Ala
120 125 130

act cgt gag gag tgg gag cag cgt gcg cgc gct ggt gag gat cca gag 547
Thr Arg Glu Glu Trp Glu Gln Arg Ala Arg Ala Gly Glu Asp Pro Glu
135 140 145

gtc tat ttg gat gct ggc acg tgg gtc gcg gcg atc gct gaa gta gat 595
Val Tyr Leu Asp Ala Gly Thr Trp Val Ala Ala Ile Ala Glu Val Asp
150 155 160 165

gac aaa gca ctg ttg cag gat gcg ttg tca tct agg ccg cct gcg gtg 643
Asp Lys Ala Leu Leu Gln Asp Ala Leu Ser Ser Arg Pro Pro Ala Val
170 175 180

gaa act tat gag ggt ctt cct tcg ttg gac atg gtg gta aac att cgt 691
Glu Thr Tyr Glu Gly Leu Pro Ser Leu Asp Met Val Val Asn Ile Arg
185 190 195

gag aac ctc atg att ccc acg gtg aag atc gct cgc tgg gca gca cac 739
Glu Asn Leu Met Ile Pro Thr Val Lys Ile Ala Arg Trp Ala Ala His

```
        200                 205                 210

aag gct ggt tct ttg gcg cct acg act gcg cag cgc ctc gtg gat gcc   787
Lys Ala Gly Ser Leu Ala Pro Thr Thr Ala Gln Arg Leu Val Asp Ala
    215                 220                 225

cgt ggt gtg ctc acc aat gat gaa gtc gac gcg ctg aca cag gtg tgg   835
Arg Gly Val Leu Thr Asn Asp Glu Val Asp Ala Leu Thr Gln Val Trp
230                 235                 240                 245

act tcc gca ctg agc ttg cag tcg aaa cgt tgg atg gat cac atc cat   883
Thr Ser Ala Leu Ser Leu Gln Ser Lys Arg Trp Met Asp His Ile His
                250                 255                 260

gat caa gaa acc acc gct tgg gag ctt ccc gcg ctg caa cgt gcc act   931
Asp Gln Glu Thr Thr Ala Trp Glu Leu Pro Ala Leu Gln Arg Ala Thr
            265                 270                 275

ttt ggc gca tcg gct cgg ttg ctt tct gag gtg ttg cgg tcc gtt gaa   979
Phe Gly Ala Ser Ala Arg Leu Leu Ser Glu Val Leu Arg Ser Val Glu
        280                 285                 290

gcc cgt gaa atc gat acc aaa taggaactct gcacaattac tgg            1023
Ala Arg Glu Ile Asp Thr Lys
    295                 300


<210> 2828
<211> 300
<212> PRT
<213> Corynebacterium glutamicum

<400> 2828
Met Arg Ser Val Val Leu Glu Leu Leu Glu Asn Trp Lys Glu Ser Leu
  1               5                  10                  15

Val Leu His Pro Ser Leu Thr Glu Leu Ala Asp Ala Ala Pro Leu Ala
             20                  25                  30

Gln Asp Phe Ala Thr Val Arg Gly Val Leu Lys Glu Ser Leu Asp Leu
         35                  40                  45

Leu Gly Asn Ala Leu Asn His Gly Glu Glu Pro Ala Glu Leu Ala Gly
     50                  55                  60

Trp Leu Ser Gln Val Ile Thr Asp Val Leu His Ser Pro Gly Leu Asp
 65                  70                  75                  80

Ala His Val Val Leu Thr Gly Pro Val Gly Arg Gly Asp Ala Leu Pro
                 85                  90                  95

Thr Ser Pro Val Arg Trp Leu Ala Val Val Asp Ser Gln Glu Asp Pro
            100                 105                 110

Asn Glu Lys Ile Ser Ala Leu Leu Thr Glu Val Gly Phe Ile Ala Glu
        115                 120                 125

Pro Ile Gly Ala Ala Thr Arg Glu Glu Trp Glu Gln Arg Ala Arg Ala
    130                 135                 140

Gly Glu Asp Pro Glu Val Tyr Leu Asp Ala Gly Thr Trp Val Ala Ala
```

```
145                 150                 155                 160

Ile Ala Glu Val Asp Asp Lys Ala Leu Leu Gln Asp Ala Leu Ser Ser
                165                 170                 175

Arg Pro Pro Ala Val Glu Thr Tyr Glu Gly Leu Pro Ser Leu Asp Met
            180                 185                 190

Val Val Asn Ile Arg Glu Asn Leu Met Ile Pro Thr Val Lys Ile Ala
        195                 200                 205

Arg Trp Ala Ala His Lys Ala Gly Ser Leu Ala Pro Thr Thr Ala Gln
    210                 215                 220

Arg Leu Val Asp Ala Arg Gly Val Leu Thr Asn Asp Glu Val Asp Ala
225                 230                 235                 240

Leu Thr Gln Val Trp Thr Ser Ala Leu Ser Leu Gln Ser Lys Arg Trp
                245                 250                 255

Met Asp His Ile His Asp Gln Glu Thr Thr Ala Trp Glu Leu Pro Ala
            260                 265                 270

Leu Gln Arg Ala Thr Phe Gly Ala Ser Ala Arg Leu Leu Ser Glu Val
        275                 280                 285

Leu Arg Ser Val Glu Ala Arg Glu Ile Asp Thr Lys
    290                 295                 300
```

US20050153417A1

<210> 2829
<211> 777
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(754)
<223> RXA02620

<400> 2829

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atcgatacca aataggaact ctgcacaatt actggctaca atctcttgag atcaataggc 60

caaaacttta aggaagtaga attacgctat ggcaggagca gtg gga cgc ccc cgg   115
                                                Val Gly Arg Pro Arg
                                                  1               5

aga tca gct ccg cga cgg gca ggc aag aat cct cgc gag gag att ctt   163
Arg Ser Ala Pro Arg Arg Ala Gly Lys Asn Pro Arg Glu Glu Ile Leu
                 10                  15                  20

gac gcc tct gct gag ctt ttc acc cgt caa ggc ttc gca aca acc tcc   211
Asp Ala Ser Ala Glu Leu Phe Thr Arg Gln Gly Phe Ala Thr Thr Ser
             25                  30                  35

acg cat caa atc gct gat gcc gtg gga atc cgc caa gcc tcg ctg tat   259
Thr His Gln Ile Ala Asp Ala Val Gly Ile Arg Gln Ala Ser Leu Tyr
         40                  45                  50

tat cac ttc ccg tcc aag acg gaa atc ttc ctc acc ctg ctg aaa tct   307
Tyr His Phe Pro Ser Lys Thr Glu Ile Phe Leu Thr Leu Leu Lys Ser
```

```
     55                  60                  65

act gtc gag ccg tcc act gtg ctc gcc gaa gac tta agc acc ctg gac   355
Thr Val Glu Pro Ser Thr Val Leu Ala Glu Asp Leu Ser Thr Leu Asp
 70                  75                  80                  85

gcc gga cct gag atg cgc ctc tgg gca atc gtt gcc tcc gaa gtg cgt   403
Ala Gly Pro Glu Met Arg Leu Trp Ala Ile Val Ala Ser Glu Val Arg
                 90                  95                 100

ctg ctg ctg tcc acc aag tgg aac gtc ggt cgc ctg tac caa ctc ccc   451
Leu Leu Leu Ser Thr Lys Trp Asn Val Gly Arg Leu Tyr Gln Leu Pro
            105                 110                 115

atc gtt ggt tct gaa gag ttc gcc gag tac cac agc cag cgc gaa gcc   499
Ile Val Gly Ser Glu Glu Phe Ala Glu Tyr His Ser Gln Arg Glu Ala
        120                 125                 130

ctc acc aac gtc ttc cgc gac ctc gcc acc gaa atc gtc ggt gac gac   547
Leu Thr Asn Val Phe Arg Asp Leu Ala Thr Glu Ile Val Gly Asp Asp
    135                 140                 145

ccc cgc gca gaa ctc ccc ttc cac atc acc atg tcg gtg atc gaa atg   595
Pro Arg Ala Glu Leu Pro Phe His Ile Thr Met Ser Val Ile Glu Met
150                 155                 160                 165

cgt cgc aac gac ggc aag att cca agc ccg ctt tcc gca gac agc ctc   643
Arg Arg Asn Asp Gly Lys Ile Pro Ser Pro Leu Ser Ala Asp Ser Leu
                170                 175                 180

ccg gag acc gca att atg ctt gcc gac gcc tcc ctc gcc gtc ctc ggc   691
Pro Glu Thr Ala Ile Met Leu Ala Asp Ala Ser Leu Ala Val Leu Gly
            185                 190                 195

gcg ccg ctg ccc gcc gac cgg gtc gaa aaa acg ctt gaa cta atc aag   739
Ala Pro Leu Pro Ala Asp Arg Val Glu Lys Thr Leu Glu Leu Ile Lys
        200                 205                 210

cag gct gac gcg aaa taaccatccg cgcctgcgaa atc                    777
Gln Ala Asp Ala Lys
    215
```

US20090275090A1

<210> 2830
<211> 218
<212> PRT
<213> Corynebacterium glutamicum

<400> 2830

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Val Gly Arg Pro Arg Arg Ser Ala Pro Arg Arg Ala Gly Lys Asn Pro
  1               5                  10                  15

Arg Glu Glu Ile Leu Asp Ala Ser Ala Glu Leu Phe Thr Arg Gln Gly
             20                  25                  30

Phe Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala Val Gly Ile Arg
         35                  40                  45

Gln Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr Glu Ile Phe Leu
     50                  55                  60
```

```
Thr Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val Leu Ala Glu Asp
 65                  70                  75                  80

Leu Ser Thr Leu Asp Ala Gly Pro Glu Met Arg Leu Trp Ala Ile Val
                 85                  90                  95

Ala Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp Asn Val Gly Arg
            100                 105                 110

Leu Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe Ala Glu Tyr His
        115                 120                 125

Ser Gln Arg Glu Ala Leu Thr Asn Val Phe Arg Asp Leu Ala Thr Glu
    130                 135                 140

Ile Val Gly Asp Asp Pro Arg Ala Glu Leu Pro Phe His Ile Thr Met
145                 150                 155                 160

Ser Val Ile Glu Met Arg Arg Asn Asp Gly Lys Ile Pro Ser Pro Leu
                165                 170                 175

Ser Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu Ala Asp Ala Ser
            180                 185                 190

Leu Ala Val Leu Gly Ala Pro Leu Pro Ala Asp Arg Val Glu Lys Thr
        195                 200                 205

Leu Glu Leu Ile Lys Gln Ala Asp Ala Lys
    210                 215


<210> 2831
<211> 957
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(934)
<223> RXA02639

<400> 2831
cgaaaatgtt ggaaatcgcc gaacgggaac gtcgacaagc aaaacgcgcg gcaaaggtcg 60

ccaagaaacg caccaccttt ataaggaaaa tctttaaaaa atg att gca ctg ggt   115
                                            Met Ile Ala Leu Gly
                                              1               5

tca gcg ccc aag ctg gtt gcc tcc gat gtt gat ggc acc ctc atc aat   163
Ser Ala Pro Lys Leu Val Ala Ser Asp Val Asp Gly Thr Leu Ile Asn
                 10                  15                  20

agt tct gag cgc gtg ccg caa cgc ctg cgc gat gtg atc acg cgg atg   211
Ser Ser Glu Arg Val Pro Gln Arg Leu Arg Asp Val Ile Thr Arg Met
             25                  30                  35

acc aat cag ggc gtg acc ctg gcg ctg tcc acg ggc cgc ccg ccg cgc   259
Thr Asn Gln Gly Val Thr Leu Ala Leu Ser Thr Gly Arg Pro Pro Arg
         40                  45                  50

tgg att cat tat gtg ctg gat cag ctg agc gtg aag ccg att tgc gtc   307
```

```
Trp Ile His Tyr Val Leu Asp Gln Leu Ser Val Lys Pro Ile Cys Val
     55                  60                  65

tgc gcg aat ggc gcg gtg ctg tac gat tcc gct gcc gat gag att ctt   355
Cys Ala Asn Gly Ala Val Leu Tyr Asp Ser Ala Ala Asp Glu Ile Leu
 70                  75                  80                  85

gca gct cag acg ctt agt ccg gag gtt atg gcg agt gcc gtc atg gct   403
Ala Ala Gln Thr Leu Ser Pro Glu Val Met Ala Ser Ala Val Met Ala
                 90                  95                 100

gcg cgt gcc gct ttg gaa gag cat ggc ggg gtc agt att gct gtc gag   451
Ala Arg Ala Ala Leu Glu Glu His Gly Gly Val Ser Ile Ala Val Glu
            105                 110                 115

cgc gct gga aaa tcc gct tac gat cca gcc gat gag ctg ttt ttg gtc   499
Arg Ala Gly Lys Ser Ala Tyr Asp Pro Ala Asp Glu Leu Phe Leu Val
        120                 125                 130

acc ccg gaa tac agc cac gcg tgg ccc tca aat gat cac ggc acc ttc   547
Thr Pro Glu Tyr Ser His Ala Trp Pro Ser Asn Asp His Gly Thr Phe
    135                 140                 145

gag gaa gcc gaa gtg ctt tcc gaa cca gcc acc aaa ttg ttg atg cgc   595
Glu Glu Ala Glu Val Leu Ser Glu Pro Ala Thr Lys Leu Leu Met Arg
150                 155                 160                 165

agc gat tac ctc gat tcc aag cag ctt ttt gat atc gtc cgc gcc tcc   643
Ser Asp Tyr Leu Asp Ser Lys Gln Leu Phe Asp Ile Val Arg Ala Ser
                170                 175                 180

gtt ccc gag gat caa gtc cac gtc acc ttc tcc atg tcc ggc gga ctc   691
Val Pro Glu Asp Gln Val His Val Thr Phe Ser Met Ser Gly Gly Leu
            185                 190                 195

att gag atc gca gcg ccc ggc gtg acc aag gca ctg ggc gta tcg atg   739
Ile Glu Ile Ala Ala Pro Gly Val Thr Lys Ala Leu Gly Val Ser Met
        200                 205                 210

ctg gca gag cgc cta aag att gcg caa aag gac gtt ata acg ttc ggc   787
Leu Ala Glu Arg Leu Lys Ile Ala Gln Lys Asp Val Ile Thr Phe Gly
    215                 220                 225

gac atg ccc aac gat att gaa atg ctc cag tgg gcc ggc cgg gga gtg   835
Asp Met Pro Asn Asp Ile Glu Met Leu Gln Trp Ala Gly Arg Gly Val
230                 235                 240                 245

gcg atg ggc aac gcc cga cca gag gtc aaa gcc gtg tca gac cac atc   883
Ala Met Gly Asn Ala Arg Pro Glu Val Lys Ala Val Ser Asp His Ile
                250                 255                 260

acc cgc acc aac gac gac gcc ggt gta gca gat gta ttg gag tgg tgg   931
Thr Arg Thr Asn Asp Asp Ala Gly Val Ala Asp Val Leu Glu Trp Trp
            265                 270                 275

ttc taataggtgg tgttaaaaca ctg                                    957
Phe
```

<210> 2832

<211> 278
<212> PRT
<213> Corynebacterium glutamicum

<400> 2832

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Met Ile Ala Leu Gly Ser Ala Pro Lys Leu Val Ala Ser Asp Val Asp
  1               5                  10                  15

Gly Thr Leu Ile Asn Ser Ser Glu Arg Val Pro Gln Arg Leu Arg Asp
            20                  25                  30

Val Ile Thr Arg Met Thr Asn Gln Gly Val Thr Leu Ala Leu Ser Thr
        35                  40                  45

Gly Arg Pro Pro Arg Trp Ile His Tyr Val Leu Asp Gln Leu Ser Val
    50                  55                  60

Lys Pro Ile Cys Val Cys Ala Asn Gly Ala Val Leu Tyr Asp Ser Ala
65                  70                  75                  80

Ala Asp Glu Ile Leu Ala Ala Gln Thr Leu Ser Pro Glu Val Met Ala
                85                  90                  95

Ser Ala Val Met Ala Ala Arg Ala Ala Leu Glu Glu His Gly Gly Val
            100                 105                 110

Ser Ile Ala Val Glu Arg Ala Gly Lys Ser Ala Tyr Asp Pro Ala Asp
        115                 120                 125

Glu Leu Phe Leu Val Thr Pro Glu Tyr Ser His Ala Trp Pro Ser Asn
    130                 135                 140

Asp His Gly Thr Phe Glu Glu Ala Glu Val Leu Ser Glu Pro Ala Thr
145                 150                 155                 160

Lys Leu Leu Met Arg Ser Asp Tyr Leu Asp Ser Lys Gln Leu Phe Asp
                165                 170                 175

Ile Val Arg Ala Ser Val Pro Glu Asp Gln Val His Val Thr Phe Ser
            180                 185                 190

Met Ser Gly Gly Leu Ile Glu Ile Ala Ala Pro Gly Val Thr Lys Ala
        195                 200                 205

Leu Gly Val Ser Met Leu Ala Glu Arg Leu Lys Ile Ala Gln Lys Asp
    210                 215                 220

Val Ile Thr Phe Gly Asp Met Pro Asn Asp Ile Glu Met Leu Gln Trp
225                 230                 235                 240

Ala Gly Arg Gly Val Ala Met Gly Asn Ala Arg Pro Glu Val Lys Ala
                245                 250                 255

Val Ser Asp His Ile Thr Arg Thr Asn Asp Asp Ala Gly Val Ala Asp
            260                 265                 270

Val Leu Glu Trp Trp Phe
        275
```

<210> 2833

<211> 585
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> RXA02647

<400> 2833
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tttgcgtcga agtactttga cccttgttac agcaagcgct gtg gca ttg tcc gtg 115
Val Ala Leu Ser Val
1 5

ttc act cca gtt gcc cag gct cag tcc tct gac gca ctg aca cag ctc 163
Phe Thr Pro Val Ala Gln Ala Gln Ser Ser Asp Ala Leu Thr Gln Leu
10 15 20

tca gac aac atc acc tca tca cag atc ctt gat gat gat gga aat cca 211
Ser Asp Asn Ile Thr Ser Ser Gln Ile Leu Asp Asp Asp Gly Asn Pro
25 30 35

gtc gat gga aac gaa acc tgg cca ggc agc tct gaa ggc agc tca atg 259
Val Asp Gly Asn Glu Thr Trp Pro Gly Ser Ser Glu Gly Ser Ser Met
40 45 50

ctc agc aat ggc gac att cct gcg gcc cca agc ttg agc tcc tcc ggc 307
Leu Ser Asn Gly Asp Ile Pro Ala Ala Pro Ser Leu Ser Ser Ser Gly
55 60 65

aaa gac acc agc gat gat gac gat gaa atc agc gaa gag cag caa gca 355
Lys Asp Thr Ser Asp Asp Asp Asp Glu Ile Ser Glu Glu Gln Gln Ala
70 75 80 85

ctg atc gat cgg ttg tcc gaa atg cca gtg att ggt tcc att gtc tcc 403
Leu Ile Asp Arg Leu Ser Glu Met Pro Val Ile Gly Ser Ile Val Ser
90 95 100

cca cca gaa tgg ctt gcc att cct ttt gcg gta ctg cag gga ttg ctc 451
Pro Pro Glu Trp Leu Ala Ile Pro Phe Ala Val Leu Gln Gly Leu Leu
105 110 115

gca atc acc act ctt gct tcc acc gca gca tcc ttc atg gtg acc gtc 499
Ala Ile Thr Thr Leu Ala Ser Thr Ala Ala Ser Phe Met Val Thr Val
120 125 130

gac cca tcg ttc aag cag act ctg cgt gac atg ctc acc cag ttt ggc 547
Asp Pro Ser Phe Lys Gln Thr Leu Arg Asp Met Leu Thr Gln Phe Gly
135 140 145

atc aac gtc gac gct taaaagcaca ctgacataaa atg 585
Ile Asn Val Asp Ala
150

<210> 2834
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 2834
Val Ala Leu Ser Val Phe Thr Pro Val Ala Gln Ala Gln Ser Ser Asp
1 5 10 15

Ala Leu Thr Gln Leu Ser Asp Asn Ile Thr Ser Ser Gln Ile Leu Asp
20 25 30

Asp Asp Gly Asn Pro Val Asp Gly Asn Glu Thr Trp Pro Gly Ser Ser
35 40 45

Glu Gly Ser Ser Met Leu Ser Asn Gly Asp Ile Pro Ala Ala Pro Ser
50 55 60

Leu Ser Ser Ser Gly Lys Asp Thr Ser Asp Asp Asp Asp Glu Ile Ser
65 70 75 80

Glu Glu Gln Gln Ala Leu Ile Asp Arg Leu Ser Glu Met Pro Val Ile
85 90 95

Gly Ser Ile Val Ser Pro Pro Glu Trp Leu Ala Ile Pro Phe Ala Val
100 105 110

Leu Gln Gly Leu Leu Ala Ile Thr Thr Leu Ala Ser Thr Ala Ala Ser
115 120 125

Phe Met Val Thr Val Asp Pro Ser Phe Lys Gln Thr Leu Arg Asp Met
130 135 140

Leu Thr Gln Phe Gly Ile Asn Val Asp Ala
145 150

<210> 2835
<211> 1125
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1102)
<223> RXA02649

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atttgttctt tttggcgccg atgccgatag gtttaaaggc gtg cta aaa cga ttc 115
Val Leu Lys Arg Phe
1 5

tct cac cac tcc agc ccg caa gtt ctt tca cgg aaa gtt gtc gcg tcc 163
Ser His His Ser Ser Pro Gln Val Leu Ser Arg Lys Val Val Ala Ser
10 15 20

gca tta gct tta aca acc gcg ctg gct tta gcc gcg tgt agt tcc tca 211
Ala Leu Ala Leu Thr Thr Ala Leu Ala Leu Ala Ala Cys Ser Ser Ser
25 30 35

gcc gag ccg gac tcc cct gaa gtt gag cag gcg gtg ggt ctt gcg gtg 259
Ala Glu Pro Asp Ser Pro Glu Val Glu Gln Ala Val Gly Leu Ala Val
40 45 50

```
gat acg cca cgt gtg gtg gtt gtg gat cca ggc act ggc gat ttg cag   307
Asp Thr Pro Arg Val Val Val Val Asp Pro Gly Thr Gly Asp Leu Gln
     55                  60                  65

cgc ttg caa tac aaa gac atc gcc cct gat gcc aca cag gaa cag acc   355
Arg Leu Gln Tyr Lys Asp Ile Ala Pro Asp Ala Thr Gln Glu Gln Thr
 70                  75                  80                  85

atc aat att gct gaa ggt ttt gcc caa tcg gtg gtg aat gcg gac agc   403
Ile Asn Ile Ala Glu Gly Phe Ala Gln Ser Val Val Asn Ala Asp Ser
                 90                  95                 100

gtg gat ccg cag gca cca gcc ggt ggc gat gtc acc aca ttc cac ctt   451
Val Asp Pro Gln Ala Pro Ala Gly Gly Asp Val Thr Thr Phe His Leu
            105                 110                 115

cct gtt aaa gcc acc acc gag gaa gcg gag ttc agc gat cag gaa atg   499
Pro Val Lys Ala Thr Thr Glu Glu Ala Glu Phe Ser Asp Gln Glu Met
        120                 125                 130

gtg agc gcg act cgc gat atc tct cta ctt ttc ggt aaa cct acc tac   547
Val Ser Ala Thr Arg Asp Ile Ser Leu Leu Phe Gly Lys Pro Thr Tyr
    135                 140                 145

acc gat ctt tcc caa gtt gaa gat gtg aat tcc acc gag gga ttc acg   595
Thr Asp Leu Ser Gln Val Glu Asp Val Asn Ser Thr Glu Gly Phe Thr
150                 155                 160                 165

ctg gga atc cgc gca aca gat agt gga cag cac acc acc tta agt ttc   643
Leu Gly Ile Arg Ala Thr Asp Ser Gly Gln His Thr Thr Leu Ser Phe
                170                 175                 180

gca gcc cct gtt gat tcc act gaa act ggt cgc atg ctc atg gag caa   691
Ala Ala Pro Val Asp Ser Thr Glu Thr Gly Arg Met Leu Met Glu Gln
            185                 190                 195

tac tta ctc acg ttt acg tcc ctt ccc att gtg ttc ccc tct gac gat   739
Tyr Leu Leu Thr Phe Thr Ser Leu Pro Ile Val Phe Pro Ser Asp Asp
        200                 205                 210

att ggc gtg ggc gcg aag tgg act gtg gat agc cgt gtg aca ggc gaa   787
Ile Gly Val Gly Ala Lys Trp Thr Val Asp Ser Arg Val Thr Gly Glu
    215                 220                 225

tca acg ctg cta caa acc gtg acc tac acg atc aca ggg atc gac ggc   835
Ser Thr Leu Leu Gln Thr Val Thr Tyr Thr Ile Thr Gly Ile Asp Gly
230                 235                 240                 245

gac aaa gta aac ctc gat gtg gaa gtc tct cag cgc ccc agc atg ggt   883
Asp Lys Val Asn Leu Asp Val Glu Val Ser Gln Arg Pro Ser Met Gly
                250                 255                 260

gcg ttg gag atc acc gat gaa gaa tcg gac gag acc acc ggg cag ctc   931
Ala Leu Glu Ile Thr Asp Glu Glu Ser Asp Glu Thr Thr Gly Gln Leu
            265                 270                 275

act gtc ctt aat tcc aac acc acc tcc gtg ggc acc ttg gaa gtc gat   979
Thr Val Leu Asn Ser Asn Thr Thr Ser Val Gly Thr Leu Glu Val Asp
        280                 285                 290
```

```
ctg act cag cct tta ccc acg tca gga cag gtt tct tgg acc act cgc   1027
Leu Thr Gln Pro Leu Pro Thr Ser Gly Gln Val Ser Trp Thr Thr Arg
    295                 300                 305

gtg att tac ggc ggt tcc aat gag cag gtg cgt gtg gtg cag gat tcc   1075
Val Ile Tyr Gly Gly Ser Asn Glu Gln Val Arg Val Val Gln Asp Ser
310                 315                 320                 325

acc tct tcg gtg agc ttc gga gac cag taatttacca attagggttg         1122
Thr Ser Ser Val Ser Phe Gly Asp Gln
                330

cca                                                               1125
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<210> 2836
<211> 334
<212> PRT
<213> Corynebacterium glutamicum

<400> 2836

```
Val Leu Lys Arg Phe Ser His His Ser Ser Pro Gln Val Leu Ser Arg
  1               5                  10                  15

Lys Val Val Ala Ser Ala Leu Ala Leu Thr Thr Ala Leu Ala Leu Ala
            20                  25                  30

Ala Cys Ser Ser Ser Ala Glu Pro Asp Ser Pro Glu Val Glu Gln Ala
        35                  40                  45

Val Gly Leu Ala Val Asp Thr Pro Arg Val Val Val Val Asp Pro Gly
    50                  55                  60

Thr Gly Asp Leu Gln Arg Leu Gln Tyr Lys Asp Ile Ala Pro Asp Ala
65                  70                  75                  80

Thr Gln Glu Gln Thr Ile Asn Ile Ala Glu Gly Phe Ala Gln Ser Val
                85                  90                  95

Val Asn Ala Asp Ser Val Asp Pro Gln Ala Pro Ala Gly Gly Asp Val
            100                 105                 110

Thr Thr Phe His Leu Pro Val Lys Ala Thr Thr Glu Glu Ala Glu Phe
        115                 120                 125

Ser Asp Gln Glu Met Val Ser Ala Thr Arg Asp Ile Ser Leu Leu Phe
    130                 135                 140

Gly Lys Pro Thr Tyr Thr Asp Leu Ser Gln Val Glu Asp Val Asn Ser
145                 150                 155                 160

Thr Glu Gly Phe Thr Leu Gly Ile Arg Ala Thr Asp Ser Gly Gln His
                165                 170                 175

Thr Thr Leu Ser Phe Ala Ala Pro Val Asp Ser Thr Glu Thr Gly Arg
            180                 185                 190

Met Leu Met Glu Gln Tyr Leu Leu Thr Phe Thr Ser Leu Pro Ile Val
        195                 200                 205

Phe Pro Ser Asp Asp Ile Gly Val Gly Ala Lys Trp Thr Val Asp Ser
```

```
    210                 215                 220

Arg Val Thr Gly Glu Ser Thr Leu Leu Gln Thr Val Thr Tyr Thr Ile
225                 230                 235                 240

Thr Gly Ile Asp Gly Asp Lys Val Asn Leu Asp Val Glu Val Ser Gln
                245                 250                 255

Arg Pro Ser Met Gly Ala Leu Glu Ile Thr Asp Glu Glu Ser Asp Glu
            260                 265                 270

Thr Thr Gly Gln Leu Thr Val Leu Asn Ser Asn Thr Thr Ser Val Gly
        275                 280                 285

Thr Leu Glu Val Asp Leu Thr Gln Pro Leu Pro Thr Ser Gly Gln Val
    290                 295                 300

Ser Trp Thr Thr Arg Val Ile Tyr Gly Gly Ser Asn Glu Gln Val Arg
305                 310                 315                 320

Val Val Gln Asp Ser Thr Ser Ser Val Ser Phe Gly Asp Gln
                325                 330


<210> 2837
<211> 702
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(679)
<223> RXA02652

<400> 2837
cgcttggatt caaccaccca gcagatggcc gatggatgga aatcgtctcc ccatatccaa 60

ctgatctcca acacgcttta gacgttctcc gcgagcaata atg gat ggt gtc gat   115
                                              Met Asp Gly Val Asp
                                                1               5

aaa ggg cga cgc atc gtc gcc ctc cta gca att ctc gca ttg gtt gtc   163
Lys Gly Arg Arg Ile Val Ala Leu Leu Ala Ile Leu Ala Leu Val Val
                10                  15                  20

gtg gtt gcg atc ttg agt ttc agc gac cgc acc gcg aaa ccc atg cag   211
Val Val Ala Ile Leu Ser Phe Ser Asp Arg Thr Ala Lys Pro Met Gln
            25                  30                  35

ctc aac ggt gac atg ctc ggc caa gac aac acg gaa act tcc gtc gag   259
Leu Asn Gly Asp Met Leu Gly Gln Asp Asn Thr Glu Thr Ser Val Glu
        40                  45                  50

tac cgt cag cgg gca tcg gaa tca ttg gaa aat gcc gcg gtc ggc gaa   307
Tyr Arg Gln Arg Ala Ser Glu Ser Leu Glu Asn Ala Ala Val Gly Glu
    55                  60                  65

gaa gcc tat tca ctg gtg acg ttc aca cag ccg ctt tcg cct tcc gag   355
Glu Ala Tyr Ser Leu Val Thr Phe Thr Gln Pro Leu Ser Pro Ser Glu
70                  75                  80                  85
```

```
gcc tct aac ctt ctt aaa gga gtc ggt cgc gtc aat gcc atg gtt atg   403
Ala Ser Asn Leu Leu Lys Gly Val Gly Arg Val Asn Ala Met Val Met
                 90                  95                 100

ctc tcg gct cct gcc atg gat cta ccc gaa ccc atc gca ggc gag acc   451
Leu Ser Ala Pro Ala Met Asp Leu Pro Glu Pro Ile Ala Gly Glu Thr
            105                 110                 115

cgt gaa gat gtt ttt aac cgt caa ata aag ctt gtc gac gcc cag tta   499
Arg Glu Asp Val Phe Asn Arg Gln Ile Lys Leu Val Asp Ala Gln Leu
        120                 125                 130

tcc ggt atc ggc aac gtc cgc gcg ccg ggc gaa ctc aac ggg gta gtg   547
Ser Gly Ile Gly Asn Val Arg Ala Pro Gly Glu Leu Asn Gly Val Val
    135                 140                 145

gtt tgg gat att cct cag aaa gtt cgt gtg ttg tcc gag agc tcg ctg   595
Val Trp Asp Ile Pro Gln Lys Val Arg Val Leu Ser Glu Ser Ser Leu
150                 155                 160                 165

gtt tat agt gtc gaa acc ctg cca cct gac gcg gcg tgg ggc agt ttc   643
Val Tyr Ser Val Glu Thr Leu Pro Pro Asp Ala Ala Trp Gly Ser Phe
                170                 175                 180

ggt att cga cca gtc gat act tcg ggt act aat ttt tagaagaaaa        689
Gly Ile Arg Pro Val Asp Thr Ser Gly Thr Asn Phe
            185                 190

ttccagatgc ccc                                                   702
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<210> 2838
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 2838

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Met Asp Gly Val Asp Lys Gly Arg Arg Ile Val Ala Leu Leu Ala Ile
  1               5                  10                  15

Leu Ala Leu Val Val Val Val Ala Ile Leu Ser Phe Ser Asp Arg Thr
             20                  25                  30

Ala Lys Pro Met Gln Leu Asn Gly Asp Met Leu Gly Gln Asp Asn Thr
         35                  40                  45

Glu Thr Ser Val Glu Tyr Arg Gln Arg Ala Ser Glu Ser Leu Glu Asn
     50                  55                  60

Ala Ala Val Gly Glu Glu Ala Tyr Ser Leu Val Thr Phe Thr Gln Pro
 65                  70                  75                  80

Leu Ser Pro Ser Glu Ala Ser Asn Leu Leu Lys Gly Val Gly Arg Val
                 85                  90                  95

Asn Ala Met Val Met Leu Ser Ala Pro Ala Met Asp Leu Pro Glu Pro
            100                 105                 110

Ile Ala Gly Glu Thr Arg Glu Asp Val Phe Asn Arg Gln Ile Lys Leu
        115                 120                 125
```

```
Val Asp Ala Gln Leu Ser Gly Ile Gly Asn Val Arg Ala Pro Gly Glu
    130                 135                 140

Leu Asn Gly Val Val Val Trp Asp Ile Pro Gln Lys Val Arg Val Leu
145                 150                 155                 160

Ser Glu Ser Ser Leu Val Tyr Ser Val Glu Thr Leu Pro Pro Asp Ala
                165                 170                 175

Ala Trp Gly Ser Phe Gly Ile Arg Pro Val Asp Thr Ser Gly Thr Asn
            180                 185                 190

Phe
```

<210> 2839
<211> 1107
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1084)
<223> RXA02655

<400> 2839

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aattcgatgg agaagaaaaa gtcatggggg tcaggctagg agaaaatgat ctcatgatgg 60

ctttggaacg gtacctcgct cacgagtttg gtgaaattag atg agt cca gaa gcc   115
                                            Met Ser Pro Glu Ala
                                              1               5

aaa gaa gcc caa gat tct agg cgc aac gag atg ccc gag aaa aag cga   163
Lys Glu Ala Gln Asp Ser Arg Arg Asn Glu Met Pro Glu Lys Lys Arg
                  10                  15                  20

gcg gtg cta cgt aaa gcg att aag ttg gaa tgg gca acg atc gca tgg   211
Ala Val Leu Arg Lys Ala Ile Lys Leu Glu Trp Ala Thr Ile Ala Trp
              25                  30                  35

gtt ctt ttt tcg atc gtt ttg gta ggt gtt gtc gct ggt caa tcg cag   259
Val Leu Phe Ser Ile Val Leu Val Gly Val Val Ala Gly Gln Ser Gln
          40                  45                  50

gcc atg cgt agt gca tgg att gaa gac atg ctt tct ttg gta cca cct   307
Ala Met Arg Ser Ala Trp Ile Glu Asp Met Leu Ser Leu Val Pro Pro
      55                  60                  65

atc gct ttt ctt tta gcc tcc cga atc agc aaa gct gtg gca acc aga   355
Ile Ala Phe Leu Leu Ala Ser Arg Ile Ser Lys Ala Val Ala Thr Arg
 70                  75                  80                  85

aaa cat cca tac ggc aag cac cgg tcg att gct atc ggg cac caa gct   403
Lys His Pro Tyr Gly Lys His Arg Ser Ile Ala Ile Gly His Gln Ala
                  90                  95                 100

gca gca ctg gcc ctg ctt atc atg gga agc ctt tta att tat gaa gcg   451
Ala Ala Leu Ala Leu Leu Ile Met Gly Ser Leu Leu Ile Tyr Glu Ala
            105                 110                 115
```

```
gta tct gca ctg atc aag gga gaa agg cct ccg ata ggt tta gct att   499
Val Ser Ala Leu Ile Lys Gly Glu Arg Pro Pro Ile Gly Leu Ala Ile
        120                 125                 130

tta ttt ggc cat gac gtg tgg tca ggt tgg tta atg atc ggg gtt atg   547
Leu Phe Gly His Asp Val Trp Ser Gly Trp Leu Met Ile Gly Val Met
    135                 140                 145

att tca gtg tcg atc ccg atg gtg att gta ggg cga gta aaa ata aac   595
Ile Ser Val Ser Ile Pro Met Val Ile Val Gly Arg Val Lys Ile Asn
150                 155                 160                 165

tta gct aaa gat ctc cac gat aaa ctc ctc tat gca gac gcg gat atg   643
Leu Ala Lys Asp Leu His Asp Lys Leu Leu Tyr Ala Asp Ala Asp Met
                170                 175                 180

gcc aag gct gac tgg ggc aca gca gtc gct agc aca gta ggc gtg ctc   691
Ala Lys Ala Asp Trp Gly Thr Ala Val Ala Ser Thr Val Gly Val Leu
            185                 190                 195

gga ata gga ctg ggt ttt tgg tgg gcg gat gca gtt gca gct cta gta   739
Gly Ile Gly Leu Gly Phe Trp Trp Ala Asp Ala Val Ala Ala Leu Val
        200                 205                 210

ata tca gct tca att ctc aga gat ggc gtg ata aat atg aaa gct gct   787
Ile Ser Ala Ser Ile Leu Arg Asp Gly Val Ile Asn Met Lys Ala Ala
    215                 220                 225

ata tct gac tta ggt gat gga cga gcc atg act tat gac aat tcc gcc   835
Ile Ser Asp Leu Gly Asp Gly Arg Ala Met Thr Tyr Asp Asn Ser Ala
230                 235                 240                 245

cct cac cca tta aat gat gat gtg gaa aag gct gcc cta gag atg cat   883
Pro His Pro Leu Asn Asp Asp Val Glu Lys Ala Ala Leu Glu Met His
                250                 255                 260

tgg gtc aaa cac gcc cgc gct agg ata cgc gac caa ggc cgc tgt ttc   931
Trp Val Lys His Ala Arg Ala Arg Ile Arg Asp Gln Gly Arg Cys Phe
            265                 270                 275

cac aca gag tta ttt gtc gaa cca gta gaa gga tac aca cct gct ccg   979
His Thr Glu Leu Phe Val Glu Pro Val Glu Gly Tyr Thr Pro Ala Pro
        280                 285                 290

gaa gaa ata act tct cta gtt aag cga atc caa aac ctt gac tgg aag   1027
Glu Glu Ile Thr Ser Leu Val Lys Arg Ile Gln Asn Leu Asp Trp Lys
    295                 300                 305

ctg caa gat gtc gta gct tcc gtc gtc gaa aaa atc gac cgg ttt cag   1075
Leu Gln Asp Val Val Ala Ser Val Val Glu Lys Ile Asp Arg Phe Gln
310                 315                 320                 325

gcc cct tcg taaaacttaa ctgagaaagt gat                            1107
Ala Pro Ser
```

<210> 2840
<211> 328
<212> PRT
<213> Corynebacterium glutamicum

<400> 2840

```
Met Ser Pro Glu Ala Lys Glu Ala Gln Asp Ser Arg Arg Asn Glu Met
  1               5                  10                  15

Pro Glu Lys Lys Arg Ala Val Leu Arg Lys Ala Ile Lys Leu Glu Trp
             20                  25                  30

Ala Thr Ile Ala Trp Val Leu Phe Ser Ile Val Leu Val Gly Val Val
         35                  40                  45

Ala Gly Gln Ser Gln Ala Met Arg Ser Ala Trp Ile Glu Asp Met Leu
     50                  55                  60

Ser Leu Val Pro Pro Ile Ala Phe Leu Leu Ala Ser Arg Ile Ser Lys
 65                  70                  75                  80

Ala Val Ala Thr Arg Lys His Pro Tyr Gly Lys His Arg Ser Ile Ala
                 85                  90                  95

Ile Gly His Gln Ala Ala Ala Leu Ala Leu Leu Ile Met Gly Ser Leu
            100                 105                 110

Leu Ile Tyr Glu Ala Val Ser Ala Leu Ile Lys Gly Glu Arg Pro Pro
        115                 120                 125

Ile Gly Leu Ala Ile Leu Phe Gly His Asp Val Trp Ser Gly Trp Leu
    130                 135                 140

Met Ile Gly Val Met Ile Ser Val Ser Ile Pro Met Val Ile Val Gly
145                 150                 155                 160

Arg Val Lys Ile Asn Leu Ala Lys Asp Leu His Asp Lys Leu Leu Tyr
                165                 170                 175

Ala Asp Ala Asp Met Ala Lys Ala Asp Trp Gly Thr Ala Val Ala Ser
            180                 185                 190

Thr Val Gly Val Leu Gly Ile Gly Leu Gly Phe Trp Trp Ala Asp Ala
        195                 200                 205

Val Ala Ala Leu Val Ile Ser Ala Ser Ile Leu Arg Asp Gly Val Ile
    210                 215                 220

Asn Met Lys Ala Ala Ile Ser Asp Leu Gly Asp Gly Arg Ala Met Thr
225                 230                 235                 240

Tyr Asp Asn Ser Ala Pro His Pro Leu Asn Asp Asp Val Glu Lys Ala
                245                 250                 255

Ala Leu Glu Met His Trp Val Lys His Ala Arg Ala Arg Ile Arg Asp
            260                 265                 270

Gln Gly Arg Cys Phe His Thr Glu Leu Phe Val Glu Pro Val Glu Gly
        275                 280                 285

Tyr Thr Pro Ala Pro Glu Glu Ile Thr Ser Leu Val Lys Arg Ile Gln
    290                 295                 300

Asn Leu Asp Trp Lys Leu Gln Asp Val Val Ala Ser Val Val Glu Lys
305                 310                 315                 320
```

```
Ile Asp Arg Phe Gln Ala Pro Ser
                325

<210> 2841
<211> 387
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(364)
<223> RXA02662

<400> 2841
ccaaggtgtc accctcaccg ttgccatcgc cttcatcatc gtcaatatcg ccgtggacct 60

gctctacgtc ctggtcaatc cacgtattag gagcatctag atg cgc cgt aaa cta   115
                                            Met Arg Arg Lys Leu
                                              1               5

acc acc aca tta gaa aac aag ccc ggt gca cga ctt ggt ggc ttc cgc   163
Thr Thr Thr Leu Glu Asn Lys Pro Gly Ala Arg Leu Gly Gly Phe Arg
                  10                  15                  20

gca ctt gca cca act tca aaa atc gcg ctg gtt ttc ctt ctc ctg atc   211
Ala Leu Ala Pro Thr Ser Lys Ile Ala Leu Val Phe Leu Leu Leu Ile
              25                  30                  35

ttc ctc ctc gcg atc ttt gcc cca ctg att gct aaa tac gat cca ctg   259
Phe Leu Leu Ala Ile Phe Ala Pro Leu Ile Ala Lys Tyr Asp Pro Leu
          40                  45                  50

gcc tcc gga act cca gtc cag cct cca agc ggt gag cac tgg ttt ggt   307
Ala Ser Gly Thr Pro Val Gln Pro Pro Ser Gly Glu His Trp Phe Gly
      55                  60                  65

acc gac gcc atc ggc cgc gat att ttc tcc cgc gta gcc acg gcg cca   355
Thr Asp Ala Ile Gly Arg Asp Ile Phe Ser Arg Val Ala Thr Ala Pro
  70                  75                  80                  85

gag cct ccc tgatcattgg tcttttcgct acg                            387
Glu Pro Pro

<210> 2842
<211> 88
<212> PRT
<213> Corynebacterium glutamicum

<400> 2842
Met Arg Arg Lys Leu Thr Thr Thr Leu Glu Asn Lys Pro Gly Ala Arg
  1               5                  10                  15

Leu Gly Gly Phe Arg Ala Leu Ala Pro Thr Ser Lys Ile Ala Leu Val
              20                  25                  30

Phe Leu Leu Leu Ile Phe Leu Leu Ala Ile Phe Ala Pro Leu Ile Ala
          35                  40                  45
```

```
Lys Tyr Asp Pro Leu Ala Ser Gly Thr Pro Val Gln Pro Pro Ser Gly
     50                  55                  60

Glu His Trp Phe Gly Thr Asp Ala Ile Gly Arg Asp Ile Phe Ser Arg
 65                  70                  75                  80

Val Ala Thr Ala Pro Glu Pro Pro
                 85
```

<210> 2843
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> RXA02665

<400> 2843

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caaggcgacc caatggcgtt taaagtaaca acccccattg atatgatgct ggcacaacgc 60

atcaccgacg aagccgaacc cacaatattt gaggtaccag gtg act aac cca atc   115
                                            Val Thr Asn Pro Ile
                                              1               5

atc ccc cgc gta gga atc gcc aca gac gcc cac caa atc gaa gcg gga   163
Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His Gln Ile Glu Ala Gly
                 10                  15                  20

aaa ccc tgc tgg atc gcc tgc ctc ctc ttt gaa ggc gtc gac ggc tgc   211
Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu Gly Val Asp Gly Cys
             25                  30                  35

gaa ggc cac tcc gac ggt gat gtt gta gct cat gca att gtg gat gct   259
Glu Gly His Ser Asp Gly Asp Val Val Ala His Ala Ile Val Asp Ala
         40                  45                  50

ctc ctt tct gcc tct ggt ctg ggg gat ttg ggc tct ttc gtt ggt gtg   307
Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly Ser Phe Val Gly Val
     55                  60                  65

ggg aga cct gaa tac gat ggt gtt tct ggt aca cag ttg ttg aag gaa   355
Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr Gln Leu Leu Lys Glu
 70                  75                  80                  85

gtt cgg gag ctg ctt tcg gca cac ggg tac gtc att gga aat gtc gcc   403
Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val Ile Gly Asn Val Ala
             90                  95                 100

gcc caa ctg gtt ggc caa acc ccc aaa ttt gga ccc cgc cgc gaa gaa   451
Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly Pro Arg Arg Glu Glu
        105                 110                 115

gca caa caa gtc atc tcc gaa atc atc ggc gca cca tgc tca ctg tct   499
Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala Pro Cys Ser Leu Ser
    120                 125                 130

gcc acc acc act gat cac atg gga ttc act ggt cgc agc gag ggt cgt   547
```

```
Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly Arg Ser Glu Gly Arg
    135                 140                 145

gca tcg gta gca acg gca gtg gtg tgg aag gct taagttttct gtagggattg 600
Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala
150                 155                 160

ggc                                                               603


<210> 2844
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 2844
Val Thr Asn Pro Ile Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His
  1               5                  10                  15

Gln Ile Glu Ala Gly Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu
            20                  25                  30

Gly Val Asp Gly Cys Glu Gly His Ser Asp Gly Asp Val Val Ala His
         35                  40                  45

Ala Ile Val Asp Ala Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly
     50                  55                  60

Ser Phe Val Gly Val Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr
 65                  70                  75                  80

Gln Leu Leu Lys Glu Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val
                85                  90                  95

Ile Gly Asn Val Ala Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly
            100                 105                 110

Pro Arg Arg Glu Glu Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala
        115                 120                 125

Pro Cys Ser Leu Ser Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly
    130                 135                 140

Arg Ser Glu Gly Arg Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala
145                 150                 155                 160


<210> 2845
<211> 705
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(682)
<223> RXA02670

<400> 2845
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ccgtttaatc aaccgactgt gtgaatgcgc ttaaacggac tagggttgtg agcagcatat 60

ccagattttt ctggataaat cctggaattt cttaaaacca atg gag gac gaa tcc   115
                                            Met Glu Asp Glu Ser
                                              1               5

gtg aag tcc ctg aac ttg gct gcc cgt cgt ggc gcg ctc gtg acc gtg   163
Val Lys Ser Leu Asn Leu Ala Ala Arg Arg Gly Ala Leu Val Thr Val
                 10                  15                  20

gct gct gcg tca gct ctt gcg ctt gca tcc tgc agt gcc gga cag atc   211
Ala Ala Ala Ser Ala Leu Ala Leu Ala Ser Cys Ser Ala Gly Gln Ile
             25                  30                  35

acc cag acc tca agc cag gtt gca gca gtt gat ggc aac cag gca ggc   259
Thr Gln Thr Ser Ser Gln Val Ala Ala Val Asp Gly Asn Gln Ala Gly
         40                  45                  50

tcc gcg aac gac cca gtt ctg gtg cgt gat gta acc gtg cac ctc acc   307
Ser Ala Asn Asp Pro Val Leu Val Arg Asp Val Thr Val His Leu Thr
     55                  60                  65

acc gac ggc gaa gct gga gta aag ttc acc gcc atc aac cag gac acc   355
Thr Asp Gly Glu Ala Gly Val Lys Phe Thr Ala Ile Asn Gln Asp Thr
 70                  75                  80                  85

tct cac act tct cac acc ctt gag tcc gtc acc gtt gac ggc gaa gag   403
Ser His Thr Ser His Thr Leu Glu Ser Val Thr Val Asp Gly Glu Glu
                 90                  95                 100

gtt gag ctt gat gat gca gag cca atc gag cgc aac tgc tcc ctc gtt   451
Val Glu Leu Asp Asp Ala Glu Pro Ile Glu Arg Asn Cys Ser Leu Val
             105                 110                 115

gca gac atc cag tcc gaa ctg gat ctg atc gag gag cca gaa gtt ggc   499
Ala Asp Ile Gln Ser Glu Leu Asp Leu Ile Glu Glu Pro Glu Val Gly
         120                 125                 130

tgc atc cag cac gta gca act tct ctg gag aac cca ggt ttc gca tac   547
Cys Ile Gln His Val Ala Thr Ser Leu Glu Asn Pro Gly Phe Ala Tyr
     135                 140                 145

ggc gga gtc gtg cca gtt gag ttc gtc ttc gac acc ggt gcg atc acc   595
Gly Gly Val Val Pro Val Glu Phe Val Phe Asp Thr Gly Ala Ile Thr
150                 155                 160                 165

atc gat gcc acc gtt tcc gca cct gtc ctc gag tca ggc gta gaa aac   643
Ile Asp Ala Thr Val Ser Ala Pro Val Leu Glu Ser Gly Val Glu Asn
                170                 175                 180

cgc gag gtc ggc gga gac act gca gag gca agc cac cac taagcctctc    692
Arg Glu Val Gly Gly Asp Thr Ala Glu Ala Ser His His
            185                 190

aaagctgctt gaa                                                   705


<210> 2846
<211> 194
<212> PRT
<213> Corynebacterium glutamicum
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<400> 2846
Met Glu Asp Glu Ser Val Lys Ser Leu Asn Leu Ala Ala Arg Arg Gly
1 5 10 15

Ala Leu Val Thr Val Ala Ala Ala Ser Ala Leu Ala Leu Ala Ser Cys
20 25 30

Ser Ala Gly Gln Ile Thr Gln Thr Ser Ser Gln Val Ala Ala Val Asp
35 40 45

Gly Asn Gln Ala Gly Ser Ala Asn Asp Pro Val Leu Val Arg Asp Val
50 55 60

Thr Val His Leu Thr Thr Asp Gly Glu Ala Gly Val Lys Phe Thr Ala
65 70 75 80

Ile Asn Gln Asp Thr Ser His Thr Ser His Thr Leu Glu Ser Val Thr
85 90 95

Val Asp Gly Glu Glu Val Glu Leu Asp Asp Ala Glu Pro Ile Glu Arg
100 105 110

Asn Cys Ser Leu Val Ala Asp Ile Gln Ser Glu Leu Asp Leu Ile Glu
115 120 125

Glu Pro Glu Val Gly Cys Ile Gln His Val Ala Thr Ser Leu Glu Asn
130 135 140

Pro Gly Phe Ala Tyr Gly Gly Val Val Pro Val Glu Phe Val Phe Asp
145 150 155 160

Thr Gly Ala Ile Thr Ile Asp Ala Thr Val Ser Ala Pro Val Leu Glu
165 170 175

Ser Gly Val Glu Asn Arg Glu Val Gly Gly Asp Thr Ala Glu Ala Ser
180 185 190

His His

<210> 2847
<211> 1221
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1198)
<223> RXA02672

<400> 2847
agcagtcatc cccggaggct caggcatcaa acaaacaagc ctgagagtca tcgaagcttc 60

aacacttgcc gaagcacttg cagcagtaag cttataaagc atg aca cca aca acc 115
Met Thr Pro Thr Thr
1 5

act cct gta tca aac cca gat gcc ctt tcc act gga act cag gat gtg 163
Thr Pro Val Ser Asn Pro Asp Ala Leu Ser Thr Gly Thr Gln Asp Val

```
                  10                  15                  20

cac acc ctc aaa gga acg ttg cag cgc ctc gcc cca ggc aca cca ctt   211
His Thr Leu Lys Gly Thr Leu Gln Arg Leu Ala Pro Gly Thr Pro Leu
             25                  30                  35

cgc gat ggc tta gac cgc atc gtc cga gga cac acc ggc gcg tta atc   259
Arg Asp Gly Leu Asp Arg Ile Val Arg Gly His Thr Gly Ala Leu Ile
         40                  45                  50

gtc att ggt gat gat gaa aac gtc tcc tcg atc tgc gac ggc ggc ttt   307
Val Ile Gly Asp Asp Glu Asn Val Ser Ser Ile Cys Asp Gly Gly Phe
     55                  60                  65

gaa ttc gac gtt tcg ttt gct gca acc cga ctc cgc gag ctg tgc aag   355
Glu Phe Asp Val Ser Phe Ala Ala Thr Arg Leu Arg Glu Leu Cys Lys
 70                  75                  80                  85

atg gat ggc gct gtc atc ttg tct tcc gac ctt gag cgt atc aaa cgc   403
Met Asp Gly Ala Val Ile Leu Ser Ser Asp Leu Glu Arg Ile Lys Arg
                 90                  95                 100

gcc aat gtt cag ctg ctg cct tca cca acc tgg cca acc cag gag tcc   451
Ala Asn Val Gln Leu Leu Pro Ser Pro Thr Trp Pro Thr Gln Glu Ser
             105                 110                 115

ggc acc cgc cac cgt tct gca gaa cgc acc gcg ctt cac acc ggt gtg   499
Gly Thr Arg His Arg Ser Ala Glu Arg Thr Ala Leu His Thr Gly Val
         120                 125                 130

cca gtg att gcg gta tcc gaa tca caa aac acc atc act ctc tac gtc   547
Pro Val Ile Ala Val Ser Glu Ser Gln Asn Thr Ile Thr Leu Tyr Val
     135                 140                 145

gag ggc aaa tcc cac atg ttg gag cag cca gct gcc ctg ctt aac cgc   595
Glu Gly Lys Ser His Met Leu Glu Gln Pro Ala Ala Leu Leu Asn Arg
150                 155                 160                 165

gcc aac caa gct ttg gga aca atg gag cgc tac cgc gat cgt ctc gat   643
Ala Asn Gln Ala Leu Gly Thr Met Glu Arg Tyr Arg Asp Arg Leu Asp
                170                 175                 180

cag gtc aat aac cgc ctt cac ctg gct gaa ctc cac agc tat gtc acc   691
Gln Val Asn Asn Arg Leu His Leu Ala Glu Leu His Ser Tyr Val Thr
             185                 190                 195

gtg att gat gtt gtt tct gtc att cag cgc gag gaa atg ctg cgc cga   739
Val Ile Asp Val Val Ser Val Ile Gln Arg Glu Glu Met Leu Arg Arg
         200                 205                 210

gtg ggt gaa atc att gat ggc gat gtt ctt gaa cta ggc aaa gac gcc   787
Val Gly Glu Ile Ile Asp Gly Asp Val Leu Glu Leu Gly Lys Asp Ala
     215                 220                 225

aag gag att cag atc cag ctc agc gaa tta cgt ggc gat aat gac cga   835
Lys Glu Ile Gln Ile Gln Leu Ser Glu Leu Arg Gly Asp Asn Asp Arg
230                 235                 240                 245

gaa cgt gaa tca atc att gct gat tac ctt gtc acc gac ggt att cct   883
Glu Arg Glu Ser Ile Ile Ala Asp Tyr Leu Val Thr Asp Gly Ile Pro
                250                 255                 260
```

```
gca gat gag gaa atc cac gca gcc ctc gaa gcg atc tca cat tta gat   931
Ala Asp Glu Glu Ile His Ala Ala Leu Glu Ala Ile Ser His Leu Asp
            265                 270                 275

gat aag gct ctg ctg aat cct gcg aac atc gcg cgt gtt ctt gga ctg   979
Asp Lys Ala Leu Leu Asn Pro Ala Asn Ile Ala Arg Val Leu Gly Leu
        280                 285                 290

cca ccg acc gag gaa gca ctt gat gag cca gtc act cct cgc ggc tac   1027
Pro Pro Thr Glu Glu Ala Leu Asp Glu Pro Val Thr Pro Arg Gly Tyr
    295                 300                 305

cgc acg ctc aac aga att cct cga gtg caa aaa ttc ctc atg gat aaa   1075
Arg Thr Leu Asn Arg Ile Pro Arg Val Gln Lys Phe Leu Met Asp Lys
310                 315                 320                 325

ctc atc gtg gaa ttc ggc aac ttg gat gca ctg ctc aat gcg tca gta   1123
Leu Ile Val Glu Phe Gly Asn Leu Asp Ala Leu Leu Asn Ala Ser Val
                330                 335                 340

gag gat cta agt gca gtc gat ggt gtg ggc tca ctg tgg gca cgc cac   1171
Glu Asp Leu Ser Ala Val Asp Gly Val Gly Ser Leu Trp Ala Arg His
            345                 350                 355

atc acc gac gga ctt ggc cgt tta agt taggttaaag gtcaccgctg         1218
Ile Thr Asp Gly Leu Gly Arg Leu Ser
        360                 365

gtg                                                               1221


<210> 2848
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

<400> 2848
Met Thr Pro Thr Thr Thr Pro Val Ser Asn Pro Asp Ala Leu Ser Thr
  1               5                  10                  15

Gly Thr Gln Asp Val His Thr Leu Lys Gly Thr Leu Gln Arg Leu Ala
             20                  25                  30

Pro Gly Thr Pro Leu Arg Asp Gly Leu Asp Arg Ile Val Arg Gly His
         35                  40                  45

Thr Gly Ala Leu Ile Val Ile Gly Asp Asp Glu Asn Val Ser Ser Ile
     50                  55                  60

Cys Asp Gly Gly Phe Glu Phe Asp Val Ser Phe Ala Ala Thr Arg Leu
 65                  70                  75                  80

Arg Glu Leu Cys Lys Met Asp Gly Ala Val Ile Leu Ser Ser Asp Leu
                 85                  90                  95

Glu Arg Ile Lys Arg Ala Asn Val Gln Leu Leu Pro Ser Pro Thr Trp
            100                 105                 110

Pro Thr Gln Glu Ser Gly Thr Arg His Arg Ser Ala Glu Arg Thr Ala
        115                 120                 125
```

```
Leu His Thr Gly Val Pro Val Ile Ala Val Ser Glu Ser Gln Asn Thr
    130                 135                 140

Ile Thr Leu Tyr Val Glu Gly Lys Ser His Met Leu Glu Gln Pro Ala
145                 150                 155                 160

Ala Leu Leu Asn Arg Ala Asn Gln Ala Leu Gly Thr Met Glu Arg Tyr
                165                 170                 175

Arg Asp Arg Leu Asp Gln Val Asn Asn Arg Leu His Leu Ala Glu Leu
            180                 185                 190

His Ser Tyr Val Thr Val Ile Asp Val Val Ser Val Ile Gln Arg Glu
        195                 200                 205

Glu Met Leu Arg Arg Val Gly Glu Ile Ile Asp Gly Asp Val Leu Glu
    210                 215                 220

Leu Gly Lys Asp Ala Lys Glu Ile Gln Ile Gln Leu Ser Glu Leu Arg
225                 230                 235                 240

Gly Asp Asn Asp Arg Glu Arg Glu Ser Ile Ile Ala Asp Tyr Leu Val
                245                 250                 255

Thr Asp Gly Ile Pro Ala Asp Glu Glu Ile His Ala Ala Leu Glu Ala
            260                 265                 270

Ile Ser His Leu Asp Asp Lys Ala Leu Leu Asn Pro Ala Asn Ile Ala
        275                 280                 285

Arg Val Leu Gly Leu Pro Pro Thr Glu Glu Ala Leu Asp Glu Pro Val
    290                 295                 300

Thr Pro Arg Gly Tyr Arg Thr Leu Asn Arg Ile Pro Arg Val Gln Lys
305                 310                 315                 320

Phe Leu Met Asp Lys Leu Ile Val Glu Phe Gly Asn Leu Asp Ala Leu
                325                 330                 335

Leu Asn Ala Ser Val Glu Asp Leu Ser Ala Val Asp Gly Val Gly Ser
            340                 345                 350

Leu Trp Ala Arg His Ile Thr Asp Gly Leu Gly Arg Leu Ser
        355                 360                 365
```

<210> 2849
<211> 1041
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1018)
<223> RXA02678

<400> 2849
ctgtgggcgc gcgaacaggg cgtcgacatg ctcgccacca attatccgga ccgtgcggcg 60

gagcttttga acgcacatcc caagcccgcc atgtacgcta atg cgc atg gca aag 115

```
                                                    Met Arg Met Ala Lys
                                                      1               5

aag act aag aag aat gaa cag ctg ccg gag ggc atg agc cgt cgt cag   163
Lys Thr Lys Lys Asn Glu Gln Leu Pro Glu Gly Met Ser Arg Arg Gln
                  10                  15                  20

gca aaa ctt gca gcc cgc gcg gct gaa cgt gca gca ctt gag cgt gaa   211
Ala Lys Leu Ala Ala Arg Ala Ala Glu Arg Ala Ala Leu Glu Arg Glu
              25                  30                  35

cct cgc cca ttc gag ggc ctg gca atg gag tca cag ctc gtt gca ctg   259
Pro Arg Pro Phe Glu Gly Leu Ala Met Glu Ser Gln Leu Val Ala Leu
          40                  45                  50

cag gaa ttc att cca tct gca acc gca ccc atc acc gtt gca ggc acc   307
Gln Glu Phe Ile Pro Ser Ala Thr Ala Pro Ile Thr Val Ala Gly Thr
      55                  60                  65

gat cgc aag atc acc ctc tgt acc gtg ctt cca ggc gca gct gcg gca   355
Asp Arg Lys Ile Thr Leu Cys Thr Val Leu Pro Gly Ala Ala Ala Ala
  70                  75                  80                  85

ctt gtc cgc gaa gaa gca ttc ggc ggc gaa gcg ttt gtt gca atg cag   403
Leu Val Arg Glu Glu Ala Phe Gly Gly Glu Ala Phe Val Ala Met Gln
                  90                  95                 100

cag gcc atc cgc tcc aac aac cca agc aag gac ctc gcg ttc gcg ctg   451
Gln Ala Ile Arg Ser Asn Asn Pro Ser Lys Asp Leu Ala Phe Ala Leu
              105                 110                 115

aac tgg gtc atc aac gca aaa gcc ggc gag tca ctg gcc acc gcc aca   499
Asn Trp Val Ile Asn Ala Lys Ala Gly Glu Ser Leu Ala Thr Ala Thr
          120                 125                 130

gcg gac ggc acc cag cca gag cta aag agc ttg ctt aac gac gcc gac   547
Ala Asp Gly Thr Gln Pro Glu Leu Lys Ser Leu Leu Asn Asp Ala Asp
      135                 140                 145

acc ctc gaa atc acc act cac cag gac ttc aac tgg tgg ctg gcg gaa   595
Thr Leu Glu Ile Thr Thr His Gln Asp Phe Asn Trp Trp Leu Ala Glu
150                 155                 160                 165

aac gac aac ctc tcc cca gaa gtt gcg cag cac atg cag gca gcc aat   643
Asn Asp Asn Leu Ser Pro Glu Val Ala Gln His Met Gln Ala Ala Asn
                  170                 175                 180

gac tcc atc ctg cct tca cac gaa gtc gaa gca gac gtc cca ggc gct   691
Asp Ser Ile Leu Pro Ser His Glu Val Glu Ala Asp Val Pro Gly Ala
              185                 190                 195

gtt tgg tgg gtc aac cca ggc gga aaa gcg cac atc cgt tgg gtc cgc   739
Val Trp Trp Val Asn Pro Gly Gly Lys Ala His Ile Arg Trp Val Arg
          200                 205                 210

acc gaa aac gaa acc gca ctg ttc aac gct ttg gca cgc atc gca gca   787
Thr Glu Asn Glu Thr Ala Leu Phe Asn Ala Leu Ala Arg Ile Ala Ala
      215                 220                 225

cgt ggc gag ctg aat ctc ggc gaa gaa act aag ttc gct ggt gct ttc   835
Arg Gly Glu Leu Asn Leu Gly Glu Glu Thr Lys Phe Ala Gly Ala Phe
```

```
230                 235                 240                 245

cgc acc cac ggc atc gtc gtc cca gtg tgg gat ctc gat cct gag cgt   883
Arg Thr His Gly Ile Val Val Pro Val Trp Asp Leu Asp Pro Glu Arg
                250                 255                 260

cca tcc acc gat tac gcc gat gtt ttg gtt gca ctc aac gag aag atc   931
Pro Ser Thr Asp Tyr Ala Asp Val Leu Val Ala Leu Asn Glu Lys Ile
            265                 270                 275

gtc gct gaa ctg gat aac gat gca cag ctc aac gcc gac gag cgc cgt   979
Val Ala Glu Leu Asp Asn Asp Ala Gln Leu Asn Ala Asp Glu Arg Arg
        280                 285                 290

cag ctg gag aac atc aag tcc cgc cag gtg acc atc cgc taaaatctct   1028
Gln Leu Glu Asn Ile Lys Ser Arg Gln Val Thr Ile Arg
    295                 300                 305

taaaaacact tca                                                  1041
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SEQUENCE LISTING

<210> 2850
<211> 306
<212> PRT
<213> Corynebacterium glutamicum

<400> 2850

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Met Arg Met Ala Lys Lys Thr Lys Lys Asn Glu Gln Leu Pro Glu Gly
  1               5                  10                  15

Met Ser Arg Arg Gln Ala Lys Leu Ala Ala Arg Ala Ala Glu Arg Ala
             20                  25                  30

Ala Leu Glu Arg Glu Pro Arg Pro Phe Glu Gly Leu Ala Met Glu Ser
         35                  40                  45

Gln Leu Val Ala Leu Gln Glu Phe Ile Pro Ser Ala Thr Ala Pro Ile
     50                  55                  60

Thr Val Ala Gly Thr Asp Arg Lys Ile Thr Leu Cys Thr Val Leu Pro
 65                  70                  75                  80

Gly Ala Ala Ala Ala Leu Val Arg Glu Glu Ala Phe Gly Gly Glu Ala
                 85                  90                  95

Phe Val Ala Met Gln Gln Ala Ile Arg Ser Asn Asn Pro Ser Lys Asp
            100                 105                 110

Leu Ala Phe Ala Leu Asn Trp Val Ile Asn Ala Lys Ala Gly Glu Ser
        115                 120                 125

Leu Ala Thr Ala Thr Ala Asp Gly Thr Gln Pro Glu Leu Lys Ser Leu
    130                 135                 140

Leu Asn Asp Ala Asp Thr Leu Glu Ile Thr Thr His Gln Asp Phe Asn
145                 150                 155                 160

Trp Trp Leu Ala Glu Asn Asp Asn Leu Ser Pro Glu Val Ala Gln His
                165                 170                 175

Met Gln Ala Ala Asn Asp Ser Ile Leu Pro Ser His Glu Val Glu Ala
```

```
            180                 185                 190

Asp Val Pro Gly Ala Val Trp Trp Val Asn Pro Gly Gly Lys Ala His
        195                 200                 205

Ile Arg Trp Val Arg Thr Glu Asn Glu Thr Ala Leu Phe Asn Ala Leu
    210                 215                 220

Ala Arg Ile Ala Ala Arg Gly Glu Leu Asn Leu Gly Glu Glu Thr Lys
225                 230                 235                 240

Phe Ala Gly Ala Phe Arg Thr His Gly Ile Val Val Pro Val Trp Asp
                245                 250                 255

Leu Asp Pro Glu Arg Pro Ser Thr Asp Tyr Ala Asp Val Leu Val Ala
            260                 265                 270

Leu Asn Glu Lys Ile Val Ala Glu Leu Asp Asn Asp Ala Gln Leu Asn
        275                 280                 285

Ala Asp Glu Arg Arg Gln Leu Glu Asn Ile Lys Ser Arg Gln Val Thr
    290                 295                 300

Ile Arg
305


<210> 2851
<211> 801
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(778)
<223> RXA02683

<400> 2851
gacggtttct tctgtcatga cggaaactcc tacttatacc tcttcatcta ggtcggtgga 60

atctaccgcg gggacgatcg ctgcctcgga ggaagccacg atg acg cta ctg gag   115
                                              Met Thr Leu Leu Glu
                                                1               5

aat agt tcg ggg gat ccg gga tct gat tct ggg ggt gca cgc tat agc   163
Asn Ser Ser Gly Asp Pro Gly Ser Asp Ser Gly Gly Ala Arg Tyr Ser
                10                  15                  20

ctc aat tcg ctc aaa gtt tct gag cag gcc gcg gct aac gcc gtc tta   211
Leu Asn Ser Leu Lys Val Ser Glu Gln Ala Ala Ala Asn Ala Val Leu
            25                  30                  35

aag gcc gtg ctt aac gac gtc tcc tac caa gag ttc gca gac tcc tcc   259
Lys Ala Val Leu Asn Asp Val Ser Tyr Gln Glu Phe Ala Asp Ser Ser
        40                  45                  50

tac tta gaa atc aca gga acg ccc tcc gcc gac gga aca tgg ggc atc   307
Tyr Leu Glu Ile Thr Gly Thr Pro Ser Ala Asp Gly Thr Trp Gly Ile
    55                  60                  65

tca ttt ggc gga cct tcc gaa tcg gcc tcc gtg gaa ttc tcc gac ggc   355
```

```
Ser Phe Gly Gly Pro Ser Glu Ser Ala Ser Val Glu Phe Ser Asp Gly
 70                  75                  80                  85

agc atc agc ttc tcc cct gtt gac atg aca gtg ccc gca aca cga ttg   403
Ser Ile Ser Phe Ser Pro Val Asp Met Thr Val Pro Ala Thr Arg Leu
                 90                  95                 100

cct cag atg ggc gca ttt tat gaa acc ctg acc gaa gaa caa tta ggc   451
Pro Gln Met Gly Ala Phe Tyr Glu Thr Leu Thr Glu Glu Gln Leu Gly
            105                 110                 115

atg ctg gag act ggc ctc gcg gtt tcc acc gtg gat tcg agc caa cag   499
Met Leu Glu Thr Gly Leu Ala Val Ser Thr Val Asp Ser Ser Gln Gln
        120                 125                 130

gaa atg ctt ctg gac ttg gtc tcc aac tcg atc ggc ctg gca gat act   547
Glu Met Leu Leu Asp Leu Val Ser Asn Ser Ile Gly Leu Ala Asp Thr
    135                 140                 145

gaa acc act gcg act gca att agt aaa atc cga gca acg ctt tcc gag   595
Glu Thr Thr Ala Thr Ala Ile Ser Lys Ile Arg Ala Thr Leu Ser Glu
150                 155                 160                 165

acc tac ctg ttc gga acc ccc gac gga tta acc ttg gcg ctt agt ggc   643
Thr Tyr Leu Phe Gly Thr Pro Asp Gly Leu Thr Leu Ala Leu Ser Gly
                170                 175                 180

cca cac gtt gat ttc gaa gtc tcc cac cag ggc agc acc gcg aaa att   691
Pro His Val Asp Phe Glu Val Ser His Gln Gly Ser Thr Ala Lys Ile
            185                 190                 195

act tac cgc gat cca agc acc gac acc tta acc gcc gaa gat cgg gta   739
Thr Tyr Arg Asp Pro Ser Thr Asp Thr Leu Thr Ala Glu Asp Arg Val
        200                 205                 210

gat acc gca agt gtg gct gct gct ccg ccg gag gtt gtt taggcgtttg    788
Asp Thr Ala Ser Val Ala Ala Ala Pro Pro Glu Val Val
    215                 220                 225

ccgagaaatt ttc                                                   801


<210> 2852
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 2852
Met Thr Leu Leu Glu Asn Ser Ser Gly Asp Pro Gly Ser Asp Ser Gly
  1               5                  10                  15

Gly Ala Arg Tyr Ser Leu Asn Ser Leu Lys Val Ser Glu Gln Ala Ala
             20                  25                  30

Ala Asn Ala Val Leu Lys Ala Val Leu Asn Asp Val Ser Tyr Gln Glu
         35                  40                  45

Phe Ala Asp Ser Ser Tyr Leu Glu Ile Thr Gly Thr Pro Ser Ala Asp
     50                  55                  60

Gly Thr Trp Gly Ile Ser Phe Gly Gly Pro Ser Glu Ser Ala Ser Val
```

```
 65                  70                  75                  80

Glu Phe Ser Asp Gly Ser Ile Ser Phe Ser Pro Val Asp Met Thr Val
                 85                  90                  95

Pro Ala Thr Arg Leu Pro Gln Met Gly Ala Phe Tyr Glu Thr Leu Thr
            100                 105                 110

Glu Glu Gln Leu Gly Met Leu Glu Thr Gly Leu Ala Val Ser Thr Val
        115                 120                 125

Asp Ser Ser Gln Gln Glu Met Leu Leu Asp Leu Val Ser Asn Ser Ile
    130                 135                 140

Gly Leu Ala Asp Thr Glu Thr Thr Ala Thr Ala Ile Ser Lys Ile Arg
145                 150                 155                 160

Ala Thr Leu Ser Glu Thr Tyr Leu Phe Gly Thr Pro Asp Gly Leu Thr
                165                 170                 175

Leu Ala Leu Ser Gly Pro His Val Asp Phe Glu Val Ser His Gln Gly
            180                 185                 190

Ser Thr Ala Lys Ile Thr Tyr Arg Asp Pro Ser Thr Asp Thr Leu Thr
        195                 200                 205

Ala Glu Asp Arg Val Asp Thr Ala Ser Val Ala Ala Ala Pro Pro Glu
    210                 215                 220

Val Val
225
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US20090203102A1

<210> 2853
<211> 780
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(757)
<223> RXA02685

<400> 2853

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tagcagcatt tgtggaaaga gctgtggcat gagtagttca gtaatgtcac cgcgtcgaat 60

aaaggcggaa atacttatcg ttttagccat caccttggc atg agc ggc ctg cga   115
                                          Met Ser Gly Leu Arg
                                            1               5

tca atc ctg cgc ctc atc gac gat ctc ctc gca ccg gtt gcg ctc aac   163
Ser Ile Leu Arg Leu Ile Asp Asp Leu Leu Ala Pro Val Ala Leu Asn
                10                  15                  20

gac cag caa gtt gca ctg aat gcc tca atg gca aac tcc gca tgg ctg   211
Asp Gln Gln Val Ala Leu Asn Ala Ser Met Ala Asn Ser Ala Trp Leu
            25                  30                  35

gat ctc acc ttg caa ttg tgt tcc gcc gga gtg ctg ttt tcc tgg gga   259
Asp Leu Thr Leu Gln Leu Cys Ser Ala Gly Val Leu Phe Ser Trp Gly
        40                  45                  50
```

```
gca cta gcg atc tac ctg cta ggt gaa cgt ttt cag tgg att aaa ccc   307
Ala Leu Ala Ile Tyr Leu Leu Gly Glu Arg Phe Gln Trp Ile Lys Pro
     55                  60                  65

aaa gac tgg gca tgg ggt gca ggc ctt gca gca ctc att ggt att cca   355
Lys Asp Trp Ala Trp Gly Ala Gly Leu Ala Ala Leu Ile Gly Ile Pro
 70                  75                  80                  85

ggg tta atc ttc tac gcc agt gct gtt cat ttg ggg ctg tcc aaa cag   403
Gly Leu Ile Phe Tyr Ala Ser Ala Val His Leu Gly Leu Ser Lys Gln
                 90                  95                 100

gtt gtg ccc acc acg ttg gaa acc tgg tgg gaa atc cca gta ctt ctt   451
Val Val Pro Thr Thr Leu Glu Thr Trp Trp Glu Ile Pro Val Leu Leu
            105                 110                 115

atc tgg tca gct gcc aac gcc ttt ggt gaa gag atc gtg gta gtc atg   499
Ile Trp Ser Ala Ala Asn Ala Phe Gly Glu Glu Ile Val Val Val Met
        120                 125                 130

tgg ttt ttc acc agg ctg cgc cag ctg aag tgg agt gtg cct gca gtt   547
Trp Phe Phe Thr Arg Leu Arg Gln Leu Lys Trp Ser Val Pro Ala Val
    135                 140                 145

atc gtg aca tct tca gta cta cgc ggt tcc tat cac ctc tac cag gga   595
Ile Val Thr Ser Ser Val Leu Arg Gly Ser Tyr His Leu Tyr Gln Gly
150                 155                 160                 165

atc tct gca ggc ttg ggc aac atc atc atg gga gta gcg ttc gcg tac   643
Ile Ser Ala Gly Leu Gly Asn Ile Ile Met Gly Val Ala Phe Ala Tyr
                170                 175                 180

ttc tat cac cgc acg ggc aaa atc tgg cca ctg gta atc gct cac ttc   691
Phe Tyr His Arg Thr Gly Lys Ile Trp Pro Leu Val Ile Ala His Phe
            185                 190                 195

ttg att gat gcg gtg gct ttt gtg ggc tac tcc gca att ggc ggg aat   739
Leu Ile Asp Ala Val Ala Phe Val Gly Tyr Ser Ala Ile Gly Gly Asn
        200                 205                 210

tta agt tgg tta ggg ctt taaactgaag ttcctatttt att                 780
Leu Ser Trp Leu Gly Leu
    215
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<210> 2854
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

<400> 2854

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Met Ser Gly Leu Arg Ser Ile Leu Arg Leu Ile Asp Asp Leu Leu Ala
  1               5                  10                  15

Pro Val Ala Leu Asn Asp Gln Gln Val Ala Leu Asn Ala Ser Met Ala
             20                  25                  30

Asn Ser Ala Trp Leu Asp Leu Thr Leu Gln Leu Cys Ser Ala Gly Val
         35                  40                  45
```

```
Leu Phe Ser Trp Gly Ala Leu Ala Ile Tyr Leu Leu Gly Glu Arg Phe
     50                  55                  60

Gln Trp Ile Lys Pro Lys Asp Trp Ala Trp Gly Ala Gly Leu Ala Ala
 65                  70                  75                  80

Leu Ile Gly Ile Pro Gly Leu Ile Phe Tyr Ala Ser Ala Val His Leu
                 85                  90                  95

Gly Leu Ser Lys Gln Val Val Pro Thr Thr Leu Glu Thr Trp Trp Glu
            100                 105                 110

Ile Pro Val Leu Leu Ile Trp Ser Ala Ala Asn Ala Phe Gly Glu Glu
        115                 120                 125

Ile Val Val Val Met Trp Phe Phe Thr Arg Leu Arg Gln Leu Lys Trp
    130                 135                 140

Ser Val Pro Ala Val Ile Val Thr Ser Ser Val Leu Arg Gly Ser Tyr
145                 150                 155                 160

His Leu Tyr Gln Gly Ile Ser Ala Gly Leu Gly Asn Ile Ile Met Gly
                165                 170                 175

Val Ala Phe Ala Tyr Phe Tyr His Arg Thr Gly Lys Ile Trp Pro Leu
            180                 185                 190

Val Ile Ala His Phe Leu Ile Asp Ala Val Ala Phe Val Gly Tyr Ser
        195                 200                 205

Ala Ile Gly Gly Asn Leu Ser Trp Leu Gly Leu
    210                 215
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<210> 2855
<211> 792
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(769)
<223> RXA02688

<400> 2855

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gtgcggaaga cagcacgccc caaaccgacc aactagctaa gctacacaag gcggacgaat 60

gggttcgcgc agcaagcgaa ggaaggaaac ttaactagcc atg gcc ggc cgg att   115
                                        Met Ala Gly Arg Ile
                                          1               5

att ttg cta cga cac ggg cag act cac aac aac gtc aaa cac ctc ctg   163
Ile Leu Leu Arg His Gly Gln Thr His Asn Asn Val Lys His Leu Leu
                 10                  15                  20

gac acc cgc cca cca gga gct gaa ctc acc gac ctg ggc cgt aaa caa   211
Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp Leu Gly Arg Lys Gln
             25                  30                  35

gcc ctt gaa gtt ggc cac gaa cta gcc acc tac tcc ggt gag cgc ctc   259
Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr Ser Gly Glu Arg Leu
```

```
         40                  45                  50

gcc cat gtg tac agc tcc atc gtg ttg cgc gcc caa caa acc gcc gtg   307
Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala Gln Gln Thr Ala Val
     55                  60                  65

ctt gcc acc tct acc ttt gaa aaa gct cgc gac atg cag tcc ggt gcg   355
Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp Met Gln Ser Gly Ala
 70                  75                  80                  85

att cca ctc gac gtt gtg gaa ggc att cag gaa atc aac gtc ggc gac   403
Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu Ile Asn Val Gly Asp
                 90                  95                 100

ttt gaa atg cgc ggc gat gaa gaa gcc cac atg aat tac tcc cgc gca   451
Phe Glu Met Arg Gly Asp Glu Glu Ala His Met Asn Tyr Ser Arg Ala
            105                 110                 115

ctc aac ggc tgg ctt cac ggg gat cct gcc gct ggt ctt ccc ggc ggt   499
Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala Gly Leu Pro Gly Gly
        120                 125                 130

gag acc tac aaa gac gtg ctg aac cgc tac cag ccg act ctt gat cga   547
Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln Pro Thr Leu Asp Arg
    135                 140                 145

atc atg gac agc cac gac ctt gac gac gac cgc gac gtt gcc gtt gtc   595
Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg Asp Val Ala Val Val
150                 155                 160                 165

agc cac ggc gcc gtc atc cgc atc gtg gca aca cac gca act ggt gtg   643
Ser His Gly Ala Val Ile Arg Ile Val Ala Thr His Ala Thr Gly Val
                170                 175                 180

gat ccc aac ttt gcg ttc aac acc tac ctg ggc aac tgc cgc ttc gtg   691
Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly Asn Cys Arg Phe Val
            185                 190                 195

gtg ctg gag cca aac ggt aag aaa ttc agc caa tgg gat gtt gtg cgc   739
Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln Trp Asp Val Val Arg
        200                 205                 210

tgg act gac agc cca ctg cca tgg cag gag taattgagac caaaggctcg     789
Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu
    215                 220

gat                                                               792
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US 20050059097 A1

<210> 2856
<211> 223
<212> PRT
<213> Corynebacterium glutamicum

<400> 2856

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Met Ala Gly Arg Ile Ile Leu Leu Arg His Gly Gln Thr His Asn Asn
  1               5                  10                  15

Val Lys His Leu Leu Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp
             20                  25                  30
```

```
Leu Gly Arg Lys Gln Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr
          35                  40                  45

Ser Gly Glu Arg Leu Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala
     50                  55                  60

Gln Gln Thr Ala Val Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp
 65                  70                  75                  80

Met Gln Ser Gly Ala Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu
                 85                  90                  95

Ile Asn Val Gly Asp Phe Glu Met Arg Gly Asp Glu Glu Ala His Met
            100                 105                 110

Asn Tyr Ser Arg Ala Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala
        115                 120                 125

Gly Leu Pro Gly Gly Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln
    130                 135                 140

Pro Thr Leu Asp Arg Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg
145                 150                 155                 160

Asp Val Ala Val Val Ser His Gly Ala Val Ile Arg Ile Val Ala Thr
                165                 170                 175

His Ala Thr Gly Val Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly
            180                 185                 190

Asn Cys Arg Phe Val Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln
        195                 200                 205

Trp Asp Val Val Arg Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu
    210                 215                 220
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US-10-605-042-2857

<210> 2857
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXA02689

<400> 2857

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gtgaagttcc cccacctcag ccagagcgcg atccgctccg tgacactgca ggaacgacag 60

catccgcgga ggtcggagta cctgtagagg agaacgctcc atg att gaa gtc agc   115
                                            Met Ile Glu Val Ser
                                              1               5

gac gaa cgc ttc gag gaa ctg gtc gaa cta gcc ttc gac caa gtt ccc   163
Asp Glu Arg Phe Glu Glu Leu Val Glu Leu Ala Phe Asp Gln Val Pro
                 10                  15                  20

cag caa ttc ctg gat cat atg cgc aac gtg gtt tta ctc att gag gat   211
Gln Gln Phe Leu Asp His Met Arg Asn Val Val Leu Leu Ile Glu Asp
             25                  30                  35
```

```
ttc aac cca gat tcg cct tat atc ttg ggt tta tac cac ggc gtt gct   259
Phe Asn Pro Asp Ser Pro Tyr Ile Leu Gly Leu Tyr His Gly Val Ala
         40                  45                  50

ctc aca gag cgc aca ttc aac cac ggt ggc ctg ccg gat tcc atc acc   307
Leu Thr Glu Arg Thr Phe Asn His Gly Gly Leu Pro Asp Ser Ile Thr
     55                  60                  65

att tat aaa ggt gcg ttg caa aat tac tgc aat tca gag gaa caa cta   355
Ile Tyr Lys Gly Ala Leu Gln Asn Tyr Cys Asn Ser Glu Glu Gln Leu
 70                  75                  80                  85

gtg gag cag gtg cgg gtg acc gtg ctg cat gag att ggg cat tat ttt   403
Val Glu Gln Val Arg Val Thr Val Leu His Glu Ile Gly His Tyr Phe
                 90                  95                 100

ggc ctc ggc gaa gag gac ctg cac agg ctc gga tac gcc taaaacgcct    452
Gly Leu Gly Glu Glu Asp Leu His Arg Leu Gly Tyr Ala
            105                 110

cattaggtgc aca                                                   465
```

CONFIDENTIAL

<210> 2858
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 2858

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Met Ile Glu Val Ser Asp Glu Arg Phe Glu Glu Leu Val Glu Leu Ala
  1               5                  10                  15

Phe Asp Gln Val Pro Gln Gln Phe Leu Asp His Met Arg Asn Val Val
             20                  25                  30

Leu Leu Ile Glu Asp Phe Asn Pro Asp Ser Pro Tyr Ile Leu Gly Leu
         35                  40                  45

Tyr His Gly Val Ala Leu Thr Glu Arg Thr Phe Asn His Gly Gly Leu
     50                  55                  60

Pro Asp Ser Ile Thr Ile Tyr Lys Gly Ala Leu Gln Asn Tyr Cys Asn
 65                  70                  75                  80

Ser Glu Glu Gln Leu Val Glu Gln Val Arg Val Thr Val Leu His Glu
                 85                  90                  95

Ile Gly His Tyr Phe Gly Leu Gly Glu Glu Asp Leu His Arg Leu Gly
            100                 105                 110

Tyr Ala
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<210> 2859
<211> 1221
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(1198)
<223> RXA02690

<400> 2859
tttccttgta ccgaaccgac cgatattctt taaaaacatt ggttacacgc tccgaagatc 60

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tctgacgtga acccattttg gtggcatgat ggtgtcaatt atg agt aca aac ttt   115
                                             Met Ser Thr Asn Phe
                                               1               5

gac act tcg acg tct cca gag ggt gaa acc aag aag aac tct tct ttc   163
Asp Thr Ser Thr Ser Pro Glu Gly Glu Thr Lys Lys Asn Ser Ser Phe
                  10                  15                  20

cgc act gcg gcc tct gtg cag acc atg ctt gtt gca gct ttg gca gca   211
Arg Thr Ala Ala Ser Val Gln Thr Met Leu Val Ala Ala Leu Ala Ala
              25                  30                  35

acg gct gct gtt ggc gtg tac tcc tac aac acg gac aat tca gca aac   259
Thr Ala Ala Val Gly Val Tyr Ser Tyr Asn Thr Asp Asn Ser Ala Asn
          40                  45                  50

ggc ggc gaa tcc ccc aca gga cct gag caa agt aca gtg tcc acc acc   307
Gly Gly Glu Ser Pro Thr Gly Pro Glu Gln Ser Thr Val Ser Thr Thr
      55                  60                  65

gca act att gcc tca ttt acc act gct gac gtg ggc caa tgt gca acc   355
Ala Thr Ile Ala Ser Phe Thr Thr Ala Asp Val Gly Gln Cys Ala Thr
  70                  75                  80                  85

tgg gat gtt aac aat gaa ggt cta gtg tct ggt ttt gaa caa acc agc   403
Trp Asp Val Asn Asn Glu Gly Leu Val Ser Gly Phe Glu Gln Thr Ser
                  90                  95                 100

tgc gat caa gag cac cgc ttt gaa att tct gct cgg gaa aac ttg gca   451
Cys Asp Gln Glu His Arg Phe Glu Ile Ser Ala Arg Glu Asn Leu Ala
             105                 110                 115

act tac cca agt tcg gaa ttc ggt ccg gac gca gct cca cca aac ctc   499
Thr Tyr Pro Ser Ser Glu Phe Gly Pro Asp Ala Ala Pro Pro Asn Leu
         120                 125                 130

acc cgt cag gcg cag ctg cgt gaa gag ctc tgc caa tct cct acc ttg   547
Thr Arg Gln Ala Gln Leu Arg Glu Glu Leu Cys Gln Ser Pro Thr Leu
     135                 140                 145

gcg tat ttg aat aac cgt ttc gat cca tcg ggg cgc tac acc atc gcc   595
Ala Tyr Leu Asn Asn Arg Phe Asp Pro Ser Gly Arg Tyr Thr Ile Ala
150                 155                 160                 165

ccg atc ctg cca cct gcg gaa gcg tgg gct gcg gga gat cgc acc atg   643
Pro Ile Leu Pro Pro Ala Glu Ala Trp Ala Ala Gly Asp Arg Thr Met
                170                 175                 180

ctc tgt gga ctt cag gca acc gac gct tca ggc act cca caa ctc acc   691
Leu Cys Gly Leu Gln Ala Thr Asp Ala Ser Gly Thr Pro Gln Leu Thr
            185                 190                 195

gtc gga ccg ata gca gcc aat gac cag gca cgc gtt ttt gaa acc ggc   739
Val Gly Pro Ile Ala Ala Asn Asp Gln Ala Arg Val Phe Glu Thr Gly
```

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        200                 205                 210

gcc tgc gtg aag gtg gaa tcc tcc gca gag ttc cgc caa gtt gat tgc   787
Ala Cys Val Lys Val Glu Ser Ser Ala Glu Phe Arg Gln Val Asp Cys
    215                 220                 225

acg gaa gat cac cac ctc gaa tca att ttg aca gtc aac ctt ggt gtc   835
Thr Glu Asp His His Leu Glu Ser Ile Leu Thr Val Asn Leu Gly Val
230                 235                 240                 245

ccc ttc cca cag ggc gcg ccc agc acg gat gag cag aac aat ttc ctc   883
Pro Phe Pro Gln Gly Ala Pro Ser Thr Asp Glu Gln Asn Asn Phe Leu
                250                 255                 260

gga aac acc tgc acc caa gca tcc att gat tac cta ggc tcc gaa gaa   931
Gly Asn Thr Cys Thr Gln Ala Ser Ile Asp Tyr Leu Gly Ser Glu Glu
            265                 270                 275

aac gtc tac caa tcc acc ctg cag acc ttc tgg cca acg att acc tcc   979
Asn Val Tyr Gln Ser Thr Leu Gln Thr Phe Trp Pro Thr Ile Thr Ser
        280                 285                 290

aac tcc tgg ttg ggc ggt tca cac agc gtg aac tgc ttc ctc atg tca   1027
Asn Ser Trp Leu Gly Gly Ser His Ser Val Asn Cys Phe Leu Met Ser
    295                 300                 305

cca tcc acc gag ggt gct gca aca ttt aac acc ctc aac ggt tca gcg   1075
Pro Ser Thr Glu Gly Ala Ala Thr Phe Asn Thr Leu Asn Gly Ser Ala
310                 315                 320                 325

act ggc aca ttc acc atc aac ggt gaa gtt ccc cca cct cag cca gag   1123
Thr Gly Thr Phe Thr Ile Asn Gly Glu Val Pro Pro Pro Gln Pro Glu
                330                 335                 340

cgc gat ccg ctc cgt gac act gca gga acg aca gca tcc gcg gag gtc   1171
Arg Asp Pro Leu Arg Asp Thr Ala Gly Thr Thr Ala Ser Ala Glu Val
            345                 350                 355

gga gta cct gta gag gag aac gct cca tgattgaagt cagcgacgaa         1218
Gly Val Pro Val Glu Glu Asn Ala Pro
        360                 365

cgc                                                              1221


<210> 2860
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

<400> 2860
Met Ser Thr Asn Phe Asp Thr Ser Thr Ser Pro Glu Gly Glu Thr Lys
  1               5                  10                  15

Lys Asn Ser Ser Phe Arg Thr Ala Ala Ser Val Gln Thr Met Leu Val
             20                  25                  30

Ala Ala Leu Ala Ala Thr Ala Ala Val Gly Val Tyr Ser Tyr Asn Thr
         35                  40                  45

Asp Asn Ser Ala Asn Gly Gly Glu Ser Pro Thr Gly Pro Glu Gln Ser
```

```
     50                  55                  60

Thr Val Ser Thr Thr Ala Thr Ile Ala Ser Phe Thr Thr Ala Asp Val
 65                  70                  75                  80

Gly Gln Cys Ala Thr Trp Asp Val Asn Asn Glu Gly Leu Val Ser Gly
                 85                  90                  95

Phe Glu Gln Thr Ser Cys Asp Gln Glu His Arg Phe Glu Ile Ser Ala
            100                 105                 110

Arg Glu Asn Leu Ala Thr Tyr Pro Ser Ser Glu Phe Gly Pro Asp Ala
        115                 120                 125

Ala Pro Pro Asn Leu Thr Arg Gln Ala Gln Leu Arg Glu Glu Leu Cys
    130                 135                 140

Gln Ser Pro Thr Leu Ala Tyr Leu Asn Asn Arg Phe Asp Pro Ser Gly
145                 150                 155                 160

Arg Tyr Thr Ile Ala Pro Ile Leu Pro Pro Ala Glu Ala Trp Ala Ala
                165                 170                 175

Gly Asp Arg Thr Met Leu Cys Gly Leu Gln Ala Thr Asp Ala Ser Gly
            180                 185                 190

Thr Pro Gln Leu Thr Val Gly Pro Ile Ala Ala Asn Asp Gln Ala Arg
        195                 200                 205

Val Phe Glu Thr Gly Ala Cys Val Lys Val Glu Ser Ser Ala Glu Phe
    210                 215                 220

Arg Gln Val Asp Cys Thr Glu Asp His His Leu Glu Ser Ile Leu Thr
225                 230                 235                 240

Val Asn Leu Gly Val Pro Phe Pro Gln Gly Ala Pro Ser Thr Asp Glu
                245                 250                 255

Gln Asn Asn Phe Leu Gly Asn Thr Cys Thr Gln Ala Ser Ile Asp Tyr
            260                 265                 270

Leu Gly Ser Glu Glu Asn Val Tyr Gln Ser Thr Leu Gln Thr Phe Trp
        275                 280                 285

Pro Thr Ile Thr Ser Asn Ser Trp Leu Gly Gly Ser His Ser Val Asn
    290                 295                 300

Cys Phe Leu Met Ser Pro Ser Thr Glu Gly Ala Ala Thr Phe Asn Thr
305                 310                 315                 320

Leu Asn Gly Ser Ala Thr Gly Thr Phe Thr Ile Asn Gly Glu Val Pro
                325                 330                 335

Pro Pro Gln Pro Glu Arg Asp Pro Leu Arg Asp Thr Ala Gly Thr Thr
            340                 345                 350

Ala Ser Ala Glu Val Gly Val Pro Val Glu Glu Asn Ala Pro
        355                 360                 365
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<210> 2861

<211> 1359
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1336)
<223> RXA02700

<400> 2861
tgacaactga tgcggacgac aacgatcgaa tttatagtca aacccctcgt gcacgcagcg 60

aagtctcggt aggggggagaa gttacagtaa gggcgtttta gtg gtt ccc tcg ttg 115
Val Val Pro Ser Leu
1 5

cag caa tgg cga aaa cct gct ctc atc ctg gcc att ttg acg gtg cta 163
Gln Gln Trp Arg Lys Pro Ala Leu Ile Leu Ala Ile Leu Thr Val Leu
10 15 20

ggc gta ctc ctg acc cat tgg ttc gcc tgg cca ctc acc tgg ccg ctg 211
Gly Val Leu Leu Thr His Trp Phe Ala Trp Pro Leu Thr Trp Pro Leu
25 30 35

ggg ctg cgt ctt ccc gtt gat gta gag gtg tac tgg cag ggt gcg cgc 259
Gly Leu Arg Leu Pro Val Asp Val Glu Val Tyr Trp Gln Gly Ala Arg
40 45 50

gag ttt tgg ctc gcc gat gat ctc tac gac atc agg tat gac acc act 307
Glu Phe Trp Leu Ala Asp Asp Leu Tyr Asp Ile Arg Tyr Asp Thr Thr
55 60 65

ttc gac aac ttg ccg ttc acc tat ccc cct ttc ggt gcg ttg gtg ttc 355
Phe Asp Asn Leu Pro Phe Thr Tyr Pro Pro Phe Gly Ala Leu Val Phe
70 75 80 85

acc cca ttg tgg tgg att cat gac ctc ttt ggt ctt ctc gtc acc gaa 403
Thr Pro Leu Trp Trp Ile His Asp Leu Phe Gly Leu Leu Val Thr Glu
90 95 100

cgt gtc ttc gcg cta atc acg ctg ctc acc acc tac gct gtg gca gtt 451
Arg Val Phe Ala Leu Ile Thr Leu Leu Thr Thr Tyr Ala Val Ala Val
105 110 115

ttc ctg ctc cgc ctg gcc ggc gtg cgc gat cgt gtg tgg gaa ttc gtc 499
Phe Leu Leu Arg Leu Ala Gly Val Arg Asp Arg Val Trp Glu Phe Val
120 125 130

gca ttc gca gcc ctg ctc gtg tcc gcg ccg gtg tat ttc aca ctc aat 547
Ala Phe Ala Ala Leu Leu Val Ser Ala Pro Val Tyr Phe Thr Leu Asn
135 140 145

att ggg caa ata aac gtc atg ctc atg gct tta acg ctt ttc gac gtc 595
Ile Gly Gln Ile Asn Val Met Leu Met Ala Leu Thr Leu Phe Asp Val
150 155 160 165

gcc ctc ccc cgc agc acg cgc cat tca ggc gtg ctc aaa tac gtg cca 643
Ala Leu Pro Arg Ser Thr Arg His Ser Gly Val Leu Lys Tyr Val Pro
170 175 180

ctc ggc gta ctc acc ggc att gcc gct gcg atc aaa cta acc cca cta 691

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Leu Gly Val Leu Thr Gly Ile Ala Ala Ala Ile Lys Leu Thr Pro Leu
            185                 190                 195

gtg ttc ggg ctg tat ttc ctc atc ctg tgg gtc gtg act aaa tca cca   739
Val Phe Gly Leu Tyr Phe Leu Ile Leu Trp Val Val Thr Lys Ser Pro
        200                 205                 210

cgc gga ctg ttt gga atg att ggt ggc ttc ctc ggg gca tcc ggg ctt   787
Arg Gly Leu Phe Gly Met Ile Gly Gly Phe Leu Gly Ala Ser Gly Leu
    215                 220                 225

gca att att ttc cga cca tcc att agc atc caa tat ttc acc gac gtg   835
Ala Ile Ile Phe Arg Pro Ser Ile Ser Ile Gln Tyr Phe Thr Asp Val
230                 235                 240                 245

ctg ttt acc gca gaa cgc atc ggc gac ctc cac ttc gca cgc aat gtc   883
Leu Phe Thr Ala Glu Arg Ile Gly Asp Leu His Phe Ala Arg Asn Val
                250                 255                 260

tcc atc cgt gcg gtt ttg gaa cga ctc ccc gaa ctt ggt tcc gca gca   931
Ser Ile Arg Ala Val Leu Glu Arg Leu Pro Glu Leu Gly Ser Ala Ala
            265                 270                 275

tct atc atg tgg ctt gtt gct gtg gcg cta gtg atc atc gca gtc gca   979
Ser Ile Met Trp Leu Val Ala Val Ala Leu Val Ile Ile Ala Val Ala
        280                 285                 290

gtt gct gct tac cga atc ctg cgg acg gat ctc tcc gcg cac aat cgt   1027
Val Ala Ala Tyr Arg Ile Leu Arg Thr Asp Leu Ser Ala His Asn Arg
    295                 300                 305

ctg ctg gct gtt tcc ctc gtg tcg ctc gtt gca ctg ttg tgc tcc ccc   1075
Leu Leu Ala Val Ser Leu Val Ser Leu Val Ala Leu Leu Cys Ser Pro
310                 315                 320                 325

gtc agt tgg tac cac cac tgg gtg tgg ctt ggt ccg tta atc gtc gct   1123
Val Ser Trp Tyr His His Trp Val Trp Leu Gly Pro Leu Ile Val Ala
                330                 335                 340

ctc tgg cta act caa cac cgc tgg ctg gct cta tgg ggc gca ttc gcc   1171
Leu Trp Leu Thr Gln His Arg Trp Leu Ala Leu Trp Gly Ala Phe Ala
            345                 350                 355

gtg aca ttc gga tca ttc cac aat ttc cta ccc tca gaa aac aat atg   1219
Val Thr Phe Gly Ser Phe His Asn Phe Leu Pro Ser Glu Asn Asn Met
        360                 365                 370

gag ctc acc tgg ccg tgg tgg atg cat gtc ctc gca gca cat tat ttg   1267
Glu Leu Thr Trp Pro Trp Trp Met His Val Leu Ala Ala His Tyr Leu
    375                 380                 385

atc ttc tcc gca gtg gtt act gcc gta ttt agt tgt ggg aaa atg ccc   1315
Ile Phe Ser Ala Val Val Thr Ala Val Phe Ser Cys Gly Lys Met Pro
390                 395                 400                 405

caa aaa aca gag ctt tcc cac taatcgatca ggagtatcac atc             1359
Gln Lys Thr Glu Leu Ser His
                410
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<210> 2862

<211> 412
<212> PRT
<213> Corynebacterium glutamicum

<400> 2862

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Val Val Pro Ser Leu Gln Gln Trp Arg Lys Pro Ala Leu Ile Leu Ala
  1               5                  10                  15

Ile Leu Thr Val Leu Gly Val Leu Leu Thr His Trp Phe Ala Trp Pro
             20                  25                  30

Leu Thr Trp Pro Leu Gly Leu Arg Leu Pro Val Asp Val Glu Val Tyr
         35                  40                  45

Trp Gln Gly Ala Arg Glu Phe Trp Leu Ala Asp Asp Leu Tyr Asp Ile
     50                  55                  60

Arg Tyr Asp Thr Thr Phe Asp Asn Leu Pro Phe Thr Tyr Pro Pro Phe
 65                  70                  75                  80

Gly Ala Leu Val Phe Thr Pro Leu Trp Trp Ile His Asp Leu Phe Gly
                 85                  90                  95

Leu Leu Val Thr Glu Arg Val Phe Ala Leu Ile Thr Leu Leu Thr Thr
            100                 105                 110

Tyr Ala Val Ala Val Phe Leu Leu Arg Leu Ala Gly Val Arg Asp Arg
        115                 120                 125

Val Trp Glu Phe Val Ala Phe Ala Ala Leu Leu Val Ser Ala Pro Val
    130                 135                 140

Tyr Phe Thr Leu Asn Ile Gly Gln Ile Asn Val Met Leu Met Ala Leu
145                 150                 155                 160

Thr Leu Phe Asp Val Ala Leu Pro Arg Ser Thr Arg His Ser Gly Val
                165                 170                 175

Leu Lys Tyr Val Pro Leu Gly Val Leu Thr Gly Ile Ala Ala Ala Ile
            180                 185                 190

Lys Leu Thr Pro Leu Val Phe Gly Leu Tyr Phe Leu Ile Leu Trp Val
        195                 200                 205

Val Thr Lys Ser Pro Arg Gly Leu Phe Gly Met Ile Gly Gly Phe Leu
    210                 215                 220

Gly Ala Ser Gly Leu Ala Ile Ile Phe Arg Pro Ser Ile Ser Ile Gln
225                 230                 235                 240

Tyr Phe Thr Asp Val Leu Phe Thr Ala Glu Arg Ile Gly Asp Leu His
                245                 250                 255

Phe Ala Arg Asn Val Ser Ile Arg Ala Val Leu Glu Arg Leu Pro Glu
            260                 265                 270

Leu Gly Ser Ala Ala Ser Ile Met Trp Leu Val Ala Val Ala Leu Val
        275                 280                 285

Ile Ile Ala Val Ala Val Ala Ala Tyr Arg Ile Leu Arg Thr Asp Leu
    290                 295                 300
```

```
Ser Ala His Asn Arg Leu Leu Ala Val Ser Leu Val Ser Leu Val Ala
305                 310                 315                 320

Leu Leu Cys Ser Pro Val Ser Trp Tyr His His Trp Val Trp Leu Gly
                325                 330                 335

Pro Leu Ile Val Ala Leu Trp Leu Thr Gln His Arg Trp Leu Ala Leu
            340                 345                 350

Trp Gly Ala Phe Ala Val Thr Phe Gly Ser Phe His Asn Phe Leu Pro
        355                 360                 365

Ser Glu Asn Asn Met Glu Leu Thr Trp Pro Trp Trp Met His Val Leu
    370                 375                 380

Ala Ala His Tyr Leu Ile Phe Ser Ala Val Val Thr Ala Val Phe Ser
385                 390                 395                 400

Cys Gly Lys Met Pro Gln Lys Thr Glu Leu Ser His
                405                 410
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20030207000003

<210> 2863
<211> 1423
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1408)
<223> RXA02701

<400> 2863

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cccactaatc gatcaggagt atcacatctc catgatttaa gattaaaact ttgtctaaac 60

acgaacggtg ttttcatgtt taagaaaagg actcctggtt ttg acg aac ccc cag   115
                                              Leu Thr Asn Pro Gln
                                                1               5

aca gca cat gct gcc gcg tct gac tcc gca tcc cag aag gag gct cct   163
Thr Ala His Ala Ala Ala Ser Asp Ser Ala Ser Gln Lys Glu Ala Pro
                  10                  15                  20

aat cct tca ctc tcc atc act gta ggt att aaa gat ctg ctg ggg ctg   211
Asn Pro Ser Leu Ser Ile Thr Val Gly Ile Lys Asp Leu Leu Gly Leu
              25                  30                  35

ctt tca gtt ctt ggc att gca gcg ggg ctg ata gcc aac aag att ctc   259
Leu Ser Val Leu Gly Ile Ala Ala Gly Leu Ile Ala Asn Lys Ile Leu
          40                  45                  50

atc gaa cgc tac aac tgg cgc atc gat gcc gca gtt tac cgc gaa ggc   307
Ile Glu Arg Tyr Asn Trp Arg Ile Asp Ala Ala Val Tyr Arg Glu Gly
      55                  60                  65

gcg tta gcg ctg gtc aac ggg gaa tca ctg tac gcg cag ccg ttt gat   355
Ala Leu Ala Leu Val Asn Gly Glu Ser Leu Tyr Ala Gln Pro Phe Asp
  70                  75                  80                  85

atg ggt gat att tca cta ccc ttt atc tac cca ccg att ggt gcc atc   403
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```
Met Gly Asp Ile Ser Leu Pro Phe Ile Tyr Pro Pro Ile Gly Ala Ile
                 90                  95                 100

ctg ttt gcg cct tgg ggg tac ttt gat ttc atc aca gtt gaa ctt gcg   451
Leu Phe Ala Pro Trp Gly Tyr Phe Asp Phe Ile Thr Val Glu Leu Ala
            105                 110                 115

gga aac ctt gtt gtc ata ggc tca tcc ctg ctg tta tta ctg tgc ctg   499
Gly Asn Leu Val Val Ile Gly Ser Ser Leu Leu Leu Leu Leu Cys Leu
        120                 125                 130

tat ctt gtc acc aac gct gtt ctt agc ggt cga gac aag ctg ttg gcc   547
Tyr Leu Val Thr Asn Ala Val Leu Ser Gly Arg Asp Lys Leu Leu Ala
    135                 140                 145

ttc acc atc gct gcg att tcc tgg ccg atc gct ctc ttt gca gag cca   595
Phe Thr Ile Ala Ala Ile Ser Trp Pro Ile Ala Leu Phe Ala Glu Pro
150                 155                 160                 165

gtg ttt ttg aac gct gac ttg ggc caa atc aac att ttg atc atg gct   643
Val Phe Leu Asn Ala Asp Leu Gly Gln Ile Asn Ile Leu Ile Met Ala
                170                 175                 180

ttg gtt gtc atg gac ctg ctt ccg att aag cgc aga atc ccc cga ggt   691
Leu Val Val Met Asp Leu Leu Pro Ile Lys Arg Arg Ile Pro Arg Gly
            185                 190                 195

gtc ctg att ggc ctt gca gcc gcc atc aaa atc act ccg ctg gcc atg   739
Val Leu Ile Gly Leu Ala Ala Ala Ile Lys Ile Thr Pro Leu Ala Met
        200                 205                 210

ctg ttg tat ttc ctg gtg aag aag gat ttc cgc gga atc atc aat gcg   787
Leu Leu Tyr Phe Leu Val Lys Lys Asp Phe Arg Gly Ile Ile Asn Ala
    215                 220                 225

gtg atc tca cta ctt gcc ttc act gct atc ggt gct gtg ctc gca tgg   835
Val Ile Ser Leu Leu Ala Phe Thr Ala Ile Gly Ala Val Leu Ala Trp
230                 235                 240                 245

gaa aac acc aaa gag ttc ttc tct tca acc ctt ctc aac tta agt gct   883
Glu Asn Thr Lys Glu Phe Phe Ser Ser Thr Leu Leu Asn Leu Ser Ala
                250                 255                 260

gaa ggc gat tca ggc gta gac acc acg ttc caa tcc aac agc tcg att   931
Glu Gly Asp Ser Gly Val Asp Thr Thr Phe Gln Ser Asn Ser Ser Ile
            265                 270                 275

cag gcc atg ctg tat cgc tgg tgg acc tca aag gca gat gcc gaa gca   979
Gln Ala Met Leu Tyr Arg Trp Trp Thr Ser Lys Ala Asp Ala Glu Ala
        280                 285                 290

tcc tca ctg ccc acc atc ttg tgg atc gta ctg tcc ctg att gct gtg   1027
Ser Ser Leu Pro Thr Ile Leu Trp Ile Val Leu Ser Leu Ile Ala Val
    295                 300                 305

gcg gcc gtt gcc tac cta atg cac caa ctc ttc tcc aga gga ttg cac   1075
Ala Ala Val Ala Tyr Leu Met His Gln Leu Phe Ser Arg Gly Leu His
310                 315                 320                 325

gtt gag gca gtc atg gtt aac gcc atg ctc atg cta ctt atc tcc ccc   1123
Val Glu Ala Val Met Val Asn Ala Met Leu Met Leu Leu Ile Ser Pro
```

```
                330                 335                 340

atc tca tgg tct cac cac tgg gtg tgg cta ccg ctg tgg gct gtg gtg   1171
Ile Ser Trp Ser His His Trp Val Trp Leu Pro Leu Trp Ala Val Val
            345                 350                 355

ttc ttc gtt cga tac cgc cag cac cgc tct cac ccg aag ttc ttg ttg   1219
Phe Phe Val Arg Tyr Arg Gln His Arg Ser His Pro Lys Phe Leu Leu
        360                 365                 370

tgg agc gga gtt atc ttg agc gtc atg ctg ctg atg ctg cca cca aaa   1267
Trp Ser Gly Val Ile Leu Ser Val Met Leu Leu Met Leu Pro Pro Lys
    375                 380                 385

tgg tgg ttt ggc cgc gat ggc gtc aac gtc ttc gaa ctg aat ttc tgg   1315
Trp Trp Phe Gly Arg Asp Gly Val Asn Val Phe Glu Leu Asn Phe Trp
390                 395                 400                 405

gag aaa cta ctc atc tct gac tgg acg tgg ctc tcc atc ggg ctc atg   1363
Glu Lys Leu Leu Ile Ser Asp Trp Thr Trp Leu Ser Ile Gly Leu Met
                410                 415                 420

atc acc ttg ggt ctt ggg ctg aaa gca ttt ccc aaa ata tcc aaa       1408
Ile Thr Leu Gly Leu Gly Leu Lys Ala Phe Pro Lys Ile Ser Lys
            425                 430                 435

tagataaagg tgtgg                                                 1423


<210> 2864
<211> 436
<212> PRT
<213> Corynebacterium glutamicum

<400> 2864
Leu Thr Asn Pro Gln Thr Ala His Ala Ala Ala Ser Asp Ser Ala Ser
  1               5                  10                  15

Gln Lys Glu Ala Pro Asn Pro Ser Leu Ser Ile Thr Val Gly Ile Lys
             20                  25                  30

Asp Leu Leu Gly Leu Leu Ser Val Leu Gly Ile Ala Ala Gly Leu Ile
         35                  40                  45

Ala Asn Lys Ile Leu Ile Glu Arg Tyr Asn Trp Arg Ile Asp Ala Ala
     50                  55                  60

Val Tyr Arg Glu Gly Ala Leu Ala Leu Val Asn Gly Glu Ser Leu Tyr
 65                  70                  75                  80

Ala Gln Pro Phe Asp Met Gly Asp Ile Ser Leu Pro Phe Ile Tyr Pro
                 85                  90                  95

Pro Ile Gly Ala Ile Leu Phe Ala Pro Trp Gly Tyr Phe Asp Phe Ile
            100                 105                 110

Thr Val Glu Leu Ala Gly Asn Leu Val Val Ile Gly Ser Ser Leu Leu
        115                 120                 125

Leu Leu Leu Cys Leu Tyr Leu Val Thr Asn Ala Val Leu Ser Gly Arg
    130                 135                 140
```

```
Asp Lys Leu Leu Ala Phe Thr Ile Ala Ala Ile Ser Trp Pro Ile Ala
145                 150                 155                 160

Leu Phe Ala Glu Pro Val Phe Leu Asn Ala Asp Leu Gly Gln Ile Asn
                165                 170                 175

Ile Leu Ile Met Ala Leu Val Val Met Asp Leu Leu Pro Ile Lys Arg
            180                 185                 190

Arg Ile Pro Arg Gly Val Leu Ile Gly Leu Ala Ala Ala Ile Lys Ile
        195                 200                 205

Thr Pro Leu Ala Met Leu Leu Tyr Phe Leu Val Lys Lys Asp Phe Arg
    210                 215                 220

Gly Ile Ile Asn Ala Val Ile Ser Leu Leu Ala Phe Thr Ala Ile Gly
225                 230                 235                 240

Ala Val Leu Ala Trp Glu Asn Thr Lys Glu Phe Phe Ser Ser Thr Leu
                245                 250                 255

Leu Asn Leu Ser Ala Glu Gly Asp Ser Gly Val Asp Thr Thr Phe Gln
            260                 265                 270

Ser Asn Ser Ser Ile Gln Ala Met Leu Tyr Arg Trp Trp Thr Ser Lys
        275                 280                 285

Ala Asp Ala Glu Ala Ser Ser Leu Pro Thr Ile Leu Trp Ile Val Leu
    290                 295                 300

Ser Leu Ile Ala Val Ala Ala Val Ala Tyr Leu Met His Gln Leu Phe
305                 310                 315                 320

Ser Arg Gly Leu His Val Glu Ala Val Met Val Asn Ala Met Leu Met
                325                 330                 335

Leu Leu Ile Ser Pro Ile Ser Trp Ser His His Trp Val Trp Leu Pro
            340                 345                 350

Leu Trp Ala Val Val Phe Phe Val Arg Tyr Arg Gln His Arg Ser His
        355                 360                 365

Pro Lys Phe Leu Leu Trp Ser Gly Val Ile Leu Ser Val Met Leu Leu
    370                 375                 380

Met Leu Pro Pro Lys Trp Trp Phe Gly Arg Asp Gly Val Asn Val Phe
385                 390                 395                 400

Glu Leu Asn Phe Trp Glu Lys Leu Leu Ile Ser Asp Trp Thr Trp Leu
                405                 410                 415

Ser Ile Gly Leu Met Ile Thr Leu Gly Leu Gly Leu Lys Ala Phe Pro
            420                 425                 430

Lys Ile Ser Lys
        435
```

<210> 2865
<211> 918

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(895)
<223> RXA02712

<400> 2865
ctgaaacggc ttcggaagct gaaattgaag aaaacccacg tgccgcacct gtgaaggtgc 60

gcgcaatcga aagaatcggc aacaactcag gagacctctc atg acc atg aca aat 115
Met Thr Met Thr Asn
1 5

ggc tcc cgc aca gag tcg gga aag att cgc gat cga cgt gtc gct gac 163
Gly Ser Arg Thr Glu Ser Gly Lys Ile Arg Asp Arg Arg Val Ala Asp
10 15 20

gct gat cca cgg tat ggc cgt cgc gtc tcg gtg agt agg gat ttc tcc 211
Ala Asp Pro Arg Tyr Gly Arg Arg Val Ser Val Ser Arg Asp Phe Ser
25 30 35

aca gcg gaa gct tcg ggg agg ggc gcg tcg ata agc acg caa cct cgt 259
Thr Ala Glu Ala Ser Gly Arg Gly Ala Ser Ile Ser Thr Gln Pro Arg
40 45 50

cgt gac atg gcg ccg gaa agg cgc cac aca acc cgg gcc cta gtg aac 307
Arg Asp Met Ala Pro Glu Arg Arg His Thr Thr Arg Ala Leu Val Asn
55 60 65

cct ggc gtg caa cca acg cgt aag cgt ttg atg cag cac aag ctg ggc 355
Pro Gly Val Gln Pro Thr Arg Lys Arg Leu Met Gln His Lys Leu Gly
70 75 80 85

tct cag cag gtt atg tcg gtg cgt ggt cgc cgc gtt gag gca aaa cgt 403
Ser Gln Gln Val Met Ser Val Arg Gly Arg Arg Val Glu Ala Lys Arg
90 95 100

gct gat cct aag gtg atc cag ctg tct gtg ctg gtg gtt atc ctg ctg 451
Ala Asp Pro Lys Val Ile Gln Leu Ser Val Leu Val Val Ile Leu Leu
105 110 115

tgc gtt ggt gtt ggc gcg acc atg ggt ctg tcc gga acg tct aca cag 499
Cys Val Gly Val Gly Ala Thr Met Gly Leu Ser Gly Thr Ser Thr Gln
120 125 130

cag act ttc cag ttg cag gaa ctt cag gca act gaa acg gat ttg agc 547
Gln Thr Phe Gln Leu Gln Glu Leu Gln Ala Thr Glu Thr Asp Leu Ser
135 140 145

aat cgc att gag tcg ctc aac cga gat gtg gaa gat gct cgc tca gca 595
Asn Arg Ile Glu Ser Leu Asn Arg Asp Val Glu Asp Ala Arg Ser Ala
150 155 160 165

gca acc ttg gca gcg aat gct acg gag atg ggc ttg gta tcc cca gtg 643
Ala Thr Leu Ala Ala Asn Ala Thr Glu Met Gly Leu Val Ser Pro Val
170 175 180

gaa cct ggc gtg ctc gca gtg cag gaa aac ggt gat gtt gtg gag gag 691
Glu Pro Gly Val Leu Ala Val Gln Glu Asn Gly Asp Val Val Glu Glu

```
            185                 190                 195

cgc gaa gca aat cca gag aca cgc cct ata gtt gac atc aat gga caa   739
Arg Glu Ala Asn Pro Glu Thr Arg Pro Ile Val Asp Ile Asn Gly Gln
        200                 205                 210

cag acc cga cca aat cgg gca tca agc aac cct gac gag act aac gca   787
Gln Thr Arg Pro Asn Arg Ala Ser Ser Asn Pro Asp Glu Thr Asn Ala
    215                 220                 225

gtg act gaa aac ctc cag gcg att cca caa gaa gca gca gct ccg ccg   835
Val Thr Glu Asn Leu Gln Ala Ile Pro Gln Glu Ala Ala Ala Pro Pro
230                 235                 240                 245

tat cag acc aac act gtt cct tat gct gca acc acc gga caa gca ggt   883
Tyr Gln Thr Asn Thr Val Pro Tyr Ala Ala Thr Thr Gly Gln Ala Gly
                250                 255                 260

ggc gca ggg cag tgactttccc cagcaatggc aga                        918
Gly Ala Gly Gln
            265
```

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<210> 2866
<211> 265
<212> PRT
<213> Corynebacterium glutamicum

<400> 2866

```
Met Thr Met Thr Asn Gly Ser Arg Thr Glu Ser Gly Lys Ile Arg Asp
  1               5                  10                  15

Arg Arg Val Ala Asp Ala Asp Pro Arg Tyr Gly Arg Arg Val Ser Val
             20                  25                  30

Ser Arg Asp Phe Ser Thr Ala Glu Ala Ser Gly Arg Gly Ala Ser Ile
         35                  40                  45

Ser Thr Gln Pro Arg Arg Asp Met Ala Pro Glu Arg Arg His Thr Thr
     50                  55                  60

Arg Ala Leu Val Asn Pro Gly Val Gln Pro Thr Arg Lys Arg Leu Met
 65                  70                  75                  80

Gln His Lys Leu Gly Ser Gln Gln Val Met Ser Val Arg Gly Arg Arg
                 85                  90                  95

Val Glu Ala Lys Arg Ala Asp Pro Lys Val Ile Gln Leu Ser Val Leu
            100                 105                 110

Val Val Ile Leu Leu Cys Val Gly Val Gly Ala Thr Met Gly Leu Ser
        115                 120                 125

Gly Thr Ser Thr Gln Gln Thr Phe Gln Leu Gln Glu Leu Gln Ala Thr
    130                 135                 140

Glu Thr Asp Leu Ser Asn Arg Ile Glu Ser Leu Asn Arg Asp Val Glu
145                 150                 155                 160

Asp Ala Arg Ser Ala Ala Thr Leu Ala Ala Asn Ala Thr Glu Met Gly
                165                 170                 175
```

```
Leu Val Ser Pro Val Glu Pro Gly Val Leu Ala Val Gln Glu Asn Gly
            180                 185                 190

Asp Val Val Glu Glu Arg Glu Ala Asn Pro Glu Thr Arg Pro Ile Val
        195                 200                 205

Asp Ile Asn Gly Gln Gln Thr Arg Pro Asn Arg Ala Ser Ser Asn Pro
    210                 215                 220

Asp Glu Thr Asn Ala Val Thr Glu Asn Leu Gln Ala Ile Pro Gln Glu
225                 230                 235                 240

Ala Ala Ala Pro Pro Tyr Gln Thr Asn Thr Val Pro Tyr Ala Ala Thr
                245                 250                 255

Thr Gly Gln Ala Gly Gly Ala Gly Gln
            260                 265


<210> 2867
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> RXA02714

<400> 2867
cgcggtggtc ttgcatgaga ggccactacg caccctcaga gacaaactga atggttggtt 60

ctgtttatgc cactgagttg ctgggaaggg gacttcaagg atg ttc ctt ggt acc   115
                                          Met Phe Leu Gly Thr
                                            1               5

tat acc ccg aaa ctc gat gac aaa ggc agg ctg act ctt cca gca aag   163
Tyr Thr Pro Lys Leu Asp Asp Lys Gly Arg Leu Thr Leu Pro Ala Lys
                10                  15                  20

ttc cgt gag gac ctt gcg ggg gga ttg atg gtc act aaa ggt caa gac   211
Phe Arg Glu Asp Leu Ala Gly Gly Leu Met Val Thr Lys Gly Gln Asp
            25                  30                  35

cac agt ctc gcg gtt tat ccg aag gaa gaa ttt gca gca agg gct cgc   259
His Ser Leu Ala Val Tyr Pro Lys Glu Glu Phe Ala Ala Arg Ala Arg
        40                  45                  50

aag gca gct gca gtt tct agg aca aac cct gag gct cgt gcg ttt atc   307
Lys Ala Ala Ala Val Ser Arg Thr Asn Pro Glu Ala Arg Ala Phe Ile
    55                  60                  65

cga aac ctt gca gca agc gcg gat gaa caa cga ccc gac ggc cag ggg   355
Arg Asn Leu Ala Ala Ser Ala Asp Glu Gln Arg Pro Asp Gly Gln Gly
70                  75                  80                  85

cgc atc acc ctt tcg gca gcg cac cgc aca tat gcg ggg ctg aca aaa   403
Arg Ile Thr Leu Ser Ala Ala His Arg Thr Tyr Ala Gly Leu Thr Lys
                90                  95                  100
```

```
gag tgt gtc gtt atc ggt tcg gtg gat ttt ctg gag att tgg gac gct   451
Glu Cys Val Val Ile Gly Ser Val Asp Phe Leu Glu Ile Trp Asp Ala
            105                 110                 115

caa gcc tgg gcc gcg tat cag gaa gag acg gag gct gcc ttc tca gca   499
Gln Ala Trp Ala Ala Tyr Gln Glu Glu Thr Glu Ala Ala Phe Ser Ala
        120                 125                 130

gct gaa gat gac gtc ctt gga gga ttg ctc tgatagttgg gcaatgcttc     549
Ala Glu Asp Asp Val Leu Gly Gly Leu Leu
    135                 140

gaa                                                               552
```

<210> 2868
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 2868

```
Met Phe Leu Gly Thr Tyr Thr Pro Lys Leu Asp Asp Lys Gly Arg Leu
  1               5                  10                  15

Thr Leu Pro Ala Lys Phe Arg Glu Asp Leu Ala Gly Gly Leu Met Val
             20                  25                  30

Thr Lys Gly Gln Asp His Ser Leu Ala Val Tyr Pro Lys Glu Glu Phe
         35                  40                  45

Ala Ala Arg Ala Arg Lys Ala Ala Ala Val Ser Arg Thr Asn Pro Glu
     50                  55                  60

Ala Arg Ala Phe Ile Arg Asn Leu Ala Ala Ser Ala Asp Glu Gln Arg
 65                  70                  75                  80

Pro Asp Gly Gln Gly Arg Ile Thr Leu Ser Ala Ala His Arg Thr Tyr
                 85                  90                  95

Ala Gly Leu Thr Lys Glu Cys Val Val Ile Gly Ser Val Asp Phe Leu
            100                 105                 110

Glu Ile Trp Asp Ala Gln Ala Trp Ala Ala Tyr Gln Glu Glu Thr Glu
        115                 120                 125

Ala Ala Phe Ser Ala Ala Glu Asp Asp Val Leu Gly Gly Leu Leu
    130                 135                 140
```

<210> 2869
<211> 513
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(490)
<223> RXA02715

<400> 2869

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gtttttgtcg ttattggcat aacggggaac attctggata ttctgggcgt taataaggca 60
```

```
tagaagaaaa aatgtctcta ctaaccaccg ggaggacatc gtg tcg ctt tca gag   115
                                             Val Ser Leu Ser Glu
                                               1               5

cag gag caa cgc gca ctg cgc gaa att gag caa gcg ctc atg gca gat   163
Gln Glu Gln Arg Ala Leu Arg Glu Ile Glu Gln Ala Leu Met Ala Asp
                 10                  15                  20

gat ccg aaa ttt gga aaa gcg gtt gca agt aac aat ggc cta gca ggc   211
Asp Pro Lys Phe Gly Lys Ala Val Ala Ser Asn Asn Gly Leu Ala Gly
             25                  30                  35

ggt ggg ttt acc ctt cgg gga atc gca ctt ttc gta ctc gga ctt gtc   259
Gly Gly Phe Thr Leu Arg Gly Ile Ala Leu Phe Val Leu Gly Leu Val
         40                  45                  50

ctt ctt gtt gcc ggc gtc gca tta agc cag caa aca ttg tgg ttc gtt   307
Leu Leu Val Ala Gly Val Ala Leu Ser Gln Gln Thr Leu Trp Phe Val
     55                  60                  65

gcg ctc gga att atc gga ttc tta gtc atg ttc gga tcg gga gtg tgg   355
Ala Leu Gly Ile Ile Gly Phe Leu Val Met Phe Gly Ser Gly Val Trp
 70                  75                  80                  85

atg ctg cgc ggg ggc ggc tcc aac aaa atc tcc gtc aca tcc cgc act   403
Met Leu Arg Gly Gly Gly Ser Asn Lys Ile Ser Val Thr Ser Arg Thr
                 90                  95                 100

tcc aat gcg aag aat cgc caa cag ggc aat tcc acc att ggg gac aaa   451
Ser Asn Ala Lys Asn Arg Gln Gln Gly Asn Ser Thr Ile Gly Asp Lys
             105                 110                 115

atg gaa gaa aac ttc cgt cga cga ttc gag ggc aat aag taagaagtaa    500
Met Glu Glu Asn Phe Arg Arg Arg Phe Glu Gly Asn Lys
         120                 125                 130

ctgaataagt ctt                                                   513
```

<210> 2870
<211> 130
<212> PRT
<213> Corynebacterium glutamicum

<400> 2870

```
Val Ser Leu Ser Glu Gln Glu Gln Arg Ala Leu Arg Glu Ile Glu Gln
  1               5                  10                  15

Ala Leu Met Ala Asp Asp Pro Lys Phe Gly Lys Ala Val Ala Ser Asn
             20                  25                  30

Asn Gly Leu Ala Gly Gly Gly Phe Thr Leu Arg Gly Ile Ala Leu Phe
         35                  40                  45

Val Leu Gly Leu Val Leu Leu Val Ala Gly Val Ala Leu Ser Gln Gln
     50                  55                  60

Thr Leu Trp Phe Val Ala Leu Gly Ile Ile Gly Phe Leu Val Met Phe
 65                  70                  75                  80
```

```
Gly Ser Gly Val Trp Met Leu Arg Gly Gly Gly Ser Asn Lys Ile Ser
                  85                  90                  95

Val Thr Ser Arg Thr Ser Asn Ala Lys Asn Arg Gln Gln Gly Asn Ser
             100                 105                 110

Thr Ile Gly Asp Lys Met Glu Glu Asn Phe Arg Arg Arg Phe Glu Gly
         115                 120                 125

Asn Lys
    130
```

<210> 2871
<211> 861
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(838)
<223> RXA02721

<400> 2871

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ccgtgatgat cgtcgtgacg atcgccgcga tgaccgcgga gacgacctgg atgtacccag 60

cttcctccag taattaagaa ggagaataga cttatccact atg gat agt ctt gac   115
                                           Met Asp Ser Leu Asp
                                             1               5

ccc cgc aac cgc ccc gtc cgc aag gtc ttc acg acc cgt gcc ggc ggg   163
Pro Arg Asn Arg Pro Val Arg Lys Val Phe Thr Thr Arg Ala Gly Gly
                  10                  15                  20

gtt tcg cag tcc ccg tat gct tcc ttc aac ctt ggt gat cac gtc ggc   211
Val Ser Gln Ser Pro Tyr Ala Ser Phe Asn Leu Gly Asp His Val Gly
              25                  30                  35

gac gat cct caa gct gtg gca tcc aac cgc aat cgc ttg gct gac atc   259
Asp Asp Pro Gln Ala Val Ala Ser Asn Arg Asn Arg Leu Ala Asp Ile
          40                  45                  50

atc ggt ttg tcc cca gac aag gtg gtg tac atg gag caa att cat tcc   307
Ile Gly Leu Ser Pro Asp Lys Val Val Tyr Met Glu Gln Ile His Ser
      55                  60                  65

aat acc gtc aca gtc att gat gaa gcc cca gcg gat ggc cag gct gta   355
Asn Thr Val Thr Val Ile Asp Glu Ala Pro Ala Asp Gly Gln Ala Val
  70                  75                  80                  85

gag gcc acc gat gcg cta gtg acc acg caa cga ggg cta gcg ctg gcc   403
Glu Ala Thr Asp Ala Leu Val Thr Thr Gln Arg Gly Leu Ala Leu Ala
                  90                  95                 100

gtt ttg gtt gct gat tgc gtg cca gtg ctg ctg tca gac acc gac gct   451
Val Leu Val Ala Asp Cys Val Pro Val Leu Leu Ser Asp Thr Asp Ala
             105                 110                 115

ggc gtg att gcg gca gtg cat gca ggc cgc atg gga gcc cgc aat ggc   499
Gly Val Ile Ala Ala Val His Ala Gly Arg Met Gly Ala Arg Asn Gly
         120                 125                 130
```

```
atc gta gct aaa acc att gcg aag atg gag gag ctc ggc gcg aaa ccc   547
Ile Val Ala Lys Thr Ile Ala Lys Met Glu Glu Leu Gly Ala Lys Pro
    135                 140                 145

agc cgc att cat gcg ctc atg ggt gca gcg gca tcg ggt gcg aac tac   595
Ser Arg Ile His Ala Leu Met Gly Ala Ala Ala Ser Gly Ala Asn Tyr
150                 155                 160                 165

gag gtc cca gag gcc atg gcg cgc gat gtg gaa gcc aaa ctt cca ggt   643
Glu Val Pro Glu Ala Met Ala Arg Asp Val Glu Ala Lys Leu Pro Gly
                170                 175                 180

tcc att gcg cgt acg aca aaa ggc acc aca gga ctg gac atc cgc gca   691
Ser Ile Ala Arg Thr Thr Lys Gly Thr Thr Gly Leu Asp Ile Arg Ala
            185                 190                 195

ggg ctg ctg cgt caa atg ctc agc ctg ggt gtg caa atg att gat tct   739
Gly Leu Leu Arg Gln Met Leu Ser Leu Gly Val Gln Met Ile Asp Ser
        200                 205                 210

gat cca cgc tgc acc atc gaa gac gaa gat ctg ttt tct tac cgc cgc   787
Asp Pro Arg Cys Thr Ile Glu Asp Glu Asp Leu Phe Ser Tyr Arg Arg
    215                 220                 225

gaa ggc acg aca ggc cgc cag gcc ggc gtg gtg tgg ctg cca aag gag   835
Glu Gly Thr Thr Gly Arg Gln Ala Gly Val Val Trp Leu Pro Lys Glu
230                 235                 240                 245

gca taaattggag cgccgcgaag agc                                    861
Ala
```

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<210> 2872
<211> 246
<212> PRT
<213> Corynebacterium glutamicum

<400> 2872

```
Met Asp Ser Leu Asp Pro Arg Asn Arg Pro Val Arg Lys Val Phe Thr
  1               5                  10                  15

Thr Arg Ala Gly Gly Val Ser Gln Ser Pro Tyr Ala Ser Phe Asn Leu
            20                  25                  30

Gly Asp His Val Gly Asp Asp Pro Gln Ala Val Ala Ser Asn Arg Asn
        35                  40                  45

Arg Leu Ala Asp Ile Ile Gly Leu Ser Pro Asp Lys Val Val Tyr Met
    50                  55                  60

Glu Gln Ile His Ser Asn Thr Val Thr Val Ile Asp Glu Ala Pro Ala
65                  70                  75                  80

Asp Gly Gln Ala Val Glu Ala Thr Asp Ala Leu Val Thr Thr Gln Arg
                85                  90                  95

Gly Leu Ala Leu Ala Val Leu Val Ala Asp Cys Val Pro Val Leu Leu
            100                 105                 110
```

```
Ser Asp Thr Asp Ala Gly Val Ile Ala Ala Val His Ala Gly Arg Met
        115                 120                 125

Gly Ala Arg Asn Gly Ile Val Ala Lys Thr Ile Ala Lys Met Glu Glu
    130                 135                 140

Leu Gly Ala Lys Pro Ser Arg Ile His Ala Leu Met Gly Ala Ala Ala
145                 150                 155                 160

Ser Gly Ala Asn Tyr Glu Val Pro Glu Ala Met Ala Arg Asp Val Glu
                165                 170                 175

Ala Lys Leu Pro Gly Ser Ile Ala Arg Thr Thr Lys Gly Thr Thr Gly
            180                 185                 190

Leu Asp Ile Arg Ala Gly Leu Leu Arg Gln Met Leu Ser Leu Gly Val
        195                 200                 205

Gln Met Ile Asp Ser Asp Pro Arg Cys Thr Ile Glu Asp Glu Asp Leu
    210                 215                 220

Phe Ser Tyr Arg Arg Glu Gly Thr Thr Gly Arg Gln Ala Gly Val Val
225                 230                 235                 240

Trp Leu Pro Lys Glu Ala
                245
```

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<210> 2873
<211> 735
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(712)
<223> RXA02725

<400> 2873

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gaaagcccgc tgcacatcgg tgtggcgggt tttctcatgc ccagatattg accttgtcac 60

tgtgtcaagg cattgaataa gtgccatgaa cataagtgcc atg gac aac ttc gaa   115
                                              Met Asp Asn Phe Glu
                                                1               5

cat tca aat gca tct atc cgt tta caa gca gcg ttg gcc gca gga act   163
His Ser Asn Ala Ser Ile Arg Leu Gln Ala Ala Leu Ala Ala Gly Thr
                  10                  15                  20

gct gag gac acc act gcg atc gat att ctt ttg tac cgc agt ggg gta   211
Ala Glu Asp Thr Thr Ala Ile Asp Ile Leu Leu Tyr Arg Ser Gly Val
             25                  30                  35

gaa gaa gac ttc ttt gtg cgc gac atg ata acg tgg gcg ctc acc cgc   259
Glu Glu Asp Phe Phe Val Arg Asp Met Ile Thr Trp Ala Leu Thr Arg
         40                  45                  50

atg cca gtt gat gac gtg ttt acc tca ctg gtc gct gat ttg gat tct   307
Met Pro Val Asp Asp Val Phe Thr Ser Leu Val Ala Asp Leu Asp Ser
     55                  60                  65
```

```
gag gta cct gat cga cca ttc ggt gca agt caa gca ctc cac aca ctc   355
Glu Val Pro Asp Arg Pro Phe Gly Ala Ser Gln Ala Leu His Thr Leu
 70                  75                  80                  85

tcc aag tta agg gtc gcg cag tcg tgg cag gaa ttg caa gca cgg cct   403
Ser Lys Leu Arg Val Ala Gln Ser Trp Gln Glu Leu Gln Ala Arg Pro
                 90                  95                 100

tgg ctt ttg cac cgg gag gac acc gcc caa act gcg tgg cga acc ttt   451
Trp Leu Leu His Arg Glu Asp Thr Ala Gln Thr Ala Trp Arg Thr Phe
            105                 110                 115

gtg gga ctg gtc cca gat gat cag acc gca tgg ttg gcg cac caa ttg   499
Val Gly Leu Val Pro Asp Asp Gln Thr Ala Trp Leu Ala His Gln Leu
        120                 125                 130

ctc caa gaa ttg gat aaa gga acg cct gaa att cag cgg agt tta agt   547
Leu Gln Glu Leu Asp Lys Gly Thr Pro Glu Ile Gln Arg Ser Leu Ser
    135                 140                 145

cgg gcg atg gcg gaa ttg gag ggg agg gag gcg tcg ata agc gtg ctt   595
Arg Ala Met Ala Glu Leu Glu Gly Arg Glu Ala Ser Ile Ser Val Leu
150                 155                 160                 165

cta ggc gct tta acg agc gcg cac gcg gtg gcc acc gcc aag ctc att   643
Leu Gly Ala Leu Thr Ser Ala His Ala Val Ala Thr Ala Lys Leu Ile
                170                 175                 180

gcg gat ccg gac tcc gat ttc atg gct gat ctg gag gaa gcg cgg cgc   691
Ala Asp Pro Asp Ser Asp Phe Met Ala Asp Leu Glu Glu Ala Arg Arg
            185                 190                 195

gtg gat aat atg ggt gca tgc tgatcggtga ggtgtccaag ctc            735
Val Asp Asn Met Gly Ala Cys
        200
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US20050009050A1

<210> 2874
<211> 204
<212> PRT
<213> Corynebacterium glutamicum

<400> 2874

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Met Asp Asn Phe Glu His Ser Asn Ala Ser Ile Arg Leu Gln Ala Ala
  1               5                  10                  15

Leu Ala Ala Gly Thr Ala Glu Asp Thr Thr Ala Ile Asp Ile Leu Leu
             20                  25                  30

Tyr Arg Ser Gly Val Glu Glu Asp Phe Phe Val Arg Asp Met Ile Thr
         35                  40                  45

Trp Ala Leu Thr Arg Met Pro Val Asp Asp Val Phe Thr Ser Leu Val
     50                  55                  60

Ala Asp Leu Asp Ser Glu Val Pro Asp Arg Pro Phe Gly Ala Ser Gln
 65                  70                  75                  80

Ala Leu His Thr Leu Ser Lys Leu Arg Val Ala Gln Ser Trp Gln Glu
                 85                  90                  95
```

```
Leu Gln Ala Arg Pro Trp Leu Leu His Arg Glu Asp Thr Ala Gln Thr
            100                 105                 110

Ala Trp Arg Thr Phe Val Gly Leu Val Pro Asp Asp Gln Thr Ala Trp
        115                 120                 125

Leu Ala His Gln Leu Leu Gln Glu Leu Asp Lys Gly Thr Pro Glu Ile
    130                 135                 140

Gln Arg Ser Leu Ser Arg Ala Met Ala Glu Leu Glu Gly Arg Glu Ala
145                 150                 155                 160

Ser Ile Ser Val Leu Leu Gly Ala Leu Thr Ser Ala His Ala Val Ala
                165                 170                 175

Thr Ala Lys Leu Ile Ala Asp Pro Asp Ser Asp Phe Met Ala Asp Leu
            180                 185                 190

Glu Glu Ala Arg Arg Val Asp Asn Met Gly Ala Cys
        195                 200
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<210> 2875
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> RXA02727

<400> 2875

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gatcagttcc tagatctcgt tgaggacgcc ctcgttcagt tccaagagga aaacgaagac 60

ctaaagcagc aggtcgaaga gctagaggcg caggttgccg gtg gtc ctt ctt ccg   115
                                            Val Val Leu Leu Pro
                                              1               5

ctg cta gtt cct caa ctg cag gtg cag cca cag ttg cag ctt cca agt   163
Leu Leu Val Pro Gln Leu Gln Val Gln Pro Gln Leu Gln Leu Pro Ser
                10                  15                  20

ctg ttg acg agg cag cgc tgc gca agg aaa tca aag aga agc tgc gct   211
Leu Leu Thr Arg Gln Arg Cys Ala Arg Lys Ser Lys Arg Ser Cys Ala
            25                  30                  35

ccg aat acg gca tcc aag ctc gat gat gcc tcc aag gcc gct cag aag   259
Pro Asn Thr Ala Ser Lys Leu Asp Asp Ala Ser Lys Ala Ala Gln Lys
        40                  45                  50

gct caa aac gat gcg aag tcc gct caa gat cag cta cag cgt gca caa   307
Ala Gln Asn Asp Ala Lys Ser Ala Gln Asp Gln Leu Gln Arg Ala Gln
    55                  60                  65

gct gac gca aag gca gct cgc gac gaa gct gaa aag gcc aag gct gaa   355
Ala Asp Ala Lys Ala Ala Arg Asp Glu Ala Glu Lys Ala Lys Ala Glu
70                  75                  80                  85

gct aag tca gca gca tcc tcc agc acc act aag gca gca gcg gtt ggc   403
Ala Lys Ser Ala Ala Ser Ser Ser Thr Thr Lys Ala Ala Ala Val Gly
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```
                  90                  95                 100

gct gtc ggc gct ggc acc gga gca gca gtt gct aca ggt gct gca aat   451
Ala Val Gly Ala Gly Thr Gly Ala Ala Val Ala Thr Gly Ala Ala Asn
            105                 110                 115

gtg gac acc cac atg cag gca gcg aag gtt ctg gga ctc gca cag gaa   499
Val Asp Thr His Met Gln Ala Ala Lys Val Leu Gly Leu Ala Gln Glu
        120                 125                 130

atg gca gac cgc ctg acc tca gag gct cgc tcc gaa tcc aag tcc atg   547
Met Ala Asp Arg Leu Thr Ser Glu Ala Arg Ser Glu Ser Lys Ser Met
    135                 140                 145

ctg gac gag gct cgc gaa gca gca gag aag cag atc gag gaa gca aac   595
Leu Asp Glu Ala Arg Glu Ala Ala Glu Lys Gln Ile Glu Glu Ala Asn
150                 155                 160                 165

agc acc tcc aac cgc act ctg gaa gat gct cgc gca aac gct gag aag   643
Ser Thr Ser Asn Arg Thr Leu Glu Asp Ala Arg Ala Asn Ala Glu Lys
                170                 175                 180

cag atc gct gaa gcg cag aac cgc gct gac act ctg gtc aac gaa gct   691
Gln Ile Ala Glu Ala Gln Asn Arg Ala Asp Thr Leu Val Asn Glu Ala
            185                 190                 195

gac gct aag gct aag aac ctg gtt tcc gaa gcc gag aag aag tcc gca   739
Asp Ala Lys Ala Lys Asn Leu Val Ser Glu Ala Glu Lys Lys Ser Ala
        200                 205                 210

gcc acc ctg gcc gca tcc acc tct cgt gca gaa gct cag atc cgt caa   787
Ala Thr Leu Ala Ala Ser Thr Ser Arg Ala Glu Ala Gln Ile Arg Gln
    215                 220                 225

gcc gag gac aag gca aac gcc ctc cag gca gac gca gag cgc aag cac   835
Ala Glu Asp Lys Ala Asn Ala Leu Gln Ala Asp Ala Glu Arg Lys His
230                 235                 240                 245

acc gaa acc atg gct gca gtc aag gaa cag cag aat gct ctg gag acc   883
Thr Glu Thr Met Ala Ala Val Lys Glu Gln Gln Asn Ala Leu Glu Thr
                250                 255                 260

cgc atc gcg gaa ctg cag acc ttc gag cgt gag tac cgc acc cgt ctg   931
Arg Ile Ala Glu Leu Gln Thr Phe Glu Arg Glu Tyr Arg Thr Arg Leu
            265                 270                 275

aag tcc ctc ctc gag ggc cag ctg gaa gaa ctc cac gca cgt ggc tcc   979
Lys Ser Leu Leu Glu Gly Gln Leu Glu Glu Leu His Ala Arg Gly Ser
        280                 285                 290

tct gca cca acc aac aac aag cca tct ggt gag taaaaagaaa gattagttat 1032
Ser Ala Pro Thr Asn Asn Lys Pro Ser Gly Glu
    295                 300

ctt                                                               1035


<210> 2876
<211> 304
<212> PRT
<213> Corynebacterium glutamicum
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<400> 2876

```
Val Val Leu Leu Pro Leu Leu Val Pro Gln Leu Gln Val Gln Pro Gln
  1               5                  10                  15

Leu Gln Leu Pro Ser Leu Leu Thr Arg Gln Arg Cys Ala Arg Lys Ser
            20                  25                  30

Lys Arg Ser Cys Ala Pro Asn Thr Ala Ser Lys Leu Asp Asp Ala Ser
        35                  40                  45

Lys Ala Ala Gln Lys Ala Gln Asn Asp Ala Lys Ser Ala Gln Asp Gln
    50                  55                  60

Leu Gln Arg Ala Gln Ala Asp Ala Lys Ala Ala Arg Asp Glu Ala Glu
65                  70                  75                  80

Lys Ala Lys Ala Glu Ala Lys Ser Ala Ala Ser Ser Ser Thr Thr Lys
                85                  90                  95

Ala Ala Ala Val Gly Ala Val Gly Ala Gly Thr Gly Ala Ala Val Ala
            100                 105                 110

Thr Gly Ala Ala Asn Val Asp Thr His Met Gln Ala Ala Lys Val Leu
        115                 120                 125

Gly Leu Ala Gln Glu Met Ala Asp Arg Leu Thr Ser Glu Ala Arg Ser
    130                 135                 140

Glu Ser Lys Ser Met Leu Asp Glu Ala Arg Glu Ala Ala Glu Lys Gln
145                 150                 155                 160

Ile Glu Glu Ala Asn Ser Thr Ser Asn Arg Thr Leu Glu Asp Ala Arg
                165                 170                 175

Ala Asn Ala Glu Lys Gln Ile Ala Glu Ala Gln Asn Arg Ala Asp Thr
            180                 185                 190

Leu Val Asn Glu Ala Asp Ala Lys Ala Lys Asn Leu Val Ser Glu Ala
        195                 200                 205

Glu Lys Lys Ser Ala Ala Thr Leu Ala Ala Ser Thr Ser Arg Ala Glu
    210                 215                 220

Ala Gln Ile Arg Gln Ala Glu Asp Lys Ala Asn Ala Leu Gln Ala Asp
225                 230                 235                 240

Ala Glu Arg Lys His Thr Glu Thr Met Ala Ala Val Lys Glu Gln Gln
                245                 250                 255

Asn Ala Leu Glu Thr Arg Ile Ala Glu Leu Gln Thr Phe Glu Arg Glu
            260                 265                 270

Tyr Arg Thr Arg Leu Lys Ser Leu Leu Glu Gly Gln Leu Glu Glu Leu
        275                 280                 285

His Ala Arg Gly Ser Ser Ala Pro Thr Asn Asn Lys Pro Ser Gly Glu
    290                 295                 300
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<210> 2877
<211> 828
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(805)
<223> RXA02735

<400> 2877
gaggagcttc gccacatgga tccagatttg ggctaccagc acgcactatc cggcttgtcc 60

agcgtcaagc tggaaaccgt ctaaggagaa atacaacact atg gtt gat gta gta 115
Met Val Asp Val Val
1 5

cgc gca cgc gat act gaa gat ttg gtt gca cag gct gcc tcc aaa ttc 163
Arg Ala Arg Asp Thr Glu Asp Leu Val Ala Gln Ala Ala Ser Lys Phe
10 15 20

att gag gtt gtt gaa gca gca act gcc aat aat ggc acc gca cag gta 211
Ile Glu Val Val Glu Ala Ala Thr Ala Asn Asn Gly Thr Ala Gln Val
25 30 35

gtg ctc acc ggt ggt ggc gcc ggc atc aag ttg ctg gaa aag ctc agc 259
Val Leu Thr Gly Gly Gly Ala Gly Ile Lys Leu Leu Glu Lys Leu Ser
40 45 50

gtt gat gcg gct gac ctt gcc tgg gat cgc att cat gtg ttc ttc ggc 307
Val Asp Ala Ala Asp Leu Ala Trp Asp Arg Ile His Val Phe Phe Gly
55 60 65

gat gag cgc aat gtc cct gtc agt gat tct gag tcc aat gag ggc cag 355
Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu Ser Asn Glu Gly Gln
70 75 80 85

gct cgt gag gca ctg ttg tcc aag gtt tct atc cct gaa gcc aac att 403
Ala Arg Glu Ala Leu Leu Ser Lys Val Ser Ile Pro Glu Ala Asn Ile
90 95 100

cac gga tat ggt ctc ggc gac gta gat ctt gca gag gca gcc cgc gct 451
His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala Glu Ala Ala Arg Ala
105 110 115

tac gaa gct gtg ttg gat gaa ttc gca cca aac ggc ttt gat ctt cac 499
Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn Gly Phe Asp Leu His
120 125 130

ctg ctc ggc atg ggt ggc gaa ggc cat atc aac tcc ctg ttc cct cac 547
Leu Leu Gly Met Gly Gly Glu Gly His Ile Asn Ser Leu Phe Pro His
135 140 145

acc gat gca gtc aag gaa tcc tcc gca aag gtc atc gcg gtg ttt gat 595
Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val Ile Ala Val Phe Asp
150 155 160 165

tcc cct aag cct cct tca gag cgt gca act cta acc ctt cct gcg gtt 643
Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu Thr Leu Pro Ala Val

```
                170                 175                 180

cac tcc gca aag cgc gtg tgg ttg ctg gtt tct ggt gcg gag aag gct   691
His Ser Ala Lys Arg Val Trp Leu Leu Val Ser Gly Ala Glu Lys Ala
            185                 190                 195

gag gca gct gcg gcg atc gtc aac ggt gag cct gct gtt gag tgg cct   739
Glu Ala Ala Ala Ala Ile Val Asn Gly Glu Pro Ala Val Glu Trp Pro
        200                 205                 210

gct gct gga gct acc gga tct gag gaa acg gta ttg ttc ttg gct gat   787
Ala Ala Gly Ala Thr Gly Ser Glu Glu Thr Val Leu Phe Leu Ala Asp
    215                 220                 225

gat gct gca gga aat ctc taagcagcgc cagctctaac aag                 828
Asp Ala Ala Gly Asn Leu
230                 235
```

US20050003474A1

<210> 2878
<211> 235
<212> PRT
<213> Corynebacterium glutamicum

<400> 2878

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Met Val Asp Val Val Arg Ala Arg Asp Thr Glu Asp Leu Val Ala Gln
  1               5                  10                  15

Ala Ala Ser Lys Phe Ile Glu Val Val Glu Ala Ala Thr Ala Asn Asn
             20                  25                  30

Gly Thr Ala Gln Val Val Leu Thr Gly Gly Gly Ala Gly Ile Lys Leu
         35                  40                  45

Leu Glu Lys Leu Ser Val Asp Ala Ala Asp Leu Ala Trp Asp Arg Ile
     50                  55                  60

His Val Phe Phe Gly Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu
 65                  70                  75                  80

Ser Asn Glu Gly Gln Ala Arg Glu Ala Leu Leu Ser Lys Val Ser Ile
                 85                  90                  95

Pro Glu Ala Asn Ile His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala
            100                 105                 110

Glu Ala Ala Arg Ala Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn
        115                 120                 125

Gly Phe Asp Leu His Leu Leu Gly Met Gly Gly Glu Gly His Ile Asn
    130                 135                 140

Ser Leu Phe Pro His Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val
145                 150                 155                 160

Ile Ala Val Phe Asp Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu
                165                 170                 175

Thr Leu Pro Ala Val His Ser Ala Lys Arg Val Trp Leu Leu Val Ser
            180                 185                 190
```

```
Gly Ala Glu Lys Ala Glu Ala Ala Ala Ile Val Asn Gly Glu Pro
        195                 200                 205

Ala Val Glu Trp Pro Ala Ala Gly Ala Thr Gly Ser Glu Glu Thr Val
    210                 215                 220

Leu Phe Leu Ala Asp Asp Ala Ala Gly Asn Leu
225             230                 235


<210> 2879
<211> 1080
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1057)
<223> RXA02736

<400> 2879
cagaggatta cccagcgggt acgtggggtc caaagagcgc tgatgaaatg ctttcccgca 60

acggtcacac ctggcgcagg ccataattta ggggcaaaaa atg atc ttt gaa ctt   115
                                          Met Ile Phe Glu Leu
                                            1               5

ccg gat acc acc acc cag caa att tcc aag acc cta act cga ctg cgt   163
Pro Asp Thr Thr Thr Gln Gln Ile Ser Lys Thr Leu Thr Arg Leu Arg
                  10                  15                  20

gaa tcg ggc acc cag gtc acc acc ggc cga gtg ctc acc ctc atc gtg   211
Glu Ser Gly Thr Gln Val Thr Thr Gly Arg Val Leu Thr Leu Ile Val
              25                  30                  35

gtc act gac tcc gaa agc gat gtc gct gca gtt acc gag tcc acc aat   259
Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val Thr Glu Ser Thr Asn
          40                  45                  50

gaa gcc tcg cgc gag cac cca tct cgc gtg atc att ttg gtg gtt ggc   307
Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile Ile Leu Val Val Gly
      55                  60                  65

gat aaa act gca gaa aac aaa gtt gac gca gaa gtc cgt atc ggt ggc   355
Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu Val Arg Ile Gly Gly
  70                  75                  80                  85

gac gct ggt gct tcc gag atg atc atc atg cat ctc aac gga cct gtc   403
Asp Ala Gly Ala Ser Glu Met Ile Ile Met His Leu Asn Gly Pro Val
                  90                  95                 100

gct gac aag ctc cag tat gtc gtc aca cca ctg ttg ctt cct gac acc   451
Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu Leu Leu Pro Asp Thr
              105                 110                 115

ccc atc gtt gct tgg tgg cca ggt gaa tca cca aag aat cct tcc cag   499
Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro Lys Asn Pro Ser Gln
          120                 125                 130

gac cca att gga cgc atc gca caa cga cgc atc act gat gct ttg tac   547
Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile Thr Asp Ala Leu Tyr
```

```
    135                 140                 145

gac cgt gat gac gca cta gaa gat cgt gtt gag aac tat cac cca ggt   595
Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu Asn Tyr His Pro Gly
150                 155                 160                 165

gat acc gac atg acg tgg gcg cgc ctt acc cag tgg cgg gga ctt gtt   643
Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln Trp Arg Gly Leu Val
                170                 175                 180

gcc tcc tca ttg gat cac cca cca cac agc gaa atc act tcc gtg agg   691
Ala Ser Ser Leu Asp His Pro Pro His Ser Glu Ile Thr Ser Val Arg
            185                 190                 195

ctg acc ggt gca agc ggc agt acc tcg gtg gat ttg gct gca ggc tgg   739
Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp Leu Ala Ala Gly Trp
        200                 205                 210

ttg gcg cgg agg ctg aaa gtg cct gtg atc cgc gag gtg aca gat gct   787
Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg Glu Val Thr Asp Ala
    215                 220                 225

ccc acc gtg cca acc gat gag ttt ggt act cca ctg ctg gct atc cag   835
Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro Leu Leu Ala Ile Gln
230                 235                 240                 245

cgc ctg gag atc gtt cgc acc acc ggc tcg atc atc atc acc atc tat   883
Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile Ile Ile Thr Ile Tyr
                250                 255                 260

gac gct cat acc ctt cag gta gag atg ccg gaa tcc ggc aat gcc cca   931
Asp Ala His Thr Leu Gln Val Glu Met Pro Glu Ser Gly Asn Ala Pro
            265                 270                 275

tcg ctg gtg gct att ggt cgt cga agt gag tcc gac tgc ttg tct gag   979
Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser Asp Cys Leu Ser Glu
        280                 285                 290

gag ctt cgc cac atg gat cca gat ttg ggc tac cag cac gca cta tcc   1027
Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr Gln His Ala Leu Ser
    295                 300                 305

ggc ttg tcc agc gtc aag ctg gaa acc gtc taaggagaaa tacaacacta     1077
Gly Leu Ser Ser Val Lys Leu Glu Thr Val
310                 315

tgg                                                               1080


<210> 2880
<211> 319
<212> PRT
<213> Corynebacterium glutamicum

<400> 2880
Met Ile Phe Glu Leu Pro Asp Thr Thr Thr Gln Gln Ile Ser Lys Thr
  1               5                  10                  15

Leu Thr Arg Leu Arg Glu Ser Gly Thr Gln Val Thr Thr Gly Arg Val
             20                  25                  30
```

```
Leu Thr Leu Ile Val Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val
          35                  40                  45

Thr Glu Ser Thr Asn Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile
      50                  55                  60

Ile Leu Val Val Gly Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu
 65                  70                  75                  80

Val Arg Ile Gly Gly Asp Ala Gly Ala Ser Glu Met Ile Ile Met His
                 85                  90                  95

Leu Asn Gly Pro Val Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu
            100                 105                 110

Leu Leu Pro Asp Thr Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro
        115                 120                 125

Lys Asn Pro Ser Gln Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile
    130                 135                 140

Thr Asp Ala Leu Tyr Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu
145                 150                 155                 160

Asn Tyr His Pro Gly Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln
                165                 170                 175

Trp Arg Gly Leu Val Ala Ser Ser Leu Asp His Pro Pro His Ser Glu
            180                 185                 190

Ile Thr Ser Val Arg Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp
        195                 200                 205

Leu Ala Ala Gly Trp Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg
    210                 215                 220

Glu Val Thr Asp Ala Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro
225                 230                 235                 240

Leu Leu Ala Ile Gln Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile
                245                 250                 255

Ile Ile Thr Ile Tyr Asp Ala His Thr Leu Gln Val Glu Met Pro Glu
            260                 265                 270

Ser Gly Asn Ala Pro Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser
        275                 280                 285

Asp Cys Leu Ser Glu Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr
    290                 295                 300

Gln His Ala Leu Ser Gly Leu Ser Ser Val Lys Leu Glu Thr Val
305                 310                 315
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<210> 2881
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(574)
<223> RXA02751

<400> 2881
ggtgtcttct tgtcaaataa ccactgttta tagggcaatt ctttggcaat gtacccaact 60

cattacccac ctgctgattc aaagagtaga tttaaatagt gtg ctt ccg att gcc 115
Val Leu Pro Ile Ala
1 5

tcc ggt aac gat gac cgg aat tta atc cgt tat gtc gac ggt ggt cga 163
Ser Gly Asn Asp Asp Arg Asn Leu Ile Arg Tyr Val Asp Gly Gly Arg
10 15 20

ttt gat gaa atc atg ctc acc gga gac ctc act ggc ctg agc agt ttt 211
Phe Asp Glu Ile Met Leu Thr Gly Asp Leu Thr Gly Leu Ser Ser Phe
25 30 35

ctt acc aac gct ggc ccg aac gcc cgg gat gat ttt gat ctc acg gtg 259
Leu Thr Asn Ala Gly Pro Asn Ala Arg Asp Asp Phe Asp Leu Thr Val
40 45 50

ctc atg cgc gct gcc gag gca ggc aac ctc atg gtt gtt gcc cgc ttg 307
Leu Met Arg Ala Ala Glu Ala Gly Asn Leu Met Val Val Ala Arg Leu
55 60 65

tta gat tta ggt gcc aat ccc cga ctc acc aat cct cgt ggt gtc acg 355
Leu Asp Leu Gly Ala Asn Pro Arg Leu Thr Asn Pro Arg Gly Val Thr
70 75 80 85

gcc cta cat atc gca gcg atc gcc ggg gac gat ggc att gtg gaa tgc 403
Ala Leu His Ile Ala Ala Ile Ala Gly Asp Asp Gly Ile Val Glu Cys
90 95 100

ctc att gat gca ggc gct gaa gtc gat gct gta gat gat caa ggt cgc 451
Leu Ile Asp Ala Gly Ala Glu Val Asp Ala Val Asp Asp Gln Gly Arg
105 110 115

act ccc cta tgg aac gca gcg gct cat cat ctg cct gat tct gcg gtg 499
Thr Pro Leu Trp Asn Ala Ala Ala His His Leu Pro Asp Ser Ala Val
120 125 130

gtg gat gtg ctg ctt cgc gca ggt gcg aat gtg aat ctg cgc gat tgc 547
Val Asp Val Leu Leu Arg Ala Gly Ala Asn Val Asn Leu Arg Asp Cys
135 140 145

aat gga gtc agc cca gaa gac atg ctg tagaagcatt ctttagcagg 594
Asn Gly Val Ser Pro Glu Asp Met Leu
150 155

att 597

<210> 2882
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 2882
Val Leu Pro Ile Ala Ser Gly Asn Asp Asp Arg Asn Leu Ile Arg Tyr

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  1               5                  10                  15

Val Asp Gly Gly Arg Phe Asp Glu Ile Met Leu Thr Gly Asp Leu Thr
            20                  25                  30

Gly Leu Ser Ser Phe Leu Thr Asn Ala Gly Pro Asn Ala Arg Asp Asp
        35                  40                  45

Phe Asp Leu Thr Val Leu Met Arg Ala Ala Glu Ala Gly Asn Leu Met
    50                  55                  60

Val Val Ala Arg Leu Leu Asp Leu Gly Ala Asn Pro Arg Leu Thr Asn
65                  70                  75                  80

Pro Arg Gly Val Thr Ala Leu His Ile Ala Ala Ile Ala Gly Asp Asp
                85                  90                  95

Gly Ile Val Glu Cys Leu Ile Asp Ala Gly Ala Glu Val Asp Ala Val
            100                 105                 110

Asp Asp Gln Gly Arg Thr Pro Leu Trp Asn Ala Ala Ala His His Leu
        115                 120                 125

Pro Asp Ser Ala Val Val Asp Val Leu Leu Arg Ala Gly Ala Asn Val
    130                 135                 140

Asn Leu Arg Asp Cys Asn Gly Val Ser Pro Glu Asp Met Leu
145                 150                 155


<210> 2883
<211> 1014
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(991)
<223> RXA02756

<400> 2883
cgtgacggtt gttgcaattc cataactaaa cgagctttga ttaacaagtc cttgtattgt 60

gtaaatcgct tattgcacac aattgaaaaa ggacattgtt atg aca agc cct tat   115
                                               Met Thr Ser Pro Tyr
                                                 1               5

gga tcc caa tac cca ggc gac gac aac aat aat tgg aac tcc cag ttc   163
Gly Ser Gln Tyr Pro Gly Asp Asp Asn Asn Asn Trp Asn Ser Gln Phe
                10                  15                  20

ggc aac cct tcc ggc gag cag aac tac ggt cag ccc tac ggt gcg cca   211
Gly Asn Pro Ser Gly Glu Gln Asn Tyr Gly Gln Pro Tyr Gly Ala Pro
            25                  30                  35

tat gga cag cct tac ggg cag cca ttt gat caa gga ttc aac gcc tac   259
Tyr Gly Gln Pro Tyr Gly Gln Pro Phe Asp Gln Gly Phe Asn Ala Tyr
        40                  45                  50

agt tct ccc atc cca cct gag gtc cca cag cct tcc atg cag gag gct   307
Ser Ser Pro Ile Pro Pro Glu Val Pro Gln Pro Ser Met Gln Glu Ala
```

```
     55                  60                  65

cag tgg cgc tcc ttt gac ctt gga act gtt ttt ggt cag gca tgg aag   355
Gln Trp Arg Ser Phe Asp Leu Gly Thr Val Phe Gly Gln Ala Trp Lys
 70                  75                  80                  85

ggc ttt acc gca acg tgg cag gca tgg gtg ctg tct gca ctg atc tac   403
Gly Phe Thr Ala Thr Trp Gln Ala Trp Val Leu Ser Ala Leu Ile Tyr
                 90                  95                 100

ttc gcg gtg ttg ctt gtg ctg atg ttt gcg tgg atc ctc ccg atg gtt   451
Phe Ala Val Leu Leu Val Leu Met Phe Ala Trp Ile Leu Pro Met Val
            105                 110                 115

agt gtg ctc gca gcg acc tca tct ggt tct gat tcc gca gct att gca   499
Ser Val Leu Ala Ala Thr Ser Ser Gly Ser Asp Ser Ala Ala Ile Ala
        120                 125                 130

gcg acg ggt ggc acc agc ttc ttc ggg ttc atg ctg atg atc gtc ctg   547
Ala Thr Gly Gly Thr Ser Phe Phe Gly Phe Met Leu Met Ile Val Leu
    135                 140                 145

gca ttc atc agt ttt gtg tac tcc ctt aac tgc tac cgc aac gcg gct   595
Ala Phe Ile Ser Phe Val Tyr Ser Leu Asn Cys Tyr Arg Asn Ala Ala
150                 155                 160                 165

cga gtt gtg cgc ggt gag cag atc acc att cag agt ttc ttc aag atg   643
Arg Val Val Arg Gly Glu Gln Ile Thr Ile Gln Ser Phe Phe Lys Met
                170                 175                 180

aag ggt ctt ggt aag gcg ctc ggt att tac atc ttg atc aat atc gtc   691
Lys Gly Leu Gly Lys Ala Leu Gly Ile Tyr Ile Leu Ile Asn Ile Val
            185                 190                 195

atc ttc atc gga atg atc ttg ctg ctc att cct gga att atc gct gcc   739
Ile Phe Ile Gly Met Ile Leu Leu Leu Ile Pro Gly Ile Ile Ala Ala
        200                 205                 210

gtg gtg ctg atc ttt gct gtt cct gtg gca ttc cag ctg cgc gac gcc   787
Val Val Leu Ile Phe Ala Val Pro Val Ala Phe Gln Leu Arg Asp Ala
    215                 220                 225

tcg atc ggt gat gcg ttt tcc gca agc tgg aag gca gtg tcc aaa aac   835
Ser Ile Gly Asp Ala Phe Ser Ala Ser Trp Lys Ala Val Ser Lys Asn
230                 235                 240                 245

gtt ggt cag gtc att ctc tta gaa ctg gct atc ttc gcg ttg agc ttc   883
Val Gly Gln Val Ile Leu Leu Glu Leu Ala Ile Phe Ala Leu Ser Phe
                250                 255                 260

ttg ggc agc gca gtg atc atc ggt atg ttg gtg acc act ccg ctt aca   931
Leu Gly Ser Ala Val Ile Ile Gly Met Leu Val Thr Thr Pro Leu Thr
            265                 270                 275

ttc ctg ctg tat gcc tac gca ttc cag acc gcc agc ggt ggt ccc atc   979
Phe Leu Leu Tyr Ala Tyr Ala Phe Gln Thr Ala Ser Gly Gly Pro Ile
        280                 285                 290

atg cag cgt cag tagcagttag ttttacttag tca                        1014
Met Gln Arg Gln
    295
```

<210> 2884
<211> 297
<212> PRT
<213> Corynebacterium glutamicum

<400> 2884

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Met Thr Ser Pro Tyr Gly Ser Gln Tyr Pro Gly Asp Asp Asn Asn Asn
  1               5                  10                  15

Trp Asn Ser Gln Phe Gly Asn Pro Ser Gly Glu Gln Asn Tyr Gly Gln
             20                  25                  30

Pro Tyr Gly Ala Pro Tyr Gly Gln Pro Tyr Gly Gln Pro Phe Asp Gln
         35                  40                  45

Gly Phe Asn Ala Tyr Ser Ser Pro Ile Pro Pro Glu Val Pro Gln Pro
     50                  55                  60

Ser Met Gln Glu Ala Gln Trp Arg Ser Phe Asp Leu Gly Thr Val Phe
 65                  70                  75                  80

Gly Gln Ala Trp Lys Gly Phe Thr Ala Thr Trp Gln Ala Trp Val Leu
                 85                  90                  95

Ser Ala Leu Ile Tyr Phe Ala Val Leu Leu Val Leu Met Phe Ala Trp
            100                 105                 110

Ile Leu Pro Met Val Ser Val Leu Ala Ala Thr Ser Ser Gly Ser Asp
        115                 120                 125

Ser Ala Ala Ile Ala Ala Thr Gly Gly Thr Ser Phe Phe Gly Phe Met
    130                 135                 140

Leu Met Ile Val Leu Ala Phe Ile Ser Phe Val Tyr Ser Leu Asn Cys
145                 150                 155                 160

Tyr Arg Asn Ala Ala Arg Val Val Arg Gly Glu Gln Ile Thr Ile Gln
                165                 170                 175

Ser Phe Phe Lys Met Lys Gly Leu Gly Lys Ala Leu Gly Ile Tyr Ile
            180                 185                 190

Leu Ile Asn Ile Val Ile Phe Ile Gly Met Ile Leu Leu Leu Ile Pro
        195                 200                 205

Gly Ile Ile Ala Ala Val Val Leu Ile Phe Ala Val Pro Val Ala Phe
    210                 215                 220

Gln Leu Arg Asp Ala Ser Ile Gly Asp Ala Phe Ser Ala Ser Trp Lys
225                 230                 235                 240

Ala Val Ser Lys Asn Val Gly Gln Val Ile Leu Leu Glu Leu Ala Ile
                245                 250                 255

Phe Ala Leu Ser Phe Leu Gly Ser Ala Val Ile Ile Gly Met Leu Val
            260                 265                 270

Thr Thr Pro Leu Thr Phe Leu Leu Tyr Ala Tyr Ala Phe Gln Thr Ala
        275                 280                 285
```

```
Ser Gly Gly Pro Ile Met Gln Arg Gln
    290                 295


<210> 2885
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(646)
<223> RXA02757

<400> 2885
ttcggatcct tcgaccgttc aggcaatgca gatcgcgttg cacattccga aacagaatcc 60

gccccggcgg acagatgtgt tggaagcggc ggcgaggagt gtg gtc aag ctt tgc   115
                                            Val Val Lys Leu Cys
                                              1               5

ctc gac gaa cga gta tcc acc gat cct gat ttt cgg gcg gcc ttg gaa   163
Leu Asp Glu Arg Val Ser Thr Asp Pro Asp Phe Arg Ala Ala Leu Glu
                 10                  15                  20

cgt tgg tac gga cac ttg att cgg aag gtg tca cgt cgc gct cgt aat   211
Arg Trp Tyr Gly His Leu Ile Arg Lys Val Ser Arg Arg Ala Arg Asn
             25                  30                  35

gcg gcg tgg gat cgg gtg caa gat tta ccc ggc gtg act gtg gaa gat   259
Ala Ala Trp Asp Arg Val Gln Asp Leu Pro Gly Val Thr Val Glu Asp
         40                  45                  50

gat gct gca aag gtt cgg gca ttt ttg ccc agc gca gtg gtg gat gtg   307
Asp Ala Ala Lys Val Arg Ala Phe Leu Pro Ser Ala Val Val Asp Val
     55                  60                  65

cct gca gat atc aaa aag ctg cag att tcc ggt acg gaa ttg cct ctc   355
Pro Ala Asp Ile Lys Lys Leu Gln Ile Ser Gly Thr Glu Leu Pro Leu
 70                  75                  80                  85

gat gag ccg aat ccg atc aac gat gaa tac ccc gtt atc tac att gat   403
Asp Glu Pro Asn Pro Ile Asn Asp Glu Tyr Pro Val Ile Tyr Ile Asp
                 90                  95                 100

gaa tcg ttg aag atg acg ctg gga aag gcc gct gcg cag gta gga cac   451
Glu Ser Leu Lys Met Thr Leu Gly Lys Ala Ala Ala Gln Val Gly His
            105                 110                 115

gca tcc atg ttg ctt gcc gcg cac caa ccg ttt gag tgg gtg gag cag   499
Ala Ser Met Leu Leu Ala Ala His Gln Pro Phe Glu Trp Val Glu Gln
        120                 125                 130

tgg gaa gca gcg gat ttt gcg ctg cac gtc agg gag att ccc tcg gag   547
Trp Glu Ala Ala Asp Phe Ala Leu His Val Arg Glu Ile Pro Ser Glu
    135                 140                 145

gag ttc ctg cgc ctt atc gag tct cct ggt gct gtt cca gtt cgc gat   595
Glu Phe Leu Arg Leu Ile Glu Ser Pro Gly Ala Val Pro Val Arg Asp
150                 155                 160                 165
```

```
ggc ggc ttt act gag gtt gcc ccc aac acc gtg acg gtt gtt gca att   643
Gly Gly Phe Thr Glu Val Ala Pro Asn Thr Val Thr Val Val Ala Ile
                170                 175                 180

cca taactaaacg agctttgatt aac                                   669
Pro
```

<210> 2886
<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 2886

```
Val Val Lys Leu Cys Leu Asp Glu Arg Val Ser Thr Asp Pro Asp Phe
  1               5                  10                  15

Arg Ala Ala Leu Glu Arg Trp Tyr Gly His Leu Ile Arg Lys Val Ser
             20                  25                  30

Arg Arg Ala Arg Asn Ala Ala Trp Asp Arg Val Gln Asp Leu Pro Gly
         35                  40                  45

Val Thr Val Glu Asp Asp Ala Ala Lys Val Arg Ala Phe Leu Pro Ser
     50                  55                  60

Ala Val Val Asp Val Pro Ala Asp Ile Lys Lys Leu Gln Ile Ser Gly
 65                  70                  75                  80

Thr Glu Leu Pro Leu Asp Glu Pro Asn Pro Ile Asn Asp Glu Tyr Pro
                 85                  90                  95

Val Ile Tyr Ile Asp Glu Ser Leu Lys Met Thr Leu Gly Lys Ala Ala
            100                 105                 110

Ala Gln Val Gly His Ala Ser Met Leu Leu Ala Ala His Gln Pro Phe
        115                 120                 125

Glu Trp Val Glu Gln Trp Glu Ala Ala Asp Phe Ala Leu His Val Arg
    130                 135                 140

Glu Ile Pro Ser Glu Glu Phe Leu Arg Leu Ile Glu Ser Pro Gly Ala
145                 150                 155                 160

Val Pro Val Arg Asp Gly Gly Phe Thr Glu Val Ala Pro Asn Thr Val
                165                 170                 175

Thr Val Val Ala Ile Pro
            180
```

<210> 2887
<211> 882
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(859)

<223> RXA02765

<400> 2887

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tctgaacttt tccgcatcga cccagatgag gtttaccccg acgacgacgc cacctgcgaa 60

ttcaacccat ggccgtatcc tcgcggattt taggagataa atg tct aat caa tta   115
                                            Met Ser Asn Gln Leu
                                              1               5

ccc gat cac gtc cgc gac gcc ttc caa gta ggt gcg gga cct gcc gaa   163
Pro Asp His Val Arg Asp Ala Phe Gln Val Gly Ala Gly Pro Ala Glu
                 10                  15                  20

caa ctc ggt caa gct tgg gac ttc gga ttc cgc gtc ggc aac act gtg   211
Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg Val Gly Asn Thr Val
             25                  30                  35

ttc gcc aaa gtg acg gcg ccg gaa gtg tcg ggc tgg tcg tcg aaa acc   259
Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly Trp Ser Ser Lys Thr
         40                  45                  50

cgc gaa acc ctg aaa cca gaa ggc gtg cgc gtc gta cga ccg atc cgc   307
Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val Val Arg Pro Ile Arg
     55                  60                  65

tcc acc gac ggc cga ttt gtg gtt gcg ggg tgg cgc gca tcg gtg ttc   355
Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp Arg Ala Ser Val Phe
 70                  75                  80                  85

tct acg gga acg atc agc aag cga gtc gat gag acg gtc gtt gcg ggt   403
Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu Thr Val Val Ala Gly
                 90                  95                 100

ctt cgt ttg gca gat gca tta gtg gat acg cat gca ccg gaa cct gtg   451
Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His Ala Pro Glu Pro Val
            105                 110                 115

gac aat gtg ttt aac cgt gct gat gtg cag gcc tgg gaa gag cag ccc   499
Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala Trp Glu Glu Gln Pro
        120                 125                 130

ggt cga atc ggt gaa ttg ttg gag ccg att aat cgc gtg aac cag gtt   547
Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn Arg Val Asn Gln Val
    135                 140                 145

ggt cat gcg gat atg ttg gcg aca acg ctg tat gcg gga act cag cca   595
Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr Ala Gly Thr Gln Pro
150                 155                 160                 165

cct gca gtg acg gat ttg gtg cca gtg ctg cgt ccg cat ggt ttc act   643
Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg Pro His Gly Phe Thr
                170                 175                 180

gcg gca ttg gtg atc gtt gat ggg ttg ctg ctg ggt gcg gtt gat gag   691
Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu Gly Ala Val Asp Glu
            185                 190                 195

gga att ctg cgg agg ttt tcg cat ttg ccg gaa att gag cag ctg gtt   739
Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu Ile Glu Gln Leu Val
        200                 205                 210
```

```
ttg agg gca ttt ttg ttc cgt cga aac ttg cag gag ttc tct gag aac   787
Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln Glu Phe Ser Glu Asn
    215                 220                 225

aac gat ccg aat gtt att tcg aac cta aac agg gtg gaa tcg aca ctc   835
Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg Val Glu Ser Thr Leu
230                 235                 240                 245

gtg tcg tat gtt tct gac aag att tgaggtatgt cggaatacaa acc         882
Val Ser Tyr Val Ser Asp Lys Ile
                250
```

<210> 2888
<211> 253
<212> PRT
<213> Corynebacterium glutamicum

<400> 2888

```
Met Ser Asn Gln Leu Pro Asp His Val Arg Asp Ala Phe Gln Val Gly
  1               5                  10                  15

Ala Gly Pro Ala Glu Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg
             20                  25                  30

Val Gly Asn Thr Val Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly
         35                  40                  45

Trp Ser Ser Lys Thr Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val
     50                  55                  60

Val Arg Pro Ile Arg Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp
 65                  70                  75                  80

Arg Ala Ser Val Phe Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu
                 85                  90                  95

Thr Val Val Ala Gly Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His
            100                 105                 110

Ala Pro Glu Pro Val Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala
        115                 120                 125

Trp Glu Glu Gln Pro Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn
    130                 135                 140

Arg Val Asn Gln Val Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr
145                 150                 155                 160

Ala Gly Thr Gln Pro Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg
                165                 170                 175

Pro His Gly Phe Thr Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu
            180                 185                 190

Gly Ala Val Asp Glu Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu
        195                 200                 205

Ile Glu Gln Leu Val Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln
    210                 215                 220
```

```
Glu Phe Ser Glu Asn Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg
225                 230                 235                 240

Val Glu Ser Thr Leu Val Ser Tyr Val Ser Asp Lys Ile
                245                 250


<210> 2889
<211> 516
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(493)
<223> RXA02766

<400> 2889
atttctcgcc gcgccgcacg gtgacgccgg ccatgttgag tgctagttcg cgcatgggta 60

acaccttact ggcgtaaggc cagggcttag actggtaccc atg aca acc tca gaa   115
                                           Met Thr Thr Ser Glu
                                             1               5

aat ttt tat gat tct gtg ggc ggc gag gaa acg ttt tcc ctc atc gtc   163
Asn Phe Tyr Asp Ser Val Gly Gly Glu Glu Thr Phe Ser Leu Ile Val
                  10                  15                  20

cac cgt ttt tat gaa cag gtc ccc aac gac gat att tta ggc ccg atg   211
His Arg Phe Tyr Glu Gln Val Pro Asn Asp Asp Ile Leu Gly Pro Met
              25                  30                  35

tat ccg ccg gat gat ttt gag ggc gcc gag cag cgt cta aag atg ttc   259
Tyr Pro Pro Asp Asp Phe Glu Gly Ala Glu Gln Arg Leu Lys Met Phe
          40                  45                  50

ctc agc cag tac tgg ggc ggc ccg aag gat tat cag gag cag cgt gga   307
Leu Ser Gln Tyr Trp Gly Gly Pro Lys Asp Tyr Gln Glu Gln Arg Gly
      55                  60                  65

cac cct cgt ctg cgc atg cgt cac gtc aat tac ccc atc ggc gtc acc   355
His Pro Arg Leu Arg Met Arg His Val Asn Tyr Pro Ile Gly Val Thr
  70                  75                  80                  85

gca gcg gag cgt tgg ctg cag ctc atg tcc aat gca ctc gac ggc gtg   403
Ala Ala Glu Arg Trp Leu Gln Leu Met Ser Asn Ala Leu Asp Gly Val
                  90                  95                 100

gat ttg acc gcg gag cag cgt gaa gcg att tgg gag cat atg gtg cgc   451
Asp Leu Thr Ala Glu Gln Arg Glu Ala Ile Trp Glu His Met Val Arg
             105                 110                 115

gcg gcc gat atg ctg atc aat tcc aac ccc gat ccg cac gct           493
Ala Ala Asp Met Leu Ile Asn Ser Asn Pro Asp Pro His Ala
         120                 125                 130

taacttctgc caaaaagtcg ttt                                        516


<210> 2890
<211> 131
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<212> PRT
<213> Corynebacterium glutamicum

<400> 2890

```
Met Thr Thr Ser Glu Asn Phe Tyr Asp Ser Val Gly Gly Glu Glu Thr
  1               5                  10                  15

Phe Ser Leu Ile Val His Arg Phe Tyr Glu Gln Val Pro Asn Asp Asp
             20                  25                  30

Ile Leu Gly Pro Met Tyr Pro Pro Asp Asp Phe Glu Gly Ala Glu Gln
         35                  40                  45

Arg Leu Lys Met Phe Leu Ser Gln Tyr Trp Gly Gly Pro Lys Asp Tyr
     50                  55                  60

Gln Glu Gln Arg Gly His Pro Arg Leu Arg Met Arg His Val Asn Tyr
 65                  70                  75                  80

Pro Ile Gly Val Thr Ala Ala Glu Arg Trp Leu Gln Leu Met Ser Asn
                 85                  90                  95

Ala Leu Asp Gly Val Asp Leu Thr Ala Glu Gln Arg Glu Ala Ile Trp
            100                 105                 110

Glu His Met Val Arg Ala Ala Asp Met Leu Ile Asn Ser Asn Pro Asp
        115                 120                 125

Pro His Ala
    130
```

<210> 2891
<211> 494
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(471)
<223> RXA02774

<400> 2891

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ccc tgc cca cca aca cag aag ctg ctc tat gca cag atg cgt gaa att   48
Pro Cys Pro Pro Thr Gln Lys Leu Leu Tyr Ala Gln Met Arg Glu Ile
  1               5                  10                  15

gca gcc gaa ctt aca gcc tgt gac gct act cgc gga ctc cat gcc gaa   96
Ala Ala Glu Leu Thr Ala Cys Asp Ala Thr Arg Gly Leu His Ala Glu
             20                  25                  30

gtg gct gcc gaa tgg ctt agt gac gcc ata acc ggc gaa ccc acc tct   144
Val Ala Ala Glu Trp Leu Ser Asp Ala Ile Thr Gly Glu Pro Thr Ser
         35                  40                  45

atc gag att gac ccc cac cgc aac ctg ttc tac gca ctt aat gtt gag   192
Ile Glu Ile Asp Pro His Arg Asn Leu Phe Tyr Ala Leu Asn Val Glu
     50                  55                  60

cac ccg cga ctc cat gaa ctc ttt gcc ggt tac gct aca cgc ctt gat   240
His Pro Arg Leu His Glu Leu Phe Ala Gly Tyr Ala Thr Arg Leu Asp
```

```
 65                  70                  75                  80

gaa ctc gac cgc gca ccg cag cag tgt gag tcg cgt caa tat ttt ctt   288
Glu Leu Asp Arg Ala Pro Gln Gln Cys Glu Ser Arg Gln Tyr Phe Leu
                 85                  90                  95

gat tat gtc tgt gct gac aac cct ttt ggc tca gac aaa cca gag ggc   336
Asp Tyr Val Cys Ala Asp Asn Pro Phe Gly Ser Asp Lys Pro Glu Gly
            100                 105                 110

att atc gtg ctg ctc gct gat cac gtg ctg gca gca gat cca gtg aca   384
Ile Ile Val Leu Leu Ala Asp His Val Leu Ala Ala Asp Pro Val Thr
        115                 120                 125

aac aag ccg gca ctc aaa tca gag gca ttc cct act gtc aca gac tat   432
Asn Lys Pro Ala Leu Lys Ser Glu Ala Phe Pro Thr Val Thr Asp Tyr
    130                 135                 140

tgc cgc act cac tct gct aaa cca aca gac att ctc att taaggatttt    481
Cys Arg Thr His Ser Ala Lys Pro Thr Asp Ile Leu Ile
145                 150                 155

agtcaccatg acg                                                   494
```

<210> 2892
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 2892

```
Pro Cys Pro Pro Thr Gln Lys Leu Leu Tyr Ala Gln Met Arg Glu Ile
  1               5                  10                  15

Ala Ala Glu Leu Thr Ala Cys Asp Ala Thr Arg Gly Leu His Ala Glu
             20                  25                  30

Val Ala Ala Glu Trp Leu Ser Asp Ala Ile Thr Gly Glu Pro Thr Ser
         35                  40                  45

Ile Glu Ile Asp Pro His Arg Asn Leu Phe Tyr Ala Leu Asn Val Glu
     50                  55                  60

His Pro Arg Leu His Glu Leu Phe Ala Gly Tyr Ala Thr Arg Leu Asp
 65                  70                  75                  80

Glu Leu Asp Arg Ala Pro Gln Gln Cys Glu Ser Arg Gln Tyr Phe Leu
                 85                  90                  95

Asp Tyr Val Cys Ala Asp Asn Pro Phe Gly Ser Asp Lys Pro Glu Gly
            100                 105                 110

Ile Ile Val Leu Leu Ala Asp His Val Leu Ala Ala Asp Pro Val Thr
        115                 120                 125

Asn Lys Pro Ala Leu Lys Ser Glu Ala Phe Pro Thr Val Thr Asp Tyr
    130                 135                 140

Cys Arg Thr His Ser Ala Lys Pro Thr Asp Ile Leu Ile
145                 150                 155
```

<210> 2893
<211> 348
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(325)
<223> RXA02775

<400> 2893
gcccccacca tctttggcac tgagattgtg ttcgattaac taccactgct gcacacacac 60

atacaacacc tctcacacac aaacaagaaa gggtcacccc atg acc acc gtt caa 115
Met Thr Thr Val Gln
1 5

gta tcc acc cgc act gtg cgc gaa cac cgt ttt act gtg cca gtg gac 163
Val Ser Thr Arg Thr Val Arg Glu His Arg Phe Thr Val Pro Val Asp
10 15 20

tac gct gtc ggc gcc acc att tca gaa atc tat gct gcc tgt gcc atg 211
Tyr Ala Val Gly Ala Thr Ile Ser Glu Ile Tyr Ala Ala Cys Ala Met
25 30 35

gcc gaa aag aaa gcc aac aac ctt ggg ctt aac act act aag gac gat 259
Ala Glu Lys Lys Ala Asn Asn Leu Gly Leu Asn Thr Thr Lys Asp Asp
40 45 50

tgg gca cga gtc act gtc act gat aat gct gtt gtg ttc att gtc gag 307
Trp Ala Arg Val Thr Val Thr Asp Asn Ala Val Val Phe Ile Val Glu
55 60 65

aat gtt atc ggg aat act tagaattgtg tgctccttaa cgg 348
Asn Val Ile Gly Asn Thr
70 75

<210> 2894
<211> 75
<212> PRT
<213> Corynebacterium glutamicum

<400> 2894
Met Thr Thr Val Gln Val Ser Thr Arg Thr Val Arg Glu His Arg Phe
1 5 10 15

Thr Val Pro Val Asp Tyr Ala Val Gly Ala Thr Ile Ser Glu Ile Tyr
20 25 30

Ala Ala Cys Ala Met Ala Glu Lys Lys Ala Asn Asn Leu Gly Leu Asn
35 40 45

Thr Thr Lys Asp Asp Trp Ala Arg Val Thr Val Thr Asp Asn Ala Val
50 55 60

Val Phe Ile Val Glu Asn Val Ile Gly Asn Thr
65 70 75

<210> 2895
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXA02776

<400> 2895
gcagcaccta gcaatgcagc cgaggcagcc ccttcaggtt ttgagccagg tacggctatt 60

caagttgtat aatccttcat tcgatgatca aacaccttcg gtg ctc tat cct gtt 115
Val Leu Tyr Pro Val
1 5

gaa gca gga acg gtg tct ctc gtt gat gta aag aaa gcg gct agc cgt 163
Glu Ala Gly Thr Val Ser Leu Val Asp Val Lys Lys Ala Ala Ser Arg
10 15 20

gcc ttt gaa cag tgg gaa aag cac aac gag tcc gct ggt gat gtc ggt 211
Ala Phe Glu Gln Trp Glu Lys His Asn Glu Ser Ala Gly Asp Val Gly
25 30 35

gat gat ctt tca ctg cag agt atc gta gat ctc att gag cgt gac act 259
Asp Asp Leu Ser Leu Gln Ser Ile Val Asp Leu Ile Glu Arg Asp Thr
40 45 50

ttc ccc acc gac gat gag caa gag ctc aat aat gtg gct ttg ctt atc 307
Phe Pro Thr Asp Asp Glu Gln Glu Leu Asn Asn Val Ala Leu Leu Ile
55 60 65

ggc gaa ctc ctg gtg agg gag gcc ggt gga gag tgg acg tcg tac atc 355
Gly Glu Leu Leu Val Arg Glu Ala Gly Gly Glu Trp Thr Ser Tyr Ile
70 75 80 85

tca aag aaa aat gat gaa gat gaa tcg ctg gag att ttc ggg gtt ttt 403
Ser Lys Lys Asn Asp Glu Asp Glu Ser Leu Glu Ile Phe Gly Val Phe
90 95 100

ggc acc ggt ggc act gaa gga tta tct gta gtg ggt aat tgagttcgca 452
Gly Thr Gly Gly Thr Glu Gly Leu Ser Val Val Gly Asn
105 110

tggttagtga aaa 465

<210> 2896
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 2896
Val Leu Tyr Pro Val Glu Ala Gly Thr Val Ser Leu Val Asp Val Lys
1 5 10 15

Lys Ala Ala Ser Arg Ala Phe Glu Gln Trp Glu Lys His Asn Glu Ser
20 25 30

Ala Gly Asp Val Gly Asp Asp Leu Ser Leu Gln Ser Ile Val Asp Leu

```
         35                  40                  45

Ile Glu Arg Asp Thr Phe Pro Thr Asp Asp Glu Gln Glu Leu Asn Asn
     50                  55                  60

Val Ala Leu Leu Ile Gly Glu Leu Leu Val Arg Glu Ala Gly Gly Glu
 65                  70                  75                  80

Trp Thr Ser Tyr Ile Ser Lys Lys Asn Asp Glu Asp Glu Ser Leu Glu
                 85                  90                  95

Ile Phe Gly Val Phe Gly Thr Gly Gly Thr Glu Gly Leu Ser Val Val
            100                 105                 110

Gly Asn
```

<210> 2897
<211> 1230
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1207)
<223> RXA02777

<400> 2897

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ggtcgcacca caccaactac tgtttcttct gtaatttgca ctgaaactat cgcctacact 60

gtcactgcta ccatcacaat cggttgctag taggctacaa atg aac cgc ccc ctt   115
                                          Met Asn Arg Pro Leu
                                            1               5

caa agt caa aat ttt tca ata acc agc gaa tgg gca aat gcc acg ttc   163
Gln Ser Gln Asn Phe Ser Ile Thr Ser Glu Trp Ala Asn Ala Thr Phe
                 10                  15                  20

aac gat atc gaa gac tct ttg gag ggg tct ttt gac atc gaa cca ggc   211
Asn Asp Ile Glu Asp Ser Leu Glu Gly Ser Phe Asp Ile Glu Pro Gly
            25                  30                  35

caa tac att gga cgc gga gaa tac ttc gta gct act tct gga acg ggt   259
Gln Tyr Ile Gly Arg Gly Glu Tyr Phe Val Ala Thr Ser Gly Thr Gly
        40                  45                  50

tcc aaa aag ttt atc aag gtg gtt ttg ggt gac ggt atc gat agc gaa   307
Ser Lys Lys Phe Ile Lys Val Val Leu Gly Asp Gly Ile Asp Ser Glu
    55                  60                  65

cta aat cgt cgc atc gaa ggt gaa att ctt gca agt agt ctc cat ctt   355
Leu Asn Arg Arg Ile Glu Gly Glu Ile Leu Ala Ser Ser Leu His Leu
70                  75                  80                  85

cca tcc aca gac cta atc tct cct gtc gta att cag tat gtg aaa gag   403
Pro Ser Thr Asp Leu Ile Ser Pro Val Val Ile Gln Tyr Val Lys Glu
                90                  95                 100

tct tct aat ttt ccc ggt gac ttc tac atc gtg tcc gac ttc aaa gac   451
Ser Ser Asn Phe Pro Gly Asp Phe Tyr Ile Val Ser Asp Phe Lys Asp
```

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            105                 110                 115

gac aca gaa act tta gag cta tct aag gct tct cta ccc ctc act gac   499
Asp Thr Glu Thr Leu Glu Leu Ser Lys Ala Ser Leu Pro Leu Thr Asp
        120                 125                 130

tta gcc aag atc gga gcg ttt ctc ttt cgt ttg gaa tct gta aca gtt   547
Leu Ala Lys Ile Gly Ala Phe Leu Phe Arg Leu Glu Ser Val Thr Val
    135                 140                 145

ccc cct caa aat cct gca agg cga gca atg gat gtt ttg gat gga ctt   595
Pro Pro Gln Asn Pro Ala Arg Arg Ala Met Asp Val Leu Asp Gly Leu
150                 155                 160                 165

tct ctt ctt gca aat aaa ggc aac att gaa aca ggc gca caa tta aca   643
Ser Leu Leu Ala Asn Lys Gly Asn Ile Glu Thr Gly Ala Gln Leu Thr
                170                 175                 180

aaa gga act ata caa gct ctt gaa atc att aat caa gaa gcg acc aac   691
Lys Gly Thr Ile Gln Ala Leu Glu Ile Ile Asn Gln Glu Ala Thr Asn
            185                 190                 195

atc gag aat gca ctt gaa aaa gta act aaa gta gga tca cgg aag ttt   739
Ile Glu Asn Ala Leu Glu Lys Val Thr Lys Val Gly Ser Arg Lys Phe
        200                 205                 210

ttc tcg cat gga gat ctt aaa ttt tct cag ttc tta att aat ggt gaa   787
Phe Ser His Gly Asp Leu Lys Phe Ser Gln Phe Leu Ile Asn Gly Glu
    215                 220                 225

acc gga aag att ttc cta tgt gac tgg gaa gaa tgc ggt agt gca cat   835
Thr Gly Lys Ile Phe Leu Cys Asp Trp Glu Glu Cys Gly Ser Ala His
230                 235                 240                 245

ttc gca aat gac cta tgt ttt ctc gca ggt gat ttg ttc tat agc aca   883
Phe Ala Asn Asp Leu Cys Phe Leu Ala Gly Asp Leu Phe Tyr Ser Thr
                250                 255                 260

att cgg gaa ctg gtg gat acc aac atc aaa aac att aaa ggc tcc tcg   931
Ile Arg Glu Leu Val Asp Thr Asn Ile Lys Asn Ile Lys Gly Ser Ser
            265                 270                 275

atc att cag gaa gcc tac gat aat gca acg ctt gag gct gta tca aaa   979
Ile Ile Gln Glu Ala Tyr Asp Asn Ala Thr Leu Glu Ala Val Ser Lys
        280                 285                 290

gta aat gca ata tta act ggc tat tcc tca gag agg ggt tac tct ctc   1027
Val Asn Ala Ile Leu Thr Gly Tyr Ser Ser Glu Arg Gly Tyr Ser Leu
    295                 300                 305

acc tcg gac gaa aaa cga atc att agt atc aga atc gga ttg gct ggt   1075
Thr Ser Asp Glu Lys Arg Ile Ile Ser Ile Arg Ile Gly Leu Ala Gly
310                 315                 320                 325

cta ttt cga ctt tac act gtg agc gct aaa tct aat gag tta cgc ccg   1123
Leu Phe Arg Leu Tyr Thr Val Ser Ala Lys Ser Asn Glu Leu Arg Pro
                330                 335                 340

cgc gaa tta gcc tta gcc tcc atc gga atg caa att act tta ggt caa   1171
Arg Glu Leu Ala Leu Ala Ser Ile Gly Met Gln Ile Thr Leu Gly Gln
            345                 350                 355
```

```
gca ccc aat ctg gtg ttt aca gat agc aag gtg gtt taagtgagga        1217
Ala Pro Asn Leu Val Phe Thr Asp Ser Lys Val Val
        360                 365

atttgcacga aac                                                   1230


<210> 2898
<211> 369
<212> PRT
<213> Corynebacterium glutamicum

<400> 2898
Met Asn Arg Pro Leu Gln Ser Gln Asn Phe Ser Ile Thr Ser Glu Trp
  1               5                  10                  15

Ala Asn Ala Thr Phe Asn Asp Ile Glu Asp Ser Leu Glu Gly Ser Phe
             20                  25                  30

Asp Ile Glu Pro Gly Gln Tyr Ile Gly Arg Gly Glu Tyr Phe Val Ala
         35                  40                  45

Thr Ser Gly Thr Gly Ser Lys Lys Phe Ile Lys Val Val Leu Gly Asp
     50                  55                  60

Gly Ile Asp Ser Glu Leu Asn Arg Arg Ile Glu Gly Glu Ile Leu Ala
 65                  70                  75                  80

Ser Ser Leu His Leu Pro Ser Thr Asp Leu Ile Ser Pro Val Val Ile
                 85                  90                  95

Gln Tyr Val Lys Glu Ser Ser Asn Phe Pro Gly Asp Phe Tyr Ile Val
            100                 105                 110

Ser Asp Phe Lys Asp Asp Thr Glu Thr Leu Glu Leu Ser Lys Ala Ser
        115                 120                 125

Leu Pro Leu Thr Asp Leu Ala Lys Ile Gly Ala Phe Leu Phe Arg Leu
    130                 135                 140

Glu Ser Val Thr Val Pro Pro Gln Asn Pro Ala Arg Arg Ala Met Asp
145                 150                 155                 160

Val Leu Asp Gly Leu Ser Leu Leu Ala Asn Lys Gly Asn Ile Glu Thr
                165                 170                 175

Gly Ala Gln Leu Thr Lys Gly Thr Ile Gln Ala Leu Glu Ile Ile Asn
            180                 185                 190

Gln Glu Ala Thr Asn Ile Glu Asn Ala Leu Glu Lys Val Thr Lys Val
        195                 200                 205

Gly Ser Arg Lys Phe Phe Ser His Gly Asp Leu Lys Phe Ser Gln Phe
    210                 215                 220

Leu Ile Asn Gly Glu Thr Gly Lys Ile Phe Leu Cys Asp Trp Glu Glu
225                 230                 235                 240

Cys Gly Ser Ala His Phe Ala Asn Asp Leu Cys Phe Leu Ala Gly Asp
                245                 250                 255
```

```
Leu Phe Tyr Ser Thr Ile Arg Glu Leu Val Asp Thr Asn Ile Lys Asn
            260                 265                 270

Ile Lys Gly Ser Ser Ile Ile Gln Glu Ala Tyr Asp Asn Ala Thr Leu
        275                 280                 285

Glu Ala Val Ser Lys Val Asn Ala Ile Leu Thr Gly Tyr Ser Ser Glu
    290                 295                 300

Arg Gly Tyr Ser Leu Thr Ser Asp Glu Lys Arg Ile Ile Ser Ile Arg
305                 310                 315                 320

Ile Gly Leu Ala Gly Leu Phe Arg Leu Tyr Thr Val Ser Ala Lys Ser
                325                 330                 335

Asn Glu Leu Arg Pro Arg Glu Leu Ala Leu Ala Ser Ile Gly Met Gln
            340                 345                 350

Ile Thr Leu Gly Gln Ala Pro Asn Leu Val Phe Thr Asp Ser Lys Val
        355                 360                 365

Val
```

<210> 2899
<211> 348
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(325)
<223> RXA02778

<400> 2899

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ctccgatttc tgaggtcagt acgcgctcct gtctaacttc taccacccag cccaaccaat 60

cgtttttcaa gggttcaccg aagcaactgt tgagcacctc atg cag gtc att gag   115
                                            Met Gln Val Ile Glu
                                              1               5

acg ctt gat ccc gat cag cgc gca gcg gtg ctc gct gca gcg ata ccg   163
Thr Leu Asp Pro Asp Gln Arg Ala Ala Val Leu Ala Ala Ala Ile Pro
                  10                  15                  20

cgc gag gct aag atc ctg ggg cga aaa gta act ctt cgc cct ggt tgg   211
Arg Glu Ala Lys Ile Leu Gly Arg Lys Val Thr Leu Arg Pro Gly Trp
              25                  30                  35

ggc aat atg cgc gta cac gtc gtg att gca gtt atc ttt atc aag ttt   259
Gly Asn Met Arg Val His Val Val Ile Ala Val Ile Phe Ile Lys Phe
          40                  45                  50

ttg caa ccg gat ctt cgc cag gcg ctg cta aca aca ggt gat gcc gta   307
Leu Gln Pro Asp Leu Arg Gln Ala Leu Leu Thr Thr Gly Asp Ala Val
      55                  60                  65

ctt gtc gaa gat gat acc tgaggcgcct tctggggcgt cga                 348
Leu Val Glu Asp Asp Thr
```

70 75

<210> 2900
<211> 75
<212> PRT
<213> Corynebacterium glutamicum

<400> 2900
Met Gln Val Ile Glu Thr Leu Asp Pro Asp Gln Arg Ala Ala Val Leu
1 5 10 15

Ala Ala Ala Ile Pro Arg Glu Ala Lys Ile Leu Gly Arg Lys Val Thr
20 25 30

Leu Arg Pro Gly Trp Gly Asn Met Arg Val His Val Val Ile Ala Val
35 40 45

Ile Phe Ile Lys Phe Leu Gln Pro Asp Leu Arg Gln Ala Leu Leu Thr
50 55 60

Thr Gly Asp Ala Val Leu Val Glu Asp Asp Thr
65 70 75

<210> 2901
<211> 402
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(379)
<223> RXA02779

<400> 2901
ctcaaaggag actgcacatc atgttcctca ccaaagatat gctcgcacgt tttcctgcaa 60

gtttgaattt gccaatgcac agtgctcaga accagaagaa atg ggc gaa tac ttc 115
Met Gly Glu Tyr Phe
1 5

cag gtc gtt caa aac atc gcc atg aca ctg ggt gct ggc gaa agc gtt 163
Gln Val Val Gln Asn Ile Ala Met Thr Leu Gly Ala Gly Glu Ser Val
10 15 20

gat ctt gtt gtc cgc gaa tac atc aac gat gtg gaa ggc aac ccg acc 211
Asp Leu Val Val Arg Glu Tyr Ile Asn Asp Val Glu Gly Asn Pro Thr
25 30 35

atc tat cac ggt atg ccg ctg cgt act gaa tac cgc gca ttc atc gac 259
Ile Tyr His Gly Met Pro Leu Arg Thr Glu Tyr Arg Ala Phe Ile Asp
40 45 50

ctt gat cac tgt gat ccg tcc gct ggt gag cct gag cct cgc tta ttg 307
Leu Asp His Cys Asp Pro Ser Ala Gly Glu Pro Glu Pro Arg Leu Leu
55 60 65

ggg gtt act ccc tac tgg cac ccc tcc gtg atg gag aaa gct ctt cgc 355
Gly Val Thr Pro Tyr Trp His Pro Ser Val Met Glu Lys Ala Leu Arg
70 75 80 85

```
ctt tgc ttc aag cga tgt tgg tgc tgaattcggt cacatcaacg atg          402
Leu Cys Phe Lys Arg Cys Trp Cys
                 90


<210> 2902
<211> 93
<212> PRT
<213> Corynebacterium glutamicum

<400> 2902
Met Gly Glu Tyr Phe Gln Val Val Gln Asn Ile Ala Met Thr Leu Gly
  1               5                  10                  15

Ala Gly Glu Ser Val Asp Leu Val Val Arg Glu Tyr Ile Asn Asp Val
             20                  25                  30

Glu Gly Asn Pro Thr Ile Tyr His Gly Met Pro Leu Arg Thr Glu Tyr
         35                  40                  45

Arg Ala Phe Ile Asp Leu Asp His Cys Asp Pro Ser Ala Gly Glu Pro
     50                  55                  60

Glu Pro Arg Leu Leu Gly Val Thr Pro Tyr Trp His Pro Ser Val Met
 65                  70                  75                  80

Glu Lys Ala Leu Arg Leu Cys Phe Lys Arg Cys Trp Cys
                 85                  90


<210> 2903
<211> 450
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(427)
<223> RXA02780

<400> 2903
atggagaaag ctcttcgcct ttgcttcaag cgatgttggt gctgaattcg gtcacatcaa 60

cgatgattac cgcacctacc gtgcccacaa agacagcctc atg tcc aag ttc cat   115
                                          Met Ser Lys Phe His
                                            1               5

aca cac cgt gat gat gtc att tca cgt atc act gca cta cta ccc cag   163
Thr His Arg Asp Asp Val Ile Ser Arg Ile Thr Ala Leu Leu Pro Gln
                 10                  15                  20

ctt cgt gca caa gag ctg caa ggt caa tgg tct gtg gac atc atg aaa   211
Leu Arg Ala Gln Glu Leu Gln Gly Gln Trp Ser Val Asp Ile Met Lys
             25                  30                  35

aac ggg gag gat ttc tac ctc att gac atg gct ctc atg tgc gag tcc   259
Asn Gly Glu Asp Phe Tyr Leu Ile Asp Met Ala Leu Met Cys Glu Ser
         40                  45                  50

gca ctg tct gaa cta ctc act gtt aca gat gag tac gcc aca gtc gag   307
```

```
Ala Leu Ser Glu Leu Leu Thr Val Thr Asp Glu Tyr Ala Thr Val Glu
     55                  60                  65

ccg agt gtc atc aat gac ttc gcc aac cag ctg gtc att gat tat gac   355
Pro Ser Val Ile Asn Asp Phe Ala Asn Gln Leu Val Ile Asp Tyr Asp
 70                  75                  80                  85

gag cac gat atg ggc ttt gat cga gac ttt cca gca ggt gtg tat aac   403
Glu His Asp Met Gly Phe Asp Arg Asp Phe Pro Ala Gly Val Tyr Asn
                 90                  95                 100

acc cga caa gca agt gct atc aac taaaaaatac acacatccac acc         450
Thr Arg Gln Ala Ser Ala Ile Asn
            105


<210> 2904
<211> 109
<212> PRT
<213> Corynebacterium glutamicum

<400> 2904
Met Ser Lys Phe His Thr His Arg Asp Asp Val Ile Ser Arg Ile Thr
  1               5                  10                  15

Ala Leu Leu Pro Gln Leu Arg Ala Gln Glu Leu Gln Gly Gln Trp Ser
             20                  25                  30

Val Asp Ile Met Lys Asn Gly Glu Asp Phe Tyr Leu Ile Asp Met Ala
         35                  40                  45

Leu Met Cys Glu Ser Ala Leu Ser Glu Leu Leu Thr Val Thr Asp Glu
     50                  55                  60

Tyr Ala Thr Val Glu Pro Ser Val Ile Asn Asp Phe Ala Asn Gln Leu
 65                  70                  75                  80

Val Ile Asp Tyr Asp Glu His Asp Met Gly Phe Asp Arg Asp Phe Pro
                 85                  90                  95

Ala Gly Val Tyr Asn Thr Arg Gln Ala Ser Ala Ile Asn
            100                 105


<210> 2905
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
<223> RXA02783

<400> 2905
acaagcttca tgcaacccat aacctcagtg ctgttttgcc taccgaaact actgactcac 60

gtgtggcaac caccgctttc gccgtacact cacactgtcg gtg gtc tct ggt tca   115
                                              Val Val Ser Gly Ser
                                                1               5
```

```
cgc gct gct gca ttc ttg aac agc aac cat att cag ggt gct gtc tcg   163
Arg Ala Ala Ala Phe Leu Asn Ser Asn His Ile Gln Gly Ala Val Ser
                 10                  15                  20

gcc act aag cac ttt gcc ctg tgc gac aac aac gac gat att cga gca   211
Ala Thr Lys His Phe Ala Leu Cys Asp Asn Asn Asp Asp Ile Arg Ala
             25                  30                  35

ctc ctg tcg gtg cgc tca cca aaa aac aat gcc cgc atg tat cgc aaa   259
Leu Leu Ser Val Arg Ser Pro Lys Asn Asn Ala Arg Met Tyr Arg Lys
         40                  45                  50

aaa ggc aca tgg gaa atc cag cgc tat gcg aca ctc ggt aac gtc cct   307
Lys Gly Thr Trp Glu Ile Gln Arg Tyr Ala Thr Leu Gly Asn Val Pro
     55                  60                  65

ggc ggt ttt act agg ctg ctg aag ttt gcc gag cac aca ctc aac gaa   355
Gly Gly Phe Thr Arg Leu Leu Lys Phe Ala Glu His Thr Leu Asn Glu
 70                  75                  80                  85

cac agc aca gta ctc aag caa tgg atc tca ttt tct gct gct gat gtc   403
His Ser Thr Val Leu Lys Gln Trp Ile Ser Phe Ser Ala Ala Asp Val
                 90                  95                 100

tct gac ggc agc ctg tat cga act gcc ggt ttt acc gcc gag caa cag   451
Ser Asp Gly Ser Leu Tyr Arg Thr Ala Gly Phe Thr Ala Glu Gln Gln
             105                 110                 115

ctt gca ccg gat tat cgc tat gtc ggt ggc gca aca ggt tgg cgc cga   499
Leu Ala Pro Asp Tyr Arg Tyr Val Gly Gly Ala Thr Gly Trp Arg Arg
         120                 125                 130

aca ccc aaa gaa agc ttc cag cgc aaa cgc ttt aga gac gac cca gcg   547
Thr Pro Lys Glu Ser Phe Gln Arg Lys Arg Phe Arg Asp Asp Pro Ala
     135                 140                 145

ttg cta tgg aac gaa tct tgg aca gag cac gaa gca gcg ctc aac aac   595
Leu Leu Trp Asn Glu Ser Trp Thr Glu His Glu Ala Ala Leu Asn Asn
150                 155                 160                 165

gag ctc tac aga atc tac gat gcc ggc aaa acc cgg tgg gtt aaa aat   643
Glu Leu Tyr Arg Ile Tyr Asp Ala Gly Lys Thr Arg Trp Val Lys Asn
                170                 175                 180

gtt gct tgattctgca gattagttac tga                                672
Val Ala
```

<210> 2906
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 2906

```
Val Val Ser Gly Ser Arg Ala Ala Ala Phe Leu Asn Ser Asn His Ile
  1               5                  10                  15

Gln Gly Ala Val Ser Ala Thr Lys His Phe Ala Leu Cys Asp Asn Asn
             20                  25                  30
```

```
Asp Asp Ile Arg Ala Leu Leu Ser Val Arg Ser Pro Lys Asn Asn Ala
          35                  40                  45

Arg Met Tyr Arg Lys Lys Gly Thr Trp Glu Ile Gln Arg Tyr Ala Thr
      50                  55                  60

Leu Gly Asn Val Pro Gly Gly Phe Thr Arg Leu Leu Lys Phe Ala Glu
 65                  70                  75                  80

His Thr Leu Asn Glu His Ser Thr Val Leu Lys Gln Trp Ile Ser Phe
                 85                  90                  95

Ser Ala Ala Asp Val Ser Asp Gly Ser Leu Tyr Arg Thr Ala Gly Phe
            100                 105                 110

Thr Ala Glu Gln Gln Leu Ala Pro Asp Tyr Arg Tyr Val Gly Gly Ala
        115                 120                 125

Thr Gly Trp Arg Arg Thr Pro Lys Glu Ser Phe Gln Arg Lys Arg Phe
    130                 135                 140

Arg Asp Asp Pro Ala Leu Leu Trp Asn Glu Ser Trp Thr Glu His Glu
145                 150                 155                 160

Ala Ala Leu Asn Asn Glu Leu Tyr Arg Ile Tyr Asp Ala Gly Lys Thr
                165                 170                 175

Arg Trp Val Lys Asn Val Ala
            180
```

US20050059097A1

<210> 2907
<211> 309
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(286)
<223> RXA02784

<400> 2907

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agctgcaact caggtagaag aaacaacagt cgcccgagtt gaacacgata cttacgacac 60

tattgctaac cagctacaag atgccggtgt ctatgacgat gtg gcc ttt gcc gaa   115
                                            Val Ala Phe Ala Glu
                                              1               5

ggc tac tac cag gaa atg gct gag gtt gta tgt gaa gca cgc gaa gag   163
Gly Tyr Tyr Gln Glu Met Ala Glu Val Val Cys Glu Ala Arg Glu Glu
                 10                  15                  20

ggt atc acc cac gag gac acc ctg cat atg ctc aat gac atg atg gca   211
Gly Ile Thr His Glu Asp Thr Leu His Met Leu Asn Asp Met Met Ala
             25                  30                  35

atg aaa cga tct ggc gaa gta ctc aat acg ctc gct gat gtt ctc tat   259
Met Lys Arg Ser Gly Glu Val Leu Asn Thr Leu Ala Asp Val Leu Tyr
         40                  45                  50

gca aat gaa tgc cct gaa tat cga atc taaattgttg gtcactctgc         306
```

```
Ala Asn Glu Cys Pro Glu Tyr Arg Ile
     55                  60

ata                                                                    309


<210> 2908
<211> 62
<212> PRT
<213> Corynebacterium glutamicum

<400> 2908
Val Ala Phe Ala Glu Gly Tyr Tyr Gln Glu Met Ala Glu Val Val Cys
  1               5                  10                  15

Glu Ala Arg Glu Glu Gly Ile Thr His Glu Asp Thr Leu His Met Leu
             20                  25                  30

Asn Asp Met Met Ala Met Lys Arg Ser Gly Glu Val Leu Asn Thr Leu
         35                  40                  45

Ala Asp Val Leu Tyr Ala Asn Glu Cys Pro Glu Tyr Arg Ile
     50                  55                  60


<210> 2909
<211> 830
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(807)
<223> RXA02786

<400> 2909
atc ctg cgc aac ctc ggc caa tcg ctg ggc agc ctg cac gcc gcc acc   48
Ile Leu Arg Asn Leu Gly Gln Ser Leu Gly Ser Leu His Ala Ala Thr
  1               5                  10                  15

gca gac cgc gaa gaa gac ttc aac att ctg ctc aac cgt atg ctg gcc   96
Ala Asp Arg Glu Glu Asp Phe Asn Ile Leu Leu Asn Arg Met Leu Ala
             20                  25                  30

aaa tac cca gcc aca gct gag atg cag aaa aac cgc gat agg ttg ctg   144
Lys Tyr Pro Ala Thr Ala Glu Met Gln Lys Asn Arg Asp Arg Leu Leu
         35                  40                  45

ccc gca gca att gag gtg ggt aaa aag ata ctt gtc gac gcc ggg gtc   192
Pro Ala Ala Ile Glu Val Gly Lys Lys Ile Leu Val Asp Ala Gly Val
     50                  55                  60

acc gtt cca gaa gtc gtc gag gag ttt gcc cgc gta gct cgg cga cgc   240
Thr Val Pro Glu Val Val Glu Glu Phe Ala Arg Val Ala Arg Arg Arg
 65                  70                  75                  80

ctg att tcc gga cgc cac cgt gcc ttc aca cct ttt gac ttg tca ccc   288
Leu Ile Ser Gly Arg His Arg Ala Phe Thr Pro Phe Asp Leu Ser Pro
                 85                  90                  95

gac aac atc atc gtg gct gaa cgc acc cac ttc ctg gac tac gaa gtt   336
```

```
Asp Asn Ile Ile Val Ala Glu Arg Thr His Phe Leu Asp Tyr Glu Val
            100                 105                 110

gcc ggt ttc agg gat gcc acc ttt gat gtt gct tgt gtg atc gca ggt   384
Ala Gly Phe Arg Asp Ala Thr Phe Asp Val Ala Cys Val Ile Ala Gly
        115                 120                 125

ttc ccg caa ttc gtg ttc agc cgc ccc atc tct gat gat gag gta gac   432
Phe Pro Gln Phe Val Phe Ser Arg Pro Ile Ser Asp Asp Glu Val Asp
    130                 135                 140

gaa ctc att gaa tcc tgg gtc caa gaa gtc cgt gga atc tgg ccc aat   480
Glu Leu Ile Glu Ser Trp Val Gln Glu Val Arg Gly Ile Trp Pro Asn
145                 150                 155                 160

gtg aac aat gaa gag cgc ctc caa gca cgt atc gtg acc gct ctc atc   528
Val Asn Asn Glu Glu Arg Leu Gln Ala Arg Ile Val Thr Ala Leu Ile
                165                 170                 175

ggc tgg gca cta tcg agt gtt gcc ttc atg aag ctc ggc tcc atc agc   576
Gly Trp Ala Leu Ser Ser Val Ala Phe Met Lys Leu Gly Ser Ile Ser
            180                 185                 190

ggc atg ctt aac ctg ctg cac gtc acc gaa gat gga aac acc act ttg   624
Gly Met Leu Asn Leu Leu His Val Thr Glu Asp Gly Asn Thr Thr Leu
        195                 200                 205

gat gtc tcc aac ctt gat gaa ctg ttg att cca cga tct gcc gaa gat   672
Asp Val Ser Asn Leu Asp Glu Leu Leu Ile Pro Arg Ser Ala Glu Asp
    210                 215                 220

gac gag ctg gtc cag caa gac ctc cac gac acg ttc tcc gcg ctt cag   720
Asp Glu Leu Val Gln Gln Asp Leu His Asp Thr Phe Ser Ala Leu Gln
225                 230                 235                 240

cga ttt gca gcg cgc ggg ctg gat tcc agg ttc cct gag gtg gca cga   768
Arg Phe Ala Ala Arg Gly Leu Asp Ser Arg Phe Pro Glu Val Ala Arg
                245                 250                 255

ttc gca gac gac gtg gtg cgt ttg ttc ctc aaa aat gac tagctgaaga    817
Phe Ala Asp Asp Val Val Arg Leu Phe Leu Lys Asn Asp
            260                 265

gcaccggttg ctt                                                   830


<210> 2910
<211> 269
<212> PRT
<213> Corynebacterium glutamicum

<400> 2910
Ile Leu Arg Asn Leu Gly Gln Ser Leu Gly Ser Leu His Ala Ala Thr
  1               5                  10                  15

Ala Asp Arg Glu Glu Asp Phe Asn Ile Leu Leu Asn Arg Met Leu Ala
             20                  25                  30

Lys Tyr Pro Ala Thr Ala Glu Met Gln Lys Asn Arg Asp Arg Leu Leu
         35                  40                  45
```

```
Pro Ala Ala Ile Glu Val Gly Lys Lys Ile Leu Val Asp Ala Gly Val
     50                  55                  60

Thr Val Pro Glu Val Val Glu Glu Phe Ala Arg Val Ala Arg Arg Arg
 65                  70                  75                  80

Leu Ile Ser Gly Arg His Arg Ala Phe Thr Pro Phe Asp Leu Ser Pro
                 85                  90                  95

Asp Asn Ile Ile Val Ala Glu Arg Thr His Phe Leu Asp Tyr Glu Val
            100                 105                 110

Ala Gly Phe Arg Asp Ala Thr Phe Asp Val Ala Cys Val Ile Ala Gly
        115                 120                 125

Phe Pro Gln Phe Val Phe Ser Arg Pro Ile Ser Asp Asp Glu Val Asp
    130                 135                 140

Glu Leu Ile Glu Ser Trp Val Gln Glu Val Arg Gly Ile Trp Pro Asn
145                 150                 155                 160

Val Asn Asn Glu Glu Arg Leu Gln Ala Arg Ile Val Thr Ala Leu Ile
                165                 170                 175

Gly Trp Ala Leu Ser Ser Val Ala Phe Met Lys Leu Gly Ser Ile Ser
            180                 185                 190

Gly Met Leu Asn Leu Leu His Val Thr Glu Asp Gly Asn Thr Thr Leu
        195                 200                 205

Asp Val Ser Asn Leu Asp Glu Leu Leu Ile Pro Arg Ser Ala Glu Asp
    210                 215                 220

Asp Glu Leu Val Gln Gln Asp Leu His Asp Thr Phe Ser Ala Leu Gln
225                 230                 235                 240

Arg Phe Ala Ala Arg Gly Leu Asp Ser Arg Phe Pro Glu Val Ala Arg
                245                 250                 255

Phe Ala Asp Asp Val Val Arg Leu Phe Leu Lys Asn Asp
            260                 265
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09/05/2005 09:50:55 PM

<210> 2911
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(646)
<223> RXA02789

<400> 2911
ttcttccgta cggctatgct taaaagctaa atttgtcttt gtgccttgca acacattaat 60

ttcttaacac taaacaatgg aaaggtaagc gggtttttct atg aag gtt tcc gcc 115
                                                Met Lys Val Ser Ala
                                                  1   5

gat aca ccc ggt cac gat gat cca ggc cca ggc cgg cgc ctt ggc tta 163

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Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly Arg Arg Leu Gly Leu
                 10                  15                  20

gat gtc ggc acc gtg cgc atc gga gtg gca gcc tct gac cgc gat gcc   211
Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala Ser Asp Arg Asp Ala
             25                  30                  35

aag ctt gcc atg cct gtg gaa acc gtt ccg cgg gaa act gga ttc aaa   259
Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg Glu Thr Gly Phe Lys
         40                  45                  50

ggg cca gac ctg gcc gat att gat cgg ttg gtc gcc atc gtt gag gaa   307
Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val Ala Ile Val Glu Glu
     55                  60                  65

tac aac gcc gtg gaa gtc att gtt ggt cta ccc aca gat ctg cag gga   355
Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro Thr Asp Leu Gln Gly
 70                  75                  80                  85

aat ggc tcc gcc agt gtg aag cat gca aag gaa att gct ttc cgc gtc   403
Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu Ile Ala Phe Arg Val
                 90                  95                 100

cgt cgg cgc ctc acc aat gct gga aag aac att ccg gta cgg ctt ggc   451
Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile Pro Val Arg Leu Gly
             105                 110                 115

gac gaa cgc ctc acc acc gtc gtg gcc acc caa gcc ttg cgg gcc tca   499
Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln Ala Leu Arg Ala Ser
         120                 125                 130

gga gtc agc gaa aaa gcg gga cgt aaa gtt att gat caa gct gcc gca   547
Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile Asp Gln Ala Ala Ala
     135                 140                 145

gta gaa atc ctt caa acc tgg ttg gat gct cgc acc cga gcc ctt gaa   595
Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg Thr Arg Ala Leu Glu
150                 155                 160                 165

cca caa tcc aca gac acc caa gat ttc gac gag aag gga aat ttc cca   643
Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu Lys Gly Asn Phe Pro
                170                 175                 180

gga tgaaccaaat ccgaaaccgc cgg                                    669
Gly
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<210> 2912
<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 2912

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Met Lys Val Ser Ala Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly
  1               5                  10                  15

Arg Arg Leu Gly Leu Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala
             20                  25                  30

Ser Asp Arg Asp Ala Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg
```

```
         35                  40                  45

Glu Thr Gly Phe Lys Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val
     50                  55                  60

Ala Ile Val Glu Glu Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro
 65                  70                  75                  80

Thr Asp Leu Gln Gly Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu
                 85                  90                  95

Ile Ala Phe Arg Val Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile
            100                 105                 110

Pro Val Arg Leu Gly Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln
        115                 120                 125

Ala Leu Arg Ala Ser Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile
    130                 135                 140

Asp Gln Ala Ala Ala Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg
145                 150                 155                 160

Thr Arg Ala Leu Glu Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu
                165                 170                 175

Lys Gly Asn Phe Pro Gly
            180
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US20050100900A1

<210> 2913
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> RXA02793

<400> 2913

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ggtggtgaat tttgatagtc caccatcaca catcgccttg atg aaa agc gcc gcc   115
                                            Met Lys Ser Ala Ala
                                              1               5

gta ccc acg ctt gat gct tta ggt gtt ttg gat cgc gtg gtg acc aaa   163
Val Pro Thr Leu Asp Ala Leu Gly Val Leu Asp Arg Val Val Thr Lys
                 10                  15                  20

gct ggt gcc ttc cca gct ggg tat tac gac gcc gat tta tcg gaa aga   211
Ala Gly Ala Phe Pro Ala Gly Tyr Tyr Asp Ala Asp Leu Ser Glu Arg
             25                  30                  35

gtc acg gac atc cca acg ctg tcc aac aag atc gac gcc agc gga cac   259
Val Thr Asp Ile Pro Thr Leu Ser Asn Lys Ile Asp Ala Ser Gly His
         40                  45                  50

gtg ttg atc tcg aaa gaa gtc gtt gtt gcc gcc aac cca gac att gtt   307
Val Leu Ile Ser Lys Glu Val Val Val Ala Ala Asn Pro Asp Ile Val
```

```
     55                  60                  65

ttc ggc gaa act gac acc atc aac cgc gca tcc atg gca tcc tcg aac   355
Phe Gly Glu Thr Asp Thr Ile Asn Arg Ala Ser Met Ala Ser Ser Asn
 70                  75                  80                  85

atc ccg gtc gtg gag gaa cca gca ttc tgt ggc agc atc gac ggc gac   403
Ile Pro Val Val Glu Glu Pro Ala Phe Cys Gly Ser Ile Asp Gly Asp
                 90                  95                 100

gtg agt ttt gat gat gtc tgg tca caa atc tcc acc tat ggc acc att   451
Val Ser Phe Asp Asp Val Trp Ser Gln Ile Ser Thr Tyr Gly Thr Ile
            105                 110                 115

ttt gat cgc tcg aca gaa gca gac gca tac att gca acg ttg aag gaa   499
Phe Asp Arg Ser Thr Glu Ala Asp Ala Tyr Ile Ala Thr Leu Lys Glu
        120                 125                 130

cgt gtt tct gaa gta tcc tcg cgg gtt act gac tcc gga aaa act gtg   547
Arg Val Ser Glu Val Ser Ser Arg Val Thr Asp Ser Gly Lys Thr Val
    135                 140                 145

gcg gtg ctc tac ccc acc atc ggc ggc gga gtc acc tac gca tac ggc   595
Ala Val Leu Tyr Pro Thr Ile Gly Gly Gly Val Thr Tyr Ala Tyr Gly
150                 155                 160                 165

cgc gga tcc atg gcc aac cca ctt gtt gcc gaa gca ggc ctg acc aac   643
Arg Gly Ser Met Ala Asn Pro Leu Val Ala Glu Ala Gly Leu Thr Asn
                170                 175                 180

gtt ttc gca gac caa tcc gaa cgc gtc ttt gag gtc acg gca gaa gaa   691
Val Phe Ala Asp Gln Ser Glu Arg Val Phe Glu Val Thr Ala Glu Glu
            185                 190                 195

ctg atc tcc gaa acc ccg act cat cat cgt ttt aca cag cga cgg ttc   739
Leu Ile Ser Glu Thr Pro Thr His His Arg Phe Thr Gln Arg Arg Phe
        200                 205                 210

ccc ttc aga cat cgt cgc aga ggt ggg caa tct cca agg gtc cag cgc   787
Pro Phe Arg His Arg Arg Arg Gly Gly Gln Ser Pro Arg Val Gln Arg
    215                 220                 225

act cac tgc tct gag tgagaacaaa gtgctgccca tac                    825
Thr His Cys Ser Glu
230
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<2910> 2914
<2911> 234
<2912> PRT
<2913> Corynebacterium glutamicum

<400> 2914

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Met Lys Ser Ala Ala Val Pro Thr Leu Asp Ala Leu Gly Val Leu Asp
  1               5                  10                  15

Arg Val Val Thr Lys Ala Gly Ala Phe Pro Ala Gly Tyr Tyr Asp Ala
             20                  25                  30

Asp Leu Ser Glu Arg Val Thr Asp Ile Pro Thr Leu Ser Asn Lys Ile
         35                  40                  45
```

```
Asp Ala Ser Gly His Val Leu Ile Ser Lys Glu Val Val Val Ala Ala
     50                  55                  60

Asn Pro Asp Ile Val Phe Gly Glu Thr Asp Thr Ile Asn Arg Ala Ser
 65                  70                  75                  80

Met Ala Ser Ser Asn Ile Pro Val Val Glu Glu Pro Ala Phe Cys Gly
                 85                  90                  95

Ser Ile Asp Gly Asp Val Ser Phe Asp Asp Val Trp Ser Gln Ile Ser
            100                 105                 110

Thr Tyr Gly Thr Ile Phe Asp Arg Ser Thr Glu Ala Asp Ala Tyr Ile
        115                 120                 125

Ala Thr Leu Lys Glu Arg Val Ser Glu Val Ser Ser Arg Val Thr Asp
    130                 135                 140

Ser Gly Lys Thr Val Ala Val Leu Tyr Pro Thr Ile Gly Gly Gly Val
145                 150                 155                 160

Thr Tyr Ala Tyr Gly Arg Gly Ser Met Ala Asn Pro Leu Val Ala Glu
                165                 170                 175

Ala Gly Leu Thr Asn Val Phe Ala Asp Gln Ser Glu Arg Val Phe Glu
            180                 185                 190

Val Thr Ala Glu Glu Leu Ile Ser Glu Thr Pro Thr His His Arg Phe
        195                 200                 205

Thr Gln Arg Arg Phe Pro Phe Arg His Arg Arg Arg Gly Gly Gln Ser
    210                 215                 220

Pro Arg Val Gln Arg Thr His Cys Ser Glu
225                 230
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5000000000

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            25                  30                  35

atc acg ttg gcg ttc tat gga gaa tta cct gat ggg gca gtc gaa gat   259
Ile Thr Leu Ala Phe Tyr Gly Glu Leu Pro Asp Gly Ala Val Glu Asp
         40                  45                  50

ctc att gag cat ctg aca agt gca gcc cga atc aat gaa gaa ttc acc   307
Leu Ile Glu His Leu Thr Ser Ala Ala Arg Ile Asn Glu Glu Phe Thr
     55                  60                  65

atc aga atc aaa ggc gca ggc tca ttt aat cgg aag aat ttg tgg atg   355
Ile Arg Ile Lys Gly Ala Gly Ser Phe Asn Arg Lys Asn Leu Trp Met
 70                  75                  80                  85

ggt gtt ggt ggt gac acc aaa gat ctg cgg cga ctg atg gct gat tgt   403
Gly Val Gly Gly Asp Thr Lys Asp Leu Arg Arg Leu Met Ala Asp Cys
                 90                  95                 100

ctg att gat cct gag gaa cgc cga cgc cag cgt gca cac ctg acc gtg   451
Leu Ile Asp Pro Glu Glu Arg Arg Arg Gln Arg Ala His Leu Thr Val
            105                 110                 115

gcg aaa cca acg cag cga cag cgc agc cgc gat tgg gat cct gtc atc   499
Ala Lys Pro Thr Gln Arg Gln Arg Ser Arg Asp Trp Asp Pro Val Ile
        120                 125                 130

ccc gat ctg gtc cac gct ctc tct ata tac gaa ggc ccc gaa tgg cca   547
Pro Asp Leu Val His Ala Leu Ser Ile Tyr Glu Gly Pro Glu Trp Pro
    135                 140                 145

gtc gat gag att gaa ctg gtg tct tct gaa cct gga aaa ggc aga agc   595
Val Asp Glu Ile Glu Leu Val Ser Ser Glu Pro Gly Lys Gly Arg Ser
150                 155                 160                 165

ggt ggg cca ctg tat aca acc gtg gcc acc att gcg ttg tca tct gcg   643
Gly Gly Pro Leu Tyr Thr Thr Val Ala Thr Ile Ala Leu Ser Ser Ala
                170                 175                 180

ctg gtt taaaggctca accgcggaac ggc                                672
Leu Val
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<210> 2916
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 2916

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Met Arg Leu Phe Ala Ser Ile Thr Pro Pro Ile Glu Val Thr Glu His
  1               5                  10                  15

Leu Ile Asn Ala Leu Arg Pro Tyr Lys Asp Asp Leu Arg Trp Ser Asp
             20                  25                  30

Pro Asp Asn Trp His Ile Thr Leu Ala Phe Tyr Gly Glu Leu Pro Asp
         35                  40                  45

Gly Ala Val Glu Asp Leu Ile Glu His Leu Thr Ser Ala Ala Arg Ile
     50                  55                  60
```

```
Asn Glu Glu Phe Thr Ile Arg Ile Lys Gly Ala Gly Ser Phe Asn Arg
 65                  70                  75                  80

Lys Asn Leu Trp Met Gly Val Gly Gly Asp Thr Lys Asp Leu Arg Arg
                 85                  90                  95

Leu Met Ala Asp Cys Leu Ile Asp Pro Glu Glu Arg Arg Arg Gln Arg
            100                 105                 110

Ala His Leu Thr Val Ala Lys Pro Thr Gln Arg Gln Arg Ser Arg Asp
        115                 120                 125

Trp Asp Pro Val Ile Pro Asp Leu Val His Ala Leu Ser Ile Tyr Glu
    130                 135                 140

Gly Pro Glu Trp Pro Val Asp Glu Ile Glu Leu Val Ser Ser Glu Pro
145                 150                 155                 160

Gly Lys Gly Arg Ser Gly Gly Pro Leu Tyr Thr Thr Val Ala Thr Ile
                165                 170                 175

Ala Leu Ser Ser Ala Leu Val
            180
```

US20070020750A1

<210> 2917
<211> 1548
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1525)
<223> RXA02798

<400> 2917

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gcatcaaaat catgtgcatt catcattgct gatcatcata gacctgttgg caaatgaatt 60

caccaattct ttaaagctct caccctcttt agggaactga atg cgg tct gta ctc   115
                                              Met Arg Ser Val Leu
                                                1               5

gac tac tgg atc atg act ctt gca cct tcc acc aat gcg gtt tcg cag   163
Asp Tyr Trp Ile Met Thr Leu Ala Pro Ser Thr Asn Ala Val Ser Gln
                10                  15                  20

caa aca aga agg aac cct tcc caa gcg ccg cga ctt ctt cat cga ctt   211
Gln Thr Arg Arg Asn Pro Ser Gln Ala Pro Arg Leu Leu His Arg Leu
            25                  30                  35

cac ttc ttt gcc ggc att atc tgc gca ccg ttg att ttc atc gct gcg   259
His Phe Phe Ala Gly Ile Ile Cys Ala Pro Leu Ile Phe Ile Ala Ala
        40                  45                  50

ctc acc gga ctg gtg tat gcg ttc tcc ccc acc att gaa agc atc tct   307
Leu Thr Gly Leu Val Tyr Ala Phe Ser Pro Thr Ile Glu Ser Ile Ser
    55                  60                  65

aat cag gaa atg ctc acg gtc tcc aag tcg gct agc gac aca gct ctt   355
Asn Gln Glu Met Leu Thr Val Ser Lys Ser Ala Ser Asp Thr Ala Leu
70                  75                  80                  85
```

```
ccg gtg cgt gaa caa gtg agc atc gcc caa gaa ctc cac ccc gat tta   403
Pro Val Arg Glu Gln Val Ser Ile Ala Gln Glu Leu His Pro Asp Leu
                 90                  95                 100

gat ctc tca ggt gtc cgg ctt ggc gat gat tcc tcc acc acc cgc gtc   451
Asp Leu Ser Gly Val Arg Leu Gly Asp Asp Ser Ser Thr Thr Arg Val
            105                 110                 115

ctc ttc gcc gac gag acg ctt gct gaa tcc aca gtc cgc gcc gtg ttt   499
Leu Phe Ala Asp Glu Thr Leu Ala Glu Ser Thr Val Arg Ala Val Phe
        120                 125                 130

gtt gat ccc tac acc ggc gag atc acc ggt gat acc acc caa tac gga   547
Val Asp Pro Tyr Thr Gly Glu Ile Thr Gly Asp Thr Thr Gln Tyr Gly
    135                 140                 145

agc tca gct gca ctg ccg ttt cgg caa tgg gtc tcg caa ggt cac cgc   595
Ser Ser Ala Ala Leu Pro Phe Arg Gln Trp Val Ser Gln Gly His Arg
150                 155                 160                 165

atg ttg tgg ctt ggt gaa cct gga cgt att tat tcc gaa ctt gcg gca   643
Met Leu Trp Leu Gly Glu Pro Gly Arg Ile Tyr Ser Glu Leu Ala Ala
                170                 175                 180

agt tgg ctc gga gtt tta gcc gta ggc ggt ttc gca tta ttg tgg ttg   691
Ser Trp Leu Gly Val Leu Ala Val Gly Gly Phe Ala Leu Leu Trp Leu
            185                 190                 195

cgc aac aaa aag ccc ggc cgc ttg aga aag atg gtg cga act ggt ggc   739
Arg Asn Lys Lys Pro Gly Arg Leu Arg Lys Met Val Arg Thr Gly Gly
        200                 205                 210

cgt ggt cga gtg aaa acg tat cgc cga cat gca gca ttg ggc acc gta   787
Arg Gly Arg Val Lys Thr Tyr Arg Arg His Ala Ala Leu Gly Thr Val
    215                 220                 225

gcg ggc ttg ggt ttt gtg ttc ctc acc ttt act ggc ctg acc tgg tca   835
Ala Gly Leu Gly Phe Val Phe Leu Thr Phe Thr Gly Leu Thr Trp Ser
230                 235                 240                 245

act tat gcg gga tcc aac atc acg gat tta cgc acc caa ctc aat tgg   883
Thr Tyr Ala Gly Ser Asn Ile Thr Asp Leu Arg Thr Gln Leu Asn Trp
                250                 255                 260

acg cag cct tcc gtt aac gct tct cta aca gct gcc cca caa gtg gac   931
Thr Gln Pro Ser Val Asn Ala Ser Leu Thr Ala Ala Pro Gln Val Asp
            265                 270                 275

atg cat gat gaa cac gca ggt cat cac atg cat atg gag tcg gca acc   979
Met His Asp Glu His Ala Gly His His Met His Met Glu Ser Ala Thr
        280                 285                 290

tca ggc tca ggt tct ata gat ctg gta gcg gcc acg gct atc tcc gaa   1027
Ser Gly Ser Gly Ser Ile Asp Leu Val Ala Ala Thr Ala Ile Ser Glu
    295                 300                 305

tta cgc act ccc ctc acc att act ccc cca gca caa gat ggc ctc gcg   1075
Leu Arg Thr Pro Leu Thr Ile Thr Pro Pro Ala Gln Asp Gly Leu Ala
310                 315                 320                 325
```

```
tgg act gcc aca gaa aac cgc gac gcc tac cga ttc acc act gac acc   1123
Trp Thr Ala Thr Glu Asn Arg Asp Ala Tyr Arg Phe Thr Thr Asp Thr
                330                 335                 340

atc gct gtt gat ggc gac acc gga atg ctg acc aac cgt ttg aat tcc   1171
Ile Ala Val Asp Gly Asp Thr Gly Met Leu Thr Asn Arg Leu Asn Ser
            345                 350                 355

act gat tgg cca tta gct gct caa gcg agt gca tgg ctc atc cag ctt   1219
Thr Asp Trp Pro Leu Ala Ala Gln Ala Ser Ala Trp Leu Ile Gln Leu
        360                 365                 370

cac atg ggc acc ctg ttt ggc ctt ccc aac cag gtt gta ctt ggg ctg   1267
His Met Gly Thr Leu Phe Gly Leu Pro Asn Gln Val Val Leu Gly Leu
    375                 380                 385

ttg gct gcc tca ata atc gtg atg atc ggc ctt ggg tat tgg atg ctg   1315
Leu Ala Ala Ser Ile Ile Val Met Ile Gly Leu Gly Tyr Trp Met Leu
390                 395                 400                 405

tgg cag cat cgg cca cgg gaa ggt tgg cct agc gct ccc aag cgt gca   1363
Trp Gln His Arg Pro Arg Glu Gly Trp Pro Ser Ala Pro Lys Arg Ala
                410                 415                 420

gga ttt gaa aaa ccc acc tgg gga act atc gcg ttg ggt gtt gtg gtg   1411
Gly Phe Glu Lys Pro Thr Trp Gly Thr Ile Ala Leu Gly Val Val Val
            425                 430                 435

atc gcg tat ggg ctt ctc gcg cca ctt ttt gca gtt tca ctg ctc gtg   1459
Ile Ala Tyr Gly Leu Leu Ala Pro Leu Phe Ala Val Ser Leu Leu Val
        440                 445                 450

ttt att gga tta agc ctt gga gtg cgg ttt att tct cgt atg tcc ggg   1507
Phe Ile Gly Leu Ser Leu Gly Val Arg Phe Ile Ser Arg Met Ser Gly
    455                 460                 465

cgc gcg gac acg tcc aac taagaacacc aaaccacacc gcc                 1548
Arg Ala Asp Thr Ser Asn
470                 475
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<210> 2918
<211> 475
<212> PRT
<213> Corynebacterium glutamicum

<400> 2918

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Met Arg Ser Val Leu Asp Tyr Trp Ile Met Thr Leu Ala Pro Ser Thr
  1               5                  10                  15

Asn Ala Val Ser Gln Gln Thr Arg Arg Asn Pro Ser Gln Ala Pro Arg
             20                  25                  30

Leu Leu His Arg Leu His Phe Phe Ala Gly Ile Ile Cys Ala Pro Leu
         35                  40                  45

Ile Phe Ile Ala Ala Leu Thr Gly Leu Val Tyr Ala Phe Ser Pro Thr
     50                  55                  60

Ile Glu Ser Ile Ser Asn Gln Glu Met Leu Thr Val Ser Lys Ser Ala
 65                  70                  75                  80
```

```
Ser Asp Thr Ala Leu Pro Val Arg Glu Gln Val Ser Ile Ala Gln Glu
                  85                  90                  95

Leu His Pro Asp Leu Asp Leu Ser Gly Val Arg Leu Gly Asp Asp Ser
             100                 105                 110

Ser Thr Thr Arg Val Leu Phe Ala Asp Glu Thr Leu Ala Glu Ser Thr
         115                 120                 125

Val Arg Ala Val Phe Val Asp Pro Tyr Thr Gly Glu Ile Thr Gly Asp
     130                 135                 140

Thr Thr Gln Tyr Gly Ser Ser Ala Ala Leu Pro Phe Arg Gln Trp Val
145                 150                 155                 160

Ser Gln Gly His Arg Met Leu Trp Leu Gly Glu Pro Gly Arg Ile Tyr
                 165                 170                 175

Ser Glu Leu Ala Ala Ser Trp Leu Gly Val Leu Ala Val Gly Gly Phe
             180                 185                 190

Ala Leu Leu Trp Leu Arg Asn Lys Lys Pro Gly Arg Leu Arg Lys Met
         195                 200                 205

Val Arg Thr Gly Gly Arg Gly Arg Val Lys Thr Tyr Arg Arg His Ala
     210                 215                 220

Ala Leu Gly Thr Val Ala Gly Leu Gly Phe Val Phe Leu Thr Phe Thr
225                 230                 235                 240

Gly Leu Thr Trp Ser Thr Tyr Ala Gly Ser Asn Ile Thr Asp Leu Arg
                 245                 250                 255

Thr Gln Leu Asn Trp Thr Gln Pro Ser Val Asn Ala Ser Leu Thr Ala
             260                 265                 270

Ala Pro Gln Val Asp Met His Asp Glu His Ala Gly His His Met His
         275                 280                 285

Met Glu Ser Ala Thr Ser Gly Ser Gly Ser Ile Asp Leu Val Ala Ala
     290                 295                 300

Thr Ala Ile Ser Glu Leu Arg Thr Pro Leu Thr Ile Thr Pro Pro Ala
305                 310                 315                 320

Gln Asp Gly Leu Ala Trp Thr Ala Thr Glu Asn Arg Asp Ala Tyr Arg
                 325                 330                 335

Phe Thr Thr Asp Thr Ile Ala Val Asp Gly Asp Thr Gly Met Leu Thr
             340                 345                 350

Asn Arg Leu Asn Ser Thr Asp Trp Pro Leu Ala Ala Gln Ala Ser Ala
         355                 360                 365

Trp Leu Ile Gln Leu His Met Gly Thr Leu Phe Gly Leu Pro Asn Gln
     370                 375                 380

Val Val Leu Gly Leu Leu Ala Ala Ser Ile Ile Val Met Ile Gly Leu
385                 390                 395                 400
```

```
Gly Tyr Trp Met Leu Trp Gln His Arg Pro Arg Glu Gly Trp Pro Ser
                405                 410                 415

Ala Pro Lys Arg Ala Gly Phe Glu Lys Pro Thr Trp Gly Thr Ile Ala
            420                 425                 430

Leu Gly Val Val Val Ile Ala Tyr Gly Leu Leu Ala Pro Leu Phe Ala
        435                 440                 445

Val Ser Leu Leu Val Phe Ile Gly Leu Ser Leu Gly Val Arg Phe Ile
    450                 455                 460

Ser Arg Met Ser Gly Arg Ala Asp Thr Ser Asn
465                 470                 475


<210> 2919
<211> 396
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(373)
<223> RXA02799

<400> 2919
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tttttagttg atcacagata caccaatcag gagtagcgca gtg gca cgc aac att   115
                                            Val Ala Arg Asn Ile
                                              1               5

gaa gac atc cag cgc gat att gag cgc acc cgc cgt cag ttg gct tcc   163
Glu Asp Ile Gln Arg Asp Ile Glu Arg Thr Arg Arg Gln Leu Ala Ser
                  10                  15                  20

acc ctc gac gag ctg gca gac cgc agc aag cct tcc aac ttg gtc gat   211
Thr Leu Asp Glu Leu Ala Asp Arg Ser Lys Pro Ser Asn Leu Val Asp
              25                  30                  35

gac gcc aag aac cag gca acc gcg aag ctg cag gaa tca aac gta cag   259
Asp Ala Lys Asn Gln Ala Thr Ala Lys Leu Gln Glu Ser Asn Val Gln
          40                  45                  50

aag gtg ctc ctg ggc gtc gct gct gtc gtc gtc ggt gct gtt gta ttc   307
Lys Val Leu Leu Gly Val Ala Ala Val Val Val Gly Ala Val Val Phe
      55                  60                  65

agc gtt gtg cgt ggc cgt aag aag gca aac gat ctg aag gaa atc cag   355
Ser Val Val Arg Gly Arg Lys Lys Ala Asn Asp Leu Lys Glu Ile Gln
  70                  75                  80                  85

cgc ctg ctc tcc gag cgt taaattgctt ttcgacgggg cgt                396
Arg Leu Leu Ser Glu Arg
                  90


<210> 2920
<211> 91
<212> PRT
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<213> Corynebacterium glutamicum

<400> 2920

```
Val Ala Arg Asn Ile Glu Asp Ile Gln Arg Asp Ile Glu Arg Thr Arg
  1               5                  10                  15

Arg Gln Leu Ala Ser Thr Leu Asp Glu Leu Ala Asp Arg Ser Lys Pro
             20                  25                  30

Ser Asn Leu Val Asp Asp Ala Lys Asn Gln Ala Thr Ala Lys Leu Gln
         35                  40                  45

Glu Ser Asn Val Gln Lys Val Leu Leu Gly Val Ala Ala Val Val Val
     50                  55                  60

Gly Ala Val Val Phe Ser Val Val Arg Gly Arg Lys Lys Ala Asn Asp
 65                  70                  75                  80

Leu Lys Glu Ile Gln Arg Leu Leu Ser Glu Arg
                 85                  90
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<210> 2921
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(552)
<223> RXA02815

<400> 2921

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tgg ctg cgc agt acc aaa gag ttc gaa gac cag ccc gtg att ccg gca   48
Trp Leu Arg Ser Thr Lys Glu Phe Glu Asp Gln Pro Val Ile Pro Ala
  1               5                  10                  15

ttc gaa gta atc gca acg gtt gcc tct gaa ttc gca ggc gac gac ggc   96
Phe Glu Val Ile Ala Thr Val Ala Ser Glu Phe Ala Gly Asp Asp Gly
             20                  25                  30

aac tac tcc aac gaa ttc ccc gtg gaa gat cta gtc gga tac gtt gac   144
Asn Tyr Ser Asn Glu Phe Pro Val Glu Asp Leu Val Gly Tyr Val Asp
         35                  40                  45

gcc atc acc gaa gcc ggc gga tac gca gtc ctg gat ctt caa ccc gga   192
Ala Ile Thr Glu Ala Gly Gly Tyr Ala Val Leu Asp Leu Gln Pro Gly
     50                  55                  60

cgc gcc aac ttc ctc gac caa gcc aaa atg tat gaa gaa ctc ctc aaa   240
Arg Ala Asn Phe Leu Asp Gln Ala Lys Met Tyr Glu Glu Leu Leu Lys
 65                  70                  75                  80

cga cca aac gtt gga ttg gcg cta gat ccc gag tgg aaa atc gga ccc   288
Arg Pro Asn Val Gly Leu Ala Leu Asp Pro Glu Trp Lys Ile Gly Pro
                 85                  90                  95

gat gag caa ccc atg aca cga gtg ggc tct gca gat gcc gcc gaa atc   336
Asp Glu Gln Pro Met Thr Arg Val Gly Ser Ala Asp Ala Ala Glu Ile
            100                 105                 110
```

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aac gaa gta tcc cag tgg ctc gcc gac ctg acc gcc gag aac gat ctt   384
Asn Glu Val Ser Gln Trp Leu Ala Asp Leu Thr Ala Glu Asn Asp Leu
        115                 120                 125

cca caa aag gca ttt gta ctg cac caa ttc caa ttg gaa atg ctc acc   432
Pro Gln Lys Ala Phe Val Leu His Gln Phe Gln Leu Glu Met Leu Thr
    130                 135                 140

aat cgg gat caa atc aat acc gat cac ctg gaa ctg gct gtc gtg ttg   480
Asn Arg Asp Gln Ile Asn Thr Asp His Leu Glu Leu Ala Val Val Leu
145                 150                 155                 160

cac gca gat gga cac gga aac gca ggg gat aag tac gca act tgg aac   528
His Ala Asp Gly His Gly Asn Ala Gly Asp Lys Tyr Ala Thr Trp Asn
                165                 170                 175

atg ctt cgc gag gga ctg agc ccg                                  552
Met Leu Arg Glu Gly Leu Ser Pro
            180
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<210> 2922
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<213> Corynebacterium glutamicum

<400> 2922

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Trp Leu Arg Ser Thr Lys Glu Phe Glu Asp Gln Pro Val Ile Pro Ala
  1               5                  10                  15

Phe Glu Val Ile Ala Thr Val Ala Ser Glu Phe Ala Gly Asp Asp Gly
             20                  25                  30

Asn Tyr Ser Asn Glu Phe Pro Val Glu Asp Leu Val Gly Tyr Val Asp
         35                  40                  45

Ala Ile Thr Glu Ala Gly Gly Tyr Ala Val Leu Asp Leu Gln Pro Gly
     50                  55                  60

Arg Ala Asn Phe Leu Asp Gln Ala Lys Met Tyr Glu Glu Leu Leu Lys
 65                  70                  75                  80

Arg Pro Asn Val Gly Leu Ala Leu Asp Pro Glu Trp Lys Ile Gly Pro
                 85                  90                  95

Asp Glu Gln Pro Met Thr Arg Val Gly Ser Ala Asp Ala Ala Glu Ile
            100                 105                 110

Asn Glu Val Ser Gln Trp Leu Ala Asp Leu Thr Ala Glu Asn Asp Leu
        115                 120                 125

Pro Gln Lys Ala Phe Val Leu His Gln Phe Gln Leu Glu Met Leu Thr
    130                 135                 140

Asn Arg Asp Gln Ile Asn Thr Asp His Leu Glu Leu Ala Val Val Leu
145                 150                 155                 160

His Ala Asp Gly His Gly Asn Ala Gly Asp Lys Tyr Ala Thr Trp Asn
                165                 170                 175

Met Leu Arg Glu Gly Leu Ser Pro
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180

<210> 2923
<211> 370
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(370)
<223> RXA02823

<400> 2923
ttatgtntnt aaacagccag ttgggggtca tgggggagcg ccccgtgact ggttaatgcc 60

ccgatctggg acgtacagta acaacgacac tggaggtgcc atg act gtt aga aat 115
Met Thr Val Arg Asn
1 5

ccc gac cgt gag gca atc cgt cac gga aaa att acg acg gag gcg ctg 163
Pro Asp Arg Glu Ala Ile Arg His Gly Lys Ile Thr Thr Glu Ala Leu
10 15 20

cgt gag cgt ccc gca tac ccg acc tgg gca atg aag ctg acc atg gcc 211
Arg Glu Arg Pro Ala Tyr Pro Thr Trp Ala Met Lys Leu Thr Met Ala
25 30 35

atc act ggc cta atg ttt ggt ggc ttc gtt ctt gtt cac atg atc gga 259
Ile Thr Gly Leu Met Phe Gly Gly Phe Val Leu Val His Met Ile Gly
40 45 50

aac ctg aaa atc ttc atg ccg gac tac gca gcc gat tct gcg cat ccg 307
Asn Leu Lys Ile Phe Met Pro Asp Tyr Ala Ala Asp Ser Ala His Pro
55 60 65

ggt gaa gca caa gta gat gtc tac ggc gag ttc ctg cgt gag atc gga 355
Gly Glu Ala Gln Val Asp Val Tyr Gly Glu Phe Leu Arg Glu Ile Gly
70 75 80 85

tcc ccg atc ctc cca 370
Ser Pro Ile Leu Pro
90

<210> 2924
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

<400> 2924
Met Thr Val Arg Asn Pro Asp Arg Glu Ala Ile Arg His Gly Lys Ile
1 5 10 15

Thr Thr Glu Ala Leu Arg Glu Arg Pro Ala Tyr Pro Thr Trp Ala Met
20 25 30

Lys Leu Thr Met Ala Ile Thr Gly Leu Met Phe Gly Gly Phe Val Leu
35 40 45

Val His Met Ile Gly Asn Leu Lys Ile Phe Met Pro Asp Tyr Ala Ala

```
gag gat cac acc tca atg ctc acc cac ttt tcc gca gct gtc ggc atg   48
Glu Asp His Thr Ser Met Leu Thr His Phe Ser Ala Ala Val Gly Met
  1               5                  10                  15

cat gac cgc gat ccg gct cgc ttc cca ggc cag ggc gac ggt tcc tac   96
His Asp Arg Asp Pro Ala Arg Phe Pro Gly Gln Gly Asp Gly Ser Tyr
             20                  25                  30

ccg gat ctt ttt tgg ctg tac aaa aac gcc ctc aac ctg gtc att agc   144
Pro Asp Leu Phe Trp Leu Tyr Lys Asn Ala Leu Asn Leu Val Ile Ser
         35                  40                  45

tca gtg ttg ttc acc cgt gag cag atg gac aac atg ctc gat cag atg   192
Ser Val Leu Phe Thr Arg Glu Gln Met Asp Asn Met Leu Asp Gln Met
     50                  55                  60

gat gaa cac ttc acg cgc gcg ggt atc ccg cgc atc gcg att aat att   240
Asp Glu His Phe Thr Arg Ala Gly Ile Pro Arg Ile Ala Ile Asn Ile
 65                  70                  75                  80

gag cgc cgc gac gac gcc ctg atg aac ggc tcc ctc gag cgt gcg cta   288
Glu Arg Arg Asp Asp Ala Leu Met Asn Gly Ser Leu Glu Arg Ala Leu
                 85                  90                  95

gag ctg caa gag ctt atc gac gcc tcc cag cac gac gat ccc ttc gac   336
Glu Leu Gln Glu Leu Ile Asp Ala Ser Gln His Asp Asp Pro Phe Asp
            100                 105                 110

gac tgc cca acc tgc caa att gca gga aaa gcg gca ctc gca atg gca   384
Asp Cys Pro Thr Cys Gln Ile Ala Gly Lys Ala Ala Leu Ala Met Ala
        115                 120                 125

gca gat gat tac gac gaa acc caa aac ctc gtc tcc caa atc atc agc   432
Ala Asp Asp Tyr Asp Glu Thr Gln Asn Leu Val Ser Gln Ile Ile Ser
    130                 135                 140

tac gga tcc atc ggc tgc gtc atg gaa cca gag acc acc ctc gct gcg   480
Tyr Gly Ser Ile Gly Cys Val Met Glu Pro Glu Thr Thr Leu Ala Ala
145                 150                 155                 160

ttc atg ctg cgt gtg ctt aag tcc ggc gat gct gat tat gcc cgc tac   528
Phe Met Leu Arg Val Leu Lys Ser Gly Asp Ala Asp Tyr Ala Arg Tyr
                165                 170                 175

ctg caa gat gtc agt gcg aag gca aac cca gaa ttc cag tcc ctt gat   576
Leu Gln Asp Val Ser Ala Lys Ala Asn Pro Glu Phe Gln Ser Leu Asp
            180                 185                 190

tcc gtt gga cgc cac cta gaa ttc ctc ggc atc act gga               615
Ser Val Gly Arg His Leu Glu Phe Leu Gly Ile Thr Gly
        195                 200                 205
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<210> 2930
<211> 205
<212> PRT
<213> Corynebacterium glutamicum

<400> 2930
Glu Asp His Thr Ser Met Leu Thr His Phe Ser Ala Ala Val Gly Met
  1   5   10   15

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His Asp Arg Asp Pro Ala Arg Phe Pro Gly Gln Gly Asp Gly Ser Tyr
             20                  25                  30

Pro Asp Leu Phe Trp Leu Tyr Lys Asn Ala Leu Asn Leu Val Ile Ser
         35                  40                  45

Ser Val Leu Phe Thr Arg Glu Gln Met Asp Asn Met Leu Asp Gln Met
     50                  55                  60

Asp Glu His Phe Thr Arg Ala Gly Ile Pro Arg Ile Ala Ile Asn Ile
 65                  70                  75                  80

Glu Arg Arg Asp Asp Ala Leu Met Asn Gly Ser Leu Glu Arg Ala Leu
                 85                  90                  95

Glu Leu Gln Glu Leu Ile Asp Ala Ser Gln His Asp Asp Pro Phe Asp
            100                 105                 110

Asp Cys Pro Thr Cys Gln Ile Ala Gly Lys Ala Ala Leu Ala Met Ala
        115                 120                 125

Ala Asp Asp Tyr Asp Glu Thr Gln Asn Leu Val Ser Gln Ile Ile Ser
    130                 135                 140

Tyr Gly Ser Ile Gly Cys Val Met Glu Pro Glu Thr Thr Leu Ala Ala
145                 150                 155                 160

Phe Met Leu Arg Val Leu Lys Ser Gly Asp Ala Asp Tyr Ala Arg Tyr
                165                 170                 175

Leu Gln Asp Val Ser Ala Lys Ala Asn Pro Glu Phe Gln Ser Leu Asp
            180                 185                 190

Ser Val Gly Arg His Leu Glu Phe Leu Gly Ile Thr Gly
        195                 200                 205
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<210> 2931
<211> 499
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(499)
<223> RXA02848

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aaccccagcg cgtttcagaa tgtgaatttc ttctagttac atg cag atc gtt ctg   115
                                              Met Gln Ile Val Leu
                                                1               5

gct tcg cag tcc ccg tcc cgc cga aga atc ctc aat tcg gcg ggc gtc   163
Ala Ser Gln Ser Pro Ser Arg Arg Arg Ile Leu Asn Ser Ala Gly Val
                10                  15                  20

gag ccc ctc atc cac cca gct gat gtt gat gag gac gcg ctc ctt cac   211
Glu Pro Leu Ile His Pro Ala Asp Val Asp Glu Asp Ala Leu Leu His
```

```
     50                  55                  60

Asp Ser Ala His Pro Gly Glu Ala Gln Val Asp Val Tyr Gly Glu Phe
 65                  70                  75                  80

Leu Arg Glu Ile Gly Ser Pro Ile Leu Pro
                 85                  90


<210> 2925
<211> 523
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(523)
<223> RXA02827

<400> 2925
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gcgggtagga agaagcagcc gtgtcgcata tgcttacttt atg tat gag cag cag   115
                                        Met Tyr Glu Gln Gln
                                          1               5

aag atc ctt aac gaa gtc agt gaa aaa cgt ctt cag gca atc aaa gat   163
Lys Ile Leu Asn Glu Val Ser Glu Lys Arg Leu Gln Ala Ile Lys Asp
                 10                  15                  20

ttt aca gaa ctg gga tct gga ttc aag att gcg atg cgg gat ctt tcc   211
Phe Thr Glu Leu Gly Ser Gly Phe Lys Ile Ala Met Arg Asp Leu Ser
             25                  30                  35

att cgc ggt gca ggt aat ctc tta ggt gct cag cag cat gga ttt att   259
Ile Arg Gly Ala Gly Asn Leu Leu Gly Ala Gln Gln His Gly Phe Ile
         40                  45                  50

gat gca gtc ggt ttc gat atg tat tct caa atg cta agc gaa gct gtt   307
Asp Ala Val Gly Phe Asp Met Tyr Ser Gln Met Leu Ser Glu Ala Val
     55                  60                  65

tnt cgt aaa caa gga aag aat agt caa gtg gag aag ncc nct gtt gag   355
Xaa Arg Lys Gln Gly Lys Asn Ser Gln Val Glu Lys Xaa Xaa Val Glu
 70                  75                  80                  85

atc gac cnc ggt gtc gat gcg tat cta cct gaa aca tac gtg gca gat   403
Ile Asp Xaa Gly Val Asp Ala Tyr Leu Pro Glu Thr Tyr Val Ala Asp
                 90                  95                 100

can cgg cag aaa atc gag atc tat aaa cga att cgt gaa ctt gat tcg   451
Xaa Arg Gln Lys Ile Glu Ile Tyr Lys Arg Ile Arg Glu Leu Asp Ser
            105                 110                 115

caa gaa atg cta gat gaa cta gaa gat gat ctg ctc gac cgt ttt gga   499
Gln Glu Met Leu Asp Glu Leu Glu Asp Asp Leu Leu Asp Arg Phe Gly
        120                 125                 130

gaa can cca gaa gaa gta gca cat                                  523
Glu Xaa Pro Glu Glu Val Ala His
    135                 140
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<210> 2926
<211> 141
<212> PRT
<213> Corynebacterium glutamicum

<400> 2926
Met Tyr Glu Gln Gln Lys Ile Leu Asn Glu Val Ser Glu Lys Arg Leu
1 5 10 15

Gln Ala Ile Lys Asp Phe Thr Glu Leu Gly Ser Gly Phe Lys Ile Ala
20 25 30

Met Arg Asp Leu Ser Ile Arg Gly Ala Gly Asn Leu Leu Gly Ala Gln
35 40 45

Gln His Gly Phe Ile Asp Ala Val Gly Phe Asp Met Tyr Ser Gln Met
50 55 60

Leu Ser Glu Ala Val Xaa Arg Lys Gln Gly Lys Asn Ser Gln Val Glu
65 70 75 80

Lys Xaa Xaa Val Glu Ile Asp Xaa Gly Val Asp Ala Tyr Leu Pro Glu
85 90 95

Thr Tyr Val Ala Asp Xaa Arg Gln Lys Ile Glu Ile Tyr Lys Arg Ile
100 105 110

Arg Glu Leu Asp Ser Gln Glu Met Leu Asp Glu Leu Glu Asp Asp Leu
115 120 125

Leu Asp Arg Phe Gly Glu Xaa Pro Glu Glu Val Ala His
130 135 140

<210> 2927
<211> 356
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(342)
<223> RXA02842

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<400> 2927
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Asp Ala Gly Phe Val Tyr Phe Gly Glu Ile Asp Asp Ala Gly His Ile
1 5 10 15

ttc ggc ctg gca ggc gac gaa tac cga ggg ggg att cgc agg gtc gac 96
Phe Gly Leu Ala Gly Asp Glu Tyr Arg Gly Gly Ile Arg Arg Val Asp
20 25 30

acc cac gtg aag aaa gtt ctt tct gaa gtg tca cga cgc tcc gac gag 144
Thr His Val Lys Lys Val Leu Ser Glu Val Ser Arg Arg Ser Asp Glu
35 40 45

ctc ggg gag gac tgg ctg gta gtg atc aca act gat cat ggt cac ctt 192
Leu Gly Glu Asp Trp Leu Val Val Ile Thr Thr Asp His Gly His Leu

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     50                  55                  60

gat gag ggc ggg cac ggc ggc acc acc gat cgg gag cga gaa tcc tgg   240
Asp Glu Gly Gly His Gly Gly Thr Thr Asp Arg Glu Arg Glu Ser Trp
 65                  70                  75                  80

atc atc acg tgg agc ccg cac cgg gaa ctg cca cag tgg cct gaa gaa   288
Ile Ile Thr Trp Ser Pro His Arg Glu Leu Pro Gln Trp Pro Glu Glu
                 85                  90                  95

att gcg ccg cnt gag ctg gca gaa ctg atg ctt gtg gag cgc cga acc   336
Ile Ala Pro Xaa Glu Leu Ala Glu Leu Met Leu Val Glu Arg Arg Thr
            100                 105                 110

ttg agg tgattgtcac taaa                                          356
Leu Arg
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<210> 2928
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 2928

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Asp Ala Gly Phe Val Tyr Phe Gly Glu Ile Asp Asp Ala Gly His Ile
  1               5                  10                  15

Phe Gly Leu Ala Gly Asp Glu Tyr Arg Gly Gly Ile Arg Arg Val Asp
             20                  25                  30

Thr His Val Lys Lys Val Leu Ser Glu Val Ser Arg Arg Ser Asp Glu
         35                  40                  45

Leu Gly Glu Asp Trp Leu Val Val Ile Thr Thr Asp His Gly His Leu
     50                  55                  60

Asp Glu Gly Gly His Gly Gly Thr Thr Asp Arg Glu Arg Glu Ser Trp
 65                  70                  75                  80

Ile Ile Thr Trp Ser Pro His Arg Glu Leu Pro Gln Trp Pro Glu Glu
                 85                  90                  95

Ile Ala Pro Xaa Glu Leu Ala Glu Leu Met Leu Val Glu Arg Arg Thr
            100                 105                 110

Leu Arg
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<210> 2929
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (1)..(615)
<223> RXA02845

<400> 2929

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            25                  30                  35

tcc ctc aac ggc tct gcg ccg gag gag atc gtc cgc cag ctt gcg ctg   259
Ser Leu Asn Gly Ser Ala Pro Glu Glu Ile Val Arg Gln Leu Ala Leu
        40                  45                  50

gct aaa gca cag gtg gtt gcg ccg tcc tat ccg ggc gac gtc gtc atc   307
Ala Lys Ala Gln Val Val Ala Pro Ser Tyr Pro Gly Asp Val Val Ile
     55                  60                  65

ggt ggc gat tcc atg ctg ctt atc gac gcc acc ctc caa ggc aag ccg   355
Gly Gly Asp Ser Met Leu Leu Ile Asp Ala Thr Leu Gln Gly Lys Pro
 70                  75                  80                  85

cac acc cgc gaa gcc acc atc gaa aga tgg aaa caa caa cgc ggc aac   403
His Thr Arg Glu Ala Thr Ile Glu Arg Trp Lys Gln Gln Arg Gly Asn
                90                  95                 100

aag gcc aca ctg atc acc ggc cac gcc atc atc ttt ggc gat gaa gtg   451
Lys Ala Thr Leu Ile Thr Gly His Ala Ile Ile Phe Gly Asp Glu Val
            105                 110                 115

atc gtg gag tcc tcc tcc acc aac att cat ttc gcc gag gcc agc gat   499
Ile Val Glu Ser Ser Ser Thr Asn Ile His Phe Ala Glu Ala Ser Asp
        120                 125                 130


<210> 2932
<211> 133
<212> PRT
<213> Corynebacterium glutamicum

<400> 2932
Met Gln Ile Val Leu Ala Ser Gln Ser Pro Ser Arg Arg Arg Ile Leu
  1               5                  10                  15

Asn Ser Ala Gly Val Glu Pro Leu Ile His Pro Ala Asp Val Asp Glu
            20                  25                  30

Asp Ala Leu Leu His Ser Leu Asn Gly Ser Ala Pro Glu Glu Ile Val
        35                  40                  45

Arg Gln Leu Ala Leu Ala Lys Ala Gln Val Val Ala Pro Ser Tyr Pro
     50                  55                  60

Gly Asp Val Val Ile Gly Gly Asp Ser Met Leu Leu Ile Asp Ala Thr
 65                  70                  75                  80

Leu Gln Gly Lys Pro His Thr Arg Glu Ala Thr Ile Glu Arg Trp Lys
                85                  90                  95

Gln Gln Arg Gly Asn Lys Ala Thr Leu Ile Thr Gly His Ala Ile Ile
            100                 105                 110

Phe Gly Asp Glu Val Ile Val Glu Ser Ser Ser Thr Asn Ile His Phe
        115                 120                 125

Ala Glu Ala Ser Asp
    130
```

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